

- (B) Polypeptide Sequence
- Pat. Appln. SEQ ID NO 4278
 - Ceres seq_id 1580122
 - Location of start within SEQ ID NO 4275: at 28 nt.

- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
- Eukaryotic protein kinase domain
 - Location within SEQ ID NO 4278: from 1 to 86 aa.

- (Dp) Related Amino Acid Sequences

Maximum Length Sequence:

related to:

Clone IDs:

342142

- (Ac) cDNA Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 4279
- Ceres seq_id 1580127

- (B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 4280
- Ceres seq_id 1580128
- Location of start within SEQ ID NO 4279: at 1 nt.

- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
- Sperm histone P2
 - Location within SEQ ID NO 4280: from 43 to 101 aa.

- (Dp) Related Amino Acid Sequences

- (B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 4281
- Ceres seq_id 1580129
- Location of start within SEQ ID NO 4279: at 65 nt.

- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- (Dp) Related Amino Acid Sequences

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 874 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..874
- (D) OTHER INFORMATION: / Ceres Seq. ID 1565539

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

atcactaaca	aaacacacat	caaaaaacgat	tttacaagaa	aaaaatatca	gaaaaaatgt	60
cagagaccac	caagaatgcc	ttccaagccg	gtcaggccgc	tggcaaaagt	gaggagaaga	120
gcaatgttct	gtggacaag	gccaaaggatg	ctgctgctgc	agctggagct	tccgcgcaac	180
aggcgggaaa	gagtatatcg	gatgcggcag	tgggaggtgc	tccatctggt	cctgaagctg	240
gccctcgaac	aatgaaattc	cttgacaatt	tccatgtgca	aacaaagaga	gagcatgttt	300
tgttgggaga	taacgagaat	ggtgagaacg	atgaggaagg	cggtgaggtt	gcaaacccaa	360
aatggatcac	cattaaaGca	gctctgctGc	tactgttagg	agctgccatt	gcagctgcat	420
ttgctgatcc	tttagtcgac	actgttaaca	acttctccgc	agccacaggg	attccgtctt	480
tcttcatttc	cttcactgct	ttgcctttgg	ccaccaattc	aagtgaagcc	gtgtctgcca	540
tcactcttcg	atccccgaaa	aagatcagaa	ccgcctcttt	aactttctcc	gagctatgcg	600
gtggagtgac	aatgaacaac	attctgtgtc	tctcgggtgt	cttagcaatc	gtctacgttc	660
gaggactgac	atgggaactc	tcatacaga	agtggtgtag	tctcatcggt	tgtctcgtga	720
tggcggtgtt	cgcgagtttc	cgacacaact	atcctctttg	gacatgtttc	atagcttaact	780
tgctttacc	attctccttg	ggctcgtgtc	atattcttga	ttactggttt	ggctcgtcgt	840
agatatcaat	ctctgttcaa	agagtttgtt	ctac			

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 261 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..261
- (D) OTHER INFORMATION: / Ceres Seq. ID 1565540

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Ser	Glu	Thr	Asn	Lys	Asn	Ala	Phe	Gln	Ala	Gly	Gln	Ala	Ala	Gly
1				5					10				15		
Lys	Ala	Glu	Glu	Lys	Ser	Asn	Val	Leu	Leu	Asp	Lys	Ala	Lys	Asp	Ala
				20					25				30		
Ala	Ala	Ala	Ala	Gly	Ala	Ser	Ala	Gln	Gln	Ala	Gly	Lys	Ser	Ile	Ser
				35					40				45		
Asp	Ala	Ala	Val	Gly	Gly	Ala	Pro	Ser	Gly	Pro	Glu	Ala	Gly	Pro	Arg
				50					55				60		
Thr	Met	Lys	Phe	Leu	Asp	Asn	Phe	His	Val	Gln	Thr	Lys	Arg	Glu	His
				65					70				75		80
Ala	Leu	Leu	Gly	Asp	Asn	Glu	Asn	Gly	Glu	Asn	Asp	Glu	Glu	Gly	Gly
				85					90				95		
Glu	Val	Ala	Asn	Pro	Lys	Trp	Ile	Thr	Ile	Lys	Ala	Ala	Leu	Leu	Leu
				100					105				110		
Leu	Leu	Gly	Ala	Ala	Ile	Ala	Ala	Ala	Phe	Ala	Asp	Pro	Leu	Val	Asp
				115					120				125		
Thr	Val	Asn	Asn	Phe	Ser	Ala	Ala	Thr	Gly	Ile	Pro	Ser	Phe	Phe	Ile
				130					135				140		
Ser	Phe	Ile	Ala	Leu	Pro	Leu	Ala	Thr	Asn	Ser	Ser	Glu	Ala	Val	Ser
				145					150				155		160
Ala	Ile	Ile	Phe	Ala	Ser	Arg	Lys	Lys	Ile	Arg	Thr	Ala	Ser	Leu	Thr
				165					170				175		

Phe Ser Glu Leu Cys Gly Gly Val Thr Met Asn Asn Ile Leu Cys Leu
180 185 190
Ser Val Phe Leu Ala Ile Val Tyr Val Arg Gly Leu Thr Trp Asn Phe
195 200 205
Ser Ser Glu Val Leu Val Ile Leu Ile Val Cys Leu Val Met Gly Gly
210 215 220
Phe Ala Ser Phe Arg Thr Thr Tyr Pro Leu Trp Thr Cys Phe Ile Ala
225 230 235 240
Tyr Leu Leu Tyr Pro Phe Ser Leu Gly Leu Val Tyr Ile Leu Asp Tyr
245 250 255
Trp Phe Gly Trp Ser
260

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 196 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..196
- (D) OTHER INFORMATION: / Ceres Seq. ID 1565541

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met Lys Phe Leu Asp Asn Phe His Val Gln Thr Lys Arg Glu His Ala
1 5 10 15
Leu Leu Gly Asp Asn Glu Asn Gly Glu Asn Asp Glu Glu Gly Glu
20 25 30
Val Ala Asn Pro Lys Trp Ile Thr Ile Lys Ala Ala Leu Leu Leu
35 40 45
Leu Gly Ala Ala Ile Ala Ala Ala Phe Ala Asp Pro Leu Val Asp Thr
50 55 60
Val Asn Asn Phe Ser Ala Ala Thr Gly Ile Pro Ser Phe Phe Ile Ser
65 70 75 80
Phe Ile Ala Leu Pro Leu Ala Thr Asn Ser Ser Glu Ala Val Ser Ala
85 90 95
Ile Ile Phe Ala Ser Arg Lys Lys Ile Arg Thr Ala Ser Leu Thr Phe
100 105 110
Ser Glu Leu Cys Gly Gly Val Thr Met Asn Asn Ile Leu Cys Leu Ser
115 120 125
Val Phe Leu Ala Ile Val Tyr Val Arg Gly Leu Thr Trp Asn Phe Ser
130 135 140
Ser Glu Val Leu Val Ile Leu Ile Val Cys Leu Val Met Gly Gly Phe
145 150 155 160
Ala Ser Phe Arg Thr Thr Tyr Pro Leu Trp Thr Cys Phe Ile Ala Tyr
165 170 175
Leu Leu Tyr Pro Phe Ser Leu Gly Leu Val Tyr Ile Leu Asp Tyr Trp
180 185 190
Phe Gly Trp Ser
195

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 598 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..598
- (D) OTHER INFORMATION: / Ceres Seq. ID 1565546

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

aaatttcaat	tttaagata	aaagtaaatg	aactggtaag	ccaChgnnttt	tggttctgct	60
cttaccgttc	tcccaacttc	catatccaaa	ctgaaaagaca	ctgggttttg	ttttgtcggg	120
aaaaggagaa	acttcaaaaa	gatgcccact	ttgaatctct	tcactaacat	accagtgcac	180
gccgtcactt	gctcagacat	cctcaaggac	gccactaagg	ccgtcgctaa	aatcatcggc	240
aaacctgaat	ccatgtgat	gatactgctt	aacagtggag	tgcccattgc	atttgcgggt	300
acctagggaac	ctgctgcata	tgagaaattg	atatctattg	ggggattagg	acctggcgta	360
aacgggaagc	ttagcgagac	gatatctgag	attctccaaa	ttaagctctc	catagacagc	420
tctcgctttt	atacaaaatt	ctacgattct	ccgcgacctt	tcttcggtta	caatggatca	480
actttctgaa	aagaggcgaa	ttcaaccttg	taatgatatt	tggttagaa	ctgtttgctt	540
attcatttca	aaagctgtaa	ttctgaacca	taattataa	ttttacctcc	ctcaaaagc	

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 54 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..54

(D) OTHER INFORMATION: / Ceres Seq. ID 1565547

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Ile	Ser	Ile	Leu	Lys	Ile	Lys	Val	Asn	Glu	Leu	Val	Ser	His	Xaa	Phe	
1			5						10					15		
Trp	Phe	Cys	Ser	Tyr	Arg	Tyr	Pro	Asn	Phe	His	Ile	Gln	Thr	Glu	Arg	
			20					25					30			
His	Trp	Phe	Trp	Phe	Cys	Arg	Glu	Lys	Glu	Lys	Leu	Gln	Lys	Asp	Ala	
			35				40					45				
His	Phe	Glu	Ser	Leu	His											
			50													

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 54 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..54

(D) OTHER INFORMATION: / Ceres Seq. ID 1565548

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met	Pro	Thr	Leu	Asn	Leu	Phe	Thr	Asn	Ile	Pro	Val	Asp	Ala	Val	Thr	
1			5						10				15			
Cys	Ser	Asp	Ile	Leu	Lys	Asp	Ala	Thr	Lys	Ala	Val	Ala	Lys	Ile	Ile	
			20					25					30			
Gly	Lys	Pro	Glu	Ser	Tyr	Val	Met	Ile	Leu	Leu	Asn	Ser	Gly	Val	Pro	
			35				40					45				
Ile	Ala	Phe	Ala	Gly	Thr											
			50													

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 35 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..35

(D) OTHER INFORMATION: / Ceres Seq. ID 1565549
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:
Met Asp Gln Leu Ser Glu Lys Arg Arg Ile Gln Pro Cys Asn Asp Ile
1 5 10 15
Trp Val Arg Thr Val Cys Leu Phe Ile Ser Lys Ala Val Ile Leu Asn
20 25 30
His Asn Leu
35

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1285 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1285

(D) OTHER INFORMATION: / Ceres Seq. ID 1565556

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

gcagacgaat gtttttgggt tgcagaattt gctgaaatct attcaacgta tacagaggct 60
ggagctgggg aagaaaagga ttgctatagg agggagacgt cggaaataggt ttgggtatgcc 120
agaatactat ggatgggaag gcgagtaagt gaaatggttt agagaagact gtaccttcttt 180
gttgccctaa ggcctatggca tgtgtacctg aggatgatgc taagtgtcac tccactgttg 240
ttttctgggtg gttttcggaa cctcaccctc gctctgggaa aaaagggcggc aaagcagctc 300
atttcaacaa cccatagtgt ccaggagaag cacactcact gaaagtgtgag aaagtcttgt 360
tcaaagacaa gtccgatttt caggaaagtc tagtgttgcg gtcagccacg tacggaaaagg 420
tgcttgctct agatggatc gtacagctga ccgaaaaaga tgaatgtgca tatcaggaga 480
tgatagccca tctgccttta tgcctctata cttccctcaa aaatgttctt gttgttggtg 540
gaggtgatgg tgggtgtctt cgagagattt ctcgccatag ttctgttgag gttattgata 600
tctgtgagat agacaagaat gttatagatg tgtctaagaa gttcttcccc gagttagcgg 660
ttgggtttga cgatcctcgt gttcaacctc acattgggtga tgcgtgctga ttcttcocga 720
aatccctctg agggaaagat gatgccatca ttgttgattc ttcagatccc gtaggctcgt 780
ctcttgccgt tggttgagaag cctttcttcg agacactggc tagagcggtg aagcctgggg 840
gagttctttg taacatggca gaaagtatgt ggtccatac tcatcttatt gaagatatga 900
tctccatttg ccgtcaaaaca tcaaaaagtg ttcatctatg gtggagcagc gtcccacat 960
atccaaagcg cgtgattggg ttgctcttgt gctctactga aggaccagct gttgacttca 1020
agaaaccaat caacctatt gagaaactag acggtgcgat gacccataaa agagaattga 1080
agttctataa ctctgatatg cacagagccg catttgcctt gccacattc Ctcgggagag 1140
aagttagcttc acttctggct tcttgacttc tgtttggctc taccatatcc ctcatatcaa 1200
actttgtaga actcttgaag aggaataata aatcattgaa ggctttgtat ctctaagttt 1260
actcctttat aaaaagactt atatt

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 359 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..359

(D) OTHER INFORMATION: / Ceres Seq. ID 1565557

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Met Glu Gly Asp Val Gly Ile Gly Leu Val Cys Gln Asn Thr Met Asp
1 5 10 15
Gly Lys Ala Ser Asn Gly Asn Gly Leu Glu Lys Thr Val Pro Ser Cys
20 25 30
Cys Leu Lys Ala Met Ala Cys Val Pro Glu Asp Asp Ala Lys Cys His
35 40 45
Ser Thr Val Val Ser Gly Trp Phe Ser Glu Pro His Pro Arg Ser Gly

1	Met	Asp	Gly	Lys	5	Ala	Ser	Asn	Gly	10	Asn	Gly	Leu	Glu	Lys	15	Thr	Val	Pro	20
Ser	Cys	Cys	Leu	Lys	20	Ala	Met	Ala	Cys	25	Val	Pro	Glu	Asp	30	Asp	Ala	Lys	35	Pro
Cys	His	Ser	Thr	Val	35	Val	Ser	Gly	Trp	40	Phe	Ser	Glu	Pro	45	His	Pro	Arg	50	Pro
Ser	Gly	Lys	Lys	Gly	50	Gly	Lys	55	Ala	Val	Tyr	Phe	Asn	60	Asn	Pro	Met	Tsp	65	Pro
Pro	Gly	Glu	Ala	His	65	Ser	Leu	70	Lys	Val	Glu	Lys	75	Val	Leu	Phe	Lys	80	85	Pro

Lys Ser Asp Phe Gln Glu Val Leu Val Phe Glu Ser Ala Thr Tyr Gly
85 90 95
Lys Val Leu Val Leu Asp Gly Ile Val Gln Leu Thr Glu Lys Asp Glu
100 105 110
Cys Ala Tyr Gln Glu Met Ile Ala His Leu Pro Leu Cys Ser Ile Ser
115 120 125
Ser Pro Lys Asn Val Leu Val Val Gly Gly Gly Asp Gly Gly Val Leu
130 135 140
Arg Glu Ile Ser Arg His Ser Ser Val Glu Val Ile Asp Ile Cys Glu
145 150 155 160
Ile Asp Lys Met Val Ile Asp Val Ser Lys Lys Phe Phe Pro Glu Leu
165 170 175
Ala Val Gly Phe Asp Asp Pro Arg Val Gln Leu His Ile Gly Asp Ala
180 185 190
Ala Glu Phe Leu Arg Lys Ser Pro Glu Gly Lys Tyr Asp Ala Ile Ile
195 200 205
Val Asp Ser Ser Asp Pro Val Gly Pro Ala Leu Ala Leu Val Glu Lys
210 215 220
Pro Phe Phe Glu Thr Leu Ala Arg Ala Leu Lys Pro Gly Gly Val Leu
225 230 235 240
Cys Asn Met Ala Glu Ser Met Trp Leu His Thr His Leu Ile Glu Asp
245 250 255
Met Ile Ser Ile Cys Arg Gln Thr Phe Lys Ser Val His Tyr Ala Trp
260 265 270
Ser Ser Val Pro Thr Tyr Pro Ser Gly Val Ile Gly Phe Val Leu Cys
275 280 285
Ser Thr Glu Gly Pro Ala Val Asp Phe Lys Asn Pro Ile Asn Pro Ile
290 295 300
Glu Lys Leu Asp Gly Ala Met Thr His Lys Arg Glu Leu Lys Phe Tyr
305 310 315 320
Asn Ser Asp Met His Arg Ala Ala Phe Ala Leu Pro Thr Phe Leu Arg
325 330 335
Arg Glu Val Ala Ser Leu Leu Ala Ser
340 345

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 323 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..323
- (D) OTHER INFORMATION: / Ceres Seq. ID 1565559

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Met Ala Cys Val Pro Glu Asp Asp Ala Lys Cys His Ser Thr Val Val
1 5 10 15
Ser Gly Trp Phe Ser Glu Pro His Pro Arg Ser Gly Lys Lys Gly Gly
20 25 30
Lys Ala Val Tyr Phe Asn Asn Pro Met Trp Pro Gly Glu Ala His Ser
35 40 45
Leu Lys Val Glu Lys Val Leu Phe Lys Asp Lys Ser Asp Phe Gln Glu
50 55 60
Val Leu Val Phe Glu Ser Ala Thr Tyr Gly Lys Val Leu Val Leu Asp
65 70 75 80
Gly Ile Val Gln Leu Thr Glu Lys Asp Glu Cys Ala Tyr Gln Glu Met
85 90 95
Ile Ala His Leu Pro Leu Cys Ser Ile Ser Ser Pro Lys Asn Val Leu
100 105 110
Val Val Gly Gly Gly Asp Gly Gly Val Leu Arg Glu Ile Ser Arg His

115										120										125																			
Ser	Ser	Val	Glu	Val	Ile	Asp	Ile	Cys	Glu	Ile	Asp	Lys	Met	Val	Ile	Ser	Ser	Val	Glu	Val	Ile	Asp	Lys	Met	Val	Ile	Ser	Ser	Val	Glu	Val	Ile	Asp	Lys	Met	Val	Ile		
130							135									140																							
Asp	Val	Ser	Lys	Lys	Phe	Phe	Pro	Glu	Leu	Ala	Val	Gly	Phe	Asp	Asp	145																							
145							150									155																							
Pro	Arg	Val	Gln	Leu	His	Ile	Gly	Asp	Ala	Ala	Glu	Phe	Leu	Arg	Lys	160																							
							165									170																							
Ser	Pro	Glu	Gly	Lys	Tyr	Asp	Ala	Ile	Ile	Val	Asp	Ser	Ser	Asp	Pro	175																							
							180									185																							
Val	Gly	Pro	Ala	Leu	Ala	Leu	Val	Glu	Lys	Pro	Phe	Phe	Glu	Thr	Leu	190																							
							195									200																							
Ala	Arg	Ala	Leu	Lys	Pro	Gly	Gly	Val	Leu	Cys	Asn	Met	Ala	Glu	Ser	205																							
							210									215																							
Met	Trp	Leu	His	Thr	His	Leu	Ile	Glu	Asp	Met	Ile	Ser	Ile	Cys	Arg	220																							
							225									230																							
Gln	Thr	Phe	Lys	Ser	Val	His	Tyr	Ala	Trp	Ser	Ser	Val	Pro	Thr	Tyr	235																							
							240									245																							
Pro	Ser	Gly	Val	Ile	Gly	Phe	Val	Leu	Cys	Ser	Thr	Glu	Gly	Pro	Ala	250																							
							255									260																							
Val	Asp	Phe	Lys	Asn	Pro	Ile	Asn	Pro	Ile	Glu	Lys	Leu	Asp	Gly	Ala	265																							
							270									275																							
Met	Thr	His	Lys	Arg	Glu	Leu	Lys	Phe	Tyr	Asn	Ser	Asp	Met	His	Arg	280																							
							285									290																							
Ala	Ala	Phe	Ala	Leu	Pro	Thr	Phe	Leu	Arg	Arg	Glu	Val	Ala	Ser	Leu	295																							
							300									305																							
Leu	Ala	Ser					310									315																							

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1485 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1485
- (D) OTHER INFORMATION: / Ceres Seq. ID 1565568

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

aacacctag	ttctgtttc	ctaacaagg	ctctactttt	tcttttagta	actactatgg	60
ctcatttct	cgagacacag	gaaccctcgg	tattctccgg	gaagaaacga	aacgatcgcg	120
atgacaacga	cggtgacgac	ttgtgttgca	agaaatcagc	actggcggtg	tgtgatcgcg	180
accctgcag	ggccatagcg	aatatccgac	atgagtttgg	ggagcacggg	ggagtaaacaa	240
tgtccatga	agcctccgac	accttcacgg	tcattggaac	ggatccatgt	aggcggtatgt	300
tcacggaga	actgggacgg	gacaacgaac	tctacgtata	cagccgacac	ttcaacccca	360
ccgtgctcaa	ctcagccggt	cagatggtgt	ctctcgaagg	cacccgaagt	gcctactgta	420
ccctatcgcg	tatgtcggcg	atatcgtcag	tgatgtgtga	actgtgcagc	agcgaggagac	480
acgtggctgc	ggcaagcacg	ctctacggag	gaacacacgc	tttgtctctc	catcttctgc	540
cacggacatg	taacataacc	acctccttgc	ttgacataac	ggaccatggc	gcggtggcaa	600
acggcatcgt	tgagggttag	acacaggttc	tctactttga	gtcgggtggc	aaccgcagcg	660
tgactgtggt	tgacatacct	gaactgagcc	gtatggcaca	cgagaaggcg	gtgacggtgg	720
tggtggacaa	cacattcggc	cccatgtgtc	tgctctccgc	caagcttgga	cgagatgtgg	780
tggttcacag	tatctccaag	ttcatcagtg	gtggggctga	catcatcgca	ggggccgctgt	840
gtggagtgga	gaagctgggt	gaagagagat	atggatcttc	gtggcggtat	ctctgatctgt	900
ctaggtccca	ccatgaacgc	caagtggtgt	ttcgagctgt	ccgagcgaat	ccctcactgt	960
ggcctacgca	tgagagagca	cagccacaga	gcccaagtgc	atgctgagag	aatgagggat	1020
ttgggatgta	aagtcatata	tccaggggtc	gagaccaccc	cgcagcacaa	gctcttcaaa	1080
ggtatggtga	atagagacata	tggatacggg	ggattgtgtg	cgatagacat	ggagacagag	1140
ggaaagccca	acaagctcat	ggcatatctc	cagaacgcga	ctcagtttgg	cttgatggcc	1200
gtcagtttgg	gttactacga	gacactcatg	tcttgcctcg	ggagcagcac	cagcagcgag	1260
cttgaccctc	cgcagaagga	agctgcaggg	atctctcctg	gtcttgttacg	aatatcggtg	1320

gggtatgtgg gtacattgga gcagaagtgg acacaattcg agaagcattc ctcagaatgt 1380
aaaatgtott cttctatata tgaagggtttt ctttccccc aataccaaca attcatcatc 1440
tgcggatatat gtatgatgtg gccaatgttc agtctcttat ttgtgc

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 316 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..316
- (D) OTHER INFORMATION: / Ceres Seq. ID 1565569

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Met	Ala	His	Phe	Leu	Glu	Thr	Gln	Glu	Pro	Leu	Val	Phe	Ser	Gly	Lys
1			5					10						15	
Lys	Arg	Asn	Asp	Arg	Asp	Asp	Asn	Asp	Gly	Asp	Ala	Leu	Val	Ala	Lys
			20					25						30	
Lys	Ser	Ala	Leu	Ala	Val	Cys	Asp	Ala	Asp	Pro	Ala	Ala	Ala	Ile	Ala
			35				40					45			
Asn	Ile	Arg	His	Glu	Phe	Gly	Glu	His	Gly	Gly	Val	Asn	Met	Ser	Ile
			50				55					60			
Glu	Ala	Ser	Ala	Thr	Phe	Thr	Val	Met	Glu	Pro	Asp	Thr	Met	Arg	Arg
			65				70					75			80
Met	Phe	Thr	Gly	Glu	Leu	Gly	Pro	Asp	Asn	Asp	Phe	Tyr	Val	Tyr	Ser
															95
Arg	His	Phe	Asn	Pro	Thr	Val	Leu	Asn	Leu	Ser	Arg	Gln	Met	Ala	Ala
															110
Leu	Glu	Gly	Thr	Gln	Ala	Ala	Tyr	Cys	Thr	Ser	Ser	Gly	Met	Ser	Ala
															125
Ile	Ser	Ser	Val	Met	Leu	Gln	Leu	Cys	Ser	Ser	Gly	Gly	His	Val	Val
															140
Ala	Ala	Ser	Thr	Leu	Tyr	Gly	Gly	Thr	His	Ala	Leu	Leu	Ser	His	Phe
															155
Leu	Pro	Arg	Thr	Cys	Asn	Ile	Thr	Thr	Ser	Phe	Val	Asp	Ile	Thr	Asp
															170
His	Gly	Ala	Val	Ala	Asn	Ala	Ile	Val	Glu	Gly	Arg	Thr	Gln	Val	Leu
															185
Tyr	Phe	Glu	Ser	Val	Ala	Asn	Pro	Thr	Leu	Thr	Val	Ala	Asp	Ile	Pro
															200
Glu	Leu	Ser	Arg	Met	Ala	His	Glu	Lys	Gly	Val	Thr	Val	Val	Val	Asp
															215
Asn	Thr	Phe	Ala	Pro	Met	Val	Leu	Ser	Pro	Ala	Lys	Leu	Gly	Ala	Asp
															230
Val	Val	Val	His	Ser	Ile	Ser	Lys	Phe	Ile	Ser	Gly	Gly	Ala	Asp	Ile
															245
Ile	Ala	Gly	Ala	Val	Cys	Gly	Ser	Glu	Lys	Leu	Val	Glu	Arg	Asp	Asp
															260
Gly	Ser	Ser	Trp	Arg	Ile	Ser	Asp	Ala	Ser	Arg	Ser	His	His	Glu	Arg
															275
Gln	Gly	Gly	Phe	Arg	Ala	Leu	Arg	Ala	Asn	Pro	Ser	Leu	Gly	Pro	Thr
															290
His	Glu	Arg	Ala	Gln	Pro	Gln	Ser	Pro	Ser	Val	Cys				
															310

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 255 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..255
 (D) OTHER INFORMATION: / Ceres Seq. ID 1565570
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

```
Met Ser Ile Glu Ala Ser Ala Thr Phe Thr Val Met Glu Pro Asp Thr
1      5      10      15
Met Arg Arg Met Phe Thr Gly Glu Leu Gly Pro Asp Asn Asp Phe Tyr
      20      25      30
Val Tyr Ser Arg His Phe Asn Pro Thr Val Leu Asn Leu Ser Arg Gln
      35      40      45
Met Ala Ala Leu Glu Gly Thr Gln Ala Ala Tyr Cys Thr Ser Ser Gly
50      55      60
Met Ser Ala Ile Ser Ser Val Met Leu Gln Leu Cys Ser Ser Gly Gly
65      70      75      80
His Val Val Ala Ala Ser Thr Leu Tyr Gly Gly Thr His Ala Leu Leu
      85      90      95
Ser His Phe Leu Pro Arg Thr Cys Asn Ile Thr Thr Ser Phe Val Asp
      100      105      110
Ile Thr Asp His Gly Ala Val Ala Asn Ala Ile Val Glu Gly Arg Thr
      115      120      125
Gln Val Leu Tyr Phe Glu Ser Val Ala Asn Pro Thr Leu Thr Val Ala
130      135      140
Asp Ile Pro Glu Leu Ser Arg Met Ala His Glu Lys Gly Val Thr Val
145      150      155      160
Val Val Asp Asn Thr Phe Ala Pro Met Val Leu Ser Pro Ala Lys Leu
      165      170      175
Gly Ala Asp Val Val Val His Ser Ile Ser Lys Phe Ile Ser Gly Gly
      180      185      190
Ala Asp Ile Ile Ala Gly Ala Val Cys Gly Ser Glu Lys Leu Val Glu
195      200      205
Arg Asp Asp Gly Ser Ser Trp Arg Ile Ser Asp Ala Ser Arg Ser His
210      215      220
His Glu Arg Gln Gly Gly Phe Arg Ala Leu Arg Ala Asn Pro Ser Leu
225      230      235      240
Gly Pro Thr His Glu Arg Ala Gln Pro Gln Ser Pro Ser Val Cys
      245      250      255
```

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 244 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
 (B) LOCATION: 1..244
 (D) OTHER INFORMATION: / Ceres Seq. ID 1565571

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

```
Met Glu Pro Asp Thr Met Arg Arg Met Phe Thr Gly Glu Leu Gly Pro
1      5      10      15
Asp Asn Asp Phe Tyr Val Tyr Ser Arg His Phe Asn Pro Thr Val Leu
      20      25      30
Asn Leu Ser Arg Gln Met Ala Ala Leu Glu Gly Thr Gln Ala Ala Tyr
35      40      45
Cys Thr Ser Ser Gly Met Ser Ala Ile Ser Ser Val Met Leu Gln Leu
50      55      60
Cys Ser Ser Gly Gly His Val Val Ala Ala Ser Thr Leu Tyr Gly Gly
65      70      75      80
Thr His Ala Leu Leu Ser His Phe Leu Pro Arg Thr Cys Asn Ile Thr
```


(2) INFORMATION FOR SEO ID NO:16:

(A) LENGTH: 751 base pairs

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ix) FEATURE:

(B) LOCATION: 1..751

(D) OTHER INFORMATION: / Ceres Seq. ID 1565576

```
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:
```

aaaggagaag	gaacattcac	tctacacgcg	ttcaactctt	tccagaatac	gaaaaatttc	60
acagocaaat	ttttctcgag	aaaaactcgaa	gaagacaaaa	tgcggataca	gctaaccgat	120
cagcagattc	ccgagattcaa	ggaagctctg	agcctattcg	acaagaacgg	agatggtgtg	180
atcacccaca	aggagctctg	gactgtgatg	agatcacctg	ggcagacacc	gcagagaagg	240
gagctccagg	atattgtcaa	tgaatgtgat	gcagacggga	acgggcacat	agatttccct	300
gagttctctg	acctaatgct	caactgaagt	aaagacacat	attcagagaa	agagcttaag	360
gaagacctca	ggggttttga	caggagcagc	aacggcttca	tctcggcgcg	tgagctctgt	420
cagctgatga	caaatctctg	ggagaagttg	accgatgatg	aagtcgtcaa	gatcatcoga	480
gagcctgatg	tcgatgtgtg	tggtagaagt	aactatgaag	agcttgtcta	agatcatgat	540
gcaaatgatg	attctcttta	ttccctcgaa	tcttaagcat	gtttttcttt	tacattcttt	600
aaactgagaa	agtaatttta	tfgaacacaaa	agaaacacag	agatttgtct	octgtgtgtg	660
tttgtctctg	Agtagatttt	tgttaacgct	gctctctctt	tgccttttgg	ttttgttatt	720
ctgcttgccc	tttgcaotca	ctaatctgtt	t			

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

```
(ix) FEATURE:
```

(A) NAME/KEY: peptide

(B) LOCATION: 1..182

(D) OTHER INFORMATION: / Ceres Seq. ID 1565577

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Lys Gly Glu Gly Thr Phe Thr Leu Thr Arg Phe Asn Phe Leu Gln Lys
1 5 10 15
Gln Glu Asn Phe Thr Ala Lys Phe Phe Ser Arg Lys Ser Glu Glu Asp

20 25 30
Lys Met Ala Asp Gln Leu Thr Asp Asp Gln Ile Ser Glu Phe Lys Glu
35 40 45
Ala Phe Ser Leu Phe Asp Lys Asp Gly Asp Gly Cys Ile Thr Thr Lys
50 55 60
Glu Leu Gly Thr Val Met Arg Ser Leu Gly Gln Asn Pro Thr Glu Ala
65 70 75 80
Glu Leu Gln Asp Met Ile Asn Glu Val Asp Ala Asp Gly Asn Gly Thr
85 90 95
Ile Asp Phe Pro Glu Phe Leu Asn Leu Met Ala Arg Lys Met Lys Asp
100 105 110
Thr Asp Ser Glu Glu Glu Leu Lys Glu Ala Phe Arg Val Phe Asp Lys
115 120 125
Asp Gln Asn Gly Phe Ile Ser Ala Ala Glu Leu Arg His Val Met Thr
130 135 140
Asn Leu Gly Glu Lys Leu Thr Asp Glu Glu Val Asp Glu Met Ile Arg
145 150 155 160
Glu Ala Asp Val Asp Gly Asp Gly Gln Ile Asn Tyr Glu Glu Phe Val
165 170 175
Lys Val Met Met Ala Lys
180

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 149 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..149
- (D) OTHER INFORMATION: / Ceres Seq. ID 1565578

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Met Ala Asp Gln Leu Thr Asp Asp Gln Ile Ser Glu Phe Lys Glu Ala
1 5 10 15
Phe Ser Leu Phe Asp Lys Asp Gly Asp Gly Cys Ile Thr Thr Lys Glu
20 25 30
Leu Gly Thr Val Met Arg Ser Leu Gly Gln Asn Pro Thr Glu Ala Glu
35 40 45
Leu Gln Asp Met Ile Asn Glu Val Asp Ala Asp Gly Asn Gly Thr Ile
50 55 60
Asp Phe Pro Glu Phe Leu Asn Leu Met Ala Arg Lys Met Lys Asp Thr
65 70 75 80
Asp Ser Glu Glu Glu Leu Lys Glu Ala Phe Arg Val Phe Asp Lys Asp
85 90 95
Gln Asn Gly Phe Ile Ser Ala Ala Glu Leu Arg His Val Met Thr Asn
100 105 110
Leu Gly Glu Lys Leu Thr Asp Glu Glu Val Asp Glu Met Ile Arg Glu
115 120 125
Ala Asp Val Asp Gly Asp Gly Gln Ile Asn Tyr Glu Glu Phe Val Lys
130 135 140
Val Met Met Ala Lys
145

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1..113
(D) OTHER INFORMATION: / Ceres Seq. ID 1565579
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:
Met Arg Ser Leu Gly Gln Asn Pro Thr Glu Ala Glu Leu Gln Asp Met
1 5 10 15
Ile Asn Glu Val Asp Ala Asp Gly Asn Gly Thr Ile Asp Phe Pro Glu
20 25 30
Phe Leu Asn Leu Met Ala Arg Lys Met Lys Asp Thr Asp Ser Glu Glu
35 40 45
Glu Leu Lys Glu Ala Phe Arg Val Phe Asp Lys Asp Gln Asn Gly Phe
50 55 60
Ile Ser Ala Ala Glu Leu Arg His Val Met Thr Asn Leu Gly Glu Lys
65 70 75 80
Leu Thr Asp Glu Glu Val Asp Glu Met Ile Arg Glu Ala Asp Val Asp
85 90 95
Gly Asp Gly Gln Ile Asn Tyr Glu Glu Phe Val Lys Val Met Met Ala
100 105 110
Lys

(2) INFORMATION FOR SEQ ID NO:20:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1602 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:

(A) NAME/KEY: -
(B) LOCATION: 1..1602
(D) OTHER INFORMATION: / Ceres Seq. ID 1565612
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:
agctactact gttgaagcga ttctcactaa aaccctcgaa cacatcgcc ttatctcttt 60
ctctagatct actgcgtatg gctactatca ccgttgttaa ggctagacag atctctcgaca 120
gtcgtgttaa tccacaccgt gaggtggata tccacacgtc aaatgggtgtt aaggtttacag 180
cagctgttcc aagtggagct tccactggta tctatgaggg tcttgagctg agggatggag 240
gatctgacta ccttggaag ggtgtatcta aggctgttgg caatgtgaac aacatcatcg 300
ggccagcaact tattggaag gacccaactc agcagactgc tattgacaac ttcatgtgtc 360
atgaacttga cggaaccctaa aacgagtggg ggtggtgcaa gcaaaagctt ggagccaagt 420
cgattcttgc tgtgtctctt gctgtctgca aagctggggc tgtgtgcagc ggcattctctc 480
tatacaagca cattgccaac ctgtctggta accccaagt ttgtctacca gttcctcgct 540
tcaacgtcat caatgggtgga tcccatgccg gaacaagct tgctatgcag gagtttatga 600
tctcctctgt tggagctgct tctttcaagg gagccatgaa gatgggtgtg gaagtttacc 660
accacttgaa gtctgtgatt aagaagaagt acggccagga tgcaccaaat ttggtgtgat 720
aaggtggggt tgcaccaaac attcaggaga acaaggaggg tcttgaattg ctcaagactg 780
ctatcgagaa ggctggatgc actggaaaagg ttgtcattgg aatggatggt gccgcttcag 840
agttctactc agaagacaag acctacgact tgaacttcaa agaagagaac aacaatggct 900
ctcagaagat tctcgtgat gctctaaaagg acctgtacaa gtccctttgtc gctgagtacc 960
caatcgtgtc cattgaggag ccatttgacc aagatgactg ggagcactat gctaagatga 1020
ccaatcagtg tggaaaccgag gtccagaTtt gtcggtgatg atttgttggt cactaacccc 1080
aagagagattg ctaaggccaat cgccgagaag tcttgcgaat ctctctcttt gaaggttaac 1140
caaatcggat ctgtaaccga gagtatcgag gcaggttaaga tgcgaagaa acgaggttgg 1200
ggagtgtatg ccagccacag aagtggtgaa accgaggaca cattcatctg tgacttagcc 1260
gttggtctgt ctactggaca aatcaaaaac ggtgctcctt cgagatccga gctgcttgcc 1320
aagtaacaac agcttttgcg tattgaggag gagtgggatg cagaggcaat ttacgtctga 1380
gtcaacttcc gcaaacctgt agaacctacg taatggagac ttttagaagc aaagtgtgtc 1440
tctttgtgac gaggagaaga tgacctgagt ttgatcattt gcttttaatta aataaaacgt 1500
tctgttttga tttctttttt gtttgggttc ttactgtctt ttgtgaaccc tttttgggaa 1560
aagttactca tttttgtaag ggaacatga gaatgctcg cc

(2) INFORMATION FOR SEQ ID NO:21:
(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 351 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..351
(D) OTHER INFORMATION: / Ceres Seq. ID 1565613
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:
Leu Leu Leu Leu Lys Arg Phe Ser Leu Lys Pro Ser Asn Thr Ser Pro
1 5 10 15
Leu Ser Leu Ser Leu Asp Leu Leu Ala Met Ala Thr Ile Thr Val Val
20 25 30
Lys Ala Arg Gln Ile Phe Asp Ser Arg Gly Asn Pro Thr Val Glu Val
35 40 45
Asp Ile His Thr Ser Asn Gly Val Lys Val Thr Ala Ala Val Pro Ser
50 55 60
Gly Ala Ser Thr Gly Ile Tyr Glu Ala Leu Glu Leu Arg Asp Gly Gly
65 70 75 80
Ser Asp Tyr Leu Gly Lys Gly Val Ser Lys Ala Val Gly Asn Val Asn
85 90 95
Asn Ile Ile Gly Pro Ala Leu Ile Gly Lys Asp Pro Thr Gln Gln Thr
100 105 110
Ala Ile Asp Asn Phe Met Val His Glu Leu Asp Gly Thr Gln Asn Glu
115 120 125
Trp Gly Trp Cys Lys Gln Lys Leu Gly Ala Asn Ala Ile Leu Ala Val
130 135 140
Ser Leu Ala Val Cys Lys Ala Gly Ala Val Val Ser Gly Ile Pro Leu
145 150 155 160
Tyr Lys His Ile Ala Asn Leu Ala Gly Asn Pro Lys Ile Val Leu Pro
165 170 175
Val Pro Ala Phe Asn Val Ile Asn Gly Gly Ser His Ala Gly Asn Lys
180 185 190
Leu Ala Met Gln Glu Phe Met Ile Leu Pro Val Gly Ala Ala Ser Phe
195 200 205
Lys Gly Ala Met Lys Met Gly Val Glu Val Tyr His His Leu Lys Ser
210 215 220
Val Ile Lys Lys Lys Tyr Gly Gln Asp Ala Thr Asn Val Gly Asp Glu
225 230 235 240
Gly Gly Phe Ala Pro Asn Ile Gln Glu Asn Lys Glu Gly Leu Glu Leu
245 250 255
Leu Lys Thr Ala Ile Glu Lys Ala Gly Tyr Thr Gly Lys Val Val Ile
260 265 270
Gly Met Asp Val Ala Ala Ser Glu Phe Tyr Ser Glu Asp Lys Thr Tyr
275 280 285
Asp Leu Asn Phe Lys Glu Glu Asn Asn Asn Gly Ser Gln Lys Ile Ser
290 295 300
Gly Asp Ala Leu Lys Asp Leu Tyr Lys Ser Phe Val Ala Glu Tyr Pro
305 310 315 320
Ile Val Ser Ile Glu Asp Pro Phe Asp Gln Asp Asp Trp Glu His Tyr
325 330 335
Ala Lys Met Thr Thr Glu Cys Gly Thr Glu Val Gln Ile Cys Arg
340 345 350

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 326 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..326

(D) OTHER INFORMATION: / Ceres Seq. ID 1565614

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Met Ala Thr Ile Thr Val Val Lys Ala Arg Gln Ile Phe Asp Ser Arg
1 5 10 15
Gly Asn Pro Thr Val Glu Val Asp Ile His Thr Ser Asn Gly Val Lys
20 25 30
Val Thr Ala Ala Val Pro Ser Gly Ala Ser Thr Gly Ile Tyr Glu Ala
35 40 45
Leu Glu Leu Arg Asp Gly Gly Ser Asp Tyr Leu Gly Lys Gly Val Ser
50 55 60
Lys Ala Val Gly Asn Val Asn Asn Ile Ile Gly Pro Ala Leu Ile Gly
65 70 75 80
Lys Asp Pro Thr Gln Gln Thr Ala Ile Asp Asn Phe Met Val His Glu
85 90 95
Leu Asp Gly Thr Gln Asn Glu Trp Gly Trp Cys Lys Gln Lys Leu Gly
100 105 110
Ala Asn Ala Ile Leu Ala Val Ser Leu Ala Val Cys Lys Ala Gly Ala
115 120 125
Val Val Ser Gly Ile Pro Leu Tyr Lys His Ile Ala Asn Leu Ala Gly
130 135 140
Asn Pro Lys Ile Val Leu Pro Val Pro Ala Phe Asn Val Ile Asn Gly
145 150 155 160
Gly Ser His Ala Gly Asn Lys Leu Ala Met Gln Glu Phe Met Ile Leu
165 170 175
Pro Val Gly Ala Ala Ser Phe Lys Gly Ala Met Lys Met Gly Val Glu
180 185 190
Val Tyr His His Leu Lys Ser Val Ile Lys Lys Lys Tyr Gly Gln Asp
195 200 205
Ala Thr Asn Val Gly Asp Glu Gly Gly Phe Ala Pro Asn Ile Gln Glu
210 215 220
Asn Lys Glu Gly Leu Glu Leu Lys Thr Ala Ile Glu Lys Ala Gly
225 230 235 240
Tyr Thr Gly Lys Val Val Ile Gly Met Asp Val Ala Ala Ser Glu Phe
245 250 255
Tyr Ser Glu Asp Lys Thr Tyr Asp Leu Asn Phe Lys Glu Glu Asn Asn
260 265 270
Asn Gly Ser Gln Lys Ile Ser Gly Asp Ala Leu Lys Asp Leu Tyr Lys
275 280 285
Ser Phe Val Ala Glu Tyr Pro Ile Val Ser Ile Glu Asp Pro Phe Asp
290 295 300
Gln Asp Asp Trp Glu His Tyr Ala Lys Met Thr Thr Glu Cys Gly Thr
305 310 315 320
Glu Val Gln Ile Cys Arg
325

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 234 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..234

(D) OTHER INFORMATION: / Ceres Seq. ID 1565615

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Met Val His Glu Leu Asp Gly Thr Gln Asn Glu Trp Gly Trp Cys Lys
1 5 10 15

Gln Lys Leu Gly Ala Asn Ala Ile Leu Ala Val Ser Leu Ala Val Cys
20 25 30
Lys Ala Gly Ala Val Val Ser Gly Ile Pro Leu Tyr Lys His Ile Ala
35 40 45
Asn Leu Ala Gly Asn Pro Lys Ile Val Leu Pro Val Pro Ala Phe Asn
50 55 60
Val Ile Asn Gly Gly Ser His Ala Gly Asn Lys Leu Ala Met Gln Glu
65 70 75 80
Phe Met Ile Leu Pro Val Gly Ala Ala Ser Phe Lys Gly Ala Met Lys
85 90 95
Met Gly Val Glu Val Tyr His His Leu Lys Ser Val Ile Lys Lys Lys
100 105 110
Tyr Gly Gln Asp Ala Thr Asn Val Gly Asp Glu Gly Gly Phe Ala Pro
115 120 125
Asn Ile Gln Glu Asn Lys Gly Gly Leu Glu Leu Lys Thr Ala Ile
130 135 140
Glu Lys Ala Gly Tyr Thr Gly Lys Val Val Ile Gly Met Asp Val Ala
145 150 155 160
Ala Ser Glu Phe Tyr Ser Glu Asp Lys Thr Tyr Asp Leu Asn Phe Lys
165 170 175
Glu Glu Asn Asn Asn Gly Ser Gln Lys Ile Ser Gly Asp Ala Leu Lys
180 185 190
Asp Leu Tyr Lys Ser Phe Val Ala Glu Tyr Pro Ile Val Ser Ile Glu
195 200 205
Asp Pro Phe Asp Gln Asp Asp Trp Glu His Tyr Ala Lys Met Thr Thr
210 215 220
Glu Cys Gly Thr Glu Val Gln Ile Cys Arg
225 230

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1292 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1292
- (D) OTHER INFORMATION: / Ceres Seq. ID 1565616

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

ataaaaatca	ttatccaaaa	aagtgcaccc	ttcttcgcgc	tagaaaaacat	tcggtaacc	60
atgtccgaa	gaatcacttg	ttcttcttca	cttggtctcac	ctctctctctt	ctctccgttc	120
tttgcgaac	tcctctgctc	ttactcctca	ccgaccaccca	tcgccgtctc	aggccgcaac	180
attcgcgcac	tatcaactcc	aaccactctt	cggtgcattt	gttccacactc	ttcatctgaa	240
atcatctccg	agcatctctc	gttctgcagg	gtttacaaaag	acggtctgat	cgaacgtctt	300
tcggcaccgc	aaacagtcgc	gggttctctc	aaaccacgaa	acgacgtctg	ttcaaaagac	360
gttgtctact	caacggggca	taacctctcc	gttctgtctc	ttctccctca	caaatcaaca	420
caactgcgcg	ccggtaacaa	actccctcta	cttatctact	cccacggcgg	agcttgagata	480
aacgaatccc	ctttctcccc	aatctaccac	aatttctcca	cggaggtagt	taaatccgct	540
aactgcctcg	ccgtctcggg	tcaataccgc	cgtgcaccgc	aagatccggg	tcgggtctgc	600
tatgaagata	catggtctgc	tattcaatgg	attttctcac	attccgatgg	atctggtgaa	660
gaagattgga	ttacaacaata	cgtgatgttc	gaaaaagttt	ttctcgcggc	agatagtgc	720
ggtggttaata	tatctcatca	catggtgatg	agagctggta	aagagaagct	taagcctgaa	780
atcaaaagga	ctgtgattgt	gcataccagc	atttggggga	aagatccggg	cgatgagcac	840
gatgtgcaag	atagagagat	cagagacgga	gttgacagaa	tttggggaaa	aattgtgagt	900
ccgaatagt	ttgatggagc	ggatgatccg	tggtttaatg	tggttggtac	cgggtcggat	960
ttttccggga	tgggatgtga	gaagggtttt	gttgaggtgg	ctgggaaaag	tgtgttttgg	1020
cggaagagat	tagCttacgc	ggagaagcta	aagaagagtg	ggtggaagag	agaggtggaq	1080
gtgattgagg	aagaagatga	agaacattgc	ttccatctct	taaatccaag	ttctgaaaat	1140
gtccccagct	tcattgaagag	actgtgggag	tttatcaactg	gttaaacattg	ttctttgtgt	1200
gacacgaata	aattttgatg	taacctttga	atttgatttg	gttagataat	tatggttaag	1260

gaattaaata caggaataac tctgttctga ct

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 394 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..394

(D) OTHER INFORMATION: / Ceres Seq. ID 1565617

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

Ile	Lys	Ile	Ile	Ile	Gln	Lys	Ser	Ala	Thr	Ser	Phe	Ala	Val	Glu	Asn	
1				5					10					15		
Ile	Pro	Val	Thr	Met	Leu	Arg	Arg	Ile	Thr	Cys	Ser	Ser	Ser	Leu	Ala	
				20					25					30		
Ser	Pro	Ser	Leu	Phe	Leu	Arg	Phe	Arg	Gln	Leu	Pro	Arg	Ser	Tyr		
				35					40					45		
Ser	Ser	Pro	Thr	Thr	Ile	Ala	Val	Ser	Gly	Arg	Asn	Ile	Arg	Arg	Leu	
				50					55					60		
Ser	Thr	Pro	Thr	Thr	Leu	Arg	Cys	Ile	Cys	Ser	His	Ser	Ser	Ser	Glu	
65					70				75					80		
Ile	Ile	Ser	Glu	His	Pro	Pro	Phe	Val	Arg	Val	Tyr	Lys	Asp	Gly	Arg	
				85					90					95		
Ile	Glu	Arg	Leu	Ser	Gly	Thr	Glu	Thr	Val	Pro	Ala	Ser	Leu	Asn	Pro	
				100					105					110		
Arg	Asn	Asp	Val	Val	Ser	Lys	Asp	Val	Val	Tyr	Ser	Pro	Gly	His	Asn	
				115					120					125		
Leu	Ser	Val	Arg	Leu	Phe	Leu	Pro	His	Lys	Ser	Thr	Gln	Leu	Ala	Ala	
				130					135					140		
Gly	Asn	Lys	Leu	Pro	Leu	Leu	Ile	Tyr	Phe	His	Gly	Gly	Ala	Trp	Ile	
145					150				155					160		
Asn	Glu	Ser	Pro	Phe	Ser	Pro	Ile	Tyr	His	Asn	Phe	Leu	Thr	Glu	Val	
				165					170					175		
Val	Lys	Ser	Ala	Asn	Cys	Leu	Ala	Val	Ser	Val	Gln	Tyr	Arg	Arg	Ala	
				180					185					190		
Pro	Glu	Asp	Pro	Val	Pro	Ala	Ala	Tyr	Glu	Asp	Thr	Trp	Ser	Ala	Ile	
				195					200					205		
Gln	Trp	Ile	Phe	Ser	His	Ser	Asp	Gly	Ser	Gly	Glu	Glu	Asp	Trp	Ile	
									215					220		
Asn	Lys	Tyr	Ala	Asp	Phe	Glu	Lys	Val	Phe	Leu	Ala	Gly	Asp	Ser	Ala	
225					230				235					240		
Gly	Gly	Asn	Ile	Ser	His	His	Met	Ala	Met	Arg	Ala	Gly	Lys	Glu	Lys	
				245					250					255		
Leu	Lys	Pro	Arg	Ile	Lys	Gly	Thr	Val	Ile	Val	His	Pro	Ala	Ile	Trp	
				260					265					270		
Gly	Lys	Asp	Pro	Val	Asp	Glu	His	Asp	Val	Gln	Asp	Arg	Glu	Ile	Arg	
				275					280					285		
Asp	Gly	Val	Ala	Glu	Ile	Trp	Glu	Lys	Ile	Val	Ser	Pro	Asn	Ser	Val	
				290					295					300		
Asp	Gly	Ala	Asp	Asp	Pro	Trp	Phe	Asn	Val	Val	Gly	Ser	Gly	Ser	Asp	
305					310				315					320		
Phe	Ser	Gly	Met	Gly	Cys	Glu	Lys	Val	Leu	Val	Glu	Val	Ala	Gly	Lys	
				325					330					335		
Asp	Val	Phe	Trp	Arg	Gln	Gly	Leu	Ala	Tyr	Ala	Glu	Lys	Leu	Lys	Lys	
				340					345					350		
Ser	Gly	Trp	Lys	Gly	Glu	Val	Glu	Val	Ile	Glu	Glu	Glu	Asp	Glu	Glu	
				355					360					365		
His	Cys	Phe	His	Leu	Leu	Asn	Pro	Ser	Ser	Glu	Asn	Ala	Pro	Ser	Phe	
				370					375					380		

370

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1179 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1179

(D) OTHER INFORMATION: / Ceres Seq. ID 1565633

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

```
atcttaatta tactgatctt tatcgttgac tagatttaag aaacaaaaata ataagatgggt    60
tagggcacaat atagtgagca tggttctcct gatgcacgcc atcgttgggt ttcccttttca    120
tgcgaggggga ttaagtatga cttactacat gatgagctgt cctttcgctg aacagattgt    180
gaagaacagt gttaacaaat ctcttcaagc cgatcccaact ttagccogctg gtcttatccg    240
tatgtgtgtc cagcactggt tcatcgaggg atgtgatgag tcaattctgc tagattcaac    300
gaaagacaac actgcggaaa aggattcgcc tgcgaatctg agtctacgtg gctacgagat    360
catcgatgat gcaaaggaga aaatcgagaa tagatgtcca ggagttgtat catgcgagaa    420
tatagtgtgc atggctgcta gagatgctgt cttttgggct ggtggtccat attatgacat    480
accgaaagga aggtttgatg gtaaaagatc aaagatagaa gatcacagaa atctaccttc    540
accttttctt aatgcctctc aactcattca aacttttggc caacgttggt tcactccaca    600
agatgttgtt gctctctctg gagcacatac cctaggagtt gcacgatgct cctccttcaa    660
ggctagactt accgtcccaag actcttctatt agactcgact ttgcaaacac ctctctctaa    720
aacatgcagc gggggtgaca atgcagagca accctttgat gCtaacgcgca acgatttcca    780
caatgcttac ttcaatgcgc ttcagatgaa atcaggagtc ccttttccag accaaacttt    840
attcaacaca ccaaggacca ggaatcttgt taacggctat gcatttaacc aaagccaagt    900
ctctcttgat ttocaaacgg ccatgcgcaa gatgagcaat ctgtatgta aacttggtct    960
tcaaggtgaa gtccgtcaaa attgtcggag tattaattag cttagaccac atctacttacc    1020
gatttttgtt tttataataa gttctctact cttgtatat gaagaatcat gaattcttca    1080
ggctactatg taataaattgt gtactctcgt aatagcagt tgtatactta ttgcttgtgt    1140
ggttcagata tccatcaaaa agtaataatac tttggttgc
```

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 314 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..314

(D) OTHER INFORMATION: / Ceres Seq. ID 1565634

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

```
Met Val Arg Ala Asn Ile Val Ser Met Val Leu Leu Met His Ala Ile
1      5      10      15
Val Gly Phe Pro Phe His Ala Arg Gly Leu Ser Met Thr Tyr Tyr Met
20      25      30
Met Ser Cys Pro Phe Ala Glu Gln Ile Val Lys Asn Ser Val Asn Asn
35      40      45
Ala Leu Gln Ala Asp Pro Thr Leu Ala Ala Gly Leu Ile Arg Met Leu
50      55      60
Phe His Asp Cys Phe Ile Glu Gly Cys Asp Ala Ser Ile Leu Leu Asp
65      70      75      80
Ser Thr Lys Asp Asn Thr Ala Glu Lys Asp Ser Pro Ala Asn Leu Ser
85      90      95
Leu Arg Gly Tyr Glu Ile Ile Asp Asp Ala Lys Glu Lys Ile Glu Asn
100      105      110
Arg Cys Pro Gly Val Val Ser Cys Ala Asp Ile Val Ala Met Ala Ala
115      120      125
```

Arg Asp Ala Val Phe Trp Ala Gly Gly Pro Tyr Tyr Asp Ile Pro Lys
130 135 140
Gly Arg Phe Asp Gly Lys Arg Ser Lys Ile Glu Asp Thr Arg Asn Leu
145 150 155 160
Pro Ser Pro Phe Leu Asn Ala Ser Gln Leu Ile Gln Thr Phe Gly Gln
165 170 175
Arg Gly Phe Thr Pro Gln Asp Val Val Ala Leu Ser Gly Ala His Thr
180 185 190
Leu Gly Val Ala Arg Cys Ser Ser Phe Lys Ala Arg Leu Thr Val Pro
195 200 205
Asp Ser Ser Leu Asp Ser Thr Phe Ala Asn Thr Leu Ser Lys Thr Cys
210 215 220
Ser Ala Gly Asp Asn Ala Glu Gln Pro Phe Asp Ala Thr Arg Asn Asp
225 230 235 240
Phe Asp Asn Ala Tyr Phe Asn Ala Leu Gln Met Lys Ser Gly Val Leu
245 250 255
Phe Ser Asp Gln Thr Leu Phe Asn Thr Pro Arg Thr Arg Asn Leu Val
260 265 270
Asn Gly Tyr Ala Leu Asn Gln Ala Lys Phe Phe Phe Asp Phe Gln Gln
275 280 285
Ala Met Arg Lys Met Ser Asn Leu Asp Val Lys Leu Gly Ser Gln Gly
290 295 300
Glu Val Arg Gln Asn Cys Arg Ser Ile Asn
305 310

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 306 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..306

(D) OTHER INFORMATION: / Ceres Seq. ID 1565635

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

Met Val Leu Leu Met His Ala Ile Val Gly Phe Pro Phe His Ala Arg
1 5 10 15
Gly Leu Ser Met Thr Tyr Tyr Met Met Ser Cys Pro Phe Ala Glu Gln
20 25 30
Ile Val Lys Asn Ser Val Asn Asn Ala Leu Gln Ala Asp Pro Thr Leu
35 40 45
Ala Ala Gly Leu Ile Arg Met Leu Phe His Asp Cys Phe Ile Glu Gly
50 55 60
Cys Asp Ala Ser Ile Leu Leu Asp Ser Thr Lys Asp Asn Thr Ala Glu
65 70 75 80
Lys Asp Ser Pro Ala Asn Leu Ser Leu Arg Gly Tyr Glu Ile Ile Asp
85 90 95
Asp Ala Lys Glu Lys Ile Glu Asn Arg Cys Pro Gly Val Val Ser Cys
100 105 110
Ala Asp Ile Val Ala Met Ala Ala Arg Asp Ala Val Phe Trp Ala Gly
115 120 125
Gly Pro Tyr Tyr Asp Ile Pro Lys Gly Arg Phe Asp Gly Lys Arg Ser
130 135 140
Lys Ile Glu Asp Thr Arg Asn Leu Pro Ser Pro Phe Leu Asn Ala Ser
145 150 155 160
Gln Leu Ile Gln Thr Phe Gly Gln Arg Gly Phe Thr Pro Gln Asp Val
165 170 175
Val Ala Leu Ser Gly Ala His Thr Leu Gly Val Ala Arg Cys Ser Ser
180 185 190
Phe Lys Ala Arg Leu Thr Val Pro Asp Ser Ser Leu Asp Ser Thr Phe

195	200	205
Ala Asn Thr Leu Ser Lys Thr Cys Ser Ala Gly Asp Asn Ala Glu Gln		
210	215	220
Pro Phe Asp Ala Thr Arg Asn Asp Phe Asp Asn Ala Tyr Phe Asn Ala		
225	230	235
Leu Gln Met Lys Ser Gly Val Leu Phe Ser Asp Gln Thr Leu Phe Asn		
245	250	255
Thr Pro Arg Thr Arg Asn Leu Val Asn Gly Tyr Ala Leu Asn Gln Ala		
260	265	270
Lys Phe Phe Phe Asp Phe Gln Gln Ala Met Arg Lys Met Ser Asn Leu		
275	280	285
Asp Val Lys Leu Gly Ser Gln Gly Glu Val Arg Gln Asn Cys Arg Ser		
290	295	300
Ile Asn		
305		

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 302 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..302

(D) OTHER INFORMATION: / Ceres Seq. ID 1565636

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

Met His Ala Ile Val Gly Phe Pro Phe His Ala Arg Gly Leu Ser Met	
1	5 10 15
Thr Tyr Tyr Met Met Ser Cys Pro Phe Ala Glu Gln Ile Val Lys Asn	
	20 25 30
Ser Val Asn Asn Ala Leu Gln Ala Asp Pro Thr Leu Ala Ala Gly Leu	
	35 40 45
Ile Arg Met Leu Phe His Asp Cys Phe Ile Glu Gly Cys Asp Ala Ser	
	50 55 60
Ile Leu Leu Asp Ser Thr Lys Asp Asn Thr Ala Glu Lys Asp Ser Pro	
	65 70 75 80
Ala Asn Leu Ser Leu Arg Gly Tyr Glu Ile Asp Asp Ala Lys Glu	
	85 90 95
Lys Ile Glu Asn Arg Cys Pro Gly Val Val Ser Cys Ala Asp Ile Val	
	100 105 110
Ala Met Ala Ala Arg Asp Ala Val Phe Trp Ala Gly Gly Pro Tyr Tyr	
	115 120 125
Asp Ile Pro Lys Gly Arg Phe Asp Gly Lys Arg Ser Lys Ile Glu Asp	
	130 135 140
Thr Arg Asn Leu Pro Ser Pro Phe Leu Asn Ala Ser Gln Leu Ile Gln	
	145 150 155 160
Thr Phe Gly Gln Arg Gly Phe Thr Pro Gln Asp Val Val Ala Leu Ser	
	165 170 175
Gly Ala His Thr Leu Gly Val Ala Arg Cys Ser Ser Phe Lys Ala Arg	
	180 185 190
Leu Thr Val Pro Asp Ser Ser Leu Asp Ser Thr Phe Ala Asn Thr Leu	
	195 200 205
Ser Lys Thr Cys Ser Ala Gly Asp Asn Ala Glu Gln Pro Phe Asp Ala	
	210 215 220
Thr Arg Asn Asp Phe Asp Asn Ala Tyr Phe Asn Ala Leu Gln Met Lys	
	225 230 235 240
Ser Gly Val Leu Phe Ser Asp Gln Thr Leu Phe Asn Thr Pro Arg Thr	
	245 250 255
Arg Asn Leu Val Asn Gly Tyr Ala Leu Asn Gln Ala Lys Phe Phe Phe	
	260 265 270

Asp Phe Gln Gln Ala Met Arg Lys Met Ser Asn Leu Asp Val Lys Leu
275 280 285
Gly Ser Gln Gly Glu Val Arg Gln Asn Cys Arg Ser Ile Asn
290 295 300

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1200 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1200
- (D) OTHER INFORMATION: / Ceres Seq. ID 1565643

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

gaaatctcct	atccattctt	ctcgtctctg	caaaatcccc	acttcacgaa	tcgcaaaaaga	60
tcaaggttta	ttgatctatt	gcgaaattag	ggtttgtaa	ttcgaatcgg	agattaataa	120
tagattttgt	gatggagtgt	tcatacgcga	tagaagaatc	ttgatttcga	tctcgatgaa	180
attaggagtc	gagggtattt	atttataatt	aagatggtga	atattaaaag	ccctttacgg	240
ctattcatag	aggattctat	taaggaatta	attaggggtt	tcaggagaca	aaggatcaaa	300
tggagaaatg	catttctctt	tggttctata	atgactacca	ttgtgttctt	gcttcataca	360
ccaacgtttt	cagtctcttc	tgatgaagaa	gaacccgagt	cttcttcgcc	tatttacttg	420
aatggtcttc	tgcatttgaa	tatccatatt	gtagtagtg	aagcaaaaag	tgaaaaattt	480
catactctta	gaacaagaac	tcctattgtg	caattgaatg	cttctgaagc	aagtgaagct	540
gttatttcga	gaaaaaggcg	aaaaaggaaa	aaaaagaaag	agacaaaaga	tgatctgatt	600
ctcaactgac	ctctctcagc	accacgacat	gtctatctt	ccctcagagag	acgtgtcttt	660
tccttgcacc	cgaagaaaag	tcttacttat	gcaaaaactg	agattoacgc	tgccccggag	720
gtcataaagt	acacagatct	atttgcctca	ttgtttgaaa	acctctctgt	tttcaaaaag	780
agctatgagc	tattggaact	gatactaaag	gtctacatat	atCctgacgc	agacaaccac	840
atctctcagc	aaccgcattt	gaacggtata	tatgcttcag	aaggttggtt	tatgaagcta	900
atggagtcga	acacacagtt	tgctacaaaag	aaccctgaga	aggctcaatt	gttctacatg	960
ccatatagtg	tgaacacagt	tcagaaaaat	atctttgttc	ctggatcaca	taacatcaaa	1020
ccctttatct	ctcttcttag	aGactacgtc	aacatgctct	ccatcaataa	ccctctctgg	1080
aaccgcactc	atgggtcaga	tcatttctct	gtcgtctgcc	acgattgggt	atcgaaaatg	1140
ttctctatgt	aaagaccaat	gggtttactt	ccctcatttt	tatgttatga	tctctatttc	1200

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 312 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..312
- (D) OTHER INFORMATION: / Ceres Seq. ID 1565644

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Met Val Asn Ile Lys Ser Pro Leu Arg Leu Phe Ile Glu Asp Ser Ile	
1 5 10 15	
Lys Glu Leu Ile Arg Gly Phe Arg Arg Gln Arg Ile Lys Trp Arg Asn	
20 25 30	
Ala Phe Leu Leu Gly Ser Ile Met Thr Thr Ile Val Val Leu Leu His	
35 40 45	
Thr Pro Thr Phe Ser Val Phe Ser Asp Glu Glu Thr Thr Glu Ser Ser	
50 55 60	
Ser Pro Ile Tyr Leu Asn Gly Ser Leu His Leu Asn Ile His Ile Val	
65 70 75 80	
Ser Ser Glu Ala Lys Val Glc Asn Phe His Thr Leu Arg Thr Arg Thr	
85 90 95	

Pro Ile Val Gln Leu Asn Ala Ser Glu Ala Ser Glu Ala Val Ile Ser
100 105 110
Arg Lys Arg Arg Lys Arg Lys Lys Arg Lys Lys Thr Lys Asp Asp Leu
115 120 125
Ile Leu Thr Asp Pro Pro Pro Ala Pro Arg His Val Leu Ser Ser Ser
130 135 140
Glu Arg Arg Ala Leu Ser Leu Pro Pro Lys Lys Ala Leu Thr Tyr Ala
145 150 155 160
Lys Leu Glu Ile Gln Arg Ala Pro Glu Val Ile Asn Asp Thr Asp Leu
165 170 175
Phe Ala Pro Leu Phe Arg Asn Leu Ser Val Phe Lys Arg Ser Tyr Glu
180 185 190
Leu Met Glu Leu Ile Leu Lys Val Tyr Ile Tyr Pro Asp Gly Asp Lys
195 200 205
Pro Ile Phe His Glu Pro His Leu Asn Gly Ile Tyr Ala Ser Glu Gly
210 215 220
Trp Phe Met Lys Leu Met Glu Ser Asn Thr Gln Phe Val Thr Lys Asn
225 230 235 240
Pro Glu Lys Ala His Leu Phe Tyr Met Pro Tyr Ser Val Lys Gln Leu
245 250 255
Gln Lys Ser Ile Phe Val Pro Gly Ser His Asn Ile Lys Pro Leu Ser
260 265 270
Ile Phe Leu Arg Asp Tyr Val Asn Met Leu Ser Ile Lys Tyr Pro Phe
275 280 285
Trp Asn Arg Thr His Gly Ser Asp His Phe Leu Val Ala Cys His Asp
290 295 300
Trp Val Ser Lys Met Phe Leu Cys
305 310

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 273 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..273

(D) OTHER INFORMATION: / Ceres Seq. ID 1565645

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

Met Thr Thr Ile Val Val Leu Leu His Thr Pro Thr Phe Ser Val Phe
1 5 10 15
Ser Asp Glu Glu Glu Thr Glu Ser Ser Ser Pro Ile Tyr Leu Asn Gly
20 25 30
Ser Leu His Leu Asn Ile His Ile Val Ser Ser Glu Ala Lys Val Glu
35 40 45
Asn Phe His Thr Leu Arg Thr Arg Thr Pro Ile Val Gln Leu Asn Ala
50 55 60
Ser Glu Ala Ser Glu Ala Val Ile Ser Arg Lys Arg Arg Lys Arg Lys
65 70 75 80
Lys Arg Lys Lys Thr Lys Asp Asp Leu Ile Leu Thr Asp Pro Pro Pro
85 90 95
Ala Pro Arg His Val Leu Ser Ser Ser Glu Arg Arg Ala Leu Ser Leu
100 105 110
Pro Pro Lys Lys Ala Leu Thr Tyr Ala Lys Leu Glu Ile Gln Arg Ala
115 120 125
Pro Glu Val Ile Asn Asp Thr Asp Leu Phe Ala Pro Leu Phe Arg Asn
130 135 140
Leu Ser Val Phe Lys Arg Ser Tyr Glu Leu Met Glu Leu Ile Leu Lys
145 150 155 160
Val Tyr Ile Tyr Pro Asp Gly Asp Lys Pro Ile Phe His Glu Pro His

	165		170		175
Leu Asn Gly Ile Tyr Ala Ser Glu Gly Trp Phe Met Lys Leu Met Glu					
	180		185		190
Ser Asn Thr Gln Phe Val Thr Lys Asn Pro Glu Lys Ala His Leu Phe					
	195		200		205
Tyr Met Pro Tyr Ser Val Lys Gln Leu Gln Lys Ser Ile Phe Val Pro					
	210		215		220
Gly Ser His Asn Ile Lys Pro Leu Ser Ile Phe Leu Arg Asp Tyr Val					
	225		230		235
Asn Met Leu Ser Ile Lys Tyr Pro Phe Trp Asn Arg Thr His Gly Ser					
	240		245		250
Asp His Phe Leu Val Ala Cys His Asp Trp Val Ser Lys Met Phe Leu					
	255		260		265
					270

Cys

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1231 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1231

(D) OTHER INFORMATION: / Ceres Seq. ID 1565646

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

aacaaaaga atcacgacat tgaatcttct ttcattttct tcctcaagac atagtagcat	60
aagamaatga agatatcatc actaggatgg gtcttagtcc ttattcttcat ctctattacc	120
attgttttga gtgcaccagc acctaaacct cctaaacctc agcctgcacc agcacctaca	180
ctctcotaac ctaagcccac accagcacct acacctccta aaacctaaacc caaacaggaca	240
ctcacacctc ctaaacctaa gcccacacca gcacctacac ctctctaaacc taagcctgca	300
ccagcaccag caccagcacc aacaccagca ccgaaacctc aaacctgcacc taacaccagca	360
ccagttggag aagttgagga cgaaccggag tttagctacg agacgaaagg aaacaaggggg	420
ccagcgaaat ggggaacact acatgcagag tggaaaatgt gtggaatagg caaaatgcaa	480
tctctatttg atcttcggga caaaaatgtg gtatgttagta ataaatttgg attgctctgt	540
agccagtatc tgccttctaa taccaccatt aagaacagag gcatgatatt catgttgaaa	600
ttcaaaggag gcaataaagg tattgggtgc actatccgtg gtactagata tcaacttcaa	660
caacttcatt ggcactctcc ttccgaacat acaatcaatg gcaaaaggtt tgcgctagag	720
gaacacttgg ttcatgagag taaagatava cGctacgctg ttgtcgcttt ctattacaat	780
ctcggagact ctgaccctct ctctcttttc ttggaaaaaac aattgaagaa gataactgat	840
acacatgcgt ccgagggaaca tgtcggaaatc attgatccca aaaaactcag ttttgaatca	900
aaacattatt atagatatct cggatcaact actgctctcc catgttctcga aaatgttatt	960
tggttcgctt ccaaagagat tcgcactgtg tcaagtaaac aagtgaagct tctccgtgtg	1020
gctgtacacg atgcttccaga tctaaatgcc aggcgcgttc aagcagtcac aaagcgcaag	1080
gtatatattt acaaacacaa ggtaagtta atgaagaatc actgtaatat aagttctttac	1140
tagtaattct taattcttta tatatgtaca ttatgaattg tacactaaaa tgatgttttt	1200
agggataaac tgatgactgt gttttgttat t	

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 358 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..358

(D) OTHER INFORMATION: / Ceres Seq. ID 1565647

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

Met Lys Ile Ser Ser Leu Gly Trp Val Leu Val Leu Ile Phe Ile Ser

1 5 10 15
Ile Thr Ile Val Ser Ser Ala Pro Ala Pro Lys Pro Pro Lys Pro Lys
20 25 30
Pro Ala Pro Ala Pro Thr Pro Pro Lys Pro Lys Pro Thr Pro Ala Pro
35 40 45
Thr Pro Pro Lys Pro Lys Pro Lys Pro Ala Pro Thr Pro Pro Lys Pro
50 55 60
Lys Pro Thr Pro Ala Pro Thr Pro Pro Lys Pro Lys Pro Ala Pro Ala
65 70 75 80
Pro Ala Pro Ala Pro Thr Pro Ala Pro Lys Pro Lys Pro Ala Pro Lys
85 90 95
Pro Ala Pro Gly Gly Glu Val Glu Asp Glu Thr Glu Phe Ser Tyr Glu
100 105 110
Thr Lys Gly Asn Lys Gly Pro Ala Lys Trp Gly Thr Leu His Ala Glu
115 120 125
Trp Lys Met Cys Gly Ile Gly Lys Met Gln Ser Pro Ile Asp Leu Arg
130 135 140
Asp Lys Asn Val Val Val Ser Asn Lys Phe Gly Leu Leu Arg Ser Gln
145 150 155 160
Tyr Leu Pro Ser Asn Thr Thr Ile Lys Asn Arg Gly His Asp Ile Met
165 170 175
Leu Lys Phe Lys Gly Gly Asn Lys Gly Ile Gly Val Thr Ile Arg Gly
180 185 190
Thr Arg Tyr Gln Leu Gln Gln Leu His Trp His Ser Pro Ser Glu His
195 200 205
Thr Ile Asn Gly Lys Arg Phe Ala Leu Glu Glu His Leu Val His Glu
210 215 220
Ser Lys Asp Xaa Arg Tyr Ala Val Val Ala Phe Leu Tyr Asn Leu Gly
225 230 235 240
Ala Ser Asp Pro Phe Leu Phe Ser Leu Glu Lys Gln Leu Lys Lys Ile
245 250 255
Thr Asp Thr His Ala Ser Glu Glu His Val Gly Ile Ile Asp Pro Lys
260 265 270
Lys Leu Ser Phe Glu Ser Lys His Tyr Tyr Arg Tyr Ser Gly Ser Leu
275 280 285
Thr Ala Pro Pro Cys Ser Glu Asn Val Ile Trp Ser Val Ser Lys Glu
290 295 300
Ile Arg Thr Val Ser Ser Lys Gln Val Lys Leu Leu Arg Val Ala Val
305 310 315 320
His Asp Ala Ser Asp Ser Asn Ala Arg Pro Leu Gln Ala Val Asn Lys
325 330 335
Arg Lys Val Tyr Leu Tyr Lys Pro Lys Val Lys Leu Met Lys Lys Tyr
340 345 350
Cys Asn Ile Ser Ser Tyr
355

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 220 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..228

(D) OTHER INFORMATION: / Ceres Seq. ID 1565648

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Met Cys Gly Ile Gly Lys Met Gln Ser Pro Ile Asp Leu Arg Asp Lys
1 5 10 15
Asn Val Val Val Ser Asn Lys Phe Gly Leu Leu Arg Ser Gln Tyr Leu
20 25 30

Pro Ser Asn Thr Thr Ile Lys Asn Arg Gly His Asp Ile Met Leu Lys
35 40 45
Phe Lys Gly Gly Asn Lys Gly Ile Gly Val Thr Ile Arg Gly Thr Arg
50 55 60
Tyr Gln Leu Gln Gln Leu His Trp His Ser Pro Ser Glu His Thr Ile
65 70 75 80
Asn Gly Lys Arg Phe Ala Leu Glu Glu His Leu Val His Glu Ser Lys
85 90 95
Asp Xaa Arg Tyr Ala Val Val Ala Phe Leu Tyr Asn Leu Gly Ala Ser
100 105 110
Asp Pro Phe Leu Phe Ser Leu Glu Lys Gln Leu Lys Lys Ile Thr Asp
115 120 125
Thr His Ala Ser Glu Glu His Val Gly Ile Ile Asp Pro Lys Lys Leu
130 135 140
Ser Phe Glu Ser Lys His Tyr Tyr Arg Tyr Ser Gly Ser Leu Thr Ala
145 150 155 160
Pro Pro Cys Ser Glu Asn Val Ile Trp Ser Val Ser Lys Glu Ile Arg
165 170 175
Thr Val Ser Ser Lys Gln Val Lys Leu Leu Arg Val Ala Val His Asp
180 185 190
Ala Ser Asp Ser Asn Ala Arg Pro Leu Gln Ala Val Asn Lys Arg Lys
195 200 205
Val Tyr Leu Tyr Lys Pro Lys Val Lys Leu Met Lys Lys Tyr Cys Asn
210 215 220
Ile Ser Ser Tyr
225

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 222 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..222

(D) OTHER INFORMATION: / Ceres Seq. ID 1565649

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

Met Gln Ser Pro Ile Asp Leu Arg Asp Lys Asn Val Val Ser Asn
1 5 10 15
Lys Phe Gly Leu Leu Arg Ser Gln Tyr Leu Pro Ser Asn Thr Thr Ile
20 25 30
Lys Asn Arg Gly His Asp Ile Met Leu Lys Phe Lys Gly Gly Asn Lys
35 40 45
Gly Ile Gly Val Thr Ile Arg Gly Thr Arg Tyr Gln Leu Gln Gln Leu
50 55 60
His Trp His Ser Pro Ser Glu His Thr Ile Asn Gly Lys Arg Phe Ala
65 70 75 80
Leu Glu Glu His Leu Val His Glu Ser Lys Asp Xaa Arg Tyr Ala Val
85 90 95
Val Ala Phe Leu Tyr Asn Leu Gly Ala Ser Asp Pro Phe Leu Phe Ser
100 105 110
Leu Glu Lys Gln Leu Lys Lys Ile Thr Asp Thr His Ala Ser Glu Glu
115 120 125
His Val Gly Ile Ile Asp Pro Lys Lys Leu Ser Phe Glu Ser Lys His
130 135 140
Tyr Tyr Arg Tyr Ser Gly Ser Leu Thr Ala Pro Pro Cys Ser Glu Asn
145 150 155 160
Val Ile Trp Ser Val Ser Lys Glu Ile Arg Thr Val Ser Ser Lys Gln
165 170 175
Val Lys Leu Leu Arg Val Ala Val His Asp Ala Ser Asp Ser Asn Ala

	180		185		190
Arg Pro Leu Gln Ala Val Asn Lys Arg Lys Val Tyr Leu Tyr Lys Pro					
	195		200		205
Lys Val Lys Leu Met Lys Lys Tyr Cys Asn Ile Ser Ser Tyr					
	210		215		220

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 943 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..943
- (D) OTHER INFORMATION: / Ceres Seq. ID 1565650

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

aatttctttc	gagcaaaact	catttctcaa	tttcttttga	ttttgatcgc	ttcgaagaac	60
gaatcaattt	aggcctgcc	caaacaaacc	ctagaatacg	acaacgcacg	acgcagaaga	120
agtcgaagaa	gactactact	ataaacgacg	aagatcatta	cttcaactct	caatcgagct	180
tttaaatatt	cagatcgtag	aagaaaatcg	aacttttgat	tctaaaacgc	atgagaccga	240
ttcaatcgcc	tccaggagtt	tccgttcccg	tgaaaaacgc	tccccctcgc	cgctctgata	300
ttaccttacc	gcttctctaa	cgcgatgttt	ctctcgtctg	acctcttctc	ctccacaccta	360
cttccggtgg	ttcccggtgg	tctagtggat	ctgcgcgcgc	ttctgggtgt	tcggcgctct	420
caacgaacac	tacacagctc	atagaaacga	agaactattc	ggatttagtg	agaggtaacc	480
gtatcggaag	cggagaggtg	ggaacgggat	acaaagtgtg	tcaccgctcg	agttctctgc	540
tatatgcact	taagggtgata	tacggttaac	acgaagagac	tgtgagacgt	cagatctgtg	600
gagagatcga	gattttacga	gatgtgaatc	atccaaacat	ttcacacacg	ttggaagata	660
ccaccagacg	tgcataaact	acacctcgag	catttcaacg	tgagcgacaa	ccatctctgc	720
ggaaaaatcc	caagtgcggg	tctccttcag	acctttgaac	catctgcctt	cgctcacacac	780
atctgtcttt	gtggaaactcc	ccttaaggct	tgttaatttg	gtttaaactt	ggcggaagaa	840
taaaaaattat	gttgaatatg	ttatgatgat	gtgttcatta	tcaccgcgca	accaagttta	900
ttgtttcttt	gttatgaatt	taattttaat	gcaagaattg	ggt		

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 148 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..148
- (D) OTHER INFORMATION: / Ceres Seq. ID 1565651

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

Met Arg Pro Ile Gln Ser Pro Pro Gly Val Ser Val Pro Val Lys Ser									
1	5		10		15				
Arg Pro Arg Arg Arg Pro Asp Leu Thr Leu Pro Leu Pro Gln Arg Asp									
	20		25		30				
Val Ser Leu Ala Val Pro Leu Pro Leu Pro Thr Ser Gly Gly Ser									
	35		40		45				
Gly Gly Ser Ser Gly Ser Ala Pro Ser Ser Gly Gly Ser Ala Ser Ser									
	50		55		60				
Thr Asn Thr Asn Ser Ile Glu Ala Lys Asn Tyr Ser Asp Leu Val									
	65		70		75				
Arg Gly Asn Arg Ile Gly Ser Gly Xaa Gly Gly Thr Val Tyr Lys Val									
	85		90		95				
Ile His Arg Pro Ser Ser Arg Leu Tyr Ala Leu Lys Val Ile Tyr Gly									
	100		105		110				
Asn His Glu Glu Thr Val Arg Arg Gln Ile Cys Arg Glu Ile Glu Ile									
	115		120		125				

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Leu Arg Asp Val Asn His Pro Asn Ile Ser Gln Arg Leu Glu Asp Thr
130 135 140

Thr Ser Thr Asp

145

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1383 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1383

(D) OTHER INFORMATION: / Ceres Seq. ID 1565658

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

```
aattcccatt cgtgtttttt cggattgcga gaatcctacg ttatttcttc acttttcacg 60
atcccaggga catcttagac cccaaatggt Gbktcgtcga tgttctttgg aaactgggttc 120
ctctataact gtccggatca gaaacacagc ctctctcagc aacagatgcc attttgcaga 180
tagttctcga ggcaatggct gctacttcat ctaacgtcct ttgcaatgct agcgagtcag 240
atctttgtct tgatgattcc gctgcatttc tacttaaatt tgtagccatt gcttcgattc 300
tcttagctgg agctgctggt gtaactatac cactcattgg caggaaccgt cgtttccttc 360
aaactgattg taatctcttt gtgactgcta aagcttttgc agctgggtgg attctcgcca 420
cgtgttttgt tcataatgtt gcgggtggca cggaagcttt gaagaaccog tgcctaccgg 480
atttcccttg gtctaagttt cctttcccgg gattcttttg gatgattgct gctttgatca 540
ctctgtttgt ggatttcagt gggactcagt actatgaacg gaagcaagag agggaagcta 600
gtgagtcctg tgaacccgtt ggccgtgaac aatcaccggg tattgttgtt cccatgattg 660
gagaaggaaac gaatgatggg aaagtgtttt gtgaagaaga cagtgttggt attcacattg 720
ttggcatcca tgctcatgct gctcatcata gacatagtc tctcctcggt catgattcat 780
gtgaaggaca cagtaaaaac gacattggtc atgctcatgc tcatggggac gggcatggac 840
acggacatgg acacgtacac ggggttttgg atgctgttaa tggagctagg catatcgttg 900
tttctcaggt ttggagcttt ggaattgtgt caacttccat aatcatcggt ctatcccttg 960
gagtatctca gtctccttgc acaatccggc ctctaatcgc agcactatcc ttccaccaat 1020
tctttgaagg atttgcgctc ggtggatgca tctcccaagc gcaattcagg aacaaatcag 1080
cgaccataat ggcttgtttt ttccgctcca caaccocgat agggatcggg attggaacga 1140
cagtgcgctc gctcttcaat tctcacagtg tcggagcatt ggtcactgaa ggtatcttgg 1200
actcgctctc agccggaaatt cttgtgtaca tggctttagt ggatctcata gctgctgatt 1260
tcttgagtac aaaaatgagg tgtaacttta ggcttcaaat tgtatcttat gtaatgttgg 1320
tcttaggagc tggactcatg tcttctcttg ccatttgggc ttaattagag tataagattc 1380
cac
```

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 453 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..453

(D) OTHER INFORMATION: / Ceres Seq. ID 1565659

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

```
Phe Pro Phe Val Phe Phe Arg Ile Ala Arg Ile Leu Arg Tyr Phe Phe
1 5 10 15
Thr Phe His Asp Pro Glu Asp Ile Leu Asp Pro Lys Cys Xaa Xaa Val
20 25 30
Asp Val Leu Trp Lys Leu Val Pro Leu Tyr Leu Phe Gly Ser Glu Thr
35 40 45
Gln Ser Leu Ser Ala Thr Glu Ser Ile Leu Gln Ile Val Pro Glu Ala
50 55 60
Met Ala Ala Thr Ser Ser Asn Val Leu Cys Asn Ala Ser Glu Ser Asp
```

65		70		75		80
Leu Cys Leu Asp Asp Ser Ala Ala Phe Leu Leu Lys Phe Val Ala Ile						
	85			90		95
Ala Ser Ile Leu Leu Ala Gly Ala Ala Gly Val Thr Ile Pro Leu Ile						
	100			105		110
Gly Arg Asn Arg Arg Phe Leu Gln Thr Asp Gly Asn Leu Phe Val Thr						
	115			120		125
Ala Lys Ala Phe Ala Ala Gly Val Ile Leu Ala Thr Cys Phe Val His						
	130			135		140
Met Leu Ala Gly Gly Thr Glu Ala Leu Lys Asn Pro Cys Leu Pro Asp						
	145			150		155
Phe Pro Trp Ser Lys Phe Pro Phe Pro Gly Phe Phe Ala Met Ile Ala						
	165			170		175
Ala Leu Ile Thr Leu Phe Val Asp Phe Met Gly Thr Gln Tyr Glu						
	180			185		190
Arg Lys Gln Glu Arg Glu Ala Ser Glu Ser Val Glu Pro Phe Gly Arg						
	195			200		205
Glu Gln Ser Pro Gly Ile Val Val Pro Met Ile Gly Glu Gly Thr Asn						
	210			215		220
Asp Gly Lys Val Phe Gly Glu Glu Asp Ser Gly Gly Ile His Ile Val						
	225			230		235
Gly Ile His Ala His Ala Ala His His Arg His Ser His Pro Gly						
	245			250		255
His Asp Ser Cys Glu Gly His Ser Lys Ile Asp Ile Gly His Ala His						
	260			265		270
Ala His Gly His Gly His Gly His Gly His Gly His Val His Gly Gly						
	275			280		285
Leu Asp Ala Val Asn Gly Ala Arg His Ile Val Val Ser Gln Val Leu						
	290			295		300
Glu Leu Gly Ile Val Ser His Ser Ile Ile Ile Gly Leu Ser Leu Gly						
	305			310		315
Val Ser Gln Ser Pro Cys Thr Ile Arg Pro Leu Ile Ala Ala Leu Ser						
	325			330		335
Phe His Gln Phe Phe Glu Gly Phe Ala Leu Gly Gly Cys Ile Ser Gln						
	340			345		350
Ala Gln Phe Arg Asn Lys Ser Ala Thr Ile Met Ala Cys Phe Phe Ala						
	355			360		365
Leu Thr Thr Pro Ile Gly Ile Gly Ile Gly Thr Ala Val Ala Ser Ser						
	370			375		380
Phe Asn Ser His Ser Val Gly Ala Leu Val Thr Glu Gly Ile Leu Asp						
	385			390		395
Ser Leu Ser Ala Gly Ile Leu Val Tyr Met Ala Leu Val Asp Leu Ile						
	405			410		415
Ala Ala Asp Phe Leu Ser Thr Lys Met Arg Cys Asn Phe Arg Leu Gln						
	420			425		430
Ile Val Ser Tyr Val Met Leu Phe Leu Gly Ala Gly Leu Met Ser Ser						
	435			440		445
Leu Ala Ile Trp Ala						
	450					

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 389 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..389
- (D) OTHER INFORMATION: / Ceres Seq. ID 1565660

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

```

Met Ala Ala Thr Ser Ser Asn Val Leu Cys Asn Ala Ser Glu Ser Asp
1      5      10      15
Leu Cys Leu Asp Asp Ser Ala Ala Phe Leu Leu Lys Phe Val Ala Ile
20      25      30
Ala Ser Ile Leu Leu Ala Gly Ala Ala Gly Val Thr Ile Pro Leu Ile
35      40      45
Gly Arg Asn Arg Arg Phe Leu Gln Thr Asp Gly Asn Leu Phe Val Thr
50      55      60
Ala Lys Ala Phe Ala Ala Gly Val Ile Leu Ala Thr Cys Phe Val His
65      70      75      80
Met Leu Ala Gly Gly Thr Glu Ala Leu Lys Asn Pro Cys Leu Pro Asp
85      90      95
Phe Pro Trp Ser Lys Phe Pro Phe Pro Gly Phe Phe Ala Met Ile Ala
100     105     110
Ala Leu Ile Thr Leu Phe Val Asp Phe Met Gly Thr Gln Tyr Tyr Glu
115     120     125
Arg Lys Gln Glu Arg Glu Ala Ser Glu Ser Val Glu Pro Phe Gly Arg
130     135     140
Glu Gln Ser Pro Gly Ile Val Val Pro Met Ile Gly Glu Gly Thr Asn
145     150     155     160
Asp Gly Lys Val Phe Gly Glu Glu Asp Ser Gly Gly Ile His Ile Val
165     170     175
Gly Ile His Ala His Ala Ala His His Arg His Ser His Pro Pro Gly
180     185     190
His Asp Ser Cys Glu Gly His Ser Lys Ile Asp Ile Gly His Ala His
195     200     205
Ala His Gly His Gly His Gly His Gly His Gly His Val His Gly Gly
210     215     220
Leu Asp Ala Val Asn Gly Ala Arg His Ile Val Val Ser Gln Val Leu
225     230     235     240
Glu Leu Gly Ile Val Ser His Ser Ile Ile Ile Gly Leu Ser Leu Gly
245     250     255
Val Ser Gln Ser Pro Cys Thr Ile Arg Pro Leu Ile Ala Ala Leu Ser
260     265     270
Phe His Gln Phe Phe Glu Gly Phe Ala Leu Gly Gly Cys Ile Ser Gln
275     280     285
Ala Gln Phe Arg Asn Lys Ser Ala Thr Ile Met Ala Cys Phe Phe Ala
290     295     300
Leu Thr Thr Pro Ile Gly Ile Gly Ile Gly Thr Ala Val Ala Ser Ser
305     310     315     320
Phe Asn Ser His Ser Val Gly Ala Leu Val Thr Glu Gly Ile Leu Asp
325     330     335
Ser Leu Ser Ala Gly Ile Leu Val Tyr Met Ala Leu Val Asp Leu Ile
340     345     350
Ala Ala Asp Phe Leu Ser Thr Lys Met Arg Cys Asn Phe Arg Leu Gln
355     360     365
Ile Val Ser Tyr Val Met Leu Phe Leu Gly Ala Gly Leu Met Ser Ser
370     375     380
Leu Ala Ile Trp Ala
385

```

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 309 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..309
- (D) OTHER INFORMATION: / Ceres Seq. ID 1565661

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

Met	Leu	Ala	Gly	Gly	Thr	Glu	Ala	Leu	Lys	Asn	Pro	Cys	Leu	Pro	Asp
1			5						10				15		
Phe	Pro	Trp	Ser	Lys	Phe	Pro	Phe	Pro	Gly	Phe	Phe	Ala	Met	Ile	Ala
			20					25					30		
Ala	Leu	Ile	Thr	Leu	Phe	Val	Asp	Phe	Met	Gly	Thr	Gln	Tyr	Tyr	Glu
			35				40					45			
Arg	Lys	Gln	Glu	Arg	Glu	Ala	Ser	Glu	Ser	Val	Glu	Pro	Phe	Gly	Arg
			50			55					60				
Glu	Gln	Ser	Pro	Gly	Ile	Val	Val	Pro	Met	Ile	Gly	Glu	Gly	Thr	Asn
					70					75				80	
Asp	Gly	Lys	Val	Phe	Gly	Glu	Glu	Asp	Ser	Gly	Gly	Ile	His	Ile	Val
				85					90				95		
Gly	Ile	His	Ala	His	Ala	Ala	His	His	Arg	His	Ser	His	Pro	Pro	Gly
			100				105						110		
His	Asp	Ser	Cys	Glu	Gly	His	Ser	Lys	Ile	Asp	Ile	Gly	His	Ala	His
			115				120					125			
Ala	His	Gly	His	Gly	His	Gly	His	Gly	His	Gly	His	Val	His	Gly	Gly
			130				135					140			
Leu	Asp	Ala	Val	Asn	Gly	Ala	Arg	His	Ile	Val	Val	Ser	Gln	Val	Leu
				145		150				155				160	
Glu	Leu	Gly	Ile	Val	Ser	His	Ser	Ile	Ile	Ile	Gly	Leu	Ser	Leu	Gly
				165					170					175	
Val	Ser	Gln	Ser	Pro	Cys	Thr	Ile	Arg	Pro	Leu	Ile	Ala	Ala	Leu	Ser
				180				185					190		
Phe	His	Gln	Phe	Phe	Glu	Gly	Phe	Ala	Leu	Gly	Gly	Cys	Ile	Ser	Gln
				195			200					205			
Ala	Gln	Phe	Arg	Asn	Lys	Ser	Ala	Thr	Ile	Met	Ala	Cys	Phe	Phe	Ala
				210			215				220				
Leu	Thr	Thr	Pro	Ile	Gly	Ile	Gly	Ile	Gly	Thr	Ala	Val	Ala	Ser	Ser
				225		230				235				240	
Phe	Asn	Ser	His	Ser	Val	Gly	Ala	Leu	Val	Thr	Glu	Gly	Ile	Leu	Asp
				245				250					255		
Ser	Leu	Ser	Ala	Gly	Ile	Leu	Val	Tyr	Met	Ala	Leu	Val	Asp	Leu	Ile
			260				265						270		
Ala	Ala	Asp	Phe	Leu	Ser	Thr	Lys	Met	Arg	Cys	Asn	Phe	Arg	Leu	Gln
			275				280					285			
Ile	Val	Ser	Tyr	Val	Met	Leu	Phe	Leu	Gly	Ala	Gly	Leu	Met	Ser	Ser
			290			295					300				

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1728 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1728
- (D) OTHER INFORMATION: / Ceres Seq. ID 1565662

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

ctcgacacaca	cttctctctc	tctctctctg	cctcctttcg	gattcaaatc	tcagatctag	60
ctcaaccatg	gcgttgctcg	tcgagaagac	ctcaagtggc	cgtgaataca	aggtcaaaga	120
catgtctcaa	gccgatttgc	gtcgtctcga	actcagactc	gccgaagttg	agatgcctgg	180
actcattgct	tgtcgtaccg	aattcggacc	ttctcagcca	ttcaaaaggc	ctagaatcac	240
cggatctctt	caacatgaca	tcctaaaccgc	cgtactcact	gaaaccctaa	ctgctctcgg	300
tgtgaagtc	agatggtgtt	ctcgcacact	cttctccact	caagaccacg	ccgcgcgacg	360
catcgtctgt	gactccgcgc	ctgttttcgc	ctggaaaggt	gagactcttc	aggagtactg	420
gtggtgtacc	gagcgtgctc	tagattgggg	tccaggtggt	ggtctctgac	tgAttgttga	480

tgatggtggt	gacgctactc	ttttgattca	tgagggtggt	aaagctgagg	agatctttga	540
gaagactggt	caagttcctg	atcctacttc	tactgataac	cctgagtttc	agatcgtggt	600
gtctattatc	aaggaaggtc	ttcaagttga	tcctaagaag	taccacaaga	taaggagagag	660
acttgttggt	gtctctgagg	aaactaccac	tggtgttaag	aggctttacc	agatcgacga	720
aaatggaact	cttttgtctc	ctgcccattaa	cgtaaaccgac	ctctgcacca	agagcaaggt	780
cgacaacttg	tatggttgcc	gtcactcact	ccctgatggt	ctcatgaggg	ccactgtatgt	840
catgatcgct	ggaaggttg	ctgttatctg	tggataggt	gatgttgaa	agggttgtgc	900
tgctgcatg	aagactgctg	gtgctagagt	catgttgact	gagattgac	ccatctgtgc	960
ccctcaagct	ttgatggaag	gacttcaggt	tcttaccctt	gaggatgttg	tctcagaagc	1020
tgatatcttt	gtcaccacca	ccggtaaaca	agacatcatc	atggtogacc	acatgaggaa	1080
gatgaagaac	aacgctattg	tgtgcaacat	tggtcacttt	gacaatgaga	ttgacatgct	1140
tggaactgag	acttaccctg	gtgtgaagcg	tatcaccatc	aagccacaga	ctgcacaggtg	1200
gggtgtccca	gagaccaagg	ctggaatcat	tgtcttgct	gagggtcgct	tgatgaactt	1260
gggtgtgctg	actggtcacc	caagtttctg	gatgtcttgc	tctttcacca	accaggtgat	1320
tgcccaagctc	gagctctgga	acgagaaagc	aagcggaaag	tacgagaaga	aggtgtacgt	1380
ctctccaag	catttggtg	agaaggttgc	attacttcac	ttggcgaaag	ttggagccag	1440
gcttcaaaag	ctgtcaaaag	accaNaTctg	actacgtcag	catctccaatt	gagggaccat	1500
acaagcctcc	tcactacag	tactgagaga	gagagagagt	cgacaaagcg	gttcaggttc	1560
ggatctactt	gtggttttgt	gttgggttgt	ggggaagag	tggaacagtt	tgagatattg	1620
gtctcttgat	gaagttgacc	aatatcaggt	attaataagg	gttatgtgct	tttgaaggtt	1680
gtgctgtgtt	tctccatttt	tactgaaact	taaattagtt	tttggttt		

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 489 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..489

(D) OTHER INFORMATION: / Ceres Seq. ID 1565663

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

Ser	His	Thr	Leu	Leu	Ser	Leu	Ser	Leu	Cys	Leu	Leu	Ser	Asp	Ser	Asn
1			5						10					15	
Leu	Arg	Ser	Ser	Ser	Thr	Met	Ala	Leu	Leu	Val	Glu	Lys	Thr	Ser	Ser
			20					25					30		
Gly	Arg	Glu	Tyr	Lys	Val	Lys	Asp	Met	Ser	Gln	Ala	Asp	Phe	Gly	Arg
			35				40					45			
Leu	Glu	Leu	Glu	Leu	Ala	Glu	Val	Glu	Met	Pro	Gly	Leu	Met	Ala	Cys
			50				55					60			
Arg	Thr	Glu	Phe	Gly	Pro	Ser	Gln	Pro	Phe	Lys	Gly	Ala	Arg	Ile	Thr
65					70				75					80	
Gly	Ser	Leu	His	Met	Thr	Ile	Gln	Thr	Ala	Val	Leu	Ile	Glu	Thr	Leu
			85						90					95	
Thr	Ala	Leu	Gly	Ala	Glu	Val	Arg	Trp	Cys	Ser	Cys	Asn	Ile	Phe	Ser
			100					105					110		
Thr	Gln	Asp	His	Ala	Ala	Ala	Ile	Ala	Arg	Asp	Ser	Ala	Ala	Val	
			115				120					125			
Phe	Ala	Trp	Lys	Gly	Glu	Thr	Leu	Gln	Glu	Tyr	Trp	Trp	Cys	Thr	Glu
			130				135					140			
Arg	Ala	Leu	Asp	Trp	Gly	Pro	Gly	Gly	Pro	Asp	Leu	Ile	Val	Asp	
145					150				155					160	
Asp	Gly	Gly	Asp	Ala	Thr	Leu	Leu	Ile	His	Glu	Gly	Val	Lys	Ala	Glu
			165						170					175	
Glu	Ile	Phe	Glu	Lys	Thr	Gly	Gln	Val	Pro	Asp	Pro	Thr	Ser	Thr	Asp
			180						185					190	
Asn	Pro	Glu	Phe	Gln	Ile	Val	Leu	Ser	Ile	Ile	Lys	Glu	Gly	Leu	Gln
			195				200					205			
Val	Asp	Pro	Lys	Lys	Tyr	His	Lys	Met	Lys	Glu	Arg	Leu	Val	Gly	Val
210							215					220			

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Ser Glu Glu Thr Thr Thr Gly Val Lys Arg Leu Tyr Gln Met Gln Gln
225                230                235                240
Asn Gly Thr Leu Leu Phe Pro Ala Ile Asn Val Asn Asp Ser Val Thr
                245                250                255
Lys Ser Lys Phe Asp Asn Leu Tyr Gly Cys Arg His Ser Leu Pro Asp
                260                265                270
Gly Leu Met Arg Ala Thr Asp Val Met Ile Ala Gly Lys Val Ala Val
                275                280                285
Ile Cys Gly Tyr Gly Asp Val Gly Lys Gly Cys Ala Ala Ala Met Lys
                290                295                300
Thr Ala Gly Ala Arg Val Ile Val Thr Glu Ile Asp Pro Ile Cys Ala
305                310                315                320
Leu Gln Ala Leu Met Glu Gly Leu Gln Val Leu Thr Leu Glu Asp Val
                325                330                335
Val Ser Glu Ala Asp Ile Phe Val Thr Thr Thr Gly Asn Lys Asp Ile
                340                345                350
Ile Met Val Asp His Met Arg Lys Met Lys Asn Asn Ala Ile Val Cys
                355                360                365
Asn Ile Gly His Phe Asp Asn Glu Ile Asp Met Leu Gly Leu Glu Thr
                370                375                380
Tyr Pro Gly Val Lys Arg Ile Thr Ile Lys Pro Gln Thr Asp Arg Trp
385                390                395                400
Val Phe Pro Glu Thr Lys Ala Gly Ile Ile Val Leu Ala Glu Gly Arg
                405                410                415
Leu Met Asn Leu Gly Cys Ala Thr Gly His Pro Ser Phe Val Met Ser
                420                425                430
Cys Ser Phe Thr Asn Gln Val Ile Ala Gln Leu Glu Leu Trp Asn Glu
                435                440                445
Lys Ala Ser Gly Lys Tyr Glu Lys Lys Val Tyr Val Leu Pro Lys His
                450                455                460
Leu Asp Glu Lys Val Ala Leu Leu His Leu Gly Lys Leu Gly Ala Arg
465                470                475                480
Leu Thr Lys Leu Ser Lys Asp Xaa Ile
                485

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(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 467 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..467
- (D) OTHER INFORMATION: / Ceres Seq. ID 1565664

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

```

Met Ala Leu Leu Val Glu Lys Thr Ser Ser Gly Arg Glu Tyr Lys Val
1                5                10                15
Lys Asp Met Ser Gln Ala Asp Phe Gly Arg Leu Glu Leu Glu Leu Ala
                20                25                30
Glu Val Glu Met Pro Gly Leu Met Ala Cys Arg Thr Glu Phe Gly Pro
                35                40                45
Ser Gln Pro Phe Lys Gly Ala Arg Ile Thr Gly Ser Leu His Met Thr
                50                55                60
Ile Gln Thr Ala Val Leu Ile Glu Thr Leu Thr Ala Leu Gly Ala Glu
                65                70                75                80
Val Arg Trp Cys Ser Cys Asn Ile Phe Ser Thr Gln Asp His Ala Ala
                85                90                95
Ala Ala Ile Ala Arg Asp Ser Ala Ala Val Phe Ala Trp Lys Gly Glu
                100                105                110
Thr Leu Gln Glu Tyr Trp Trp Cys Thr Glu Arg Ala Leu Asp Trp Gly

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115 120 125
Pro Gly Gly Gly Pro Asp Leu Ile Val Asp Asp Gly Gly Asp Ala Thr
130 135 140
Leu Leu Ile His Glu Gly Val Lys Ala Glu Glu Ile Phe Glu Lys Thr
145 150 155
Gly Gln Val Pro Asp Pro Thr Ser Thr Asp Asn Pro Glu Phe Gln Ile
165 170 175
Val Leu Ser Ile Ile Lys Glu Gly Leu Gln Val Asp Pro Lys Lys Tyr
180 185 190
His Lys Met Lys Glu Arg Leu Val Gly Val Ser Glu Glu Thr Thr Thr
195 200 205
Gly Val Lys Arg Leu Tyr Gln Met Gln Gln Asn Gly Thr Leu Leu Phe
210 215 220
Pro Ala Ile Asn Val Asn Asp Ser Val Thr Lys Ser Lys Phe Asp Asn
225 230 235
Leu Tyr Gly Cys Arg His Ser Leu Pro Asp Gly Leu Met Arg Ala Thr
245 250 255
Asp Val Met Ile Ala Gly Lys Val Ala Val Ile Cys Gly Tyr Gly Asp
260 265 270
Val Gly Lys Gly Cys Ala Ala Ala Met Lys Thr Ala Gly Ala Arg Val
275 280 285
Ile Val Thr Glu Ile Asp Pro Ile Cys Ala Leu Gln Ala Leu Met Glu
290 295 300
Gly Leu Gln Val Leu Thr Leu Glu Asp Val Val Ser Glu Ala Asp Ile
305 310 315
Phe Val Thr Thr Thr Gly Asn Lys Asp Ile Ile Met Val Asp His Met
325 330 335
Arg Lys Met Lys Asn Asn Ala Ile Val Cys Asn Ile Gly His Phe Asp
340 345 350
Asn Glu Ile Asp Met Leu Gly Leu Glu Thr Tyr Pro Gly Val Lys Arg
355 360 365
Ile Thr Ile Lys Pro Gln Thr Asp Arg Trp Val Phe Pro Glu Thr Lys
370 375 380
Ala Gly Ile Ile Val Leu Ala Glu Gly Arg Leu Met Asn Leu Gly Cys
385 390 395
Ala Thr Gly His Pro Ser Phe Val Met Ser Cys Ser Phe Thr Asn Gln
405 410 415
Val Ile Ala Gln Leu Glu Leu Trp Asn Glu Lys Ala Ser Gly Lys Tyr
420 425 430
Glu Lys Lys Val Tyr Val Leu Pro Lys His Leu Asp Glu Lys Val Ala
435 440 445
Leu Leu His Leu Gly Lys Leu Gly Ala Arg Leu Thr Lys Leu Ser Lys
450 455 460
Asp Xaa Ile
465

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 449 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..449

(D) OTHER INFORMATION: / Ceres Seq. ID 1565665

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

Met Ser Gln Ala Asp Phe Gly Arg Leu Glu Leu Glu Leu Ala Glu Val
1 5 10 15
Glu Met Pro Gly Leu Met Ala Cys Arg Thr Glu Phe Gly Pro Ser Gln
20 25 30


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Pro Phe Lys Gly Ala Arg Ile Thr Gly Ser Leu His Met Thr Ile Gln
      35              40              45
Thr Ala Val Leu Ile Glu Thr Leu Thr Ala Leu Gly Ala Glu Val Arg
      50              55              60
Trp Cys Ser Cys Asn Ile Phe Ser Thr Gln Asp His Ala Ala Ala Ala
      65              70              75              80
Ile Ala Arg Asp Ser Ala Ala Val Phe Ala Trp Lys Gly Glu Thr Leu
      85              90              95
Gln Glu Tyr Trp Trp Cys Thr Glu Arg Ala Leu Asp Trp Gly Pro Gly
      100             105             110
Gly Gly Pro Asp Leu Ile Val Asp Asp Gly Gly Asp Ala Thr Leu Leu
      115             120             125
Ile His Glu Gly Val Lys Ala Glu Glu Ile Phe Glu Lys Thr Gly Gln
      130             135             140
Val Pro Asp Pro Thr Ser Thr Asp Asn Pro Glu Phe Gln Ile Val Leu
      145             150             155             160
Ser Ile Ile Lys Glu Gly Leu Gln Val Asp Pro Lys Lys Tyr His Lys
      165             170             175
Met Lys Glu Arg Leu Val Gly Val Ser Glu Glu Thr Thr Thr Gly Val
      180             185             190
Lys Arg Leu Tyr Gln Met Gln Gln Asn Gly Thr Leu Leu Phe Pro Ala
      195             200             205
Ile Asn Val Asn Asp Ser Val Thr Lys Ser Lys Phe Asp Asn Leu Tyr
      210             215             220
Gly Cys Arg His Ser Leu Pro Asp Gly Leu Met Arg Ala Thr Asp Val
      225             230             235             240
Met Ile Ala Gly Lys Val Ala Val Ile Cys Gly Tyr Gly Asp Val Gly
      245             250             255
Lys Gly Cys Ala Ala Ala Met Lys Thr Ala Gly Ala Arg Val Ile Val
      260             265             270
Thr Glu Ile Asp Pro Ile Cys Ala Leu Gln Ala Leu Met Glu Gly Leu
      275             280             285
Gln Val Leu Thr Leu Glu Asp Val Val Ser Glu Ala Asp Ile Phe Val
      290             295             300
Thr Thr Thr Gly Asn Lys Asp Ile Ile Met Val Asp His Met Arg Lys
      305             310             315             320
Met Lys Asn Asn Ala Ile Val Cys Asn Ile Gly His Phe Asp Asn Glu
      325             330             335
Ile Asp Met Leu Gly Leu Glu Thr Tyr Pro Gly Val Lys Arg Ile Thr
      340             345             350
Ile Lys Pro Gln Thr Asp Arg Trp Val Phe Pro Glu Thr Lys Ala Gly
      355             360             365
Ile Ile Val Leu Ala Glu Gly Arg Leu Met Asn Leu Gly Cys Ala Thr
      370             375             380
Gly His Pro Ser Phe Val Met Ser Cys Ser Phe Thr Asn Gln Val Ile
      385             390             395             400
Ala Gln Leu Glu Leu Trp Asn Glu Lys Ala Ser Gly Lys Tyr Glu Lys
      405             410             415
Lys Val Tyr Val Leu Pro Lys His Leu Asp Glu Lys Val Ala Leu Leu
      420             425             430
His Leu Gly Lys Leu Gly Ala Arg Leu Thr Lys Leu Ser Lys Asp Xaa
      435             440             445
Ile

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(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1415 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..1415
(D) OTHER INFORMATION: / Ceres Seq. ID 1565666

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

gtgtttgtgt	atgtgtggaa	aattaatttc	ttctccgcac	gaatcccaaa	agtttgttga	60
aatttgcttc	caagaaatct	gcaattagaa	atttcatttc	gcgcgcacgc	tcttctcttc	120
ctgattctga	tttaattccag	atgtcttcc	gagtttacg	gagattagg	cattttcgcc	180
tcgaactcgaa	ctctgtctcg	cagcttcgc	gagagagtc	tggaacacgc	accgactctc	240
cgatctcgat	cttttggta	gacggagatt	aactgggaca	aacttgacaa	aaggaggttc	300
tacattaatg	cgatggcct	cttcaactgt	gttacagtag	ctctgtatcc	tgtatcgcgt	360
gtgaaaacaa	ggcttcaagt	ttctctctaa	gagattgctg	agagaaggtc	cttttctgta	420
gttaaaggaa	ttttaaagaa	tgatggtgtt	cctggtctgt	accgaggttt	tggtactgtc	480
attacaggtg	ctgtacactgc	aagaatcata	tttctaactg	ctcttgagac	cactaagatt	540
ctctgcttta	agttgggttc	acctttggag	tttaagtgaac	ctacacaagc	cgccattgca	600
aatggaattg	ctggcatgac	agcatctctt	ttctcacagg	ctgtgtttgt	cccaattgat	660
gttgttagcc	aaaagttgat	ggtacaagga	tactcaggtc	atgctacata	tactggtggt	720
atcgatgttg	ccacaaaaat	cattaagtca	tatggtgtaa	ggggattata	cagaggggtt	780
ggctgtctgt	ttatgacct	ttctccttca	agtgccgctt	gggtggctag	ctatggatca	840
agccaaactg	ttatctggag	attcttaggt	tatggtgttg	actcggtatg	aactactgct	900
ctgtagtaag	caaaaattgt	tatggtccag	gctgctggag	gaattattgc	tggtgcaaca	960
gcactctcaa	ttacaaacac	attagacaca	atcaaaacgc	gactgcaggt	catgggacat	1020
caagaaaaat	gaccttcagc	gaaacaagtg	gtgaaaaaac	tgctagcaga	agatggcttg	1080
aaagattctc	atagggggtt	gggcccacga	ttcttttagca	tgctggcttg	gggaacctcg	1140
atgatattga	cttacgaata	cttaaaagct	ctgtgtgcaa	tagaagatta	gaagacttca	1200
ctactgtctg	ttgttttttc	ttctcttact	aactcgagta	gacggcatca	cttggattca	1260
aatctcggtg	attgggaagt	tccatgttga	caattggacc	attctttcaa	ctttggaagt	1320
tgagttcgtg	tattgtaact	attctttcaa	cttaatttgc	gtattggagt	gtattcttacc	1380
agcagaagaa	aktcGtagct	tacgtttctc	tgctt			

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 323 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..323
(D) OTHER INFORMATION: / Ceres Seq. ID 1565667

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

Met	Asp	Thr	Pro	Pro	Thr	Ser	Arg	Ile	Ala	Ser	Phe	Gly	Gln	Thr	Glu
1			5						10				15		
Ile	Asn	Trp	Asp	Lys	Leu	Asp	Lys	Arg	Arg	Phe	Tyr	Ile	Asn	Gly	Ala
			20					25					30		
Gly	Leu	Phe	Thr	Gly	Val	Thr	Val	Ala	Leu	Tyr	Pro	Val	Ser	Val	Val
			35				40				45				
Lys	Thr	Arg	Leu	Gln	Val	Ala	Ser	Lys	Glu	Ile	Ala	Glu	Arg	Ser	Ala
			50			55					60				
Phe	Ser	Val	Val	Lys	Gly	Ile	Leu	Lys	Asn	Asp	Gly	Val	Pro	Gly	Leu
			65		70			75					80		
Tyr	Arg	Gly	Phe	Gly	Thr	Val	Ile	Thr	Gly	Ala	Val	Pro	Ala	Arg	Ile
			85					90				95			
Ile	Phe	Leu	Thr	Ala	Leu	Glu	Thr	Thr	Lys	Ile	Ser	Ala	Phe	Lys	Leu
			100				105					110			
Val	Ala	Pro	Leu	Glu	Leu	Ser	Glu	Pro	Thr	Gln	Ala	Ala	Ile	Ala	Asn
			115			120					125				
Gly	Ile	Ala	Gly	Met	Thr	Ala	Ser	Leu	Phe	Ser	Gln	Ala	Val	Phe	Val
			130			135					140				
Pro	Ile	Asp	Val	Val	Ser	Gln	Lys	Leu	Met	Val	Gln	Gly	Tyr	Ser	Gly
145			150					155						160	

His Ala Thr Tyr Thr Gly Gly Ile Asp Val Ala Thr Lys Ile Ile Lys
165 170 175
Ser Tyr Gly Val Arg Gly Leu Tyr Arg Gly Phe Gly Leu Ser Val Met
180 185 190
Thr Tyr Ser Ser Pro Ser Ser Ala Ala Trp Trp Ala Ser Tyr Gly Ser Ser
195 200 205
Gln Arg Val Ile Trp Arg Phe Leu Gly Tyr Gly Asp Ser Asp Ala
210 215 220
Thr Thr Ala Pro Ser Lys Ser Lys Ile Val Met Val Gln Ala Ala Gly
225 230 235
Gly Ile Ile Ala Gly Ala Thr Ala Ser Ser Ile Thr Thr Pro Leu Asp
245 250 255
Thr Ile Lys Thr Arg Leu Gln Val Met Gly His Gln Glu Asn Arg Pro
260 265 270
Ser Ala Lys Gln Val Val Lys Lys Leu Leu Ala Glu Asp Gly Trp Lys
275 280 285
Gly Phe Tyr Arg Gly Leu Gly Pro Arg Phe Phe Ser Met Ser Ala Trp
290 295 300
Gly Thr Ser Met Ile Leu Thr Tyr Glu Tyr Leu Lys Arg Leu Cys Ala
305 310 315 320
Ile Glu Asp

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 191 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..191
- (D) OTHER INFORMATION: / Ceres Seq. ID 1565668

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

Met Thr Ala Ser Leu Phe Ser Gln Ala Val Phe Val Pro Ile Asp Val
1 5 10 15
Val Ser Gln Lys Leu Met Val Gln Gly Tyr Ser Gly His Ala Thr Tyr
20 25 30
Thr Gly Gly Ile Asp Val Ala Thr Lys Ile Ile Lys Ser Tyr Gly Val
35 40 45
Arg Gly Leu Tyr Arg Gly Phe Gly Leu Ser Val Met Thr Tyr Ser Pro
50 55 60
Ser Ser Ala Ala Trp Trp Ala Ser Tyr Gly Ser Ser Gln Arg Val Ile
65 70 75 80
Trp Arg Phe Leu Gly Tyr Gly Asp Ser Asp Ala Thr Thr Ala Pro
85 90 95
Ser Lys Ser Lys Ile Val Met Val Gln Ala Ala Gly Gly Ile Ile Ala
100 105 110
Gly Ala Thr Ala Ser Ser Ile Thr Thr Pro Leu Asp Thr Ile Lys Thr
115 120 125
Arg Leu Gln Val Met Gly His Gln Glu Asn Arg Pro Ser Ala Lys Gln
130 135 140
Val Val Lys Lys Leu Leu Ala Glu Asp Gly Trp Lys Gly Phe Tyr Arg
145 150 155 160
Gly Leu Gly Pro Arg Phe Phe Ser Met Ser Ala Trp Gly Thr Ser Met
165 170 175
Ile Leu Thr Tyr Glu Tyr Leu Lys Arg Leu Cys Ala Ile Glu Asp
180 185 190

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 amino acids

- (B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..170
(D) OTHER INFORMATION: / Ceres Seq. ID 1565669

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

Met	Val	Gln	Gly	Tyr	Ser	Gly	His	Ala	Thr	Tyr	Thr	Gly	Gly	Ile	Asp
1				5				10						15	
Val	Ala	Thr	Lys	Ile	Ile	Lys	Ser	Tyr	Gly	Val	Arg	Gly	Leu	Tyr	Arg
			20				25						30		
Gly	Phe	Gly	Leu	Ser	Val	Met	Thr	Tyr	Ser	Pro	Ser	Ser	Ala	Ala	Trp
			35				40						45		
Trp	Ala	Ser	Tyr	Gly	Ser	Ser	Gln	Arg	Val	Ile	Trp	Arg	Phe	Leu	Gly
			50				55				60				
Tyr	Gly	Gly	Asp	Ser	Asp	Ala	Thr	Thr	Ala	Pro	Ser	Lys	Ser	Lys	Ile
			65			70				75				80	
Val	Met	Val	Gln	Ala	Ala	Gly	Gly	Ile	Ile	Ala	Gly	Ala	Thr	Ala	Ser
			85						90				95		
Ser	Ile	Thr	Thr	Pro	Leu	Asp	Thr	Ile	Lys	Thr	Arg	Leu	Gln	Val	Met
			100				105					110			
Gly	His	Gln	Glu	Asn	Arg	Pro	Ser	Ala	Lys	Gln	Val	Val	Lys	Lys	Leu
			115				120					125			
Leu	Ala	Glu	Asp	Gly	Trp	Lys	Gly	Phe	Tyr	Arg	Gly	Leu	Gly	Pro	Arg
			130				135					140			
Phe	Phe	Ser	Met	Ser	Ala	Trp	Gly	Thr	Ser	Met	Ile	Leu	Thr	Tyr	Glu
			145			150				155				160	
Tyr	Leu	Lys	Arg	Leu	Cys	Ala	Ile	Glu	Asp						
			165				170								

(2) INFORMATION FOR SEQ ID NO:52:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1213 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..1213
(D) OTHER INFORMATION: / Ceres Seq. ID 1565672

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

gaccattttt	acacacagcc	aatcagagcc	ttgttttcac	gtctctttgc	gaggcgataa	60
tatttagatc	tgctcaccat	ttctcccgcc	tcgcgcgacg	aagaagaaa	atgggagaca	120
acaaccctaa	ccgatcagaa	cgagaacgtc	ttctcggaa	cgcgagaa	cttctcgagt	180
cacagatctc	aaacgggttc	aaagagtttg	caatctttag	tcaagagaca	gagccactcc	240
tcgaaggcac	cgatcaaatc	ctcgccgtcg	tcgatgtctt	actctcatca	gcaccagaga	300
atcgtatcaa	aaaccaacca	aactgggtaca	aaatccttca	gatcgaagat	ctaaatgaat	360
catcaacaga	caacgatcta	atcaagaaac	aataccgtcg	ttctgtctct	cttctccacc	420
cagacaaaaa	ccgttttccct	ttcgcgcgac	aagctttcag	attcgtgtct	gatgcatggg	480
aagttctatc	aacacccttc	aagaaatctc	aattcgatgg	agatttgaat	ctcatctcca	540
ctaaagtata	tctcaacact	cagaaatcga	agaagaaaac	aacaacgaat	gagaagatgt	600
ctacgttttg	gacggcgtgt	cgtactgtgt	acagtcttca	tgagtatcct	aggggtttatc	660
aagagtagtt	tattagatgt	caaaactgtc	aaagaGcgtt	tcacgtgtcg	agtattcctc	720
agttgcctcc	gttgatacct	ggtaaagatg	agtattattg	ttgctggggt	ttttttccga	780
tggggtttgt	tggtgggtaa	ggaggagaag	cgccattcgc	taattggagta	gatgcagcta	840
agttccctta	ttggatgcct	ccggtttttc	catccggcgg	cggttcagct	ctctccaaagt	900
gtaattgggt	tagtttttgt	ggatgggtcag	gtggagcgcg	gaagagagat	aatgagcgctg	960
tgaggagtaa	taatgggtgt	ggagttaatt	catagtgaac	accgaagaag	agaggaagag	1020
gaaggccgaa	gaagaatccg	gttttagtgt	ctcttttcaa	actccgggtca	tgattgttaa	1080

aattatggag acaaaatttt aaaggcaagt tttttaagg caaggaagtt taggtacagc 1140
gtttgtgtgc ttatgtataa cttattatg catttgtgt tattacggt gtgtaattgt 1200
gttatcttga ttt

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 347 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..347
- (D) OTHER INFORMATION: / Ceres Seq. ID 1565673

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

Pro	Phe	Leu	His	Thr	Ala	Asn	Gln	Ser	Leu	Val	Ser	Ser	Ser	Leu	Val
1			5					10					15		
Glu	Ala	Ile	Ile	Phe	Arg	Ser	Ala	His	His	Phe	Ser	Ala	Ile	Ala	Asp
			20					25					30		
Gly	Arg	Arg	Lys	Met	Gly	Asp	Asn	Asn	Pro	Asn	Arg	Ser	Glu	Ala	Glu
			35				40					45			
Arg	Leu	Leu	Gly	Ile	Ala	Gly	Lys	Leu	Leu	Glu	Ser	Arg	Asp	Leu	Asn
			50				55				60				
Gly	Ser	Lys	Glu	Phe	Ala	Ile	Leu	Ala	Gln	Glu	Thr	Glu	Pro	Leu	Leu
			65			70				75				80	
Glu	Gly	Thr	Asp	Gln	Ile	Leu	Ala	Val	Val	Asp	Val	Leu	Leu	Ser	Ser
				85					90					95	
Ala	Pro	Glu	Asn	Arg	Ile	Lys	Asn	Gln	Pro	Asn	Trp	Tyr	Lys	Ile	Leu
			100					105					110		
Gln	Ile	Glu	Asp	Leu	Asn	Glu	Ser	Ser	Thr	Asp	Asn	Asp	Leu	Ile	Lys
			115				120					125			
Lys	Gln	Tyr	Arg	Arg	Leu	Ala	Leu	Leu	His	Pro	Asp	Lys	Asn	Arg	
			130			135				140					
Phe	Pro	Phe	Ala	Asp	Gln	Ala	Phe	Arg	Phe	Val	Leu	Asp	Ala	Trp	Glu
			145			150				155				160	
Val	Leu	Ser	Thr	Pro	Ser	Lys	Lys	Ser	Gln	Phe	Asp	Gly	Asp	Leu	Asn
				165					170					175	
Leu	Ile	Phe	Thr	Lys	Val	Asn	Leu	Asn	Thr	Gln	Lys	Ser	Lys	Lys	Lys
			180					185					190		
Thr	Thr	Thr	Asn	Glu	Lys	Met	Ser	Thr	Phe	Trp	Thr	Ala	Cys	Pro	Tyr
			195				200					205			
Cys	Tyr	Ser	Leu	His	Glu	Tyr	Pro	Arg	Val	Tyr	Gln	Glu	Tyr	Cys	Ile
			210			215					220				
Arg	Cys	Gln	Asn	Cys	Gln	Arg	Ala	Phe	His	Ala	Ala	Ser	Ile	Pro	Gln
			225			230				235				240	
Leu	Pro	Pro	Leu	Ile	Pro	Gly	Lys	Asp	Glu	Tyr	Tyr	Cys	Cys	Trp	Gly
			245						250					255	
Phe	Phe	Pro	Met	Gly	Phe	Val	Gly	Gly	Lys	Gly	Gly	Glu	Ala	Ala	Ile
			260				265						270		
Ala	Asn	Gly	Val	Asp	Ala	Ala	Lys	Phe	Pro	Tyr	Trp	Met	Pro	Pro	Val
			275				280					285			
Phe	Ser	Ser	Gly	Gly	Val	Ala	Ala	Pro	Pro	Ser	Gly	Asn	Gly	Val	Ser
			290			295				300					
Phe	Asp	Gly	Trp	Ser	Gly	Gly	Ala	Ala	Lys	Arg	Asp	Asn	Glu	Ala	Val
			305			310				315				320	
Arg	Ser	Asn	Asn	Gly	Val	Gly	Val	Asn	Ser	Asp	Gly	Thr	Pro	Lys	Lys
			325					330					335		
Arg	Gly	Arg	Gly	Arg	Pro	Lys	Lys	Asn	Pro	Val					
			340				345								

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 311 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..311
(D) OTHER INFORMATION: / Ceres Seq. ID 1565674
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:
Met Gly Asp Asn Asn Pro Asn Arg Ser Glu Ala Glu Arg Leu Leu Gly
1 5 10 15
Ile Ala Glu Lys Leu Leu Glu Ser Arg Asp Leu Asn Gly Ser Lys Glu
20 25 30
Phe Ala Ile Leu Ala Gln Glu Thr Glu Pro Leu Leu Glu Gly Thr Asp
35 40 45
Gln Ile Leu Ala Val Val Asp Val Leu Leu Ser Ser Ala Pro Glu Asn
50 55 60
Arg Ile Lys Asn Gln Pro Asn Trp Tyr Lys Ile Leu Gln Ile Glu Asp
65 70 75 80
Leu Asn Glu Ser Ser Thr Asp Asn Asp Leu Ile Lys Lys Gln Tyr Arg
85 90 95
Arg Leu Ala Leu Leu His Pro Asp Lys Asn Arg Phe Pro Phe Ala
100 105 110
Asp Gln Ala Phe Arg Phe Val Leu Asp Ala Trp Glu Val Leu Ser Thr
115 120 125
Pro Ser Lys Lys Ser Gln Phe Asp Gly Asp Leu Asn Leu Ile Phe Thr
130 135 140
Lys Val Asn Leu Asn Thr Gln Lys Ser Lys Lys Lys Thr Thr Thr Asn
145 150 155 160
Glu Lys Met Ser Thr Phe Trp Thr Ala Cys Pro Tyr Cys Tyr Ser Leu
165 170 175
His Glu Tyr Pro Arg Val Tyr Gln Glu Tyr Cys Ile Arg Cys Gln Asn
180 185 190
Cys Gln Arg Ala Phe His Ala Ala Ser Ile Pro Gln Leu Pro Pro Leu
195 200 205
Ile Pro Gly Lys Asp Glu Tyr Tyr Cys Cys Trp Gly Phe Phe Pro Met
210 215 220
Gly Phe Val Gly Gly Lys Gly Gly Glu Ala Ala Ile Ala Asn Gly Val
225 230 235 240
Asp Ala Ala Lys Phe Pro Tyr Trp Met Pro Pro Val Phe Ser Ser Gly
245 250 255
Gly Val Ala Ala Pro Pro Ser Gly Asn Gly Val Ser Phe Asp Gly Trp
260 265 270
Ser Gly Gly Ala Ala Lys Arg Asp Asn Glu Ala Val Arg Ser Asn Asn
275 280 285
Gly Val Gly Val Asn Ser Asp Gly Thr Pro Lys Lys Arg Gly Arg Gly
290 295 300
Arg Pro Lys Lys Asn Pro Val
305 310
(2) INFORMATION FOR SEQ ID NO:55:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 470 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..470
(D) OTHER INFORMATION: / Ceres Seq. ID 1565683

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:
cacttagggt tcatagcagc cagagagaga gacaagttag agggatctac caaacgaagc 60
aacaatgggt aagttcttga agcagaacaa ggccgtgac cttcttcaag gacgttacgc 120
cggaagaaaa gccgtcatca tcaaatctct cgacgacggt aaccgtgac gTccttacgc 180
acactgcctc gtgcgcggac tgaagaagta cccgagcaaa gtcacccgca aagactcagc 240
taagaagaca gctaagaaat ctagggttaa gtgtttcatc aagcttggta attaccagca 300
tctgatgctc actcgtttaca cactcgacgt ggacgtgtct gtaaggacga tcacgggttac 360
cgctgcgtaa ggatttgatg atgacgggtt tctctctcac attatgatgc ttgtttgtgaa 420
ctctctctct gtctttgctg ataataata aattgttact aatataatct

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 127 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..127

(D) OTHER INFORMATION: / Ceres Seq. ID 1565684

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

Met Val Lys Phe Leu Lys Gln Asn Lys Ala Val Ile Leu Leu Gln Gly
1 5 10 15
Arg Tyr Ala Gly Lys Lys Ala Val Ile Ile Lys Ser Phe Asp Asp Gly
20 25 30
Asn Arg Asp Arg Pro Tyr Gly His Cys Leu Val Ala Gly Leu Lys Lys
35 40 45
Tyr Pro Ser Lys Val Ile Arg Lys Asp Ser Ala Lys Lys Thr Ala Lys
50 55 60
Lys Ser Arg Val Lys Cys Phe Ile Lys Leu Val Asn Tyr Gln His Leu
65 70 75 80
Met Pro Thr Arg Tyr Thr Leu Asp Val Ala Val Ser Val Arg Thr Ile
85 90 95
Thr Val Thr Val Val Glu Gly Phe Asp Asp Gly Phe Leu Phe Tyr
100 105 110
Ile Met Met Leu Phe Val Asn Ser Leu Ser Val Phe Ala Asp Lys
115 120 125

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1881 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1881

(D) OTHER INFORMATION: / Ceres Seq. ID 1565688

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

atagattata gatataaacc actgaattaa tattacggct tccaatatag gtgcatttaa 60
aacataacgt tccctctctt gtctttttat ttttgcctc tgttctttag aactgccatt 120
aacgagagtg agagagagac acacacacac agcgagtga aatgtotcog gagaagaaga 180
gtcaaaaact cctcccaata acggaatgca gagacggaga gtacgattcg atagccgccg 240
attctgacgg gactcStgct tctctcaaga agctccttc cttaacttgc gctcgtcgct 300
gttgaagctg gaagcctttt acgtggacta atcctccttc tctcgtttacc attcgtcatt 360
atctcttacc tatctcgata cgaatctctt ggtatccgc cagtctcttc acggtacgag 420
gtcgtgtctca aaatccgcga tatcgaactt gtctctcgc cagtctcttc acggtacgag 480
atctaaacata gactgttttc ttgttagtag atcactttag tttttttccg atgaactatt 540
tttaggtttt acgcggcgga ttgtgagaaa gacagttttg aggtgtttga taagtgaag 600
aagaaagtgg tagtgacgcg gaatccgatt gtgatggtgg aggcgtttgt gaagSatta 660
tcttgagggt gataaagttt tgggaacaga gattgaagtt aaccctaaaa ccaatagagc 720

cactggattt	gtgaagaagc	ctgggtgtct	tgttgggtgat	cttaagaggt	tagccatttt	780
aaaagagttt	ggtaacgaat	cacctgatct	cgccctcggg	gatcgaaact	ctgatcatga	840
tttgatgtct	ctctgcaaga	aaggttacat	gttccatgcg	accaagtcag	ccacaacgat	900
tccaaaagaa	cgcttaaaga	accgcatagt	cttccatgat	gggcggttag	cgcaacgtcc	960
aactccggtt	aacgcattta	tcacataacct	atggcttctt	tttggtttca	tcctctccat	1020
cattccggtc	tacttcaacc	tcctcttacc	tgaagatttt	gtccgttacc	ctctcagatg	1080
gctcgggagt	cacttaacca	ttcgtgggtc	tcgtctctca	cctccttccc	ctggaaactct	1140
tggaacaact	tatgtcctta	accacggtac	cgcgcttgat	cccatacgct	ttgctattgc	1200
tcctggagct	aagatctggt	gcgtcactta	cagtgtctct	cgtctctccc	ttatgtcttc	1260
tcctattctc	gctgttgccc	tcacccggtg	cogtgcacc	gatgctgcga	acatgagaaa	1320
actctctcag	aaagcgagct	tggtgatatg	tcccgaaagg	acgacgtgca	gagaaagata	1380
tcctactgaga	tttagcgctc	tattcgacga	gctaagcgac	cggatttgtgc	cagtacggat	1440
gaactgtaaa	caaggaatgt	tcaacgggac	cacagttagg	gggtgaaagt	tttgggacct	1500
ttactctctc	ttcatgaacc	caagaccaag	ctatgaagcc	actttcttgg	actgtttgcc	1560
tgaagaatgt	actgtcaacg	gtggtggcaa	gactctcata	gaggtggcta	attacgtcca	1620
gaaagtattc	ggcgcggttt	tggtgcttca	atgcaccgaa	cttactcgca	aggataaata	1680
tccttttctt	ggaggttaag	acggcaaggt	agagctctac	aacaacacca	agaagtgaag	1740
actcaaacaa	gggttttttc	ttgttatgtc	gtatacgaat	tttcatgtgt	gtaattgctg	1800
gagctctctg	catcattatg	gtacgttttt	gttatgtgta	atacagacga	tatatgtttg	1860
aataaaacta	tggttcgggtg	g				

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 297 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..297
- (D) OTHER INFORMATION: / Ceres Seq. ID 1565689

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

Met	Ser	Leu	Cys	Lys	Lys	Gly	Tyr	Met	Val	His	Ala	Thr	Lys	Ser	Ala
1				5					10					15	
Thr	Thr	Ile	Pro	Lys	Glu	Arg	Leu	Lys	Asn	Arg	Ile	Val	Phe	His	Asp
			20						25				30		
Gly	Arg	Leu	Ala	Gln	Arg	Pro	Thr	Pro	Leu	Asn	Ala	Ile	Ile	Thr	Tyr
			35				40					45			
Leu	Trp	Leu	Pro	Phe	Gly	Phe	Ile	Leu	Ser	Ile	Ile	Arg	Val	Tyr	Phe
			50			55					60				
Asn	Leu	Pro	Leu	Pro	Glu	Arg	Phe	Val	Arg	Tyr	Thr	Tyr	Glu	Met	Leu
			65			70				75				80	
Gly	Ile	His	Leu	Thr	Ile	Arg	Gly	His	Arg	Pro	Pro	Pro	Pro	Ser	Pro
			85						90					95	
Gly	Thr	Leu	Gly	Asn	Leu	Tyr	Val	Leu	Asn	His	Arg	Thr	Ala	Leu	Asp
			100					105					110		
Pro	Ile	Ile	Val	Ala	Ile	Ala	Leu	Gly	Arg	Lys	Ile	Cys	Cys	Val	Thr
			115				120					125			
Tyr	Ser	Val	Ser	Arg	Leu	Ser	Leu	Met	Leu	Ser	Pro	Ile	Pro	Ala	Val
			130				135					140			
Ala	Leu	Thr	Arg	Asp	Arg	Ala	Thr	Asp	Ala	Ala	Asn	Met	Arg	Lys	Leu
			145			150					155				160
Leu	Glu	Lys	Gly	Asp	Leu	Val	Ile	Cys	Pro	Glu	Gly	Thr	Thr	Cys	Arg
			165						170					175	
Glu	Glu	Tyr	Leu	Leu	Arg	Phe	Ser	Ala	Leu	Phe	Ala	Glu	Leu	Ser	Asp
			180					185					190		
Arg	Ile	Val	Pro	Val	Ala	Met	Asn	Cys	Lys	Gln	Gly	Met	Phe	Asn	Gly
			195				200					205			
Thr	Thr	Val	Arg	Gly	Val	Lys	Phe	Thr	Trp	Asp	Pro	Tyr	Phe	Phe	Met
			210			215						220			
Asn	Pro	Arg	Pro	Ser	Tyr	Glu	Ala	Thr	Phe	Leu	Asp	Arg	Leu	Pro	Glu

225					230					235					240
Glu	Met	Thr	Val	Asn	Gly	Gly	Gly	Lys	Thr	Pro	Ile	Glu	Val	Ala	Asn
				245					250					255	
Tyr	Val	Gln	Lys	Val	Ile	Gly	Ala	Val	Leu	Gly	Phe	Glu	Cys	Thr	Glu
			260					265					270		
Leu	Thr	Arg	Lys	Asp	Lys	Tyr	Leu	Leu	Leu	Gly	Gly	Asn	Asp	Gly	Lys
		275					280					285			
Val	Glu	Ser	Ile	Asn	Asn	Thr	Lys	Lys							
290					295										

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 289 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..289

(D) OTHER INFORMATION: / Ceres Seq. ID 1565690

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

Met	Val	His	Ala	Thr	Lys	Ser	Ala	Thr	Thr	Ile	Pro	Lys	Glu	Arg	Leu
1															
			5						10					15	
Lys	Asn	Arg	Ile	Val	Phe	His	Asp	Gly	Arg	Leu	Ala	Gln	Arg	Pro	Thr
			20					25					30		
Pro	Leu	Asn	Ala	Ile	Ile	Thr	Tyr	Leu	Trp	Leu	Pro	Phe	Gly	Phe	Ile
		35					40					45			
Leu	Ser	Ile	Ile	Arg	Val	Tyr	Phe	Asn	Leu	Pro	Leu	Pro	Glu	Arg	Phe
	50					55					60				
Val	Arg	Tyr	Thr	Tyr	Glu	Met	Leu	Gly	Ile	His	Leu	Thr	Ile	Arg	Gly
	65				70					75				80	
His	Arg	Pro	Pro	Pro	Pro	Ser	Pro	Gly	Thr	Leu	Gly	Asn	Leu	Tyr	Val
			85						90				95		
Leu	Asn	His	Arg	Thr	Ala	Leu	Asp	Pro	Ile	Ile	Val	Ala	Ile	Ala	Leu
		100					105						110		
Gly	Arg	Lys	Ile	Cys	Cys	Val	Thr	Tyr	Ser	Val	Ser	Arg	Leu	Ser	Leu
		115					120					125			
Met	Leu	Ser	Pro	Ile	Pro	Ala	Val	Ala	Leu	Thr	Arg	Asp	Arg	Ala	Thr
	130					135					140				
Asp	Ala	Ala	Asn	Met	Arg	Lys	Leu	Leu	Glu	Lys	Gly	Asp	Leu	Val	Ile
	145				150					155				160	
Cys	Pro	Glu	Gly	Thr	Thr	Cys	Arg	Glu	Glu	Tyr	Leu	Leu	Arg	Phe	Ser
			165						170					175	
Ala	Leu	Phe	Ala	Glu	Leu	Ser	Asp	Arg	Ile	Val	Pro	Val	Ala	Met	Asn
		180						185					190		
Cys	Lys	Gln	Gly	Met	Phe	Asn	Gly	Thr	Thr	Val	Arg	Gly	Val	Lys	Phe
		195					200					205			
Trp	Asp	Pro	Tyr	Phe	Phe	Phe	Met	Asn	Pro	Arg	Pro	Ser	Tyr	Glu	Ala
	210					215					220				
Thr	Phe	Leu	Asp	Arg	Leu	Pro	Glu	Glu	Met	Thr	Val	Asn	Gly	Gly	Gly
	225				230				235					240	
Lys	Thr	Pro	Ile	Glu	Val	Ala	Asn	Tyr	Val	Gln	Lys	Val	Ile	Gly	Ala
			245						250					255	
Val	Leu	Gly	Phe	Glu	Cys	Thr	Glu	Leu	Thr	Arg	Lys	Asp	Lys	Tyr	Leu
		260					265					270			
Leu	Leu	Gly	Gly	Asn	Asp	Gly	Lys	Val	Glu	Ser	Ile	Asn	Asn	Thr	Lys
		275				280						285			

Lys

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 219 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..219
(D) OTHER INFORMATION: / Ceres Seq. ID 1565691
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:
Met Leu Gly Ile His Leu Thr Ile Arg Gly His Arg Pro Pro Pro Pro
1 5 10 15
Ser Pro Gly Thr Leu Gly Asn Leu Tyr Val Leu Asn His Arg Thr Ala
20 25 30
Leu Asp Pro Ile Ile Val Ala Ile Ala Leu Gly Arg Lys Ile Cys Cys
35 40 45
Val Thr Tyr Ser Val Ser Arg Leu Ser Leu Met Leu Ser Pro Ile Pro
50 55 60
Ala Val Ala Leu Thr Arg Asp Arg Ala Thr Asp Ala Ala Asn Met Arg
65 70 75 80
Lys Leu Leu Glu Lys Gly Asp Leu Val Ile Cys Pro Glu Gly Thr Thr
85 90 95
Cys Arg Glu Glu Tyr Leu Leu Arg Phe Ser Ala Leu Phe Ala Glu Leu
100 105 110
Ser Asp Arg Ile Val Pro Val Ala Met Asn Cys Lys Gln Gly Met Phe
115 120 125
Asn Gly Thr Thr Val Arg Gly Val Lys Phe Trp Asp Pro Tyr Phe Phe
130 135 140
Phe Met Asn Pro Arg Pro Ser Tyr Glu Ala Thr Phe Leu Asp Arg Leu
145 150 155 160
Pro Glu Glu Met Thr Val Asn Gly Gly Gly Lys Thr Pro Ile Glu Val
165 170 175
Ala Asn Tyr Val Gln Lys Val Ile Gly Ala Val Leu Gly Phe Glu Cys
180 185 190
Thr Glu Leu Thr Arg Lys Asp Lys Tyr Leu Leu Leu Gly Gly Asn Asp
195 200 205
Gly Lys Val Glu Ser Ile Asn Asn Thr Lys Lys
210 215

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1065 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..1065
(D) OTHER INFORMATION: / Ceres Seq. ID 1565692
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

aaagaagaaa ttggtatccgc cgttgatcgt ccggtatctgg aacgaggaag atgagctctc 60
tatcttaaaagg ggggttagttg attacagagc taagacagga ttcaatccca aaatgattg 120
ggatgcgcttt tgtatgtttcc tcggaagttc tatcgttgag agattotcca aggatcaggt 180
tttgagtaaa atcaggaagt tgaaaaggag gtttcattgt cactcggaga aaatcaatca 240
agggaaatgat cccaaaattta ctaggcttag tgattctgaa gcctttgggt tttcttcgat 300
gattttgggga caaggtgatg atgatgggat ggataaggag cacgaggtaa acggaatagg 360
tgacgcggaaa aaccggaacta acgagagcgg ggaggagatg ttgaaggagc acgagggaga 420
agtggcttaat actgaacttt taaatgagaa tGgggcagccc aaaaacaacag agaatgggac 480
tagtagtgga aaagagagac atgatgagga caatgatgat gatgatgagt tatgcgcggt 540
gcaggatgca tttgagcgcg tgatgtcgca aggtttaagt gggttatcaa agaagttgca 600
gcttgagaag ctgatgaacc ttggaatagg taaaagaaga gagttgagtg atgaatggaa 660

agcggttatgt gttgaggaaa caagattcaa tatcaagaag cttagatttt cgcgaagct 720
tgcagaggca gctaatgata gttagatgaa accaatatgc ccttgtagca ttgggtgtg 780
tttaggttct tagtaagtca taagctctag tctgttcagt gtatttatct ttagatcctg 840
tctttcttct acctgggcaa gtgtttgtaa gatattccac ttttactca agtatccaca 900
agagccaatg tagtagagtg gcttgtgcaa gagtctagag tctagggtta ataagtgtgt 960
ttaaggcatg cttgtgtgtg tgcctaagag tgtagtgaag tagtataag aagagtgtgt 1020
gtgtgtcttg taattattat caagataatta acaatgtaga agatc

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 247 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..247

(D) OTHER INFORMATION: / Ceres Seq. ID 1565693

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

Lys Lys Lys Leu Asp Pro Pro Leu Ile Val Arg Ile Trp Asn Glu Glu
1 5 10 15
Asp Glu Leu Ser Ile Leu Lys Gly Leu Val Asp Tyr Arg Ala Lys Thr
20 25 30
Gly Phe Asn Pro Lys Ile Asp Trp Asp Ala Phe Cys Ser Phe Leu Gly
35 40 45
Ser Ser Ile Val Glu Arg Phe Ser Lys Asp Gln Val Leu Ser Lys Ile
50 55 60
Arg Lys Leu Lys Arg Arg Phe His Val His Ser Glu Lys Ile Asn Gln
65 70 75 80
Gly Asn Asp Pro Lys Lys Phe Thr Arg Ser Ser Asp Ser Glu Ala Phe Gly
85 90 95
Phe Ser Ser Met Ile Trp Gly Gln Gly Asp Asp Asp Gly Met Asp Lys
100 105 110
Glu His Glu Val Asn Gly Asn Gly Ala Ala Glu Asn Arg Thr Asn Glu
115 120 125
Ser Gly Glu Glu Met Leu Lys Glu His Glu Glu Glu Val Ala Asn Thr
130 135 140
Glu Leu Leu Asn Glu Asn Gly Ala Ala Lys Thr Thr Glu Asn Gly Thr
145 150 155 160
Ser Ser Gly Lys Glu Arg His Asp Glu Asp Asn Asp Asp Asp Asp Glu
165 170 175
Leu Cys Ala Val Gln Asp Ala Phe Glu Ala Val Met Ser Gln Gly Leu
180 185 190
Ser Gly Tyr Gln Lys Lys Leu Gln Leu Glu Lys Leu Met Asn Leu Gly
195 200 205
Asn Gly Lys Arg Arg Glu Leu Ser Asp Glu Trp Lys Ala Leu Cys Val
210 215 220
Glu Glu Thr Arg Phe Asn Ile Lys Lys Leu Arg Phe Ser Ala Lys Leu
225 230 235 240
Ala Glu Ala Ala Asn Asp Ser
245

(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 148 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..148

(D) OTHER INFORMATION: / Ceres Seq. ID 1565694

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

Met Ile Trp Gly Gln Gly Asp Asp Asp Gly Met Asp Lys Glu His Glu
1 5 10 15
Val Asn Gly Asn Gly Ala Ala Glu Asn Arg Thr Asn Glu Ser Gly Glu
20 25 30
Glu Met Leu Lys Glu His Glu Glu Val Ala Asn Thr Glu Leu Leu
35 40 45
Asn Glu Asn Gly Ala Ala Lys Thr Thr Glu Asn Gly Thr Ser Ser Gly
50 55 60
Lys Glu Arg His Asp Glu Asp Asn Asp Asp Asp Glu Leu Cys Ala
65 70 75 80
Val Gln Asp Ala Phe Glu Ala Val Met Ser Gln Gly Leu Ser Gly Tyr
85 90 95
Gln Lys Lys Leu Gln Leu Glu Lys Leu Met Asn Leu Gly Asn Gly Lys
100 105 110
Arg Arg Glu Leu Ser Asp Glu Trp Lys Ala Leu Cys Val Glu Glu Thr
115 120 125
Arg Phe Asn Ile Lys Lys Leu Arg Phe Ser Ala Lys Leu Ala Glu Ala
130 135 140

Ala Asn Asp Ser

145

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 138 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..138

(D) OTHER INFORMATION: / Ceres Seq. ID 1565695

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

Met Asp Lys Glu His Glu Val Asn Gly Asn Gly Ala Ala Glu Asn Arg
1 5 10 15
Thr Asn Glu Ser Gly Glu Glu Met Leu Lys Glu His Glu Glu Glu Val
20 25 30
Ala Asn Thr Glu Leu Leu Asn Glu Asn Gly Ala Ala Lys Thr Thr Glu
35 40 45
Asn Gly Thr Ser Ser Gly Lys Glu Arg His Asp Glu Asp Asn Asp Asp
50 55 60
Asp Asp Glu Leu Cys Ala Val Gln Asp Ala Phe Glu Ala Val Met Ser
65 70 75 80
Gln Gly Leu Ser Gly Tyr Gln Lys Lys Leu Gln Leu Glu Lys Leu Met
85 90 95
Asn Leu Gly Asn Gly Lys Arg Arg Glu Leu Ser Asp Glu Trp Lys Ala
100 105 110
Leu Cys Val Glu Glu Thr Arg Phe Asn Ile Lys Lys Leu Arg Phe Ser
115 120 125
Ala Lys Leu Ala Glu Ala Ala Asn Asp Ser
130 135

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1498 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(D) OTHER INFORMATION: / Ceres Seq. ID 1565723

[illegible]

(1) SEQUENCE CHARACTERISTICS:

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

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(ix) FEATURE:
```

(A) NAME/KEY: peptide

(B) LOCATION: 1..432

(D) OTHER INFORMATION: / Ceres Seq. ID 1565724

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

Met	Lys	Lys	Ile	5	Ser	Ser	His	Tyr	Ser	Val	Val	Ile	Ala	Ile	Leu	Val
1				5						10					15	
Val	Val	Thr	Met	Thr	Ser	Met	Cys	Gln	Ala	Val	Gly	Ser	Asn	Val	Tyr	
			20					25					30			
Pro	Leu	Ile	Leu	Val	Pro	Gly	Asn	Gly	Gly	Asn	Gln	Leu	Leu	Val	Arg	
		35					40					45				
Leu	Asp	Arg	Glu	Tyr	Lys	Pro	Ser	Ser	Val	Trp	Cys	Ser	Ser	Trp	Leu	
	50					55					60					
Tyr	Pro	Ile	His	Lys	Lys	Ser	Gly	Gly	Trp	Phe	Arg	Leu	Trp	Phe	Asp	
	65				70					75					80	
Ala	Ala	Val	Leu	Leu	Ser	Pro	Phe	Thr	Arg	Cys	Phe	Ser	Asp	Arg	Met	
				85					90					95		
Met	Leu	Tyr	Tyr	Asp	Pro	Asp	Leu	Asp	Asp	Tyr	Gln	Asn	Ala	Pro	Gly	
			100					105					110			
Val	Gln	Thr	Arg	Val	Pro	His	Phe	Gly	Ser	Thr	Lys	Ser	Leu	Leu	Tyr	
		115					120					125				
Leu	Asp	Pro	Arg	Leu	Arg	Asp	Ala	Thr	Ser	Tyr	Met	Glu	Leu	Val		
	130					135					140					
Lys	Ala	Leu	Glu	Lys	Lys	Cys	Gly	Tyr	Val	Asn	Asp	Gln	Thr	Ile	Leu	
	145				150					155					160	
Gly	Ala	Pro	Tyr	Asp	Phe	Arg	Tyr	Gly	Leu	Ala	Ala	Ser	Gly	His	Pro	

2000 2001 2002 2003 2004 2005 2006 2007 2008 2009 2010 2011 2012 2013 2014 2015 2016 2017 2018 2019 2020 2021 2022 2023 2024 2025 2026 2027 2028 2029 2030 2031 2032 2033 2034 2035 2036 2037 2038 2039 2040 2041 2042 2043 2044 2045 2046 2047 2048 2049 2050 2051 2052 2053 2054 2055 2056 2057 2058 2059 2060 2061 2062 2063 2064 2065 2066 2067 2068 2069 2070 2071 2072 2073 2074 2075 2076 2077 2078 2079 2080 2081 2082 2083 2084 2085 2086 2087 2088 2089 2090 2091 2092 2093 2094 2095 2096 2097 2098 2099 2100 2101 2102 2103 2104 2105 2106 2107 2108 2109 2110 2111 2112 2113 2114 2115 2116 2117 2118 2119 2120 2121 2122 2123 2124 2125 2126 2127 2128 2129 2130 2131 2132 2133 2134 2135 2136 2137 2138 2139 2140 2141 2142 2143 2144 2145 2146 2147 2148 2149 2150 2151 2152 2153 2154 2155 2156 2157 2158 2159 2160 2161 2162 2163 2164 2165 2166 2167 2168 2169 2170 2171 2172 2173 2174 2175 2176 2177 2178 2179 2180 2181 2182 2183 2184 2185 2186 2187 2188 2189 2190 2191 2192 2193 2194 2195 2196 2197 2198 2199 2200 2201 2202 2203 2204 2205 2206 2207 2208 2209 2210 2211 2212 2213 2214 2215 2216 2217 2218 2219 2220 2221 2222 2223 2224 2225 2226 2227 2228 2229 2230 2231 2232 2233 2234 2235 2236 2237 2238 2239 2240 2241 2242 2243 2244 2245 2246 2247 2248 2249 2250 2251 2252 2253 2254 2255 2256 2257 2258 2259 2260 2261 2262 2263 2264 2265 2266 2267 2268 2269 2270 2271 2272 2273 2274 2275 2276 2277 2278 2279 2280 2281 2282 2283 2284 2285 2286 2287 2288 2289 2290 2291 2292 2293 2294 2295 2296 2297 2298 2299 2300 2301 2302 2303 2304 2305 2306 2307 2308 2309 2310 2311 2312 2313 2314 2315 2316 2317 2318 2319 2320 2321 2322 2323 2324 2325 2326 2327 2328 2329 2330 2331 2332 2333 2334 2335 2336 2337 2338 2339 2340 2341 2342 2343 2344 2345 2346 2347 2348 2349 2350 2351 2352 2353 2354 2355 2356 2357 2358 2359 2360 2361 2362 2363 2364 2365 2366 2367 2368 2369 2370 2371 2372 2373 2374 2375 2376 2377 2378 2379 2380 2381 2382 2383 2384 2385 2386 2387 2388 2389 2390 2391 2392 2393 2394 2395 2396 2397 2398 2399 2400 2401 2402 2403 2404 2405 2406 2407 2408 2409 2410 2411 2412 2413 2414 2415 2416 2417 2418 2419 2420 2421 2422 2423 2424 2425 2426 2427 2428 2429 2430 2431 2432 2433 2434 2435 2436 2437 2438 2439 2440 2441 2442 2443 2444 2445 2446 2447 2448 2449 2450 2451 2452 2453 2454 2455 2456 2457 2458 2459 2460 2461 2462 2463 2464 2465 2466 2467 2468 2469 2470 2471 2472 2473 2474 2475 2476 2477 2478 2479 2480 2481 2482 2483 2484 2485 2486 2487 2488 2489 2490 2491 2492 2493 2494 2495 2496 2497 2498 2499 2500 2501 2502 2503 2504 2505 2506 2507 2508 2509 2510 2511 2512 2513 2514 2515 2516 2517 2518 2519 2520 2521 2522 2523 2524 2525 2526 2527 2528 2529 2530 2531 2532 2533 2534 2535 2536 2537 2538 2539 2540 2541 2542 2543 2544 2545 2546 2547 2548 2549 2550 2551 2552 2553 2554 2555 2556 2557 2558 2559 2560 2561 2562 2563 2564 2565 2566 2567 2568 2569 2570 2571 2572 2573 2574 2575 2576 2577 2578 2579 2580 2581 2582 2583 2584 2585 2586 2587 2588 2589 2590 2591 2592 2593 2594 2595 2596 2597 2598 2599 2600 2601 2602 2603 2604 2605 2606 2607 2608 2609 2610 2611 2612 2613 2614 2615 2616 2617 2618 2619 2620 2621 2622 2623 2624 2625 2626 2627 2628 2629 2630 2631 2632 2633 2634 2635 2636 2637 2638 2639 2640 2641 2642 2643 2644 2645 2646 2647 2648 2649 2650 2651 2652 2653 2654 2655 2656 2657 2658 2659 2660 2661 2662 2663 2664 2665 2666 2667 2668 2669 2670 2671 2672 2673 2674 2675 2676 2677 2678 2679 2680 2681 2682 2683 2684 2685 2686 2687 2688 2689 2690 2691 2692 2693 2694 2695 2696 2697 2698 2699 2700 2701 2702 2703 2704 2705 2706 2707 2708 2709 2710 2711 2712 2713 2714 2715 2716 2717 2718 2719 2720 2721 2722 2723 2724 2725 2726 2727 2728 2729 2730 2731 2732 2733 2734 2735 2736 2737 2738 2739 2740 2741 2742 2743 2744 2745 2746 2747 2748 2749 2750 2751 2752 2753 2754 2755 2756 2757 2758 2759 2760 2761 2762 2763 2764 2765 2766 2767 2768 2769 2770 2771 2772 2773 2774 2775 2776 2777 2778 2779 2780 2781 2782 2783 2784 2785 2786 2787 2788 2789 2790 2791 2792 2793 2794 2795 2796 2797 2798 2799 2800 2801 2802 2803 2804 2805 2806 2807 2808 2809 2810 2811 2812 2813 2814 2815 2816 2817 2818

(i) SEQUENCE CHARACTERISTICS:

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

MOLECULE TYPE: peptid

(ix) FEATURE:

(2) NDM

(A) NAME/KEY: peptide

(B) LOCATION: 1..413

(D) OTHER INFORMATION: / Ceres Seq. ID 1565725

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

Met	Thr	Ser	Met	Cys	Gln	Ala	Val	Gly	Ser	Asn	Val	Tyr	Pro	Leu	Ile
1				5					10					15	
Leu	Val	Pro	Gly	Asn	Gly	Gly	Asn	Gln	Leu	Glu	Val	Arg	Leu	Asp	Arg
			20					25					30		
Glu	Tyr	Lys	Pro	Ser	Ser	Val	Trp	Cys	Ser	Ser	Trp	Leu	Tyr	Pro	Ile
		35					40					45			
His	Lys	Lys	Ser	Gly	Gly	Trp	Phe	Arg	Leu	Trp	Phe	Asp	Ala	Ala	Val
	50					55					60				
Leu	Leu	Ser	Pro	Phe	Thr	Arg	Cys	Phe	Ser	Asp	Arg	Met	Met	Leu	Tyr
65					70					75				80	
Tyr	Asp	Pro	Asp	Leu	Asp	Asp	Tyr	Gln	Asn	Ala	Pro	Gly	Val	Gln	Thr
				85					90					95	
Arg	Val	Pro	His	Phe	Gly	Ser	Thr	Lys	Ser	Leu	Leu	Tyr	Leu	Asp	Pro
			100					105					110		

Arg Leu Arg Asp Ala Thr Ser Tyr Met Glu His Leu Val Lys Ala Leu
115 120 125
Glu Lys Lys Cys Gly Tyr Val Asn Asp Gln Thr Ile Leu Gly Ala Pro
130 135 140
Tyr Asp Phe Arg Tyr Gly Leu Ala Ala Ser Gly His Pro Ser Arg Val
145 150 155 160
Ala Ser Gln Phe Leu Gln Asp Leu Lys Gln Leu Val Glu Lys Thr Ser
165 170 175
Ser Glu Asn Glu Gly Lys Pro Val Ile Leu Leu Ser His Ser Leu Gly
180 185 190
Gly Leu Phe Val Leu His Phe Leu Asn Arg Thr Thr Pro Ser Trp Arg
195 200 205
Arg Lys Tyr Ile Lys His Phe Val Ala Leu Ala Ala Pro Trp Gly Gly
210 215 220
Thr Ile Ser Gln Met Lys Thr Phe Ala Ser Gly Asn Thr Leu Gly Val
225 230 235 240
Pro Leu Val Asn Pro Leu Leu Val Arg Arg His Gln Arg Thr Ser Glu
245 250 255
Ser Asn Gln Trp Leu Leu Pro Ser Thr Lys Val Phe His Asp Arg Thr
260 265 270
Lys Pro Leu Val Val Thr Pro Gln Val Asn Tyr Thr Ala Tyr Glu Met
275 280 285
Asp Arg Phe Phe Ala Asp Ile Gly Phe Ser Gln Gly Val Val Pro Tyr
290 295 300
Lys Thr Arg Val Leu Pro Leu Thr Glu Glu Leu Met Thr Pro Gly Val
305 310 315 320
Pro Val Thr Cys Ile Tyr Gly Arg Gly Val Asp Thr Pro Glu Val Leu
325 330 335
Met Tyr Gly Lys Gly Gly Phe Asp Lys Gln Pro Glu Ile Lys Tyr Gly
340 345 350
Asp Gly Asp Gly Thr Val Asn Leu Ala Ser Leu Ala Ala Leu Lys Val
355 360 365
Asp Ser Leu Asn Thr Val Glu Ile Asp Gly Val Ser His Thr Ser Ile
370 375 380
Leu Lys Asp Glu Ile Ala Leu Lys Glu Ile Met Lys Gln Ile Ser Ile
385 390 395 400
Ile Asn Tyr Glu Leu Ala Asn Val Asn Ala Val Asn Glu
405 410

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 410 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..410

(D) OTHER INFORMATION: / Ceres Seq. ID 1565726

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

Met Cys Gln Ala Val Gly Ser Asn Val Tyr Pro Leu Ile Leu Val Pro
1 5 10 15
Gly Asn Gly Gly Asn Gln Leu Glu Val Arg Leu Asp Arg Glu Tyr Lys
20 25 30
Pro Ser Ser Val Trp Cys Ser Ser Trp Leu Tyr Pro Ile His Lys Lys
35 40 45
Ser Gly Gly Trp Phe Arg Leu Trp Phe Asp Ala Ala Val Leu Leu Ser
50 55 60
Pro Phe Thr Arg Cys Phe Ser Asp Arg Met Met Leu Tyr Tyr Asp Pro
65 70 75 80
Asp Leu Asp Asp Tyr Gln Asn Ala Pro Gly Val Gln Thr Arg Val Pro

	85		90		95
His Phe Gly Ser Thr Lys Ser Leu Leu Tyr Leu Asp Pro Arg Leu Arg	100	105	110		
Asp Ala Thr Ser Tyr Met Glu His Leu Val Lys Ala Leu Glu Lys Lys	115	120	125		
Cys Gly Tyr Val Asn Asp Gln Thr Ile Leu Gly Ala Pro Tyr Asp Phe	130	135	140		
Arg Tyr Gly Leu Ala Ala Ser Gly His Pro Ser Arg Val Ala Ser Gln	145	150	155	160	
Phe Leu Gln Asp Leu Lys Gln Leu Val Glu Lys Thr Ser Ser Glu Asn	165	170	175		
Glu Gly Lys Pro Val Ile Leu Leu Ser His Ser Leu Gly Gly Leu Phe	180	185	190		
Val Leu His Phe Leu Asn Arg Thr Thr Pro Ser Trp Arg Arg Lys Tyr	195	200	205		
Ile Lys His Phe Val Ala Leu Ala Ala Pro Trp Gly Gly Thr Ile Ser	210	215	220		
Gln Met Lys Thr Phe Ala Ser Gly Asn Thr Leu Gly Val Pro Leu Val	225	230	235	240	
Asn Pro Leu Leu Val Arg Arg His Gln Arg Thr Ser Glu Ser Asn Gln	245	250	255		
Trp Leu Leu Pro Ser Thr Lys Val Phe His Asp Arg Thr Lys Pro Leu	260	265	270		
Val Val Thr Pro Gln Val Asn Tyr Thr Ala Tyr Glu Met Asp Arg Phe	275	280	285		
Phe Ala Asp Ile Gly Phe Ser Gln Gly Val Val Pro Tyr Lys Thr Arg	290	295	300		
Val Leu Pro Leu Thr Glu Glu Leu Met Thr Pro Gly Val Pro Val Thr	305	310	315	320	
Cys Ile Tyr Gly Arg Gly Val Asp Thr Pro Glu Val Leu Met Tyr Gly	325	330	335		
Lys Gly Gly Phe Asp Lys Gln Pro Glu Ile Lys Tyr Gly Asp Gly Asp	340	345	350		
Gly Thr Val Asn Leu Ala Ser Leu Ala Ala Leu Lys Val Asp Ser Leu	355	360	365		
Asn Thr Val Glu Ile Asp Gly Val Ser His Thr Ser Ile Leu Lys Asp	370	375	380		
Glu Ile Ala Leu Lys Glu Ile Met Lys Gln Ile Ser Ile Ile Asn Tyr	385	390	395	400	
Glu Leu Ala Asn Val Asn Ala Val Asn Glu	405	410			

(2) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1280 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1280

(D) OTHER INFORMATION: / Ceres Seq. ID 1565746

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

acaatttcagg	gaaaatcttc	aaagtgtttg	cagagaaatc	taaatctcatc	aacagttttt	60
tacaaaagaa	atggaaaacg	gagaagcaaa	acagagtgtg	ctcttctcta	ctccctataa	120
gatgggaaga	tccaatcttt	cccatagggt	tggtcttagca	ccattgacga	gacagagatc	180
gtacggaaac	gttctctcagc	ctcacgctgc	catatattac	tctcagagaa	cgactccagg	240
aggtttttct	atcaactgaag	ccactggagt	ttcagatata	gctcaaggat	atcaagatac	300
tctccggata	tggaactaaag	agcatgtgga	ggcatggaag	ccaatcgttg	atgctgtaca	360
tgccaaaggt	ggtatcttct	tctgtcagat	ctggcatgtt	ggccgcgttt	ctaatagcgg	420
gttttcagcca	aatggaaaaa	ctcctatctc	ttgttcggat	aagccattga	tgctccaaat	480

tgcgtctaat	ggcatcgatg	aagctctctt	tacccctcca	agacggcttg	gtatcgaaga	540
aatccccggc	attgtcaatg	attttaggct	tgcgtcaaga	aatgctatgg	aagctgggtt	600
tgatggagtt	gagatcatat	gagctaattg	ctatctgatt	gaccagttca	tgaaggatac	660
gggtgaatgat	agaactgatg	aatacggtgg	atcattgcaa	aaccgttgca	aatttctctt	720
agaaatagtc	gatgcagttg	ctaaggagat	cggaccagac	cgtgttgtaa	tcaggctctc	780
tccatttgct	gactacatgg	aatctggaga	cactaatcca	ggagcattag	ggctttatat	840
ggcggaatct	ttgaacaaat	acggaatcct	ctactgtcat	gtgattgaag	cgagaatgaa	900
aacaatggga	gaagtacatg	cttgtcctca	cacactaatg	ccgatgagga	aagcgtttaa	960
ggggactttt	atctccgcag	gaggtttcac	gagggaaagt	gggaatgagg	ctgtgtcaaa	1020
gggaagaact	gatttgggtg	cttatggctg	atggtttcta	gccaacccgg	acctgccaaa	1080
gaggtttccaa	gtggatgcac	cgctgaataa	gtacgataga	ccaacgtttt	acacttctga	1140
tccagtcgtc	gggttacacc	attacccttt	cctcgaatca	acagctttaa	attgttatca	1200
ataatgtaat	gtagtggtgt	tcctttatat	aagatgtaat	aagtttctgg	cttttcatit	1260
atacttttta	agtttaagcc					

(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 372 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..372
- (D) OTHER INFORMATION: / Ceres Seq. ID 1565747

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

Met	Glu	Asn	Gly	Glu	Ala	Lys	Gln	Ser	Val	Pro	Leu	Leu	Thr	Pro	Tyr
1			5					10					15		
Lys	Met	Gly	Arg	Phe	Asn	Leu	Ser	His	Arg	Val	Val	Leu	Ala	Pro	Leu
			20					25					30		
Thr	Arg	Gln	Arg	Ser	Tyr	Gly	Asn	Val	Pro	Gln	Pro	His	Ala	Ala	Ile
			35				40					45			
Tyr	Tyr	Ser	Gln	Arg	Thr	Thr	Pro	Gly	Gly	Phe	Leu	Ile	Thr	Glu	Ala
			50				55				60				
Thr	Gly	Val	Ser	Asp	Thr	Ala	Gln	Gly	Tyr	Gln	Asp	Thr	Pro	Gly	Ile
			65				70			75				80	
Trp	Thr	Lys	Glu	His	Val	Glu	Ala	Trp	Lys	Pro	Ile	Val	Asp	Ala	Val
			85						90				95		
His	Ala	Lys	Gly	Gly	Ile	Phe	Phe	Cys	Gln	Ile	Trp	His	Val	Gly	Arg
			100					105					110		
Val	Ser	Asn	Ser	Gly	Phe	Gln	Pro	Asn	Gly	Lys	Ala	Pro	Ile	Ser	Cys
			115					120				125			
Ser	Asp	Lys	Pro	Leu	Met	Pro	Gln	Ile	Arg	Ser	Asn	Gly	Ile	Asp	Glu
			130				135				140				
Ala	Leu	Phe	Thr	Pro	Pro	Arg	Arg	Leu	Gly	Ile	Glu	Glu	Ile	Pro	Gly
			145				150				155			160	
Ile	Val	Asn	Asp	Phe	Arg	Leu	Ala	Ala	Arg	Asn	Ala	Met	Glu	Ala	Gly
			165						170				175		
Phe	Asp	Gly	Val	Glu	Ile	His	Arg	Ala	Asn	Gly	Tyr	Leu	Ile	Asp	Gln
			180					185					190		
Phe	Met	Lys	Asp	Thr	Val	Asn	Asp	Arg	Thr	Asp	Glu	Tyr	Gly	Gly	Ser
			195					200				205			
Leu	Gln	Asn	Arg	Cys	Lys	Phe	Pro	Leu	Glu	Ile	Val	Asp	Ala	Val	Ala
			210				215				220				
Lys	Glu	Ile	Gly	Pro	Asp	Arg	Val	Gly	Ile	Arg	Leu	Ser	Pro	Phe	Ala
			225						235					240	
Asp	Tyr	Met	Glu	Ser	Gly	Asp	Thr	Asn	Pro	Gly	Ala	Leu	Gly	Leu	Tyr
			245						250				255		
Met	Ala	Glu	Ser	Leu	Asn	Lys	Tyr	Gly	Ile	Leu	Tyr	Cys	His	Val	Ile
			260					265				270			
Glu	Ala	Arg	Met	Lys	Thr	Met	Gly	Glu	Val	His	Ala	Cys	Pro	His	Thr

275	280	285
Leu Met Pro Met Arg Lys Ala Phe Lys Gly Thr Phe Ile Ser Ala Gly		
290	295	300
Gly Phe Thr Arg Glu Asp Gly Asn Glu Ala Val Ser Lys Gly Arg Thr		
305	310	315
Asp Leu Val Ala Tyr Gly Arg Trp Phe Leu Ala Asn Pro Asp Leu Pro		
325	330	335
Lys Arg Phe Gln Val Asp Ala Pro Leu Asn Lys Tyr Asp Arg Pro Thr		
340	345	350
Phe Tyr Thr Ser Asp Pro Val Val Gly Tyr Thr Asp Tyr Pro Phe Leu		
355	360	365
Glu Ser Thr Ala		
370		

(2) INFORMATION FOR SEQ ID NO:71:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 355 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..355

(D) OTHER INFORMATION: / Ceres Seq. ID 1565748

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

Met Gly Arg Phe Asn Leu Ser His Arg Val Val Leu Ala Pro Leu Thr	
1	10
Arg Gln Arg Ser Tyr Gly Asn Val Pro Gln Pro His Ala Ala Ile Tyr	15
20	25
Tyr Ser Gln Arg Thr Thr Pro Gly Gly Phe Leu Ile Thr Glu Ala Thr	30
35	40
Gly Val Ser Asp Thr Ala Gln Gly Tyr Gln Asp Thr Pro Gly Ile Trp	45
50	55
Thr Lys Glu His Val Glu Ala Trp Lys Pro Ile Val Asp Ala Val His	60
65	70
Ala Lys Gly Gly Ile Phe Phe Cys Gln Ile Trp His Val Gly Arg Val	75
85	90
Ser Asn Ser Gly Phe Gln Pro Asn Gly Lys Ala Pro Ile Ser Cys Ser	95
100	105
Asp Lys Pro Leu Met Pro Gln Ile Arg Ser Asn Gly Ile Asp Glu Ala	110
115	120
Leu Phe Thr Pro Pro Arg Arg Leu Gly Ile Glu Glu Ile Pro Gly Ile	125
130	135
Val Asn Asp Phe Arg Leu Ala Ala Arg Asn Ala Met Glu Ala Gly Phe	140
145	150
Asp Gly Val Glu Ile His Arg Ala Asn Gly Tyr Leu Ile Asp Gln Phe	155
165	170
Met Lys Asp Thr Val Asn Asp Arg Thr Asp Glu Tyr Gly Gly Ser Leu	175
180	185
Gln Asn Arg Cys Lys Phe Pro Leu Glu Ile Val Asp Ala Val Ala Lys	190
195	200
Glu Ile Gly Pro Asp Arg Val Gly Ile Arg Leu Ser Pro Phe Ala Asp	205
210	215
Tyr Met Glu Ser Gly Asp Thr Asn Pro Gly Ala Leu Gly Leu Tyr Met	220
225	230
Ala Glu Ser Leu Asn Lys Tyr Gly Ile Leu Tyr Cys His Val Ile Glu	235
245	250
Ala Arg Met Lys Thr Met Gly Glu Val His Ala Cys Pro His Thr Leu	255
260	265
Met Pro Met Arg Lys Ala Phe Lys Gly Thr Phe Ile Ser Ala Gly Gly	270
275	280
	285

Phe Thr Arg Glu Asp Gly Asn Glu Ala Val Ser Lys Gly Arg Thr Asp
290 295 300
Leu Val Ala Tyr Gly Arg Trp Phe Leu Ala Asn Pro Asp Leu Pro Lys
305 310 315 320
Arg Phe Gln Val Asp Ala Pro Leu Asn Lys Tyr Asp Arg Pro Thr Phe
325 330 335
Tyr Thr Ser Asp Pro Val Val Gly Tyr Thr Asp Tyr Pro Phe Leu Glu
340 345 350
Ser Thr Ala
355

(2) INFORMATION FOR SEQ ID NO:72:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 239 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..239

(D) OTHER INFORMATION: / Ceres Seq. ID 1565749

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

Met Pro Gln Ile Arg Ser Asn Gly Ile Asp Glu Ala Leu Phe Thr Pro
1 5 10 15
Pro Arg Arg Leu Gly Ile Glu Glu Ile Pro Gly Ile Val Asn Asp Phe
20 25 30
Arg Leu Ala Ala Arg Asn Ala Met Glu Ala Gly Phe Asp Gly Val Glu
35 40 45
Ile His Arg Ala Asn Gly Tyr Leu Ile Asp Gln Phe Met Lys Asp Thr
50 55 60
Val Asn Asp Arg Thr Asp Glu Tyr Gly Gly Ser Leu Gln Asn Arg Cys
65 70 75 80
Lys Phe Pro Leu Glu Ile Val Asp Ala Val Ala Lys Glu Ile Gly Pro
85 90 95
Asp Arg Val Gly Ile Arg Leu Ser Pro Phe Ala Asp Tyr Met Glu Ser
100 105 110
Gly Asp Thr Asn Pro Gly Ala Leu Gly Leu Tyr Met Ala Glu Ser Leu
115 120 125
Asn Lys Tyr Gly Ile Leu Tyr Cys His Val Ile Glu Ala Arg Met Lys
130 135 140
Thr Met Gly Glu Val His Ala Cys Pro His Thr Leu Met Pro Met Arg
145 150 155 160
Lys Ala Phe Lys Gly Thr Phe Ile Ser Ala Gly Gly Phe Thr Arg Glu
165 170 175
Asp Gly Asn Glu Ala Val Ser Lys Gly Arg Thr Asp Leu Val Ala Tyr
180 185 190
Gly Arg Trp Phe Leu Ala Asn Pro Asp Leu Pro Lys Arg Phe Gln Val
195 200 205
Asp Ala Pro Leu Asn Lys Tyr Asp Arg Pro Thr Phe Tyr Thr Ser Asp
210 215 220
Pro Val Val Gly Tyr Thr Asp Tyr Pro Phe Leu Glu Ser Thr Ala
225 230 235

(2) INFORMATION FOR SEQ ID NO:73:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1012 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1012

(D) OTHER INFORMATION: / Ceres Seq. ID 1565769

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

acttcagcaa	aaccactaca	ctttctttat	ctctcagatt	ttctcaagaa	gattgtgtgg	60
aagatgatga	gacggaagat	ttttctcttt	gggtgattcca	tcactgaaga	atccttttagt	120
gacggtggct	gggtgtcttc	ttctgcgcgt	cttctccgct	gcaaggctga	tatggtgcta	180
cgaggataca	gtggatataa	cacgaggtgg	gcactgaaag	tggtggagag	agtttttccg	240
gtggcagaag	aagacggcgg	agattctccg	gcagctgtga	ctgttttctt	tggagcggaac	300
gacgctgttc	ttccggagag	atgctcgggg	tttcagcatg	tgccacttca	cgagtacaag	360
cagaatcttc	gtctatttgt	ttcgtttctc	aagaatcgtt	ggccacaaac	ggccattatt	420
cttataactc	cgctccaat	agacgaagag	gccgcctca	gatatactta	tatcgaaaaa	480
acaacggggg	tgccggaag	aacgaatgaa	gtagccggac	tatacgcaaa	agcatgtata	540
gcagtagctg	aggaatgtca	aatttcggtc	actgatcttt	ggtccaaaaa	gcagcAaakt	600
scaaaattggs	aaacagaatg	tctatgggg	gggttacatt	tgagtccggg	cggtaacaaa	660
gtattgtttg	aagaagttagc	aaagaagctt	aaagaagaag	gcattggagc	tgaggactta	720
gcgtgtggtc	ttccctctat	agaagatgtt	gaccctaagg	atcctctcaa	atcctttgat	780
gagttttgat	gctttatatt	actaccatgc	agtttgggtc	ttctatcttt	gAttacttct	840
taatttcgat	attaatttag	ggaatgtgac	attattaggc	actttgtgag	aatctttttg	900
tgagaatctt	tttaccgttt	aggcacttgt	gagagagagg	gcactttggc	atcttttttt	960
agaggagatt	gaaccaattt	gccctggaag	tgatgaaaaa	acaataattt	tt	

(2) INFORMATION FOR SEQ ID NO:74:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 262 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..262

(D) OTHER INFORMATION: / Ceres Seq. ID 1565770

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

Thr	Ser	Ala	Lys	Pro	Leu	His	Leu	Ser	Tyr	Leu	Ser	Asp	Phe	Leu	Lys
1			5					10					15		
Lys	Ile	Val	Trp	Lys	Met	Met	Arg	Arg	Lys	Ile	Phe	Leu	Phe	Gly	Asp
		20						25				30			
Ser	Ile	Thr	Glu	Glu	Ser	Phe	Ser	Asp	Gly	Gly	Trp	Gly	Ala	Ser	Leu
		35					40				45				
Ala	Asp	Leu	Leu	Arg	Arg	Lys	Ala	Asp	Met	Val	Leu	Arg	Gly	Tyr	Ser
	50					55					60				
Gly	Tyr	Asn	Thr	Arg	Trp	Ala	Leu	Lys	Val	Val	Glu	Arg	Val	Phe	Pro
	65				70				75					80	
Val	Ala	Glu	Glu	Asp	Gly	Gly	Asp	Ser	Pro	Ala	Ala	Val	Thr	Val	Phe
			85					90					95		
Phe	Gly	Ala	Asn	Asp	Ala	Cys	Leu	Pro	Glu	Arg	Cys	Ser	Gly	Phe	Gln
		100					105						110		
His	Val	Pro	Leu	His	Glu	Tyr	Lys	Gln	Asn	Leu	Arg	Ser	Ile	Val	Ser
		115					120					125			
Phe	Leu	Lys	Asn	Arg	Trp	Pro	Gln	Thr	Ala	Ile	Ile	Leu	Ile	Thr	Pro
		130				135					140				
Pro	Pro	Ile	Asp	Glu	Glu	Ala	Arg	Leu	Arg	Tyr	Pro	Tyr	Ile	Glu	Asn
	145					150				155				160	
Thr	Thr	Gly	Leu	Pro	Glu	Arg	Thr	Asn	Glu	Val	Ala	Gly	Leu	Tyr	Ala
			165						170				175		
Lys	Ala	Cys	Ile	Ala	Val	Ala	Glu	Glu	Cys	Gln	Ile	Ser	Val	Thr	Asp
		180					185						190		
Leu	Trp	Ser	Lys	Met	Gln	Gln	Xaa	Xaa	Asn	Trp	Xaa	Thr	Glu	Cys	Leu
		195					200				205				
Trp	Asp	Gly	Leu	His	Leu	Ser	Arg	Val	Gly	Asn	Lys	Val	Leu	Phe	Glu
		210				215					220				
Glu	Val	Ala	Lys	Lys	Leu	Lys	Glu	Gly	Ile	Gly	Ala	Glu	Asp	Leu	

225 230 235 240
Ala Val Asp Leu Pro Leu Ile Glu Asp Val Asp Pro Lys Asp Pro Leu
 245 250 255
Lys Ser Phe Asp Glu Phe
 260

(2) INFORMATION FOR SEQ ID NO:75:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 241 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..241
- (D) OTHER INFORMATION: / Ceres Seq. ID 1565771

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

Met Met Arg Arg Lys Ile Phe Leu Phe Gly Asp Ser Ile Thr Glu Glu
1 5 10 15
Ser Phe Ser Asp Gly Gly Trp Gly Ala Ser Leu Ala Asp Leu Leu Arg
 20 25 30
Arg Lys Ala Asp Met Val Leu Arg Gly Tyr Ser Gly Tyr Asn Thr Arg
 35 40 45
Trp Ala Leu Lys Val Val Glu Arg Val Phe Pro Val Ala Glu Glu Asp
 50 55 60
Gly Gly Asp Ser Pro Ala Ala Val Thr Val Phe Phe Gly Ala Asn Asp
65 70 75 80
Ala Cys Leu Pro Glu Arg Cys Ser Gly Phe Gln His Val Pro Leu His
 85 90 95
Glu Tyr Lys Gln Asn Leu Arg Ser Ile Val Ser Phe Leu Lys Asn Arg
 100 105 110
Trp Pro Gln Thr Ala Ile Ile Leu Ile Thr Pro Pro Pro Ile Asp Glu
 115 120 125
Glu Ala Arg Leu Arg Tyr Pro Tyr Ile Glu Asn Thr Thr Gly Leu Pro
130 135 140
Glu Arg Thr Asn Glu Val Ala Gly Leu Tyr Ala Lys Ala Cys Ile Ala
145 150 155 160
Val Ala Glu Glu Cys Gln Ile Ser Val Thr Asp Leu Trp Ser Lys Met
 165 170 175
Gln Gln Xaa Xaa Asn Trp Xaa Thr Glu Cys Leu Trp Asp Gly Leu His
 180 185 190
Leu Ser Arg Val Gly Asn Lys Val Leu Phe Glu Glu Val Ala Lys Lys
 195 200 205
Leu Lys Glu Glu Gly Ile Gly Ala Glu Asp Leu Ala Val Asp Leu Pro
210 215 220
Leu Ile Glu Asp Val Asp Pro Lys Asp Pro Leu Lys Ser Phe Asp Glu
225 230 235 240
Phe

(2) INFORMATION FOR SEQ ID NO:76:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 240 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..240
- (D) OTHER INFORMATION: / Ceres Seq. ID 1565772

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

Met	Arg	Arg	Lys	Ile	Phe	Leu	Phe	Gly	Asp	Ser	Ile	Thr	Glu	Glu	Ser
1			5						10				15		
Phe	Ser	Asp	Gly	Trp	Gly	Ala	Ser	Leu	Ala	Asp	Leu	Leu	Arg	Arg	
		20					25					30			
Lys	Ala	Asp	Met	Val	Leu	Arg	Gly	Tyr	Ser	Gly	Tyr	Asn	Thr	Arg	Trp
		35					40					45			
Ala	Leu	Lys	Val	Val	Glu	Arg	Val	Phe	Pro	Val	Ala	Glu	Glu	Asp	Gly
	50					55				60					
Gly	Asp	Ser	Pro	Ala	Ala	Val	Thr	Val	Phe	Phe	Gly	Ala	Asn	Asp	Ala
65					70				75				80		
Cys	Leu	Pro	Glu	Arg	Cys	Ser	Gly	Phe	Gln	His	Val	Pro	Leu	His	Glu
			85						90				95		
Tyr	Lys	Gln	Asn	Leu	Arg	Ser	Ile	Val	Ser	Phe	Leu	Lys	Asn	Arg	Trp
			100					105					110		
Pro	Gln	Thr	Ala	Ile	Ile	Leu	Ile	Thr	Pro	Pro	Pro	Ile	Asp	Glu	Glu
		115					120					125			
Ala	Arg	Leu	Arg	Tyr	Pro	Tyr	Ile	Glu	Asn	Thr	Thr	Gly	Leu	Pro	Glu
	130					135					140				
Arg	Thr	Asn	Glu	Val	Ala	Gly	Leu	Tyr	Ala	Lys	Ala	Cys	Ile	Ala	Val
145					150				155					160	
Ala	Glu	Glu	Cys	Gln	Ile	Ser	Val	Thr	Asp	Leu	Trp	Ser	Lys	Met	Gln
			165					170						175	
Gln	Xaa	Xaa	Asn	Trp	Xaa	Thr	Glu	Cys	Leu	Trp	Asp	Gly	Leu	His	Leu
	180					185							190		
Ser	Arg	Val	Gly	Asn	Lys	Val	Leu	Phe	Glu	Glu	Val	Ala	Lys	Lys	Leu
	195					200						205			
Lys	Glu	Glu	Gly	Ile	Gly	Ala	Glu	Asp	Leu	Ala	Val	Asp	Leu	Pro	Leu
	210				215						220				
Ile	Glu	Asp	Val	Asp	Pro	Lys	Asp	Pro	Leu	Lys	Ser	Phe	Asp	Glu	Phe
225					230				235					240	

(2) INFORMATION FOR SEQ ID NO:77:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 976 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -

- (B) LOCATION: 1..976

- (D) OTHER INFORMATION: / Ceres Seq. ID 1565777

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

aaaaactttc	tgttatcccc	tctttctctt	attctctctc	tctcgctatc	tctccctctt	60
aaAgtttttt	ttttaaaccag	actctccctc	taagtatttc	gttcgcaatt	aaaaaagaaa	120
acaaaatctt	tataaaattt	gattttctct	ttttaccocg	attattttga	tttgactgtt	180
ttacgacagt	caatatattca	attttattat	tgggtgctga	cgtggcatgc	atccaataga	240
gtatcaccat	gaaccacaaa	acgatgcgtc	ttccccccag	tcgcgtttcta	acggcgggata	300
acgcgaaaga	acgagacgccc	tctatctcct	cgttcaccga	taatcccgccg	gaaatcgcca	360
agtttccctc	tccgcgcctc	aaacttggtc	ctccgcgggt	taatcccatat	tccaagaaat	420
cttcaaccgc	acgacgcgag	cgcgtcggct	cgaaccaact	gatgttagcc	ggttatctga	480
gccacgagta	cctcacccaa	ggcacactct	tcggagagca	atggaaccag	gctcgagccc	540
aagccgagtc	cagtaagata	aagccgagcc	atactgttga	gcccggctgag	gaatgtgagc	600
cgaaccggaa	gaggtataga	gaggttgcta	attctctcgc	gtccagatggg	gcccaactgc	660
ccggcatcgt	caatctcgcc	cagcttgccc	gattttctca	actgtgatgc	gcgtaaatccg	720
gtgtccacgt	ggagacagat	caattgtctg	tcttcggcca	acgagagacag	ccttaaaacc	780
gaaacctctt	tctctctctt	tttttttcaa	atgttttttt	agaatctctc	ctgtaaaagt	840
gactcgctgc	ctctctcttc	tctatcctgc	cttctcggca	aatcgactga	gaaaatttag	900
ggtttgttgt	tgaggtagat	gctctctctt	tgtacatcac	aaatatcaat	tagccaatgg	960
attatgtttt	cagatc					

(2) INFORMATION FOR SEQ ID NO:78:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 152 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
- (A) NAME/KEY: peptide
 - (B) LOCATION: 1..152
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1565778

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

Met Asn Thr Lys Thr Met Arg Leu Pro Pro Arg Arg Val Leu Thr Ala
1 5 10 15
Asp Lys Arg Lys Glu Arg Asp Ala Phe Ile Ser Ser Val Thr Asp Asn
20 25 30
Pro Pro Glu Ile Ala Lys Phe Pro Ser Pro Pro Pro Lys Leu Val Pro
35 40 45
Pro Pro Val Asn Pro Ile Ser Lys Lys Ser Ser Thr Ala Ala Ala Glu
50 55 60
Pro Ile Gly Ser Asn Gln Leu Met Leu Ala Gly Tyr Leu Ser His Glu
65 70 75 80
Tyr Leu Thr Gln Gly Thr Leu Phe Gly Glu Gln Trp Asn Gln Ala Arg
85 90 95
Ala Gln Ala Glu Ser Ser Lys Ile Lys Pro Ser His Thr Val Glu Pro
100 105 110
Ala Glu Glu Cys Glu Pro Lys Arg Lys Arg Tyr Arg Glu Val Ala Asn
115 120 125
Leu Leu Arg Ser Asp Gly Ala Gln Leu Pro Gly Ile Val Asn Pro Ala
130 135 140
Gln Leu Ala Arg Phe Leu Lys Leu
145 150

(2) INFORMATION FOR SEQ ID NO:79:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 147 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
- (A) NAME/KEY: peptide
 - (B) LOCATION: 1..147
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1565779

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

Met Arg Leu Pro Pro Arg Arg Val Leu Thr Ala Asp Lys Arg Lys Glu
1 5 10 15
Arg Asp Ala Phe Ile Ser Ser Val Thr Asp Asn Pro Pro Glu Ile Ala
20 25 30
Lys Phe Pro Ser Pro Pro Pro Lys Leu Val Pro Pro Pro Val Asn Pro
35 40 45
Ile Ser Lys Lys Ser Ser Thr Ala Ala Ala Glu Pro Ile Gly Ser Asn
50 55 60
Gln Leu Met Leu Ala Gly Tyr Leu Ser His Glu Tyr Leu Thr Gln Gly
65 70 75 80
Thr Leu Phe Gly Glu Gln Trp Asn Gln Ala Arg Ala Gln Ala Glu Ser
85 90 95
Ser Lys Ile Lys Pro Ser His Thr Val Glu Pro Ala Glu Glu Cys Glu
100 105 110
Pro Lys Arg Lys Arg Tyr Arg Glu Val Ala Asn Leu Leu Arg Ser Asp
115 120 125
Gly Ala Gln Leu Pro Gly Ile Val Asn Pro Ala Gln Leu Ala Arg Phe

130 135 140
Leu Lys Leu
145
(2) INFORMATION FOR SEQ ID NO:80:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 81 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..81
(D) OTHER INFORMATION: / Ceres Seq. ID 1565780
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:
Met Leu Ala Gly Tyr Leu Ser His Glu Tyr Leu Thr Gln Gly Thr Leu
1 5 10 15
Phe Gly Glu Gln Trp Asn Gln Ala Arg Ala Gln Ala Glu Ser Ser Lys
20 25 30
Ile Lys Pro Ser His Thr Val Glu Pro Ala Glu Glu Cys Glu Pro Lys
35 40 45
Arg Lys Arg Tyr Arg Glu Val Ala Asn Leu Leu Arg Ser Asp Gly Ala
50 55 60
Gln Leu Pro Gly Ile Val Asn Pro Ala Gln Leu Ala Arg Phe Leu Lys
65 70 75 80
Leu

(2) INFORMATION FOR SEQ ID NO:81:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1305 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..1305
(D) OTHER INFORMATION: / Ceres Seq. ID 1565787
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:
agccgatttc tagattctcc tccaccacca ttttaccctt cttttaaatt ccttccttca 60
atcaaaattc gaattatttc tcaaacctct tctttatata ctaaaacgtc tcaacatgaac 120
aagaagaata aatagaacaa aagaagatga acaagaacaa gattgatgtt aagatcgaga 180
cgaagaagaat atcgatggat gaggggcstg agccaatcgt ccgagtcag tccttagccg 240
agagcaacct ctccctctct cccgacccgtt acatcaaaac agcgtctcta cgcgccacca 300
cgacccaaga cgctccctacc gcgaccaaca tcccaatcat agaccttgaa ggactctctc 360
ggaagaaggg ttgtctgatt acgtcatcat ggctcggata tccggagctt gccgtgggtg 420
ggggttcttc caggtgggtga accacggggt caaacccggag ctgatggacg cggtcaggga 480
saattggaga gaggtttttc atatgcocgt taatgccaac gagacttact caaactcacc 540
aagaacctac gaaggtcatg gaagtagact aggtgttgag aaaagcaagt cttgattgga 600
gtgatattta ctttctccat ctctctctcc atcatttgaa agacttcaac aagtggtcctt 660
cttttcctcc caccataaga gaagtatcgt atgaatacgg cgaagagcta gtgaagctaa 720
gtgggagaat tatgaggta ttatogacaa acttgggact aaaaaggat aagtttcaag 780
aagcatttgg aggtgaaaac atggggcggt gtttgagggt taattattac ccaaatgcc 840
ctgcacccgt gctggctctt gctctctctc cacactccga tctggcggt atgacattc 900
tcttaccgga cgtatcaagt ttccgtctcc aggttcgtga agatgacacg tggatcaccc 960
tcaagcctca tcccctatgt ttcactgtca atattgggtga tcaaatacag atactaagca 1020
actcaacata caagagtgtg gagcatagag tgatagtga cctggacaaag gagagagattt 1080
cacttgccct ctctctcaat cctaaaaggc atattTccga tccaacctat acaagaacttt 1140
gtatcaactc ataactctcc ttatataccct cccatgacct tctcatcaga tagactcttt 1200
atcagaactc aaggtccaca aggcataatcc catgttgaat ctcatattc tcctcgttga 1260
ttgtttttct tttatttctt ccttaaaaga aaaattaagt tttttg

(2) INFORMATION FOR SEQ ID NO:82:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 97 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..97
- (D) OTHER INFORMATION: / Ceres Seq. ID 1565788

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

Met	Asn	Lys	Asn	Lys	Ile	Asp	Val	Lys	Ile	Glu	Thr	Lys	Lys	Gly	Ser	
1			5						10					15		
Met	Asp	Glu	Trp	Xaa	Glu	Pro	Ile	Val	Arg	Val	Gln	Ser	Leu	Ala	Glu	
		20						25					30			
Ser	Asn	Leu	Ser	Ser	Leu	Pro	Asp	Arg	Tyr	Ile	Lys	Pro	Ala	Ser	Leu	
		35					40					45				
Arg	Pro	Thr	Thr	Thr	Glu	Asp	Ala	Pro	Thr	Ala	Thr	Asn	Ile	Pro	Ile	
		50			55						60					
Ile	Asp	Leu	Glu	Gly	Leu	Ser	Arg	Lys	Lys	Gly	Cys	Leu	Met	Thr	Ser	
		65			70					75				80		
Ser	Trp	Leu	Gly	Tyr	Arg	Arg	Leu	Ala	Val	Gly	Gly	Gly	Ser	Ser	Arg	
			85						90					95		

Trp

(2) INFORMATION FOR SEQ ID NO:83:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 140 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..140
- (D) OTHER INFORMATION: / Ceres Seq. ID 1565789

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

Met	Arg	Val	Leu	Ser	Thr	Asn	Leu	Gly	Leu	Lys	Glu	Asp	Lys	Phe	Gln	
1			5						10					15		
Glu	Ala	Phe	Gly	Gly	Glu	Asn	Ile	Gly	Ala	Cys	Leu	Arg	Val	Asn	Tyr	
		20						25					30			
Tyr	Pro	Lys	Cys	Pro	Arg	Pro	Val	Leu	Ala	Leu	Gly	Leu	Ser	Pro	His	
		35					40					45				
Ser	Asp	Pro	Gly	Gly	Met	Thr	Ile	Leu	Leu	Pro	Asp	Asp	Gln	Val	Phe	
		50				55					60					
Gly	Leu	Gln	Val	Arg	Lys	Asp	Asp	Thr	Trp	Ile	Thr	Val	Lys	Pro	His	
		65			70					75				80		
Pro	His	Ala	Phe	Ile	Val	Asn	Ile	Gly	Asp	Gln	Ile	Gln	Ile	Leu	Ser	
			85						90					95		
Asn	Ser	Thr	Tyr	Lys	Ser	Val	Glu	His	Arg	Val	Ile	Val	Asn	Ser	Asp	
		100						105					110			
Lys	Glu	Arg	Val	Ser	Leu	Ala	Phe	Phe	Tyr	Asn	Pro	Lys	Ser	Asp	Ile	
		115					120					125				
Ser	Asp	Pro	Thr	Ile	Thr	Arg	Thr	Cys	Ile	Asn	Ser					
		130							135					140		

(2) INFORMATION FOR SEQ ID NO:84:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 87 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:

(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..87
 (D) OTHER INFORMATION: / Ceres Seq. ID 1565790
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:
Met Thr Ile Leu Leu Pro Asp Asp Gln Val Phe Gly Leu Gln Val Arg
1 5 10 15
Lys Asp Asp Thr Trp Ile Thr Val Lys Pro His Pro His Ala Phe Ile
 20 25 30
Val Asn Ile Gly Asp Gln Ile Gln Ile Leu Ser Asn Ser Thr Tyr Lys
 35 40 45
Ser Val Glu His Arg Val Ile Val Asn Ser Asp Lys Glu Arg Val Ser
 50 55 60
Leu Ala Phe Phe Tyr Asn Pro Lys Ser Asp Ile Ser Asp Pro Thr Ile
65 70 75 80
Thr Arg Thr Cys Ile Asn Ser
 85

(2) INFORMATION FOR SEQ ID NO:85:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1648 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..1648
(D) OTHER INFORMATION: / Ceres Seq. ID 1565799

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

acatgttctc tccgcgcctga atcatgtcaa tctccacacaa aagatctttg ataaaaagaa 60
ttgagcccta attccttgat gtttgttgaa tcgcacagca gataaaaaa aatggtgttg 120
gcggagctcg gcggccggat aacccgcgcc atacagcaga tgaacaatgt gacaataatc 180
gatgaaaagg ttttgaatga tttcttaaac gagattactc gcgctttgtc ccagtcocgat 240
gtttcttttg gcccttgtga aaagatgcag accaatatta agaagatcgt taacctcgac 300
gatctagcag ctggccacaa caaacgcctg atcatcgagc aggcatactt caaggaaact 360
tgtaggatcg tggatccagg aaagcctgcc ttgtccccc aaagggccaa acctagtgtg 420
tgatgtttcg tcggtttaca aggtgctgga aaaaccacaa catgtaccaa gtatgcttac 480
tatcatcaga agaaagggtt caaagcagct ctagtgtgtg cggatacttt cagggccggt 540
gccttttgatc agctgaaaca gaatgccacc aaggctaaaga tcccctttta tggaaagctac 600
acagaaatccg atcctgtgaa aattgtgtgt gagggagtgt ataggttcaa gaagaaaaag 660
tgtgatctta ttattgttga caccagtggt cgccataaac aagcagcttc tctctttgaa 720
gaaatgcgtc aagtgtgtga agcaacggaa ccagatcttg ttatatattgt tatggatagc 780
agtatgtgtc aagctgcatt tgaacaagct gaagctttta aggaaactgt atctgttgga 840
gctgtaatta ttactaaagt ggaacggcat gtggtgtgct tagcgtggtt 900
gcagctacaa aaagtctcgt gatattcatt ggaacaggag agcatatgga tgagtgtgaa 960
gtgtttgacg ttaaacattt tgtcagccgt ctcttaggaa aggggtgatt gtctggactc 1020
tggtgataac tacaagaggt ggtacctaaa gatctacaga atgaacttgt agaaaaatctc 1080
tctcagggtt actttacgtt gaagaagtat tacgaccagt tccagtgctc tctgcggatt 1140
ccacttaatc agcttttctc gatgctgcct ggaattagtg ctgaaatgat gccgaagga 1200
catggtgaag aaagccgagt gaagatgaag cgatacatga caatgatgga ttctatgaca 1260
aataaagzac ttgacagccc aaacccaaag atttttaacg agtcaaggat aatgagga 1320
gcgagagggg cagggaaggt agtaagagaa gtgatggaga ttttggaga gtacaagagg 1380
atagcaaaag caatgaaggt gatcaagatc ccaagaagac gagcatagag caaggtcata 1440
ccgcctcaga tgctaaaaa gatgggcggc atgagcggtc tgcagagctc catgaagcac 1500
atgggttcgg ctaaggacat gatgggaagt ttgtgtggcg gaggcaagta gtttctatct 1560
ttcttgCaca cagtgcagcg agggcagatg taaaactttt gttacatact gtattagtag 1620
cttataattt taacacatcc taacgacc

(2) INFORMATION FOR SEQ ID NO:86:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 479 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..479
(D) OTHER INFORMATION: / Ceres Seq. ID 1565800
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

Met	Val	Leu	Ala	Glu	Leu	Gly	Gly	Arg	Ile	Thr	Arg	Ala	Ile	Gln	Gln
1			5						10				15		
Met	Asn	Asn	Val	Thr	Ile	Ile	Asp	Glu	Lys	Val	Leu	Asn	Asp	Phe	Leu
			20					25					30		
Asn	Glu	Ile	Thr	Arg	Ala	Leu	Leu	Gln	Ser	Asp	Val	Ser	Phe	Gly	Leu
			35				40				45				
Val	Glu	Lys	Met	Gln	Thr	Asn	Ile	Lys	Lys	Ile	Val	Asn	Leu	Asp	Asp
	50					55				60					
Leu	Ala	Ala	Gly	His	Asn	Lys	Arg	Leu	Ile	Ile	Glu	Gln	Ala	Ile	Phe
	65				70				75					80	
Lys	Glu	Leu	Cys	Arg	Met	Leu	Asp	Pro	Gly	Lys	Pro	Ala	Phe	Ala	Pro
			85					90					95		
Lys	Lys	Ala	Lys	Pro	Ser	Val	Val	Met	Phe	Val	Gly	Leu	Gln	Gly	Ala
			100					105					110		
Gly	Lys	Thr	Thr	Thr	Cys	Thr	Lys	Tyr	Ala	Tyr	Tyr	His	Gln	Lys	Lys
			115					120					125		
Gly	Tyr	Lys	Ala	Ala	Leu	Val	Cys	Ala	Asp	Thr	Phe	Arg	Ala	Gly	Ala
			130				135				140				
Phe	Asp	Gln	Leu	Lys	Gln	Asn	Ala	Thr	Lys	Ala	Lys	Ile	Pro	Phe	Tyr
	145				150				155					160	
Gly	Ser	Tyr	Thr	Glu	Ser	Asp	Pro	Val	Lys	Ile	Ala	Val	Glu	Gly	Val
			165					170						175	
Asp	Arg	Phe	Lys	Lys	Glu	Lys	Cys	Asp	Leu	Ile	Ile	Val	Asp	Thr	Ser
			180					185					190		
Gly	Arg	His	Lys	Gln	Ala	Ala	Ser	Leu	Phe	Glu	Glu	Met	Arg	Gln	Val
			195				200					205			
Ala	Glu	Ala	Thr	Glu	Pro	Asp	Leu	Val	Ile	Phe	Val	Met	Asp	Ser	Ser
			210			215					220				
Ile	Gly	Gln	Ala	Ala	Phe	Glu	Gln	Ala	Glu	Ala	Phe	Lys	Glu	Thr	Val
			225		230				235					240	
Ser	Val	Gly	Ala	Val	Ile	Ile	Thr	Lys	Met	Asp	Gly	His	Ala	Lys	Gly
			245					250					255		
Gly	Gly	Ala	Leu	Ser	Ala	Val	Ala	Ala	Thr	Lys	Ser	Pro	Val	Ile	Phe
			260				265						270		
Ile	Gly	Thr	Gly	Glu	His	Met	Asp	Glu	Phe	Glu	Val	Phe	Asp	Val	Lys
			275				280					285			
Pro	Phe	Val	Ser	Arg	Leu	Leu	Gly	Lys	Gly	Asp	Trp	Ser	Gly	Leu	Val
			290			295					300				
Asp	Lys	Leu	Gln	Glu	Val	Val	Pro	Lys	Asp	Leu	Gln	Asn	Glu	Leu	Val
			305			310				315				320	
Glu	Asn	Leu	Ser	Gln	Gly	Asn	Phe	Thr	Leu	Arg	Ser	Met	Tyr	Asp	Gln
			325						330					335	
Phe	Gln	Cys	Ser	Leu	Arg	Ile	Pro	Leu	Asn	Gln	Leu	Phe	Ser	Met	Leu
			340					345					350		
Pro	Gly	Ile	Ser	Ala	Glu	Met	Met	Pro	Lys	Gly	His	Gly	Glu	Glu	Ser
			355				360					365			
Arg	Val	Lys	Met	Lys	Arg	Tyr	Met	Thr	Met	Met	Asp	Ser	Met	Thr	Asn
			370			375					380				
Lys	Glu	Leu	Asp	Ser	Pro	Asn	Pro	Lys	Ile	Phe	Asn	Glu	Ser	Arg	Ile
			385			390				395				400	
Met	Arg	Ile	Ala	Arg	Gly	Ser	Gly	Arg	Leu	Val	Arg	Glu	Val	Met	Glu

(2) INFORMATION FOR SEQ ID NO:87:

(A) LENGTH: 463 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..463

(D) OTHER INFORMATION: / Ceres Seq. ID 1565801

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

Met	Asn	Asn	Val	Thr	Ile	Ile	Asp	Glu	Lys	Val	Leu	Asn	Asp	Phe	Leu
1				5					10					15	
Asn	Glu	Ile	Thr	Arg	Ala	Leu	Leu	Gln	Ser	Asp	Val	Ser	Phe	Gly	Leu
			20					25					30		
Val	Glu	Lys	Met	Gln	Thr	Asn	Ile	Lys	Lys	Ile	Val	Asn	Leu	Asp	Asp
		35					40					45			
Leu	Ala	Ala	Gly	His	Asn	Lys	Arg	Leu	Ile	Ile	Glu	Gln	Ala	Ile	Phe
	50					55					60				
Lys	Glu	Leu	Cys	Arg	Met	Leu	Asp	Pro	Gly	Lys	Pro	Ala	Phe	Ala	Pro
65					70					75				80	
Lys	Lys	Ala	Lys	Pro	Ser	Val	Val	Met	Phe	Val	Gly	Leu	Gln	Gly	Ala
				85					90					95	
Gly	Lys	Thr	Thr	Thr	Cys	Thr	Lys	Tyr	Ala	Tyr	Tyr	His	Gln	Lys	Lys
			100					105					110		
Gly	Tyr	Lys	Ala	Ala	Leu	Val	Cys	Ala	Asp	Thr	Phe	Arg	Ala	Gly	Ala
		115				120						125			
Phe	Asp	Gln	Leu	Lys	Gln	Asn	Ala	Thr	Lys	Ala	Lys	Ile	Pro	Phe	Tyr
	130					135					140				
Gly	Ser	Tyr	Thr	Glu	Ser	Asp	Pro	Val	Lys	Ile	Ala	Val	Glu	Gly	Val
	145				150					155				160	
Asp	Arg	Phe	Lys	Lys	Glu	Lys	Cys	Asp	Leu	Ile	Ile	Val	Asp	Thr	Ser
				165					170					175	
Gly	Arg	His	Lys	Gln	Ala	Ala	Ser	Leu	Phe	Glu	Glu	Met	Arg	Gln	Val
			180					185					190		
Ala	Glu	Ala	Thr	Glu	Pro	Asp	Leu	Val	Ile	Phe	Val	Met	Asp	Ser	Ser
		195				200						205			
Ile	Gly	Gln	Ala	Ala	Phe	Glu	Gln	Ala	Glu	Ala	Phe	Lys	Glu	Thr	Val
	210					215					220				
Ser	Val	Gly	Ala	Val	Ile	Ile	Thr	Lys	Met	Asp	Gly	His	Ala	Lys	Gly
225					230					235				240	
Gly	Gly	Ala	Leu	Ser	Ala	Val	Ala	Ala	Thr	Lys	Ser	Pro	Val	Ile	Phe
				245					250					255	
Ile	Gly	Thr	Gly	Glu	His	Met	Asp	Glu	Phe	Glu	Val	Phe	Asp	Val	Lys
			260				265					270			
Pro	Phe	Val	Ser	Arg	Leu	Leu	Gly	Lys	Gly	Asp	Trp	Ser	Gly	Leu	Val
		275					280					285			
Asp	Lys	Leu	Gln	Glu	Val	Val	Pro	Lys	Asp	Leu	Gln	Asn	Glu	Leu	Val
	290					295					300				
Glu	Asn	Leu	Ser	Gln	Gly	Asn	Phe	Thr	Leu	Arg	Ser	Met	Tyr	Asp	Gln
305					310					315				320	

Phe	Gln	Cys	Ser	Leu	Arg	Ile	Pro	Leu	Asn	Gln	Leu	Phe	Ser	Met	Leu	
				325					330						335	
Pro	Gly	Ile	Ser	Ala	Glu	Met	Met	Pro	Lys	Gly	His	Gly	Glu	Glu	Ser	
				340				345						350		
Arg	Val	Lys	Met	Lys	Arg	Tyr	Met	Thr	Met	Met	Asp	Ser	Met	Thr	Asn	
				355			360					365				
Lys	Glu	Leu	Asp	Ser	Pro	Asn	Pro	Lys	Ile	Phe	Asn	Glu	Ser	Arg	Ile	
				370			375				380					
Met	Arg	Ile	Ala	Arg	Gly	Ser	Gly	Arg	Leu	Val	Arg	Glu	Val	Met	Glu	
					390					395					400	
Met	Leu	Glu	Glu	Tyr	Lys	Arg	Ile	Ala	Lys	Thr	Met	Lys	Gly	Ile	Lys	
				405				410						415		
Ile	Pro	Lys	Asn	Gly	Asp	Met	Ser	Lys	Val	Ile	Pro	Pro	Gln	Met	Leu	
				420				425						430		
Lys	Gln	Met	Gly	Gly	Met	Ser	Gly	Leu	Gln	Ser	Leu	Met	Lys	Gln	Met	
				435				440					445			
Gly	Ser	Ala	Lys	Asp	Met	Met	Gly	Met	Phe	Gly	Gly	Gly	Gly	Lys		
				450			455				460					

(2) INFORMATION FOR SEQ ID NO:88:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 428 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..428

(D) OTHER INFORMATION: / Ceres Seq. ID 1565802

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

Met	Gln	Thr	Asn	Ile	Lys	Lys	Ile	Val	Asn	Leu	Asp	Asp	Leu	Ala	Ala	
1			5					10					15			
Gly	His	Asn	Lys	Arg	Leu	Ile	Ile	Glu	Gln	Ala	Ile	Phe	Lys	Glu	Leu	
			20					25					30			
Cys	Arg	Met	Leu	Asp	Pro	Gly	Lys	Pro	Ala	Phe	Ala	Pro	Lys	Lys	Ala	
			35				40					45				
Lys	Pro	Ser	Val	Val	Met	Phe	Val	Gly	Leu	Gln	Gly	Ala	Gly	Lys	Thr	
			50				55					60				
Thr	Thr	Cys	Thr	Lys	Tyr	Ala	Tyr	Tyr	His	Gln	Lys	Lys	Gly	Tyr	Lys	
			65			70			75					80		
Ala	Ala	Leu	Val	Cys	Ala	Asp	Thr	Phe	Arg	Ala	Gly	Ala	Phe	Asp	Gln	
			85					90					95			
Leu	Lys	Gln	Asn	Ala	Thr	Lys	Ala	Lys	Ile	Pro	Phe	Tyr	Gly	Ser	Tyr	
			100					105					110			
Thr	Glu	Ser	Asp	Pro	Val	Lys	Ile	Ala	Val	Glu	Gly	Val	Asp	Arg	Phe	
			115				120					125				
Lys	Lys	Glu	Lys	Cys	Asp	Leu	Ile	Ile	Val	Asp	Thr	Ser	Gly	Arg	His	
			130			135					140					
Lys	Gln	Ala	Ala	Ser	Leu	Phe	Glu	Glu	Met	Arg	Gln	Val	Ala	Glu	Ala	
			145			150				155				160		
Thr	Glu	Pro	Asp	Leu	Val	Ile	Phe	Val	Met	Asp	Ser	Ser	Ile	Gly	Gln	
			165					170					175			
Ala	Ala	Phe	Glu	Gln	Ala	Glu	Ala	Phe	Lys	Glu	Thr	Val	Ser	Val	Gly	
			180					185					190			
Ala	Val	Ile	Ile	Thr	Lys	Met	Asp	Gly	His	Ala	Lys	Gly	Gly	Gly	Ala	
			195			200					205					
Leu	Ser	Ala	Val	Ala	Ala	Thr	Lys	Ser	Pro	Val	Ile	Phe	Ile	Gly	Thr	
			210			215					220					
Gly	Glu	His	Met	Asp	Glu	Phe	Glu	Val	Phe	Asp	Val	Lys	Pro	Phe	Val	
			225			230				235				240		
Ser	Arg	Leu	Leu	Gly	Lys	Gly	Asp	Trp	Ser	Gly	Leu	Val	Asp	Lys	Leu	

(2) INFORMATION FOR SEO ID NO:89:

(A) LENGTH: 1687 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1687

(D) OTHER INFORMATION: / Ceres Seq. ID 1565810

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

aggatacaaac	caaatctcca	tctctctcca	ttagagctgt	aagcagccat	agcctcaaaa	60
aacctctcaac	aatgtctcca	ttctgtccgc	ttttaagcaa	aactcaactc	ctctctcaac	120
caactaaccaa	atcatctcca	aactccgact	tcacctctgc	cgcgctgttc	ttcccttcca	180
aactccctgac	cgcgcgcgta	ggatcaatac	gagccggagt	aatgctctcc	gagcgggtgta	240
agctcttaga	gctcatctgt	gaagagccaa	agcgacagaga	gaagaaacac	gagcgcgcggt	300
atttgcacgc	tgttgagctg	acggctcgtg	acttgcaatg	gatcatcgta	ttaaagccgat	360
gtgtggaaac	tcaactcgga	gtgtttagta	gagataatcga	gttctccaaa	actctctaaat	420
ttactcgcgt	acgtctctgac	gaacgtctccg	tcgttaaacat	gtcgtgcgtc	attgtctctat	480
cttatcgacta	tgaacaaaaa	cgacgtatcat	gcgagctctac	gtctgtcgct	cttttcaatt	540
ccagctgttaa	cgcctctctc	atctccacgc	atattgagat	tttaaaagct	ccaaaaggaa	600
aaaggtagata	tagaacatgt	gtgtacgacg	ctccaggtgtt	gcttatcgta	gacgagcgga	660
ttaactaatgc	tggaaactgt	ctcaatgggg	gtgatctctga	ggttcttgag	ccagttgagat	720
acaatgattg	gcttgatcgt	ttcaaggttt	cgctcgtctga	tgtacgtaaa	gagttgaaga	780
cgtctaatgc	ggatgcggtg	tttgctttcc	acgtcaggaa	tcctgtctcat	aatgtgctatg	840
ctcttcttga	gactgatact	gtgtaggagac	gttttagaat	gtgttaccaa	aacctatttc	900
ttttgctcca	tcogtttaggt	gggtttaccaa	aggctgatga	tgttctctta	gattggagga	960
ttaagacaaca	cgaagaagggt	ctagaggagt	gtgtctctga	tcctggagact	acagtgtgtt	1020
cgatattccc	gtcaactatg	caltacgtcg	gtccaaaccga	agtgcatggt	caacgaaaag	1080
ctagaactcaa	tgtggtgtcg	aacttttaca	tgtgtggctg	tgatctctgt	ggagtggttc	1140
atccagtaga	gaaacgtgat	ctttaaagat	ctgatactgg	aaaagaagta	ctaaagcatg	1200
cacaggcagct	cgaacgactc	aacatctctc	ctttacgggt	tgtgcgaatc	gacaaagacg	1260
aacggcaagat	ggctttcttc	gatctctctc	ggctccaaga	tttcttgttc	attctccgga	1320
ctaatgactgc	ccacattggca	aagaacaacg	aaaaccgcgc	agacgctgtt	atgtgccacg	1380
gttgatggaaa	agttcttgtg	gattactatg	agagcttgac	tcctggcggtt	aatgtgtaga	1440
taccagaagt	gtgtccggtg	taagacaaaa	ctgttgtgtt	caaaattgtaa	cgtttgtgtt	1500
ctgaagcctt	gtagcaacaa	ctattgttgt	atttggaagat	aagcctgatt	ataactctgc	1560

ttgacctttt tccaaataaa atacagaaga aaaaaagact gtttttcggtt tgcaagataa 1620
tttacgaaac ttgtaataatt tgggcctcaa actttgtacc atattaatga aacgattgtg 1680
tttaccat

(2) INFORMATION FOR SEQ ID NO:90:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 463 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..463
- (D) OTHER INFORMATION: / Ceres Seq. ID 1565811

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

Met	Ala	Ser	Met	Ala	Ala	Val	Leu	Ser	Lys	Thr	Pro	Phe	Leu	Ser	Gln
1			5						10				15		
Pro	Leu	Thr	Lys	Ser	Ser	Pro	Asn	Ser	Asp	Leu	Pro	Phe	Ala	Ala	Val
			20					25					30		
Ser	Phe	Pro	Ser	Lys	Ser	Leu	Arg	Arg	Arg	Val	Gly	Ser	Ile	Arg	Ala
		35					40					45			
Gly	Leu	Ile	Ala	Pro	Asp	Gly	Gly	Lys	Leu	Val	Glu	Leu	Ile	Val	Glu
		50				55					60				
Glu	Pro	Lys	Arg	Arg	Glu	Lys	Lys	His	Glu	Ala	Ala	Asp	Leu	Pro	Arg
					70					75				80	
Val	Glu	Leu	Thr	Ala	Ile	Asp	Leu	Gln	Trp	Met	His	Val	Leu	Ser	Glu
					85				90				95		
Gly	Trp	Thr	Ser	Pro	Leu	Gly	Gly	Phe	Met	Arg	Glu	Ser	Glu	Phe	Leu
					100			105					110		
Gln	Thr	Leu	His	Phe	Asn	Ser	Leu	Arg	Leu	Asp	Asp	Gly	Ser	Val	Val
					115			120				125			
Asn	Met	Ser	Val	Pro	Ile	Val	Leu	Ala	Ile	Asp	Asp	Glu	Gln	Lys	Ala
					130			135				140			
Arg	Ile	Gly	Glu	Ser	Thr	Arg	Val	Ala	Leu	Phe	Asn	Ser	Asp	Gly	Asn
					145				150		155				160
Pro	Val	Ser	Ile	Leu	Ser	Asp	Ile	Glu	Ile	Tyr	Lys	His	Pro	Lys	Glu
					165				170					175	
Glu	Arg	Ile	Ala	Arg	Thr	Trp	Gly	Thr	Thr	Ala	Pro	Gly	Leu	Pro	Tyr
					180			185					190		
Val	Asp	Glu	Ala	Ile	Thr	Asn	Ala	Gly	Asn	Trp	Leu	Ile	Gly	Gly	Asp
		195					200					205			
Leu	Glu	Val	Leu	Glu	Pro	Val	Lys	Tyr	Asn	Asp	Gly	Leu	Asp	Arg	Phe
		210				215					220				
Arg	Leu	Ser	Pro	Ala	Glu	Leu	Arg	Lys	Glu	Leu	Glu	Lys	Arg	Asn	Ala
					225			230			235				240
Asp	Ala	Val	Phe	Ala	Phe	Gln	Leu	Arg	Asn	Pro	Val	His	Asn	Gly	His
					245				250				255		
Ala	Leu	Leu	Met	Thr	Asp	Thr	Arg	Arg	Arg	Leu	Leu	Glu	Met	Gly	Tyr
			260				265						270		
Lys	Asn	Pro	Ile	Leu	Leu	Leu	His	Pro	Leu	Gly	Gly	Phe	Thr	Lys	Ala
			275				280					285			
Asp	Asp	Val	Pro	Leu	Asp	Trp	Arg	Met	Lys	Gln	His	Glu	Lys	Val	Leu
			290			295					300				
Glu	Asp	Gly	Val	Leu	Asp	Pro	Glu	Thr	Thr	Val	Val	Ser	Ile	Phe	Pro
					305					310					320
Ser	Pro	Met	His	Tyr	Ala	Gly	Pro	Thr	Glu	Val	Gln	Trp	His	Ala	Lys
					325				330				335		
Ala	Arg	Ile	Asn	Ala	Gly	Ala	Asn	Phe	Tyr	Ile	Val	Gly	Arg	Asp	Pro
			340					345					350		
Ala	Gly	Met	Gly	His	Pro	Val	Glu	Lys	Arg	Asp	Leu	Tyr	Asp	Ala	Asp
			355				360					365			

His Gly Lys Lys Val Leu Ser Met Ala Pro Gly Leu Glu Arg Leu Asn
370 375 380
Ile Leu Pro Phe Arg Val Ala Ala Tyr Asp Lys Thr Gln Gly Lys Met
385 390 395
Ala Phe Phe Asp Pro Ser Arg Pro Gln Asp Phe Leu Phe Ile Ser Gly
405 410 415
Thr Lys Met Arg Thr Leu Ala Lys Asn Asn Glu Asn Pro Pro Asp Gly
420 425 430
Phe Met Cys Pro Gly Gly Trp Lys Val Leu Val Asp Tyr Tyr Glu Ser
435 440 445
Leu Thr Pro Ala Gly Asn Gly Arg Leu Pro Glu Val Val Pro Val
450 455 460

(2) INFORMATION FOR SEQ ID NO:91:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 460 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..460

(D) OTHER INFORMATION: / Ceres Seq. ID 1565812

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

Met Ala Ala Val Leu Ser Lys Thr Pro Phe Leu Ser Gln Pro Leu Thr
1 5 10 15
Lys Ser Ser Pro Asn Ser Asp Leu Pro Phe Ala Ala Val Ser Phe Pro
20 25 30
Ser Lys Ser Leu Arg Arg Arg Val Gly Ser Ile Arg Ala Gly Leu Ile
35 40 45
Ala Pro Asp Gly Gly Lys Leu Val Glu Leu Ile Val Glu Glu Pro Lys
50 55 60
Arg Arg Glu Lys Lys His Glu Ala Ala Asp Leu Pro Arg Val Glu Leu
65 70 75 80
Thr Ala Ile Asp Leu Gln Trp Met His Val Leu Ser Glu Gly Trp Thr
85 90 95
Ser Pro Leu Gly Gly Phe Met Arg Glu Ser Glu Phe Leu Gln Thr Leu
100 105 110
His Phe Asn Ser Leu Arg Leu Asp Asp Gly Ser Val Val Asn Met Ser
115 120 125
Val Pro Ile Val Leu Ala Ile Asp Asp Glu Gln Lys Ala Arg Ile Gly
130 135 140
Glu Ser Thr Arg Val Ala Leu Phe Asn Ser Asp Gly Asn Pro Val Ser
145 150 155 160
Ile Leu Ser Asp Ile Glu Ile Tyr Lys His Pro Lys Glu Glu Arg Ile
165 170 175
Ala Arg Thr Trp Gly Thr Thr Ala Pro Gly Leu Pro Tyr Val Asp Glu
180 185 190
Ala Ile Thr Asn Ala Gly Asn Trp Leu Ile Gly Gly Asp Leu Glu Val
195 200 205
Leu Glu Pro Val Lys Tyr Asn Asp Gly Leu Asp Arg Phe Arg Leu Ser
210 215 220
Pro Ala Glu Leu Arg Lys Glu Leu Glu Lys Arg Asn Ala Asp Ala Val
225 230 235 240
Phe Ala Phe Gln Leu Arg Asn Pro Val His Asn Gly His Ala Leu Leu
245 250 255
Met Thr Asp Thr Arg Arg Arg Leu Leu Glu Met Gly Tyr Lys Asn Pro
260 265 270
Ile Leu Leu Leu His Pro Leu Gly Gly Phe Thr Lys Ala Asp Asp Val
275 280 285
Pro Leu Asp Trp Arg Met Lys Gln His Glu Lys Val Leu Glu Asp Gly

290	295	300
Val Leu Asp Pro Glu Thr Thr Val Val Ser Ile Phe Pro Ser Pro Met		
305	310	315
His Tyr Ala Gly Pro Thr Glu Val Gln Trp His Ala Lys Ala Arg Ile		
	325	330
Asn Ala Gly Ala Asn Phe Tyr Ile Val Gly Arg Asp Pro Ala Gly Met		
	340	345
Gly His Pro Val Glu Lys Arg Asp Leu Tyr Asp Ala Asp His Gly Lys		
	355	360
Lys Val Leu Ser Met Ala Pro Gly Leu Glu Arg Leu Asn Ile Leu Pro		
	370	375
Phe Arg Val Ala Ala Tyr Asp Lys Thr Gln Gly Lys Met Ala Phe Phe		
385	390	395
Asp Pro Ser Arg Pro Gln Asp Phe Leu Phe Ile Ser Gly Thr Lys Met		
	405	410
Arg Thr Leu Ala Lys Asn Asn Glu Asn Pro Pro Asp Gly Phe Met Cys		
	420	425
Pro Gly Gly Trp Lys Val Leu Val Asp Tyr Tyr Glu Ser Leu Thr Pro		
	435	440
Ala Gly Asn Gly Arg Leu Pro Glu Val Val Pro Val		
450	455	460

(2) INFORMATION FOR SEQ ID NO:92:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 373 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..373

(D) OTHER INFORMATION: / Ceres Seq. ID 1565813

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

Met His Val Leu Ser Glu Gly Trp Thr Ser Pro Leu Gly Gly Phe Met		
1	5	10
Arg Glu Ser Glu Phe Leu Gln Thr Leu His Phe Asn Ser Leu Arg Leu		
	20	25
Asp Asp Gly Ser Val Val Asn Met Ser Val Pro Ile Val Leu Ala Ile		
	35	40
Asp Asp Glu Gln Lys Ala Arg Ile Gly Glu Ser Thr Arg Val Ala Leu		
	50	55
Phe Asn Ser Asp Gly Asn Pro Val Ser Ile Leu Ser Asp Ile Glu Ile		
65	70	75
Tyr Lys His Pro Lys Glu Glu Arg Ile Ala Arg Thr Trp Gly Thr Thr		
	85	90
Ala Pro Gly Leu Pro Tyr Val Asp Glu Ala Ile Thr Asn Ala Gly Asn		
	100	105
Trp Leu Ile Gly Gly Asp Leu Glu Val Leu Glu Pro Val Lys Tyr Asn		
	115	120
Asp Gly Leu Asp Arg Phe Arg Leu Ser Pro Ala Glu Leu Arg Lys Glu		
	130	135
Leu Glu Lys Arg Asn Ala Asp Ala Val Phe Ala Gln Leu Arg Asn		
145	150	155
Pro Val His Asn Gly His Ala Leu Leu Met Thr Asp Thr Arg Arg Arg		
	165	170
Leu Leu Glu Met Gly Tyr Lys Asn Pro Ile Leu Leu Leu His Pro Leu		
	180	185
Gly Gly Phe Thr Lys Ala Asp Asp Val Pro Leu Asp Trp Arg Met Lys		
	195	200
Gln His Glu Lys Val Leu Glu Asp Gly Val Leu Asp Pro Glu Thr Thr		
210	215	220

Val Val Ser Ile Phe Pro Ser Pro Met His Tyr Ala Gly Pro Thr Glu
225 230 235 240
Val Gln Trp His Ala Lys Ala Arg Ile Asn Ala Gly Ala Asn Phe Tyr
245 250 255
Ile Val Gly Arg Asp Pro Ala Gly Met Gly His Pro Val Glu Lys Arg
260 265 270
Asp Leu Tyr Asp Ala Asp His Gly Lys Lys Val Leu Ser Met Ala Pro
275 280 285
Gly Leu Glu Arg Leu Asn Ile Leu Pro Phe Arg Val Ala Ala Tyr Asp
290 295 300
Lys Thr Gln Gly Lys Met Ala Phe Phe Asp Pro Ser Arg Pro Gln Asp
305 310 315 320
Phe Leu Phe Ile Ser Gly Thr Lys Met Arg Thr Leu Ala Lys Asn Asn
325 330 335
Glu Asn Pro Pro Asp Gly Phe Met Cys Pro Gly Gly Trp Lys Val Leu
340 345 350
Val Asp Tyr Tyr Glu Ser Leu Thr Pro Ala Gly Asn Gly Arg Leu Pro
355 360 365
Glu Val Val Pro Val
370

(2) INFORMATION FOR SEQ ID NO:93:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 747 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..747
- (D) OTHER INFORMATION: / Ceres Seq. ID 1565816

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

ctcttcatta	tcttcaaaat	cgctcgagag	tgagaactct	actcttcttc	ttcttctccc	60
goccatagcta	caatgcttag	tctctcaata	gctacgcggg	ggacggCggc	gatttttctg	120
agaggaaactg	cttcggcgac	ttcaacttct	tcttcattcc	atggtgtcag	aatccagcac	180
cagggtttctg	ctcgcgtccc	cgcgccggcg	acgatatcgt	cgctcgtctcc	taaaccgtcg	240
gtgggtgatga	tgtcgaaaaa	agagggcgaa	ttgaaagaga	taagatcgaa	gacgacggag	300
cagttacaag	aggagggttg	tgaccttaaa	ggtgagctct	ttatgcttcg	tctccagaaa	360
tcggcaagga	atgagttcaa	atctagcGac	ttctgctgta	tgaagaaaaca	agttgtctcg	420
atgtgtgacg	ttaaaagaga	gagggagatc	aaagaaggga	taaagaaaaa	gttgtcgag	480
aaacttgaca	gacaatggaa	gaacaagcata	gtaccaagac	cacctccgtc	tctgaagaaa	540
cttcaagaag	aagaagctgc	agaagaaGca	gctgaagctg	ctaaatctgc	ttgaaaaaac	600
ccgctattga	tttatggtct	cttctctgtt	gtttcctcga	gatgttgta	atctctgtta	660
tttgttgctg	aaccatctg	tattgttttt	tcttttggtg	taaacacttt	ccttatcaag	720
tagtttcat	gaatccctta	aagattg				

(2) INFORMATION FOR SEQ ID NO:94:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 173 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..173
- (D) OTHER INFORMATION: / Ceres Seq. ID 1565817

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

Met	Leu	Ser	Leu	Ser	Ile	Ala	Thr	Pro	Gly	Thr	Ala	Ala	Ile	Phe	Arg
1		5						10					15		
Arg	Gly	Thr	Ala	Ser	Ala	Thr	Ser	Thr	Ser	Ser	Ser	Phe	His	Gly	Val
		20					25						30		

Arg	Ile	Gln	His	Gln	Val	Ser	Ala	Arg	Val	Pro	Ala	Ala	Ala	Thr	Ile
	35						40					45			
Ser	Ser	Ser	Ser	Pro	Lys	Pro	Ser	Val	Val	Met	Met	Ser	Lys	Arg	Glu
	50					55					60				
Ala	Glu	Leu	Lys	Glu	Ile	Arg	Ser	Lys	Thr	Thr	Glu	Gln	Leu	Gln	Glu
	65				70					75					80
Glu	Val	Val	Asp	Leu	Lys	Gly	Glu	Leu	Phe	Met	Leu	Arg	Leu	Gln	Lys
			85						90					95	
Ser	Ala	Arg	Asn	Glu	Phe	Lys	Ser	Ser	Asp	Phe	Arg	Arg	Met	Lys	Lys
			100						105				110		
Gln	Val	Ala	Arg	Met	Leu	Thr	Val	Lys	Arg	Glu	Arg	Glu	Ile	Lys	Glu
			115				120						125		
Gly	Ile	Lys	Lys	Arg	Leu	Ser	Arg	Lys	Leu	Asp	Arg	Gln	Trp	Lys	Lys
	130					135					140				
Ser	Ile	Val	Pro	Arg	Pro	Pro	Ser	Leu	Lys	Lys	Leu	Gln	Glu	Glu	
	145				150					155				160	
Glu	Ala	Ala	Glu	Glu	Ala	Ala	Glu	Ala	Ala	Lys	Ser	Ala			
			165						170						

(2) INFORMATION FOR SEQ ID NO:95:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 115 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..115

(D) OTHER INFORMATION: / Ceres Seq. ID 1565818

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

Met	Met	Ser	Lys	Arg	Glu	Ala	Glu	Leu	Lys	Glu	Ile	Arg	Ser	Lys	Thr
1			5						10					15	
Thr	Glu	Gln	Leu	Gln	Glu	Glu	Val	Val	Asp	Leu	Lys	Gly	Glu	Leu	Phe
			20					25					30		
Met	Leu	Arg	Leu	Gln	Lys	Ser	Ala	Arg	Asn	Glu	Phe	Lys	Ser	Ser	Asp
			35				40					45			
Phe	Arg	Arg	Met	Lys	Lys	Gln	Val	Ala	Arg	Met	Leu	Thr	Val	Lys	Arg
	50				55					60					
Glu	Arg	Glu	Ile	Lys	Glu	Gly	Ile	Lys	Lys	Arg	Leu	Ser	Arg	Lys	Leu
	65				70				75					80	
Asp	Arg	Gln	Trp	Lys	Lys	Ser	Ile	Val	Pro	Arg	Pro	Pro	Pro	Ser	Leu
			85					90					95		
Lys	Lys	Leu	Gln	Glu	Glu	Glu	Ala	Ala	Glu	Glu	Ala	Ala	Glu	Ala	Ala
			100				105						110		
Lys	Ser	Ala													
			115												

(2) INFORMATION FOR SEQ ID NO:96:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 114 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..114

(D) OTHER INFORMATION: / Ceres Seq. ID 1565819

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

Met	Ser	Lys	Arg	Glu	Ala	Glu	Leu	Lys	Glu	Ile	Arg	Ser	Lys	Thr	Thr
1			5						10					15	
Glu	Gln	Leu	Gln	Glu	Glu	Val	Val	Asp	Leu	Lys	Gly	Glu	Leu	Phe	Met

	20		25		30
Leu Arg Leu Gln Lys Ser Ala Arg Asn Glu Phe					Lys Ser Ser Asp Phe
35		40		45	
Arg Arg Met Lys Lys Gln Val Ala Arg Met Leu Thr Val Lys Arg Glu					
50		55		60	
Arg Glu Ile Lys Glu Gly Ile Lys Lys Arg Leu Ser Arg Lys Leu Asp					
65		70		75	80
Arg Gln Trp Lys Lys Ser Ile Val Pro Arg Pro Pro Ser Leu Lys					
	85	90		95	
Lys Leu Gln Glu Glu Glu Ala Ala Glu Glu Ala Ala Glu Ala Lys					
	100	105		110	
Ser Ala					

(2) INFORMATION FOR SEQ ID NO:97:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2216 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..2216

(D) OTHER INFORMATION: / Ceres Seq. ID 1565820

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

ggtttttcgcg gacccatcga acctttcttc tctttctctt ctgactcctt agccgacgac	60
acagagaaga agaagacgaa gacgttgagg agtcacatca aagcttaaac cttctgtgat	120
ttattctcct tttcccgagg ttcggattaa tttttcaaat tccgacgaaa ttcgctatct	180
ctctggtgctt gacgtgctta gctaaagtga gcagagagag tacaattgtt tatgtttttg	240
taaaattaag agattcttgg caaaattctg aagtagcagc agtagctgtg tttgtgtgtc	300
atagagaagt ggagcagaag aatttccgag tgtttccgtt aactcaaatg caatggacaa	360
cgctgaatat accgacacag atttgggtgt tgccgttaga aaggcccttg caactgtcca	420
aaatggagat accgacgatt atagtgcagt taaaacagtg atgtgcctta cagaagacgc	480
tgatttcgat gcagtggcac agcttgagac agtcttgaaa agtctatcac tttccgtgtg	540
ttggatagat ttagtttcat ataaagatct tcttgaagct atttttaaga tgagcttgtg	600
gtatcatagt cacagaccta gtgtaattga tgcattgggt gacctaatca tatcactggc	660
cgctactagt ggaataatct tggatccttg ttggaatag ctcgtaagaa atttcagtca	720
acctactttt aagcataaag ttccacaacac ccagtttagt aaaaagatgc aggaagtgtca	780
tcacacgggtg catgcagcctg ttccacaagt tctttattta attcctcttg ctccctggaa	840
tttagttgtt atacttgcgc agaacatgcg taaaattgac aaaaaggacc ctctctatgt	900
gacataatgt gataacctct tgaggttgga gaatagctca atcgagagaag ttgttggcac	960
cgtagattct atgatgcaa tggagaggat gctagattta gatttggtaa gtgtgattga	1020
tgactctaat ggaggcatct ttgatatgga acttgaagat cgagttgaaa gcaacttgaa	1080
tgaaggagac gagttttccag tgggggctct aaaaacaaat acttcagggt gaaatgtagt	1140
ctctggaactg ttggacaatt tgatggctct attttttcat catctagaat cctgtcaaaa	1200
ctctgtatcgt ttgatgaga tccgtgaaat tgtggtgtga gatttgcag taagcttgtt	1260
gacataatct tctccagcaa cacatgtcga cttactagga tgagtgcagt ggcttatctca	1320
gctagtctatt tgtctcgttg aagttttttg cctgcttctt ttgtggctag catgttgaaa	1380
agatttggttg acgagtgtgc ggaatatctg ggaacatgca atgatgatgt gaagccagaa	1440
gcacatcaag tgttctattc tggatgtcag gcaatctgtt atgtctgat ctccgaaatg	1500
agatccatag tggagattct tgcctttcaa tgcagtttta gatcatgtga gttcaattta	1560
tctcacaacac taaaccacat actgggtgtg tttccatctg tagtttccga gtctctttaa	1620
caagccaaag ctggtgtgtct gtccatttgt tcaRgaAtcc ttcattttg atgacctaca	1680
cgagtctgag ctctctctgt cttttggttg ctttgaagg cttgacacat tcttcccggt	1740
tgaccctgtc ttgttgaaaa tgtctagcac ctacatctcc ccgaactcca acttctgtgtc	1800
aaatgttgaaa acgacttatg gagaagatgg tgacgaagag ctttggtagt aggtcatagt	1860
gaatggagat gcagacagat cggaaggaacc tgacgatgac gtgaaacttg atagtggagt	1920
gaacacagat tctacaactc cgaaacactc tttcatgcga gaacacagaa ggctcttgaa	1980
gatgccttca agaatcagac catccactag tctctctgaa tctctcttaa tctaatagtc	2040
atagagagag ggaatgcaat tttgcaatgt aggtttctta ttacaatctc ttagctagt	2100
cgtaaactct aaaaaaaga agttgacatg agttttgtgc gagtctgtgg tattatctga	2160

tcgcagtgtg tttttagca aaattttgaa gaacatctat gaagtaatat ttatgtc

(2) INFORMATION FOR SEQ ID NO:98:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 310 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..310
- (D) OTHER INFORMATION: / Ceres Seq. ID 1565821

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

Met Gly Ala Glu Phe Pro Ser Val Pro Phe Asn Ser Asn Ala Met
1 5 10 15
Asp Asn Ala Glu Tyr Thr Asp Thr Asp Leu Val Phe Ala Val Arg Lys
20 25 30
Ala Leu Ala Ser Val Gln Asn Gly Asp Thr Asp Asp Tyr Ser Gln Leu
35 40 45
Lys Thr Val Met Cys Leu Thr Glu Asp Ala Asp Phe Asp Ala Val Ala
50 55 60
Gln Leu Glu Thr Val Leu Lys Ser Leu Ser Val Ser Val Ala Trp Ile
65 70 75 80
Asp Leu Val His His Lys Asp Leu Leu Glu Ala Ile Phe Lys Met Ser
85 90 95
Leu Trp Tyr His Ser His Arg Pro Ser Val Met Asp Ala Leu Val Asp
100 105 110
Leu Ile Ile Ser Leu Ala Ala Thr Ser Gly Lys Tyr Leu Asp Pro Cys
115 120 125
Leu Asn Met Leu Val Arg Asn Phe Ser Gln Pro Thr Phe Lys His Lys
130 135 140
Val Ser Gln Thr Gln Leu Val Lys Lys Met Gln Glu Val His Pro Arg
145 150 155 160
Val His Ala Ala Leu His Lys Ile Ser Tyr Leu Ile Pro Leu Ala Pro
165 170 175
Trp Asn Leu Val Ser Ile Leu Ala Gln Asn Met Arg Lys Ile Asp Lys
180 185 190
Lys Asp Pro Ser Ile Val Thr Tyr Val Asp Asn Leu Leu Arg Leu Glu
195 200 205
Asn Ser Ser Ile Gly Glu Val Val Gly Ser Val Ile Leu Met Met Ala
210 215 220
Met Glu Arg Met Leu Asp Leu Asp Leu Val Ser Gly Cys Asp Asp Ser
225 230 235 240
Asn Gly Gly Met Phe Asp Met Glu Leu Glu Asp Ala Val Glu Ser Thr
245 250 255
Met Asn Glu Gly Asp Glu Phe Pro Val Gly Ala Leu Lys Gln Asn Thr
260 265 270
Ser Gly Gly Asn Val Val Ser Glu Leu Leu Asp Lys Leu Met Val Leu
275 280 285
Phe Phe His His Leu Glu Ser Cys Gln Asn Ser Asp Arg Leu Asp Glu
290 295 300
Ile Leu Lys Ile Val Val
305 310

(2) INFORMATION FOR SEQ ID NO:99:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 295 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..295

(D) OTHER INFORMATION: / Ceres Seq. ID 1565822

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

Met Asp Asn Ala Glu Tyr Thr Asp Thr Asp Leu Val Phe Ala Val Arg
1 5 10 15
Lys Ala Leu Ala Ser Val Gln Asn Gly Asp Thr Asp Asp Tyr Ser Gln
20 25 30
Leu Lys Thr Val Met Cys Leu Thr Glu Asp Ala Asp Phe Asp Ala Val
35 40 45
Ala Gln Leu Glu Thr Val Leu Lys Ser Leu Ser Val Ser Val Ala Trp
50 55 60
Ile Asp Leu Val His His Lys Asp Leu Leu Glu Ala Ile Phe Lys Met
65 70 75 80
Ser Leu Trp Tyr His Ser His Arg Pro Ser Val Met Asp Ala Leu Val
85 90 95
Asp Leu Ile Ile Ser Leu Ala Ala Thr Ser Gly Lys Tyr Leu Asp Pro
100 105 110
Cys Leu Asn Met Leu Val Arg Asn Phe Ser Gln Pro Thr Phe Lys His
115 120 125
Lys Val Ser Gln Thr Gln Leu Val Lys Lys Met Gln Glu Val His Pro
130 135 140
Arg Val His Ala Ala Leu His Lys Ile Ser Tyr Leu Ile Pro Leu Ala
145 150 155 160
Pro Trp Asn Leu Val Ser Ile Leu Ala Gln Asn Met Arg Lys Ile Asp
165 170 175
Lys Lys Asp Pro Ser Ile Val Thr Tyr Val Asp Asn Leu Leu Arg Leu
180 185 190
Glu Asn Ser Ser Ile Gly Glu Val Val Gly Ser Val Ile Leu Met Met
195 200 205
Ala Met Glu Arg Met Leu Asp Leu Asp Leu Val Ser Gly Cys Asp Asp
210 215 220
Ser Asn Gly Gly Met Phe Asp Met Glu Leu Glu Asp Ala Val Glu Ser
225 230 235 240
Thr Met Asn Glu Gly Asp Glu Phe Pro Val Gly Ala Leu Lys Gln Asn
245 250 255
Thr Ser Gly Gly Asn Val Val Ser Glu Leu Leu Asp Lys Leu Met Val
260 265 270
Leu Phe Phe His His Leu Glu Ser Cys Gln Asn Ser Asp Arg Leu Asp
275 280 285
Glu Ile Leu Lys Ile Val Val
290 295

(2) INFORMATION FOR SEQ ID NO:100:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 259 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..259

(D) OTHER INFORMATION: / Ceres Seq. ID 1565823

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

Met Cys Leu Thr Glu Asp Ala Asp Phe Asp Ala Val Ala Gln Leu Glu
1 5 10 15
Thr Val Leu Lys Ser Leu Ser Val Ser Val Ala Trp Ile Asp Leu Val
20 25 30
His His Lys Asp Leu Leu Glu Ala Ile Phe Lys Met Ser Leu Trp Tyr
35 40 45
His Ser His Arg Pro Ser Val Met Asp Ala Leu Val Asp Leu Ile Ile

[illegible]

(2) INFORMATION FOR SEQ ID NO:101:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1717 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..1717
(D) OTHER INFORMATION: / Ceres Seq. ID 1565828

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

tataataaaa	cgaactctct	tgcctgattcc	atttatcggt	cttatgtgacc	ctagcgccta	60
gcgaactttc	tgcgatatact	tgcagattct	ttgcacgtct	ttaacacgtg	gtaaaaagaa	120
cttttccatc	aacatctgtgg	ctgattggcca	cgctgattct	ggaaagtctga	ccaccactgg	180
acactctgac	tacaagttgg	gtgttatatga	caagcgtctg	atttgagact	tcgaaagaa	240
ggcgtctctg	atgacaaga	ggctctccaa	tgcacgatgg	gttttgagca	aacttaaggc	300
tgaagctctg	cgtgtgatca	ctcattgatca	tgcctctctg	aagtctcgaa	ccaccaagta	360
ctactgcact	ctcattgatg	ctctcgtgtca	tcgtgatttc	atacgaagaa	tgatcactga	420
tacctccag	cgtgattgtg	ctgcctctat	catgtactcc	accactgttg	Cttttgagtg	480
tgattatctcc	aaggaatgttc	agaccctctg	cgacgctcta	cttgcttcta	gctttgggtg	540
caagcagatg	atctcgtctt	gtacaagaat	ctgtgcgaact	acccccagc	actccaaggc	600
caggtaacgt	gaatactca	aggaagtgct	tctctaactg	aagaagtggt	gttcaaccc	660
gcgacaacct	ccatttgtgc	ccatctctgg	atttgagggt	gacaaatga	ttgagaggtc	720
ccccaaactt	gactggtgaa	agggaacaac	tctcttgag	gctttgacc	agatcaacga	780
gccccaaagg	cgctcagaca	agcccacttg	tctcccaatt	caggatgtct	acaagatggt	840
tggttatgtg	acggtgcacg	ttggacctgt	tgagactggt	atgatcaagc	ctggtatggt	900
ttgtgacctt	ctgcccacag	gattgaccac	tgagctcaag	tctgttgaga	tcgacaacga	960
gtctctctct	gaggcaactc	caggtgcacaa	cgttggtgtc	aatgtttaaa	atgttgcgtt	1020
caaggacttc	aagagagggg	actcgtcact	caactccaag	gatgacctct	ccaagggtgc	1080
tgctaaactc	acctcccagg	tcatcatcat	gaaccaccc	ggtcagatgt	gtaacaggta	1140
cgcccagtc	ctggatgtcc	acaactctca	ctctcagtc	aagttctctg	agactctgac	1200
caagatctgac	agggctctct	gtaaggagat	tgaagaaggg	cttaaatctc	tgaagaatgg	1260
taactgactg	atgttcaata	gaactccaac	acgacccatg	qcttatgaga	ctctctctga	1320

gtacccacca	cttgagcgtt	tcgctgtgag	ggacatgagg	cagactgttg	cagtcggtgt	1380
tatcaagagt	gttgacaaga	aggacccaac	tgagccaag	gttaccgaag	ctgcagtcac	1440
gaagggtgcc	aagtgaactc	tgaacatcaa	aactctttcc	gctgatgaaa	tgaaggacta	1500
ttttatgttc	tttactttag	tagtttggt	tttggttggt	tgttgtgttt	accgcttcgt	1560
ttattctcgc	toggagctca	attctcgga	ttgggttcct	gacggaggt	gpcgaggtg	1620
cttgccactc	gagcttccgt	tttatttctt	ttgtttgtg	ttatgatttt	gaaccttttt	1680
ggatattcgg	ttatgatgata	tttgtgtcat	tcctgcc			

(2) INFORMATION FOR SEQ ID NO:102:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 449 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..449

(D) OTHER INFORMATION: / Ceres Seq. ID 1565829

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

Met	Gly	Lys	Lys	Lys	Phe	His	Ile	Asn	Ile	Val	Val	Ile	Gly	His	Val
1			5					10					15		
Asp	Ser	Gly	Lys	Ser	Thr	Thr	Thr	Gly	His	Leu	Ile	Tyr	Lys	Leu	Gly
			20					25					30		
Gly	Ile	Asp	Lys	Arg	Val	Ile	Glu	Arg	Phe	Glu	Lys	Glu	Ala	Ala	Glu
			35					40				45			
Met	Asn	Lys	Arg	Ser	Phe	Lys	Tyr	Ala	Trp	Val	Leu	Asp	Lys	Leu	Lys
			50					55				60			
Ala	Glu	Arg	Glu	Arg	Gly	Ile	Thr	Ile	Asp	Ile	Ala	Leu	Trp	Lys	Phe
			65					70				75			80
Glu	Thr	Thr	Lys	Tyr	Tyr	Cys	Thr	Val	Ile	Asp	Ala	Pro	Gly	His	Arg
			85					90					95		
Asp	Phe	Ile	Lys	Asn	Met	Ile	Thr	Gly	Thr	Ser	Gln	Ala	Asp	Cys	Ala
			100					105					110		
Val	Leu	Ile	Asp	Ser	Thr	Thr	Gly	Gly	Phe	Glu	Ala	Gly	Ile	Ser	
			115					120				125			
Lys	Asp	Gly	Gln	Thr	Arg	Glu	His	Ala	Leu	Leu	Ala	Phe	Thr	Leu	Gly
			130					135				140			
Val	Lys	Gln	Met	Ile	Cys	Cys	Cys	Asn	Lys	Met	Asp	Ala	Thr	Thr	Pro
			145					150				155			160
Lys	Tyr	Ser	Lys	Ala	Arg	Tyr	Asp	Glu	Ile	Ile	Lys	Glu	Val	Ser	Ser
			165					170					175		
Tyr	Leu	Lys	Lys	Val	Gly	Tyr	Asn	Pro	Asp	Lys	Ile	Pro	Phe	Val	Pro
			180					185					190		
Ile	Ser	Gly	Phe	Glu	Gly	Asp	Asn	Met	Ile	Glu	Arg	Ser	Thr	Asn	Leu
			195					200				205			
Asp	Trp	Tyr	Lys	Gly	Pro	Thr	Leu	Leu	Glu	Ala	Leu	Asp	Gln	Ile	Asn
			210					215				220			
Glu	Pro	Lys	Arg	Pro	Ser	Asp	Lys	Pro	Leu	Arg	Leu	Pro	Leu	Gln	Asp
			225					230				235			240
Val	Tyr	Lys	Ile	Gly	Gly	Ile	Gly	Thr	Val	Pro	Val	Gly	Arg	Val	Glu
			245					250					255		
Thr	Gly	Met	Ile	Lys	Pro	Gly	Met	Val	Val	Thr	Phe	Ala	Pro	Thr	Gly
			260					265					270		
Leu	Thr	Thr	Glu	Val	Lys	Ser	Val	Glu	Met	His	His	Glu	Ser	Leu	Leu
			275					280				285			
Glu	Ala	Leu	Pro	Gly	Asp	Asn	Val	Gly	Phe	Asn	Val	Lys	Asn	Val	Ala
			290					295				300			
Val	Lys	Asp	Leu	Lys	Arg	Gly	Tyr	Val	Ala	Ser	Asn	Ser	Lys	Asp	Asp
			305					310				315			320
Pro	Ala	Lys	Gly	Ala	Ala	Asn	Phe	Thr	Ser	Gln	Val	Ile	Ile	Met	Asn
			325					330					335		

His	Pro	Gly	Gln	Ile	Gly	Asn	Gly	Tyr	Ala	Pro	Val	Leu	Asp	Cys	His	
			340					345					350			
Thr	Ser	His	Ile	Ala	Val	Lys	Phe	Ser	Glu	Ile	Leu	Thr	Lys	Ile	Asp	
		355					360					365				
Arg	Arg	Ser	Gly	Lys	Glu	Ile	Glu	Lys	Glu	Pro	Lys	Phe	Leu	Lys	Asn	
		370				375					380					
Gly	Asp	Ala	Gly	Met	Val	Lys	Met	Thr	Pro	Thr	Lys	Pro	Met	Val	Val	
	385				390				395					400		
Glu	Thr	Phe	Ser	Glu	Tyr	Pro	Pro	Leu	Gly	Arg	Phe	Ala	Val	Arg	Asp	
			405					410					415			
Met	Arg	Gln	Thr	Val	Ala	Val	Gly	Val	Ile	Lys	Ser	Val	Asp	Lys	Lys	
		420						425					430			
Asp	Pro	Thr	Gly	Ala	Lys	Val	Thr	Lys	Ala	Ala	Val	Lys	Lys	Gly	Ala	
		435					440					445				

Lys

(2) INFORMATION FOR SEQ ID NO:103:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 401 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..401

(D) OTHER INFORMATION: / Ceres Seq. ID 1565830

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

Met	Asn	Lys	Arg	Ser	Phe	Lys	Tyr	Ala	Trp	Val	Leu	Asp	Lys	Leu	Lys	
1			5				10						15			
Ala	Glu	Arg	Glu	Arg	Gly	Ile	Thr	Ile	Asp	Ile	Ala	Leu	Trp	Lys	Phe	
		20					25					30				
Glu	Thr	Thr	Lys	Tyr	Tyr	Cys	Thr	Val	Ile	Asp	Ala	Pro	Gly	His	Arg	
		35				40					45					
Asp	Phe	Ile	Lys	Asn	Met	Ile	Thr	Gly	Thr	Ser	Gln	Ala	Asp	Cys	Ala	
	50				55					60						
Val	Leu	Ile	Ile	Asp	Ser	Thr	Thr	Gly	Gly	Phe	Glu	Ala	Gly	Ile	Ser	
	65			70					75				80			
Lys	Asp	Gly	Gln	Thr	Arg	Glu	His	Ala	Leu	Leu	Ala	Phe	Thr	Leu	Gly	
			85					90					95			
Val	Lys	Gln	Met	Ile	Cys	Cys	Cys	Asn	Lys	Met	Asp	Ala	Thr	Thr	Pro	
		100					105					110				
Lys	Tyr	Ser	Lys	Ala	Arg	Tyr	Asp	Glu	Ile	Ile	Lys	Glu	Val	Ser	Ser	
	115					120					125					
Tyr	Leu	Lys	Lys	Val	Gly	Tyr	Asn	Pro	Asp	Lys	Ile	Pro	Phe	Val	Pro	
	130				135						140					
Ile	Ser	Gly	Phe	Glu	Gly	Asp	Asn	Met	Ile	Glu	Arg	Ser	Thr	Asn	Leu	
	145			150					155					160		
Asp	Trp	Tyr	Lys	Gly	Pro	Thr	Leu	Leu	Glu	Ala	Leu	Asp	Gln	Ile	Asn	
			165					170					175			
Glu	Pro	Lys	Arg	Pro	Ser	Asp	Lys	Pro	Leu	Arg	Leu	Pro	Leu	Gln	Asp	
		180					185					190				
Val	Tyr	Lys	Ile	Gly	Gly	Ile	Gly	Thr	Val	Pro	Val	Gly	Arg	Val	Glu	
	195					200						205				
Thr	Gly	Met	Ile	Lys	Pro	Gly	Met	Val	Val	Thr	Phe	Ala	Pro	Thr	Gly	
	210				215						220					
Leu	Thr	Thr	Glu	Val	Lys	Ser	Val	Glu	Met	His	His	Glu	Ser	Leu	Leu	
	225				230				235					240		
Glu	Ala	Leu	Pro	Gly	Asp	Asn	Val	Gly	Phe	Asn	Val	Lys	Asn	Val	Ala	
		245						250				255				
Val	Lys	Asp	Leu	Lys	Arg	Gly	Tyr	Val	Ala	Ser	Asn	Ser	Lys	Asp	Asp	

(2) INFORMATION FOR SEO ID NO:104:

(A) LENGTH: 348 amino acids

(C) STRANDEDNESS:

(D) TOPOLOGY: lin

MOLECULE TYPE: peptid

(ix) FEATURE:

(A) NAME

(B) LOCATION: 1..348

(D) OTHER INFORMATION

SEQUENCE DESCRIPTION: SEQ ID NO:104:

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:104:
Ile Thr Gly Thr Ser Gln Ala Asp Cys Ala Val

[illegible]

Gly Asn Gly Tyr Ala Pro Val Leu Asp Cys His Thr Ser His Ile Ala
245 250 255
Val Lys Phe Ser Glu Ile Leu Thr Lys Ile Asp Arg Arg Ser Gly Lys
260 265 270
Glu Ile Glu Lys Glu Pro Lys Phe Leu Lys Asn Gly Asp Ala Gly Met
275 280 285
Val Lys Met Thr Pro Thr Lys Pro Met Val Val Glu Thr Phe Ser Glu
290 295 300
Tyr Pro Pro Leu Gly Arg Phe Ala Val Arg Asp Met Arg Gln Thr Val
305 310 315 320
Ala Val Gly Val Ile Lys Ser Val Asp Lys Lys Asp Pro Thr Gly Ala
325 330 335
Lys Val Thr Lys Ala Ala Val Lys Lys Gly Ala Lys
340 345

(2) INFORMATION FOR SEQ ID NO:105:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 635 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..635
- (D) OTHER INFORMATION: / Ceres Seq. ID 1565836

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

tctctctaca	acaaaatcag	cgacaGctca	aacgtcgata	ttttctccg	gctttcttag	60
ggttttaatt	ttctttccga	tcagagatta	atggcgactc	tagactccga	cgttaccatg	120
attctcgcgc	gagaagcctc	cagcagcgta	gccgcgtcgt	cttccaaaca	gaaagctaaag	180
cgattcgaaa	ttaagaagtg	gagcgccgtt	gctctctggg	cttgggatat	cgttgttgac	240
aactgtgcga	tctgcagaaa	ccacatcatg	gatotttgta	tcgagtgtoa	ggctaatacg	300
gccagtgcga	caagtgaaga	gtgcactgta	gcttgggggg	tttgcaatca	cgctttccac	360
tttcaactgca	tcagcagatg	gctaaagact	cgtcaagttt	gtccattgga	taacagttag	420
tgggagtttc	agaaatatgg	tcactaaatc	aacaaatggg	tccagcaagc	atgtgtctaa	480
tcgtgaagac	atcagggttca	tttggttacc	accgcgatg	ataactaaag	attgttcaag	540
tttttgcctt	tttttttgta	ctgtatttta	caatttggtg	aaacagagat	ttactgttca	600

gtgttcaacta aacctattat ggttgtgctt tgggt

(2) INFORMATION FOR SEQ ID NO:106:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 118 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..118
- (D) OTHER INFORMATION: / Ceres Seq. ID 1565837

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

Met Ala Thr Leu Asp Ser Asp Val Thr Met Ile Pro Ala Gly Glu Ala	
1 5 10 15	
Ser Ser Ser Val Ala Ala Ser Ser Ser Asn Lys Lys Ala Lys Arg Phe	
20 25 30	
Glu Ile Lys Lys Trp Ser Ala Val Ala Leu Trp Ala Trp Asp Ile Val	
35 40 45	
Val Asp Asn Cys Ala Ile Cys Arg Asn His Ile Met Asp Leu Cys Ile	
50 55 60	
Glu Cys Gln Ala Asn Gln Ala Ser Ala Thr Ser Glu Glu Cys Thr Val	
65 70 75 80	
Ala Trp Gly Val Cys Asn His Ala Phe His Phe His Cys Ile Ser Arg	
85 90 95	

Trp Leu Lys Thr Arg Gln Val Cys Pro Leu Asp Asn Ser Glu Trp Glu
100 105 110
Phe Gln Lys Tyr Gly His
115

(2) INFORMATION FOR SEQ ID NO:107:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 109 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..109
- (D) OTHER INFORMATION: / Ceres Seq. ID 1565838

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

Met Ile Pro Ala Gly Glu Ala Ser Ser Ser Val Ala Ala Ser Ser Ser
1 5 10 15
Asn Lys Lys Ala Lys Arg Phe Glu Ile Lys Lys Trp Ser Ala Val Ala
20 25 30
Leu Trp Ala Trp Asp Ile Val Val Asp Asn Cys Ala Ile Cys Arg Asn
35 40 45
His Ile Met Asp Leu Cys Ile Glu Cys Gln Ala Asn Gln Ala Ser Ala
50 55 60
Thr Ser Glu Glu Cys Thr Val Ala Trp Gly Val Cys Asn His Ala Phe
65 70 75 80
His Phe His Cys Ile Ser Arg Trp Leu Lys Thr Arg Gln Val Cys Pro
85 90 95
Leu Asp Asn Ser Glu Trp Glu Phe Gln Lys Tyr Gly His
100 105

(2) INFORMATION FOR SEQ ID NO:108:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..66
- (D) OTHER INFORMATION: / Ceres Seq. ID 1565839

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

Met Val Thr Lys Ser Thr Asn Gly Ser Ser Lys His Val Ser Asn Arg
1 5 10 15
Glu Asp Ile Arg Phe Ile Trp Leu Pro Pro His Met Ile Thr Lys Asp
20 25 30
Cys Ser Ser Phe Cys Pro Phe Phe Gly Thr Val Phe Tyr Asn Leu Trp
35 40 45
Lys Gln Arg Phe Thr Val Gln Cys Ser Leu Asn Leu Leu Trp Leu Cys
50 55 60
Phe Gly
65

(2) INFORMATION FOR SEQ ID NO:109:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1618 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -

(B) LOCATION: 1..1618

(D) OTHER INFORMATION: / Ceres Seq. ID 1565840

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

aatagattag	ttttgtactt	ctgttacgtg	gtgattatta	aaacttgtaa	taacagtata	60
atctgggtttt	gttgggtgag	attgatgatt	tcaacattgc	aaagaaggaa	gaggacattg	120
ggttctaacg	tggatttggt	ggttgctctt	tcatgctcgg	acgagctttt	acatctgtgg	180
catggggagc	tgttctgat	cggttatgta	gaaaacctgt	aatcctcata	ggaaccgctt	240
cagtggtcgt	ttttaatact	ctgttttgcc	taagtttaaa	ttctctggatg	gctattatca	300
caagattttg	ccctcggtagt	ttaacacggtt	tacttggtcc	tatcaaggct	tacgcaatgg	360
aaatattccg	tgatgagtat	caagggtttag	cactctcagc	agtttagtaca	gcttggggaa	420
ttggactccg	cattggccct	gctataggag	gttttcttgc	tcagcctgca	aagcaataatc	480
caagtttatt	cttcacaggac	tccatttttg	gcaaattttc	ctcttttttg	ccatgtctag	540
caatatccgt	ttttgcattc	ttggtagaca	tagtttcatc	aaggattccg	gaaacattgc	600
acaatcacaa	gtttaatgat	gatgagtctt	atgatgctct	caaagatttg	ctctgatgacc	660
ctgaatctaa	taaaagtggca	gagagaaagt	gaaaaagttc	tctcttgacc	aactggccat	720
taatttcaat	tatcatogta	tactgcgtct	tttcaactaca	tgatatggct	tacacagaga	780
tccttttcaat	gtgggcaaac	agtcaggaga	aatatggagg	tttgggatac	tcactctgac	840
atgttggttt	tgttcttgcc	ttttcaggct	ttgtctctct	tatctttcag	ctttcgctct	900
actcttacgc	agagaggctt	ttaggaccta	tcatagtttac	acgtatatct	gggagcctag	960
caatggctgt	cttatcatgt	taocccactaa	tagcaaaagt	atctgggtta	gtccttaccg	1020
tgaactgtaac	ttctgcacgc	gtagcaaaaga	gtgttttagg	tactttctgt	ataactggat	1080
tattcatcct	tcaaaaacag	gctgtgagac	aagaccaWag	aggagcagct	aatggaattg	1140
ccatgacagc	gatgtctctt	ttcaaaagcca	taggtccagc	agcagcagga	atcatttttt	1200
cgtggagcga	gaaacgtcag	gggtgctgct	ttctccctgg	caoccaaagt	gtattcttta	1260
tactgaatgt	ggtttttgga	cttggagttg	tattgacatt	caaacatttt	ctagctgaaa	1320
cacaagaatg	gaaaatgatg	aagattttga	tgttatctaa	attacataat	cagaatgta	1380
tgtataatat	atagatYtgt	atgtctgac	caaaagttaga	ttagaaaaat	ggcaagagaa	1440
aaagaaaaaa	aacttgtttg	aattgttgtc	atcatccttt	gtatgtttta	ggacaagtgt	1500
ttcacaataa	tttgtcta	gtgtcagaac	cattgtaaga	aggatttcaat	aatgtttttt	1560
gtacatgatg	tttcgcgaat	aatattgaca	agtcgtcaaa	tcctatcctg	agattccct	

(2) INFORMATION FOR SEQ ID NO:110:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 392 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..392

(D) OTHER INFORMATION: / Ceres Seq. ID 1565841

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

Met	Leu	Gly	Arg	Ala	Phe	Thr	Ser	Val	Ala	Trp	Gly	Leu	Val	Ala	Asp
1			5						10				15		
Arg	Tyr	Gly	Arg	Lys	Pro	Val	Ile	Leu	Ile	Gly	Thr	Ala	Ser	Val	Val
			20					25				30			
Val	Phe	Asn	Thr	Leu	Phe	Gly	Leu	Ser	Leu	Asn	Phe	Trp	Met	Ala	Ile
			35					40				45			
Ile	Thr	Arg	Phe	Cys	Leu	Gly	Ser	Phe	Asn	Gly	Leu	Leu	Gly	Pro	Ile
			50				55				60				
Lys	Ala	Tyr	Ala	Met	Glu	Ile	Phe	Arg	Asp	Glu	Tyr	Gln	Gly	Leu	Ala
65					70				75				80		
Leu	Ser	Ala	Val	Ser	Thr	Ala	Trp	Gly	Ile	Gly	Leu	Ile	Ile	Gly	Pro
					85				90				95		
Ala	Ile	Gly	Gly	Phe	Leu	Ala	Gln	Pro	Ala	Lys	Gln	Tyr	Pro	Ser	Leu
			100					105				110			
Phe	Ser	Gln	Asp	Ser	Ile	Phe	Gly	Lys	Phe	Pro	Phe	Phe	Leu	Pro	Cys
			115				120				125				
Leu	Ala	Ile	Ser	Val	Phe	Ala	Phe	Leu	Val	Thr	Ile	Val	Ser	Ser	Arg
			130				135				140				
Ile	Pro	Glu	Thr	Leu	His	Asn	His	Lys	Phe	Asn	Asp	Glu	Ser	Tyr	

145	150	155	160
Asp Ala Leu Lys Asp	Leu Ser Asp Asp	Pro Glu Ser Asn Lys Val Ala	
	165	170	175
Glu Arg Asn Gly Lys	Ser Ser Leu Leu Asn Asn Trp Pro Leu Ile Ser		
	180	185	190
Ser Ile Ile Val Tyr Cys Val Phe	Ser Leu His Asp Met Ala Tyr Thr		
	195	200	205
Glu Ile Phe Ser Leu Trp Ala Asn Ser Pro Arg Lys Tyr Gly Gly Leu			
	210	215	220
Gly Tyr Ser Thr Ala Asp Val Gly Ser Val Leu Ala Phe Ser Gly Phe			
	225	230	235
Gly Leu Leu Ile Phe Gln Leu Ser Leu Tyr Ser Tyr Ala Glu Arg Leu			
	245	250	255
Leu Gly Pro Ile Val Thr Arg Ile Ser Gly Ser Leu Ala Met Val			
	260	265	270
Val Leu Ser Cys Tyr Pro Leu Ile Ala Lys Leu Ser Gly Leu Val Leu			
	275	280	285
Thr Val Thr Val Thr Ser Ala Ser Val Ala Lys Ser Val Leu Gly Thr			
	290	295	300
Ser Ala Ile Thr Gly Leu Phe Ile Leu Gln Asn Lys Ala Val Arg Gln			
	305	310	315
Asp Xaa Arg Gly Ala Ala Asn Gly Ile Ala Met Thr Ala Met Ser Leu			
	325	330	335
Phe Lys Ala Ile Gly Pro Ala Ala Ala Gly Ile Ile Phe Ser Trp Ser			
	340	345	350
Glu Lys Arg Gln Gly Ala Ala Phe Leu Pro Gly Thr Gln Met Val Phe			
	355	360	365
Phe Ile Leu Asn Val Val Leu Ala Leu Gly Val Val Leu Thr Phe Lys			
	370	375	380
Pro Phe Leu Ala Glu Thr Gln Gln			
	385	390	

(2) INFORMATION FOR SEQ ID NO:111:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 347 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..347
- (D) OTHER INFORMATION: / Ceres Seq. ID 1565842

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

Met Ala Ile Ile Thr Arg Phe Cys Leu Gly Ser Phe Asn Gly Leu Leu	
1	5
Gly Pro Ile Lys Ala Tyr Ala Met Glu Ile Phe Arg Asp Glu Tyr Gln	
	10
	15
Gly Leu Ala Leu Ser Ala Val Ser Thr Ala Trp Gly Ile Gly Leu Ile	
	20
	25
	30
Ile Gly Pro Ala Ile Gly Gly Phe Leu Ala Gln Pro Ala Lys Gln Tyr	
	35
	40
	45
Pro Ser Leu Phe Ser Gln Asp Ser Ile Phe Gly Lys Phe Pro Phe Phe	
	50
	55
	60
Leu Pro Cys Leu Ala Ile Ser Val Phe Ala Phe Leu Val Thr Ile Val	
	65
	70
	75
	80
Ser Ser Arg Ile Pro Glu Thr Leu His Asn His Lys Phe Asn Asp Asp	
	85
	90
	95
Glu Ser Tyr Asp Ala Leu Lys Asp Leu Ser Asp Asp Pro Glu Ser Asn	
	100
	105
	110
Lys Val Ala Glu Arg Asn Gly Lys Ser Ser Leu Leu Asn Asn Trp Pro	
	115
	120
	125
	130
	135
	140

Leu Ile Ser Ser Ile Ile Val Tyr Cys Val Phe Ser Leu His Asp Met
145 150 155 160
Ala Tyr Thr Glu Ile Phe Ser Leu Trp Ala Asn Ser Pro Arg Lys Tyr
165 170 175
Gly Gly Leu Gly Tyr Ser Thr Ala Asp Val Gly Ser Val Leu Ala Phe
180 185 190
Ser Gly Phe Gly Leu Leu Ile Phe Gln Leu Ser Leu Tyr Ser Tyr Ala
195 200 205
Glu Arg Leu Leu Gly Pro Ile Ile Val Thr Arg Ile Ser Gly Ser Leu
210 215 220
Ala Met Val Val Leu Ser Cys Tyr Pro Leu Ile Ala Lys Leu Ser Gly
225 230 235 240
Leu Val Leu Thr Val Thr Val Thr Ser Ala Ser Val Ala Lys Ser Val
245 250 255
Leu Gly Thr Ser Ala Ile Thr Gly Leu Phe Ile Leu Gln Asn Lys Ala
260 265 270
Val Arg Gln Asp Xaa Arg Gly Ala Ala Asn Gly Ile Ala Met Thr Ala
275 280 285
Met Ser Leu Phe Lys Ala Ile Gly Pro Ala Ala Ala Gly Ile Ile Phe
290 295 300
Ser Trp Ser Glu Lys Arg Gln Gly Ala Ala Phe Leu Pro Gly Thr Gln
305 310 315 320
Met Val Phe Phe Ile Leu Asn Val Val Leu Ala Leu Gly Val Val Leu
325 330 335
Thr Phe Lys Pro Phe Leu Ala Glu Thr Gln Gln
340 345

(2) INFORMATION FOR SEQ ID NO:112:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 324 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..324

(D) OTHER INFORMATION: / Ceres Seq. ID 1565843

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

Met Glu Ile Phe Arg Asp Glu Tyr Gln Gly Leu Ala Leu Ser Ala Val
1 5 10 15
Ser Thr Ala Trp Gly Ile Gly Leu Ile Ile Gly Pro Ala Ile Gly Gly
20 25 30
Phe Leu Ala Gln Pro Ala Lys Gln Tyr Pro Ser Leu Phe Ser Gln Asp
35 40 45
Ser Ile Phe Gly Lys Phe Pro Phe Phe Leu Pro Cys Leu Ala Ile Ser
50 55 60
Val Phe Ala Phe Leu Val Thr Ile Val Ser Arg Ile Pro Glu Thr
65 70 75 80
Leu His Asn His Lys Phe Asn Asp Asp Glu Ser Tyr Asp Ala Leu Lys
85 90 95
Asp Leu Ser Asp Asp Pro Glu Ser Asn Lys Val Ala Glu Arg Asn Gly
100 105 110
Lys Ser Ser Leu Leu Asn Asn Trp Pro Leu Ile Ser Ser Ile Ile Val
115 120 125
Tyr Cys Val Phe Ser Leu His Asp Met Ala Tyr Thr Glu Ile Phe Ser
130 135 140
Leu Trp Ala Asn Ser Pro Arg Lys Tyr Gly Gly Leu Gly Tyr Ser Thr
145 150 155 160
Ala Asp Val Gly Ser Val Leu Ala Phe Ser Gly Phe Gly Leu Leu Ile
165 170 175
Phe Gln Leu Ser Leu Tyr Ser Tyr Ala Glu Arg Leu Leu Gly Pro Ile

	180		185		190
Ile Val Thr Arg Ile Ser Gly Ser Leu Ala Met Val Val Leu Ser Cys					
	195		200		205
Tyr Pro Leu Ile Ala Lys Leu Ser Gly Leu Val Leu Thr Val Thr Val					
	210		215		220
Thr Ser Ala Ser Val Ala Lys Ser Val Leu Gly Thr Ser Ala Ile Thr					
	225		230		235
Gly Leu Phe Ile Leu Gln Asn Lys Ala Val Arg Gln Asp Xaa Arg Gly					
			245		250
Ala Ala Asn Gly Ile Ala Met Thr Ala Met Ser Leu Phe Lys Ala Ile					
			260		265
Gly Pro Ala Ala Gly Ile Ile Phe Ser Trp Ser Glu Lys Arg Gln					
			275		280
Gly Ala Ala Phe Leu Pro Gly Thr Gln Met Val Phe Phe Ile Leu Asn					
			290		295
Val Val Leu Ala Leu Gly Val Val Leu Thr Phe Lys Pro Phe Leu Ala					
			305		310
Glu Thr Gln Gln					315
					320

(2) INFORMATION FOR SEQ ID NO:113:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1108 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1108

(D) OTHER INFORMATION: / Ceres Seq. ID 1565863

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

agattcaagc atcacacaat cgagttttta gggtttttagc ggttgctctc tcggaagcca	60
gagagaagag ggaagaggaa gtctaattcc tctgcgtttt ttgcaattag ggtttttctca	120
attggaatcg aaaaatggtga cagacaagag caagaaggcg aaaaccgaag aagaaaaacgt	180
cgagcaaatc gatgcagagc ttgtcctctc aatcgaaaaa ctccaagaga tccaagacga	240
ctctgagaag ataaaatgaaa aggctagtga tgaagtgttg gaagtggagc agaaaataaa	300
ttgtataaag aaacctgttt atgacaagcg taacgagatc atcaaaaacca tccctgattt	360
ctgggttaact gottttcttga gtcaacctgc ttttagtgaa cttttgactg aagaagacca	420
aaagattttc aaatatctta gctctcttga tgttgaggat gccaaagatg tgaatctctg	480
atactctatc actttttctc tcaatcccaa tccatttttt gaagatggaa aactgacaaa	540
gactttttac tttctcgaag aagggaacac caaaatcaac gccacgccta tcaaatggaa	600
agaggggcaa ggcctggcga atggagttaa tcatgagaag aatggaaaca aacgtgcact	660
acctgaagag agctctcttta ctgggttttag tgaatgctca cacaaggagg atgttgagga	720
tgagatgcaa gacgagcagg ttgcagatat catcaaggaa gattttgtgc ccaacctctc	780
cacctacttc aacaatgacg ctgatgaaga ggactttgat ggagacgatg atggagatga	840
agaggagaaa gaaggtgact ctgatgaaga tgaatgacga gaagacgaag ttggtgagga	900
atgatggcag ggatacccgag aaaccacaty tgctttacat tcttctctat aacagagtgt	960
gtaaagtgtt gtgtgttgaa aggtKtttta attYttaagc aaaaagtggat tatgacNac	1020
aacagacaag ctttttaatt ttatttCaCc gtaaatgta tatctgtgtg taagaaacca	1080
ttttcagcct tttgttgaaa aactctgc	

(2) INFORMATION FOR SEQ ID NO:114:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 256 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..256

(D) OTHER INFORMATION: / Ceres Seq. ID 1565864

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

Met	Val	Thr	Asp	Lys	Ser	Lys	Lys	Ala	Lys	Thr	Glu	Glu	Glu	Asn	Val
1			5						10					15	
Glu	Gln	Ile	Asp	Ala	Glu	Leu	Val	Leu	Ser	Ile	Glu	Lys	Leu	Gln	Glu
			20					25					30		
Ile	Gln	Asp	Asp	Leu	Glu	Lys	Ile	Asn	Glu	Lys	Ala	Ser	Asp	Glu	Val
			35				40				45				
Leu	Glu	Val	Glu	Gln	Lys	Tyr	Asn	Val	Ile	Arg	Lys	Pro	Val	Tyr	Asp
			50			55					60				
Lys	Arg	Asn	Glu	Ile	Ile	Lys	Thr	Ile	Pro	Asp	Phe	Thr	Leu	Thr	Ala
			65		70				75					80	
Phe	Leu	Ser	His	Pro	Ala	Leu	Gly	Glu	Leu	Thr	Glu	Glu	Asp	Gln	
			85					90					95		
Lys	Ile	Phe	Lys	Tyr	Leu	Ser	Ser	Leu	Asp	Val	Glu	Asp	Ala	Lys	Asp
			100					105					110		
Val	Lys	Ser	Gly	Tyr	Ser	Ile	Thr	Phe	Ser	Phe	Asn	Pro	Asn	Pro	Phe
			115				120						125		
Phe	Glu	Asp	Gly	Lys	Leu	Thr	Lys	Thr	Phe	Thr	Phe	Leu	Glu	Glu	Gly
			130			135					140				
Thr	Thr	Lys	Ile	Thr	Ala	Thr	Pro	Ile	Lys	Trp	Lys	Glu	Gly	Lys	Gly
			145			150					155				160
Leu	Ala	Asn	Gly	Val	Asn	His	Glu	Lys	Asn	Gly	Asn	Lys	Arg	Ala	Leu
			165					170						175	
Pro	Glu	Glu	Ser	Phe	Phe	Thr	Trp	Phe	Ser	Asp	Ala	Gln	His	Lys	Glu
			180					185					190		
Asp	Val	Glu	Asp	Glu	Met	Gln	Asp	Glu	Gln	Val	Ala	Asp	Ile	Ile	Lys
			195				200					205			
Glu	Asp	Leu	Trp	Pro	Asn	Pro	Leu	Thr	Tyr	Phe	Asn	Asn	Asp	Ala	Asp
			210			215					220				
Glu	Glu	Asp	Phe	Asp	Gly	Asp	Asp	Asp	Gly	Asp	Glu	Glu	Glu	Lys	Glu
			225			230				235				240	
Gly	Asp	Ser	Asp	Glu	Asp	Asp	Asp	Glu	Glu	Asp	Glu	Val	Gly	Glu	Glu
			245					250						255	

(2) INFORMATION FOR SEQ ID NO:115:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1710 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -

- (B) LOCATION: 1..1710

- (D) OTHER INFORMATION: / Ceres Seq. ID 1565871

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

atgcaacatt	ataaaatatt	Ttattttcat	aaccacCccc	gatatggctg	ctccacaaaa	60
gaaaccaggc	ctaagtaacg	tggagctact	ttgtaattat	aaagatttat	tgtttcccat	120
aaactggtta	aatgatttta	gaaactaaag	taaaatgagc	ttgacactag	agtttctgct	180
tcttctgatt	gtacttatct	tgagtcacca	tgctcattct	ggctctattg	tcaaatctct	240
tcctggtttt	gaaggccccc	ttccttttga	actcgaaacc	gggtacattg	gtattggtga	300
ggaagaggaa	gtgcaattat	tctactattt	catcaaatct	gagaagaatc	cagaagaaga	360
ccctctcttt	ctatggttaa	gtggaggacc	tggatgttcc	tcctttactg	gcctctcttt	420
tgagaatgga	coggtggcct	tgaagtgcga	ggttttacaat	ggaagtgttc	catcttttgt	480
ctctactaca	tattcatgga	caaagatggc	gaacataata	ttcttggatc	agccagttgg	540
atctggcttc	tcctattcaa	gaactccact	tggtgataaa	attagtgaca	ctgggtgaagt	600
taagaggatt	tatgagtttc	ttcaaaagtg	gttaagcaaa	catcaacaat	ttttttccaa	660
ccctttttac	gttgggtggag	attcttatto	aggtatgatt	gttccacccc	tagttcaaga	720
aatcggaaaa	ggtagttctg	ttaattcata	tcaatcaatc	cccatcacct	tttcttgtaa	780
tattgtttta	ttgtctgtct	ctcaataatt	aacaatatat	acaatgatgc	aggaaattat	840

```
caaaaaaatc tacaggttgt agatatattat ttgttttotta ttttttggta tttaaaaaaa    900
tattgaagat taatagtaat atgtttcttac gaaaataggg ttatatcttc ggaaccgga    960
taacagatac tgaactctga caaaactatc agattccata tgctcatgga atggcattaa    1020
tcctctgatga actatacaag tcaatggaga gaactctgcaa aggaaattat gtgaaagtgg    1080
attcacttaa cacaanaatgc tataaactaa tcaaagatta tcaaaagtgt attcataaac    1140
tgaataagta tcatatatta ttacctgact gcgataatac atctcctgat tgctttgtaa    1200
ttatataaggt atactctcat aaccttttgg gccacaaca agagcgctcg cgaagctctg    1260
caagtcaata agtggtgacc atgatatgat ggtgccttct cttgcaactc aagcctggat    1320
aagatctctc aattattcca tcaactgatga ttggaagcct tggatgataa acgatcaaat    1380
tgctggatac acgagaagtt attccaataa gatgacattt gctactatca aagcaagtct    1440
tcctttgtcca acttaattatt tgtattgtcc ttagactgca ataaaaaaga ctttttttta    1500
attgttttga gttttgtttta tttatttttt tgttaaaggg aagtgggaac acagcagagt    1560
ataaaccaaa agagacctct atcatgttca aaagatggat cagtggccag cctttgtaaa    1620
agaggatgat ggtctttggc tatgtagaat aaaactatgt aacataaaaa atgttttgtat    1680
acaatataat catctacttg gtaattaaat
```

(2) INFORMATION FOR SEQ ID NO:116:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 211 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..211

(D) OTHER INFORMATION: / Ceres Seq. ID 1565872

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

```
Met Ser Leu Thr Leu Glu Phe Leu Leu Leu Ile Val Leu Ile Leu
1 5 10 15
Ser His His Ala His Ser Gly Ser Ile Val Lys Phe Leu Pro Gly Phe
20 25 30
Glu Gly Pro Leu Pro Phe Glu Leu Glu Thr Gly Tyr Ile Gly Ile Gly
35 40 45
Glu Glu Glu Glu Val Gln Leu Phe Tyr Tyr Phe Ile Lys Ser Glu Lys
50 55 60
Asn Pro Glu Glu Asp Pro Leu Leu Leu Trp Leu Ser Gly Gly Pro Gly
65 70 75 80
Cys Ser Ser Leu Thr Gly Leu Leu Phe Glu Asn Gly Pro Val Ala Leu
85 90 95
Lys Phe Glu Val Tyr Asn Gly Ser Val Pro Ser Leu Val Ser Thr Thr
100 105 110
Tyr Ser Trp Thr Lys Met Ala Asn Ile Ile Phe Leu Asp Gln Pro Val
115 120 125
Gly Ser Gly Phe Ser Tyr Ser Arg Thr Pro Leu Val Asp Lys Ile Ser
130 135 140
Asp Thr Gly Glu Val Lys Arg Ile Tyr Glu Phe Leu Gln Lys Trp Leu
145 150 155 160
Ser Lys His Gln Gln Phe Phe Ser Asn Pro Phe Tyr Val Gly Gly Asp
165 170 175
Ser Tyr Ser Gly Met Ile Val Pro Pro Leu Val Gln Glu Ile Gly Lys
180 185 190
Gly Met Phe Val Asn Ser Tyr Gln Ser Ile Pro Ile His Phe Ser Trp
195 200 205
Asn Ile Val
210
```

(2) INFORMATION FOR SEQ ID NO:117:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1673 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1673

(D) OTHER INFORMATION: / Ceres Seq. ID 1565880

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

aatattaatt	tcttcaatta	accttgataa	gagttaaaaa	agtaaaaaac	ctcgagaaga	60
gtgtgagctg	tgggtcaacac	ttgagagggc	gcacgatgag	ctccatattg	gacgttgcaa	120
tgttgatggt	agcttttggt	gtttgtgagg	tcagccactg	gctttaccga	tgggtcaaac	180
ctaagtgcgc	tggcaagtta	ccacctggat	cgatgggttt	tccaattcatt	ggagagactc	240
tcgattttct	taagccttgt	ggagtcgaag	gtatcccaac	ctttgtccaag	aagaggatga	300
taagtgatgt	gcggttgttt	gcaacaacaa	tttttgttcc	caaaacccgt	gtttcgacag	360
atccggatgt	gatccaccag	attttccggc	aagagaacac	gtctttttgag	ctaggctatc	420
cagacataatt	tgtgaaagta	tttggaagaa	ataatttgtt	cttgaaggaa	gtgttctatc	480
acaagtacct	ccaaaaaact	actatgcaaa	tctctggctc	cgaggggttg	aagcaaacaa	540
tgttagggaa	catggacaaa	gcaacccgcg	accatattag	gtccatttgt	agccaggggg	600
gcttcaatgt	tcgtaagaaa	gttgaaaact	tggtagttag	gtacatgaca	ccaaagctga	660
taagtaacct	taaacaccag	acgcaatcaa	agcttataga	taattctaac	gccttcaatc	720
ttgatttggt	taagtctctt	ttaagactct	ctacttgcaa	agctgtccac	aaagccctca	780
agtcacgtga	agaagctatc	caggtgatga	aagacgttct	catgatgaga	aaagagacgc	840
gagagaaact	agaagacttc	tctaacacgc	tctagaagaa	actggagaaa	gacggtagct	900
ttttcgacca	aggatcggtc	ataaatctca	tcttctcttc	ggcgtttgcc	ttgagagaag	960
gtacctctag	tgtactctgt	tggccgtgta	agttcatatc	caaaagcccg	aaagtgtctg	1020
cagagctcaa	gcgtgagcat	aaggcaattg	tagacaacag	aaaagataag	gaagctggag	1080
ttagctggga	agaatataga	cacaaataga	ctttcaccaa	gatgggttag	aatgaggtGc	1140
ttgccttagc	aaacacgacc	cccttgttgt	ttcgaaagcg	gttgcaagat	gttgagatca	1200
aaggataatc	aattccgggt	ggttggaatt	tggtGgttgc	accttcagcg	gttcaattttg	1260
atctcgcaat	ctatgagaac	ccattttgag	ttaatccatg	gagatgggag	gggaaagaaa	1320
tgattttggg	atctaaaaac	tctatggcgt	ttggatatgg	agttagactt	tgtgtaggtg	1380
cagagttttc	gcggtctcaa	atggcaatct	tctccatcat	ctttgtggca	tattacgatt	1440
tctcaatggt	ccaagactcc	gagatcattc	gttcacattt	ccatcaattc	accaagagtc	1500
tgcttataaa	catctctcag	tctctaccac	agtgaaacat	gcatggatct	tccaatattt	1560
aataatcaga	tcattatatg	caataatctc	atttctGct	tccgcaaaat	ctctggagtc	1620
tttttatatg	taatatcgca	tctctataat	ttttaaaaag	tatctattct	gcc	

(2) INFORMATION FOR SEQ ID NO:118:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 479 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..479

(D) OTHER INFORMATION: / Ceres Seq. ID 1565881

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

Met	Ser	Ser	Ile	Trp	Asp	Val	Ala	Met	Leu	Met	Val	Ala	Leu	Val	Val
1				5					10				15		
Val	Arg	Ile	Ser	His	Trp	Leu	Tyr	Arg	Trp	Ser	Asn	Pro	Lys	Cys	Pro
				20				25					30		
Gly	Lys	Leu	Pro	Pro	Gly	Ser	Met	Gly	Phe	Pro	Ile	Ile	Gly	Glu	Thr
				35			40				45				
Leu	Asp	Phe	Phe	Lys	Pro	Cys	Gly	Val	Glu	Gly	Ile	Pro	Thr	Phe	Val
				50			55				60				
Lys	Lys	Arg	Met	Ile	Arg	Tyr	Gly	Pro	Leu	Phe	Arg	Thr	Asn	Ile	Phe
				65			70			75			80		
Gly	Ser	Lys	Thr	Val	Val	Ser	Thr	Asp	Pro	Asp	Val	Ile	His	Gln	Ile
				85			90					95			
Phe	Arg	Gln	Glu	Asn	Thr	Ser	Phe	Glu	Leu	Gly	Tyr	Pro	Asp	Ile	Phe
				100			105					110			
Val	Lys	Val	Phe	Gly	Lys	Asp	Asn	Leu	Phe	Leu	Lys	Glu	Val	Phe	Ile

		115						120				125					
His	Lys	Tyr	Leu	Gln	Lys	Ile	Thr	Met	Gln	Ile	Leu	Gly	Ser	Glu	Gly		
	130					135					140						
Leu	Lys	Gln	Thr	Met	Leu	Gly	Asn	Met	Asp	Lys	Ala	Thr	Arg	Asp	His		
145					150					155					160		
Ile	Arg	Ser	Ile	Ala	Ser	Gln	Gly	Ser	Phe	Asn	Val	Arg	Lys	Glu	Val		
				165					170					175			
Glu	Asn	Leu	Val	Val	Ala	Tyr	Met	Thr	Pro	Lys	Leu	Ile	Ser	Asn	Leu		
			180					185					190				
Lys	Pro	Glu	Thr	Gln	Ser	Lys	Leu	Ile	Asp	Asn	Leu	Asn	Ala	Phe	Asn		
		195						200				205					
Leu	Asp	Trp	Phe	Lys	Ser	Phe	Leu	Arg	Leu	Ser	Thr	Trp	Lys	Ala	Val		
	210					215					220						
Thr	Lys	Ala	Leu	Lys	Ser	Arg	Glu	Glu	Ala	Ile	Gln	Val	Met	Lys	Asp		
225					230					235					240		
Val	Leu	Met	Met	Arg	Lys	Glu	Thr	Arg	Glu	Lys	Gln	Glu	Asp	Phe	Leu		
				245					250					255			
Asn	Thr	Leu	Leu	Glu	Glu	Leu	Glu	Lys	Asp	Gly	Ser	Phe	Phe	Asp	Gln		
			260					265					270				
Gly	Ser	Ala	Ile	Asn	Leu	Ile	Phe	Leu	Leu	Ala	Phe	Ala	Leu	Arg	Glu		
		275					280					285					
Gly	Thr	Ser	Ser	Cys	Thr	Ala	Leu	Ala	Val	Lys	Phe	Ile	Ser	Lys	Asp		
	290					295					300						
Pro	Lys	Val	Leu	Ala	Glu	Leu	Lys	Arg	Glu	His	Lys	Ala	Ile	Val	Asp		
305					310					315					320		
Asn	Arg	Lys	Asp	Lys	Glu	Ala	Gly	Val	Ser	Trp	Glu	Glu	Tyr	Arg	His		
				325					330					335			
Asn	Met	Thr	Phe	Thr	Asn	Met	Val	Ser	Asn	Glu	Val	Leu	Arg	Leu	Ala		
			340					345					350				
Asn	Thr	Thr	Pro	Leu	Leu	Phe	Arg	Lys	Ala	Val	Gln	Asp	Val	Glu	Ile		
		355					360					365					
Lys	Gly	Tyr	Thr	Ile	Pro	Ala	Gly	Trp	Ile	Val	Ala	Val	Ala	Pro	Ser		
	370				375					380							
Ala	Val	His	Phe	Asp	Pro	Ala	Ile	Tyr	Glu	Asn	Pro	Phe	Glu	Phe	Asn		
385					390					395					400		
Pro	Trp	Arg	Trp	Glu	Gly	Lys	Glu	Met	Ile	Trp	Gly	Ser	Lys	Thr	Phe		
				405					410					415			
Met	Ala	Phe	Gly	Gly	Tyr	Gly	Val	Arg	Leu	Cys	Val	Gly	Ala	Glu	Phe		
			420					425					430				
Arg	Leu	Gln	Met	Ala	Ile	Phe	Leu	His	His	Leu	Val	Ala	Tyr	Tyr	Asp		
		435					440					44					

(2) INFORMATION FOR SEO ID NO:119:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 471 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..471

(D) OTHER INFORMATION: / Ceres Seq. ID 1565882

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

Met	Leu	Met	Val	Ala	Leu	Val	Val	Val	Arg	Ile	Ser	His	Trp	Leu	Tyr
1				5					10					15	
Arg	Trp	Ser	Asn	Pro	Lys	Cys	Pro	Gly	Lys	Leu	Pro	Pro	Gly	Ser	Met
			20					25					30		

Gly Phe Pro Ile Ile Gly Glu Thr Leu Asp Phe Phe Lys Pro Cys Gly
35 40 45
Val Glu Gly Ile Pro Thr Phe Val Lys Lys Arg Met Ile Arg Tyr Gly
50 55 60
Pro Leu Phe Arg Thr Asn Ile Phe Gly Ser Lys Thr Val Val Ser Thr
65 70 75
Asp Pro Asp Val Ile His Gln Ile Phe Arg Gln Glu Asn Thr Ser Phe
85 90 95
Glu Leu Gly Tyr Pro Asp Ile Phe Val Lys Val Phe Gly Lys Asp Asn
100 105 110
Leu Phe Leu Lys Glu Val Phe Ile His Lys Tyr Leu Gln Lys Ile Thr
115 120 125
Met Gln Ile Leu Gly Ser Glu Gly Leu Lys Gln Thr Met Leu Gly Asn
130 135 140
Met Asp Lys Ala Thr Arg Asp His Ile Arg Ser Ile Ala Ser Gln Gly
145 150 155
Ser Phe Asn Val Arg Lys Glu Val Glu Asn Leu Val Val Ala Tyr Met
165 170 175
Thr Pro Lys Leu Ile Ser Asn Leu Lys Pro Glu Thr Gln Ser Lys Leu
180 185 190
Ile Asp Asn Leu Asn Ala Phe Asn Leu Asp Trp Phe Lys Ser Phe Leu
195 200 205
Arg Leu Ser Thr Trp Lys Ala Val Thr Lys Ala Leu Lys Ser Arg Glu
210 215 220
Glu Ala Ile Gln Val Met Lys Asp Val Leu Met Met Arg Lys Glu Thr
225 230 235
Arg Glu Lys Gln Glu Asp Phe Leu Asn Thr Leu Leu Glu Glu Leu Glu
245 250 255
Lys Asp Gly Ser Phe Phe Asp Gln Gly Ser Ala Ile Asn Leu Ile Phe
260 265 270
Leu Leu Ala Phe Ala Leu Arg Glu Gly Thr Ser Ser Cys Thr Ala Leu
275 280 285
Ala Val Lys Phe Ile Ser Lys Asp Pro Lys Val Leu Ala Glu Leu Lys
290 295 300
Arg Glu His Lys Ala Ile Val Asp Asn Arg Lys Asp Lys Glu Ala Gly
305 310 315
Val Ser Trp Glu Glu Tyr Arg His Asn Met Thr Phe Thr Asn Met Val
325 330 335
Ser Asn Glu Val Leu Arg Leu Ala Asn Thr Thr Pro Leu Leu Phe Arg
340 345 350
Lys Ala Val Gln Asp Val Glu Ile Lys Gly Tyr Thr Ile Pro Ala Gly
355 360 365
Trp Ile Val Ala Val Ala Pro Ser Ala Val His Phe Asp Pro Ala Ile
370 375 380
Tyr Glu Asn Pro Phe Glu Phe Asn Pro Trp Arg Trp Glu Gly Lys Glu
385 390 395
Met Ile Trp Gly Ser Lys Thr Phe Met Ala Phe Gly Tyr Gly Val Arg
405 410 415
Leu Cys Val Gly Ala Glu Phe Ser Arg Leu Gln Met Ala Ile Phe Leu
420 425 430
His His Leu Val Ala Tyr Tyr Asp Phe Ser Met Val Gln Asp Ser Glu
435 440 445
Ile Ile Arg Ser Pro Phe His Gln Tyr Thr Lys Asp Leu Leu Ile Asn
450 455 460
Ile Ser Gln Ser Pro Thr Lys
465 470

(2) INFORMATION FOR SEQ ID NO:120:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 469 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..469
 (D) OTHER INFORMATION: / Ceres Seq. ID 1565883
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

Met	Val	Ala	Leu	Val	Val	Val	Arg	Ile	Ser	His	Trp	Leu	Tyr	Arg	Trp
1			5					10					15		
Ser	Asn	Pro	Lys	Cys	Pro	Gly	Lys	Leu	Pro	Gly	Ser	Met	Gly	Phe	
			20					25				30			
Pro	Ile	Ile	Gly	Glu	Thr	Leu	Asp	Phe	Phe	Lys	Pro	Cys	Gly	Val	Glu
			35				40					45			
Gly	Ile	Pro	Thr	Phe	Val	Lys	Arg	Met	Ile	Arg	Tyr	Gly	Pro	Leu	
			50			55				60					
Phe	Arg	Thr	Asn	Ile	Phe	Gly	Ser	Lys	Thr	Val	Ser	Thr	Asp	Pro	
65				70				75					80		
Asp	Val	Ile	His	Gln	Ile	Phe	Arg	Gln	Glu	Asn	Thr	Ser	Phe	Glu	Leu
			85					90					95		
Gly	Tyr	Pro	Asp	Ile	Phe	Val	Lys	Val	Phe	Gly	Lys	Asp	Asn	Leu	Phe
			100					105					110		
Leu	Lys	Glu	Val	Phe	Ile	His	Lys	Tyr	Leu	Gln	Lys	Ile	Thr	Met	Gln
			115				120					125			
Ile	Leu	Gly	Ser	Glu	Gly	Leu	Lys	Gln	Thr	Met	Leu	Gly	Asn	Met	Asp
			130			135				140					
Lys	Ala	Thr	Arg	Asp	His	Ile	Arg	Ser	Ile	Ala	Ser	Gln	Gly	Ser	Phe
145				150				155					160		
Asn	Val	Arg	Lys	Glu	Val	Glu	Asn	Leu	Val	Val	Ala	Tyr	Met	Thr	Pro
			165					170					175		
Lys	Leu	Ile	Ser	Asn	Leu	Lys	Pro	Glu	Thr	Gln	Ser	Lys	Leu	Ile	Asp
			180				185					190			
Asn	Leu	Asn	Ala	Phe	Asn	Leu	Asp	Trp	Phe	Lys	Ser	Phe	Leu	Arg	Leu
			195				200					205			
Ser	Thr	Trp	Lys	Ala	Val	Thr	Lys	Ala	Leu	Lys	Ser	Arg	Glu	Glu	Ala
			210			215						220			
Ile	Gln	Val	Met	Lys	Asp	Val	Leu	Met	Met	Arg	Lys	Glu	Thr	Arg	Glu
225				230				235					240		
Lys	Gln	Glu	Asp	Phe	Leu	Asn	Thr	Leu	Leu	Glu	Glu	Leu	Glu	Lys	Asp
			245					250					255		
Gly	Ser	Phe	Phe	Asp	Gln	Gly	Ser	Ala	Ile	Asn	Leu	Ile	Phe	Leu	Leu
			260			265						270			
Ala	Phe	Ala	Ileu	Arg	Glu	Gly	Thr	Ser	Ser	Cys	Thr	Ala	Leu	Ala	Val
			275				280					285			
Lys	Phe	Ile	Ser	Lys	Asp	Pro	Lys	Val	Leu	Ala	Glu	Leu	Lys	Arg	Glu
			290			295					300				
His	Lys	Ala	Ile	Val	Asp	Asn	Arg	Lys	Asp	Lys	Glu	Ala	Gly	Val	Ser
305				310				315					320		
Trp	Glu	Glu	Tyr	Arg	His	Asn	Met	Thr	Phe	Thr	Asn	Met	Val	Ser	Asn
			325					330					335		
Glu	Val	Leu	Arg	Leu	Ala	Asn	Thr	Thr	Pro	Leu	Leu	Phe	Arg	Lys	Ala
			340				345					350			
Val	Gln	Asp	Val	Glu	Ile	Lys	Gly	Tyr	Thr	Ile	Pro	Ala	Gly	Trp	Ile
			355			360					365				
Val	Ala	Val	Ala	Pro	Ser	Ala	Val	His	Phe	Asp	Pro	Ala	Ile	Tyr	Glu
			370			375				380					
Asn	Pro	Phe	Glu	Phe	Asn	Pro	Trp	Arg	Trp	Glu	Lys	Glu	Met	Ile	
385				390				395					400		
Trp	Gly	Ser	Lys	Thr	Phe	Met	Ala	Phe	Gly	Tyr	Gly	Val	Arg	Leu	Cys
			405					410					415		
Val	Gly	Ala	Glu	Phe	Ser	Arg	Leu	Gln	Met	Ala	Ile	Phe	Leu	His	His
			420				425					430			

Leu Val Ala Tyr Tyr Asp Phe Ser Met Val Gln Asp Ser Glu Ile Ile
435 440 445
Arg Ser Pro Phe His Gln Tyr Thr Lys Asp Leu Leu Ile Asn Ile Ser
450 455 460
Gln Ser Pro Thr Lys
465

(2) INFORMATION FOR SEQ ID NO:121:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2253 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..2253

(D) OTHER INFORMATION: / Ceres Seq. ID 1565898

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

attgggttct	ttctctcttt	ctccagatt	catcaatccc	tctcgtacc	gcgagagagt	60
aacaactcac	cggacgtttc	aaatccatcc	tccgataaact	atattcgttt	cgttagatct	120
agatctgagc	gtcgttgaga	gattttctgg	atctgtgata	cgttccaggga	aacatggcgga	180
cgatgaaaag	tttgataggt	ctgataaaca	aaatccagag	ggcgtgtact	gtcctcggag	240
atcatggcgg	tgaaggaatg	tcgctttggg	aagctctccc	aaccgtcgt	gtcgttggtg	300
gccagagttc	gcgaaaatct	tcagttctag	aaagtgtgtg	gggaagagat	ttctgcctc	360
gtggatctgg	tatcgttaca	aggaggccat	tggtgttgca	acttcataag	actgaagacg	420
ggacaactga	tgacgtcgag	ttcttctcat	ctcctaagaa	gagatttgc	gattttgctg	480
ctgtgcggaa	agaaattgag	gatgaaactg	atcgtattac	tggaagatca	aaacaactct	540
caaacatctc	aattcagctg	agcataatct	ctcctaattg	gtttaaactg	acgctcatag	600
attctccggg	tttgaccaag	gtcgtgtgag	atggcaaac	ggaagattt	gtccaagaca	660
ttgataaata	ggctccgtct	tatgttgaaa	agccaaattg	catcatattg	gctattttct	720
cagcaaatca	agatattgct	acctcagatg	ctataaaact	tgttagagaa	gttagaccta	780
caggcgaaa	gacttttggg	gttgcaacca	agcttgatat	catggataaa	ggaacagatt	840
gtctagatgt	tottgagggg	aggtcatacc	gtttgcaaca	tccttgggtt	ggaattgtga	900
atcgttcaca	agctgatatt	aataagagag	tcgatatgat	tgctgcacgt	agaaaagagc	960
aagaatatct	tgaacaagc	ccggaatacg	ggcaacttag	cagtagaatg	ggatcagagt	1020
atctagcaaa	actcttgtct	cagcaacttag	agactgttat	caggcgaaaa	atccccagta	1080
tgtgtgcttt	gatacaacaa	agcatcgatg	agataaatgc	agaacttgat	aggattggga	1140
gaccacttgc	agtagattca	ggagcccaac	tttacacaa	tttgaaactc	tgccgggcat	1200
ttgatctgtg	ctttaaggag	gacttgatg	gaggacgacc	tggtggagac	cgaatttatg	1260
gagtttttgc	ccatcaatta	ccagcagcct	taaaagaaat	tcctcttgat	cgacattctg	1320
ctacaaaata	tgttcagaag	gtgttttcag	aagcagatgg	ttatcagcgc	gctattttat	1380
ctcttgaaca	aggatagaca	aggctcattg	atggatccat	aagctatttc	aaaggaccag	1440
ctgaagccac	tgctgatgca	gtgcatttcg	tattgaagga	gctggtcaga	aagcgaattt	1500
cagaaaacaga	ggaactgaag	cggtttccga	ctctagcaag	cgatatagca	gctgctgcga	1560
atgaagctct	tgaagagctc	agagacgaaa	gcaggaaaa	ggttttgcgt	ctggttgata	1620
tggaactctg	ctacctcagc	gttgagttct	tcaggaaact	ccatctgaa	cccgagaaag	1680
agaaaacaaa	cccaaggaat	gccccagcac	caaacgcaga	ccctactctc	gataatcact	1740
tcagaagagt	cggatccaac	gBgagtgcat	acataaacat	ggtctgcgac	acatttgaga	1800
actctctctc	caaaagctgc	gtttactgcc	aagttagaga	agctaaagaa	tcgcttctca	1860
acttctctta	cgtctcaagt	ggcaggaaga	agaagagaga	gtcgggtgct	atgttggaag	1920
aagaccacaga	cgctgatgga	cgaagaggaa	ccttagotaa	acgggtagag	ctttacaaac	1980
aagcttagaga	cgacatcgat	cgagtggctt	ggaaagtaag	gggttttgcta	agacataattc	2040
ttttatattg	taattttctt	gtctgtgtgg	gcacactgca	ttataaatga	tatgtttgga	2100
gttctaaact	ccagctacata	caaacataca	cgcgactact	catgtttttc	tggttgccta	2160
attttatcca	accatttccc	actttttttt	gggtgtgtatc	ttcgattctt	gaatactggg	2220
ttttagaaca	gttaagacat	attttgaagt	cgc			

(2) INFORMATION FOR SEQ ID NO:122:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 614 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:

(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..614
(D) OTHER INFORMATION: / Ceres Seq. ID 1565899
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

Met	Ala	Thr	Met	Lys	Ser	Leu	Ile	Gly	Leu	Ile	Asn	Lys	Ile	Gln	Arg	
1				5					10					15		
Ala	Cys	Thr	Val	Leu	Gly	Asp	His	Gly	Gly	Glu	Gly	Met	Ser	Leu	Trp	
			20					25					30			
Glu	Ala	Leu	Pro	Thr	Val	Ala	Val	Val	Gly	Gln	Ser	Ser	Ser	Gly	Lys	
		35				40					45					
Ser	Ser	Val	Leu	Glu	Ser	Val	Val	Gly	Arg	Asp	Phe	Leu	Pro	Arg	Gly	
	50				55					60						
Ser	Gly	Ile	Val	Thr	Arg	Arg	Pro	Leu	Val	Leu	Gln	Leu	His	Lys	Thr	
65				70					75					80		
Glu	Asp	Gly	Thr	Thr	Glu	Tyr	Ala	Glu	Phe	Leu	His	Ala	Pro	Lys	Lys	
			85					90						95		
Arg	Phe	Ala	Asp	Phe	Ala	Ala	Val	Arg	Lys	Glu	Ile	Glu	Asp	Glu	Thr	
		100						105					110			
Asp	Arg	Ile	Thr	Gly	Lys	Ser	Lys	Gln	Ile	Ser	Asn	Ile	Pro	Ile	Gln	
		115					120					125				
Leu	Ser	Ile	Tyr	Ser	Pro	Asn	Val	Val	Asn	Leu	Thr	Leu	Ile	Asp	Leu	
	130				135						140					
Pro	Gly	Leu	Thr	Lys	Val	Ala	Val	Asp	Gly	Gln	Pro	Glu	Ser	Ile	Val	
	145			150					155					160		
Gln	Asp	Ile	Glu	Asn	Met	Val	Arg	Ser	Tyr	Val	Glu	Lys	Pro	Asn	Cys	
		165						170						175		
Ile	Ile	Leu	Ala	Ile	Ser	Pro	Ala	Asn	Gln	Asp	Ile	Ala	Thr	Ser	Asp	
	180						185					190				
Ala	Ile	Lys	Leu	Ala	Arg	Glu	Val	Asp	Pro	Thr	Gly	Glu	Arg	Thr	Phe	
	195						200					205				
Gly	Val	Ala	Thr	Lys	Leu	Asp	Ile	Met	Asp	Lys	Gly	Thr	Asp	Cys	Leu	
	210				215						220					
Asp	Val	Leu	Glu	Gly	Arg	Ser	Tyr	Arg	Leu	Gln	His	Pro	Trp	Val	Gly	
225					230				235					240		
Ile	Val	Asn	Arg	Ser	Gln	Ala	Asp	Ile	Asn	Lys	Arg	Val	Asp	Met	Ile	
		245						250						255		
Ala	Ala	Arg	Arg	Lys	Glu	Gln	Glu	Tyr	Phe	Glu	Thr	Ser	Pro	Glu	Tyr	
		260					265						270			
Gly	His	Leu	Ala	Ser	Arg	Met	Gly	Ser	Glu	Tyr	Leu	Ala	Lys	Leu	Leu	
	275					280						285				
Ser	Gln	His	Leu	Glu	Thr	Val	Ile	Arg	Gln	Lys	Ile	Pro	Ser	Ile	Val	
	290				295						300					
Ala	Leu	Ile	Asn	Lys	Ser	Ile	Asp	Glu	Ile	Asn	Ala	Glu	Leu	Asp	Arg	
	305			310					315					320		
Ile	Gly	Arg	Pro	Ile	Ala	Val	Asp	Ser	Gly	Ala	Gln	Leu	Tyr	Thr	Ile	
		325						330						335		
Leu	Glu	Leu	Cys	Arg	Ala	Phe	Asp	Arg	Val	Phe	Lys	Glu	His	Leu	Asp	
		340					345					350				
Gly	Gly	Arg	Pro	Gly	Gly	Asp	Arg	Ile	Tyr	Gly	Val	Phe	Asp	His	Gln	
	355					360						365				
Leu	Pro	Ala	Ala	Leu	Lys	Lys	Leu	Pro	Phe	Asp	Arg	His	Leu	Ser	Thr	
	370				375						380					
Lys	Asn	Val	Gln	Lys	Val	Val	Ser	Glu	Ala	Asp	Gly	Tyr	Gln	Pro	His	
385				390					395					400		
Leu	Ile	Ala	Pro	Glu	Gln	Gly	Tyr	Arg	Arg	Leu	Ile	Asp	Gly	Ser	Ile	
		405						410					415			
Ser	Tyr	Phe	Lys	Gly	Pro	Ala	Glu	Ala	Thr	Val	Asp	Ala	Val	His	Phe	
		420					425						430			

Val Leu Lys Glu Leu Val Arg Lys Ser Ile Ser Glu Thr Glu Glu Leu
435 440 445
Lys Arg Phe Pro Thr Leu Ala Ser Asp Ile Ala Ala Ala Asn Glu
450 455 460
Ala Leu Glu Arg Phe Arg Asp Glu Ser Arg Lys Thr Val Leu Arg Leu
465 470 475 480
Val Asp Met Glu Ser Ser Tyr Leu Thr Val Glu Phe Phe Arg Lys Leu
485 490 495
His Leu Glu Pro Glu Lys Glu Lys Pro Asn Pro Arg Asn Ala Pro Ala
500 505 510
Pro Asn Ala Asp Pro Tyr Ser Asp Asn His Phe Arg Lys Ile Gly Ser
515 520 525
Asn Xaa Ser Ala Tyr Ile Asn Met Val Cys Asp Thr Leu Arg Asn Ser
530 535 540
Leu Pro Lys Ala Val Val Tyr Cys Gln Val Arg Glu Ala Lys Arg Ser
545 550 555 560
Leu Leu Asn Phe Phe Tyr Ala Gln Val Gly Arg Lys Glu Lys Glu Lys
565 570 575
Leu Gly Ala Met Leu Asp Glu Asp Pro Gln Leu Met Glu Arg Arg Gly
580 585 590
Thr Leu Ala Lys Arg Leu Glu Leu Tyr Lys Gln Ala Arg Asp Asp Ile
595 600 605
Asp Ala Val Ala Trp Lys
610

(2) INFORMATION FOR SEQ ID NO:123:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 611 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..611

(D) OTHER INFORMATION: / Ceres Seq. ID 1565900

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

Met Lys Ser Leu Ile Gly Leu Ile Asn Lys Ile Gln Arg Ala Cys Thr
1 5 10 15
Val Leu Gly Asp His Gly Gly Glu Gly Met Ser Leu Trp Glu Ala Leu
20 25 30
Pro Thr Val Ala Val Val Gly Gly Gln Ser Ser Gly Lys Ser Ser Val
35 40 45
Leu Glu Ser Val Val Gly Arg Asp Phe Leu Pro Arg Gly Ser Gly Ile
50 55 60
Val Thr Arg Arg Pro Leu Val Leu Gln Leu His Lys Thr Glu Asp Gly
65 70 75 80
Thr Thr Glu Tyr Ala Glu Phe Leu His Ala Pro Lys Lys Arg Phe Ala
85 90 95
Asp Phe Ala Ala Val Arg Lys Glu Ile Glu Asp Glu Thr Asp Arg Ile
100 105 110
Thr Gly Lys Ser Lys Gln Ile Ser Asn Ile Pro Ile Gln Leu Ser Ile
115 120 125
Tyr Ser Pro Asn Val Val Asn Leu Thr Leu Ile Asp Leu Pro Gly Leu
130 135 140
Thr Lys Val Ala Val Asp Gly Gln Pro Glu Ser Ile Val Gln Asp Ile
145 150 155 160
Glu Asn Met Val Arg Ser Tyr Val Glu Lys Pro Asn Cys Ile Ile Leu
165 170 175
Ala Ile Ser Pro Ala Asn Gln Asp Ile Ala Thr Ser Asp Ala Ile Lys
180 185 190
Leu Ala Arg Glu Val Asp Pro Thr Gly Glu Arg Thr Phe Val Ala

195	200	205
Thr Lys Leu Asp Ile Met Asp Lys Gly Thr Asp Cys Leu Asp Val Leu		
210	215	220
Glu Gly Arg Ser Tyr Arg Leu Gln His Pro Trp Val Gly Ile Val Asn		
225	230	235
Arg Ser Gln Ala Asp Ile Asn Lys Arg Val Asp Met Ile Ala Ala Arg		
245	250	255
Arg Lys Glu Gln Glu Tyr Phe Glu Thr Ser Pro Glu Tyr Gly His Leu		
260	265	270
Ala Ser Arg Met Gly Ser Glu Tyr Leu Ala Lys Leu Leu Ser Gln His		
275	280	285
Leu Glu Thr Val Ile Arg Gln Lys Ile Pro Ser Ile Val Ala Leu Ile		
290	295	300
Asn Lys Ser Ile Asp Glu Ile Asn Ala Glu Leu Asp Arg Ile Gly Arg		
305	310	315
Pro Ile Ala Val Asp Ser Gly Ala Gln Leu Tyr Thr Ile Leu Glu Leu		
325	330	335
Cys Arg Ala Phe Asp Arg Val Phe Lys Glu His Leu Asp Gly Gly Arg		
340	345	350
Pro Gly Gly Asp Arg Ile Tyr Gly Val Phe Asp His Gln Leu Pro Ala		
355	360	365
Ala Leu Lys Lys Leu Pro Phe Asp Arg His Leu Ser Thr Lys Asn Val		
370	375	380
Gln Lys Val Val Ser Glu Ala Asp Gly Tyr Gln Pro His Leu Ile Ala		
385	390	395
Pro Glu Gln Gly Tyr Arg Arg Leu Ile Asp Gly Ser Ile Ser Tyr Phe		
405	410	415
Lys Gly Pro Ala Glu Ala Thr Val Asp Ala Val His Phe Val Leu Lys		
420	425	430
Glu Leu Val Arg Lys Ser Ile Ser Glu Thr Glu Leu Lys Arg Phe		
435	440	445
Pro Thr Leu Ala Ser Asp Ile Ala Ala Ala Asn Glu Ala Leu Glu		
450	455	460
Arg Phe Arg Asp Glu Ser Arg Lys Thr Val Leu Arg Leu Val Asp Met		
465	470	475
Glu Ser Ser Tyr Leu Thr Val Glu Phe Phe Arg Lys Leu His Leu Glu		
485	490	495
Pro Glu Lys Glu Lys Pro Asn Pro Arg Asn Ala Pro Ala Pro Asn Ala		
500	505	510
Asp Pro Tyr Ser Asp Asn His Phe Arg Lys Ile Gly Ser Asn Xaa Ser		
515	520	525
Ala Tyr Ile Asn Met Val Cys Asp Thr Leu Arg Asn Ser Leu Pro Lys		
530	535	540
Ala Val Val Tyr Cys Gln Val Arg Glu Ala Lys Arg Ser Leu Leu Asn		
545	550	555
Phe Phe Tyr Ala Gln Val Gly Arg Lys Glu Lys Glu Lys Leu Gly Ala		
565	570	575
Met Leu Asp Glu Asp Pro Gln Leu Met Glu Arg Arg Gly Thr Leu Ala		
580	585	590
Lys Arg Leu Glu Leu Tyr Lys Gln Ala Arg Asp Asp Ile Asp Ala Val		
595	600	605
Ala Trp Lys		
610		

(2) INFORMATION FOR SEQ ID NO:124:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 586 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(D) OTHER INFORMATION: / Ceres Seq. ID 1565901

1	Ser	Leu	Trp	5	Ala	Ala	Leu	Pro	Thr	Val	Ala	Val	Val	Gly	Gly	Gln
1	Ser	Ser	Gly	20	Ser	Ser	Val	Leu	Glu	Ser	Val	Val	Gly	Arg	Asp	Phe
Leu	Pro	Arg	Gly	35	Ser	Gly	Ile	Val	Thr	Arg	Arg	Pro	Leu	Val	Leu	Gln
Leu	His	Lys	Thr	50	Glu	Asp	Gly	Thr	Thr	Glu	Tyr	Ala	Glu	Phe	Leu	His
Ala	Pro	Lys	Lys	65	Arg	Phe	Ala	Asp	Phe	Ala	Ala	Val	Arg	Lys	Glu	Ile
Glu	Asp	Glu	Thr	85	Asp	Arg	Ile	Thr	Gly	Lys	Ser	Lys	Gln	Ile	Ser	Asn
Ile	Pro	Ile	Gln	100	Leu	Ser	Ile	Tyr	Ser	Pro	Asn	Val	Val	Asn	Leu	Thr
Leu	Ile	Asp	Leu	115	Pro	Gly	Leu	Thr	Lys	Val	Ala	Val	Asp	Gly	Gln	Pro
Glu	Ser	Ile	Val	130	Gln	Asp	Ile	Glu	Asn	Met	Val	Arg	Ser	Tyr	Val	Glu
Lys	Pro	Asn	Cys	145	Ile	Ile	Leu	Ala	Ile	Ser	Pro	Ala	Asn	Gln	Asp	Ile
Ala	Thr	Ser	Asp	165	Ala	Ile	Lys	Leu	Ala	Arg	Glu	Val	Asp	Pro	Thr	Gly
Glu	Arg	Thr	Phe	180	Gly	Val	Ala	Thr	Lys	Leu	Asp	Ile	Met	Asp	Lys	Gly
Thr	Asp	Cys	Leu	195	Asp	Val	Leu	Glu	Gly	Arg	Ser	Tyr	Arg	Leu	Gln	His
Pro	Trp	Val	Gly	210	Ile	Val	Asn	Arg	Ser	Gln	Ala	Asp	Ile	Asn	Lys	Arg
Val	Asp	Met	Ile	225	Ala	Ala	Arg	Arg	Lys	Glu	Gln	Glu	Tyr	Phe	Glu	Thr
Ser	Pro	Glu	Tyr	245	Gly	His	Leu	Ala	Ser	Arg	Met	Gly	Ser	Glu	Tyr	Leu
Ala	Lys	Leu	Leu	260	Ser	Gln	His	Leu	Glu	Thr	Val	Ile	Arg	Gln	Lys	Ile
Pro	Ser	Ile	Val	275	Ala	Leu	Ile	Asn	Lys	Ser	Ile	Asp	Glu	Ile	Asn	Ala
Glu	Leu	Asp	Arg	290	Ile	Gly	Arg	Pro	Ile	Ala	Val	Asp	Ser	Gly	Ala	Gln
Leu	Tyr	Thr	Ile	305	Leu	Glu	Leu	Cys	Arg	Ala	Phe	Asp	Arg	Val	Phe	Lys
Glu	His	Leu	Asp	325	Gly	Gly	Arg	Pro	Gly	Gly	Asp	Arg	Ile	Tyr	Gly	Val
Phe	Asp	His	Gln	340	Leu	Pro	Ala	Ala	Leu	Lys	Lys	Leu	Pro	Phe	Asp	Arg
His	Leu	Ser	Thr	355	Lys	Asn	Val	Gln	Lys	Val	Val	Ser	Glu	Ala	Asp	Gly
Tyr	Gln	Pro	His	370	Leu	Ile	Ala	Pro	Glu	Gln	Gly	Tyr	Arg	Arg	Leu	Ile
Asp	Gly	Ser	Ile	385	Ser	Tyr	Phe	Lys	Gly	Pro	Ala	Glu	Ala	Thr	Val	Asp
Ala	Val	His	Phe	405	Val	Leu	Lys	Glu	Leu	Val	Arg	Lys	Ser	Ile	Ser	Glu
Thr	Glu	Glu	Leu	420	Lys	Arg	Phe	Pro	Thr	Leu	Ala	Ser	Asp	Ile	Ala	Ala
Ala	Ala	Asn	Glu	435	Ala	Leu	Glu	Arg	Phe	Arg	Asp	Glu	Ser	Arg	Lys	Thr
Val	Leu	Arg	Leu	450	Val	Asp	Met	Glu	Ser	Ser	Tyr	Leu	Thr	Val	Glu	Phe

450						455										460
Phe	Arg	Lys	Leu	His	Leu	Glu	Pro	Glu	Lys	Glu	Lys	Pro	Asn	Pro	Arg	
465						470										480
Asn	Ala	Pro	Ala	Pro	Asn	Ala	Asp	Pro	Tyr	Ser	Asp	Asn	His	Phe	Arg	
						485										495
Lys	Ile	Gly	Ser	Asn	Xaa	Ser	Ala	Tyr	Ile	Asn	Met	Val	Cys	Asp	Thr	
						500										510
Leu	Arg	Asn	Ser	Ser	Leu	Pro	Lys	Ala	Val	Val	Tyr	Cys	Gln	Val	Arg	Glu
						515										525
Ala	Lys	Arg	Ser	Ser	Leu	Leu	Asn	Phe	Phe	Tyr	Ala	Gln	Val	Gly	Arg	Lys
						530										540
Glu	Lys	Glu	Lys	Leu	Gly	Ala	Met	Leu	Asp	Glu	Asp	Pro	Gln	Leu	Met	
						545										560
Glu	Arg	Arg	Gly	Thr	Leu	Ala	Lys	Arg	Leu	Glu	Leu	Tyr	Lys	Gln	Ala	
						565										575
Arg	Asp	Asp	Ile	Asp	Ala	Val	Ala	Trp	Lys							
						580										585

(2) INFORMATION FOR SEQ ID NO:125:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1152 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1152

(D) OTHER INFORMATION: / Ceres Seq. ID 1565922

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

catctctctct	tgaagctgct	tctctctcta	aattcttttt	ttttccagat	tcttctctctt	60
tcttctctct	tcttctcttat	tctgatttcg	aattttgaat	ttctctcaatg	gtctcaatcgt	120
tcttctctct	tgttcgaatc	aacaatctaa	ggaacagagt	gaatctgcgg	attttgatttc	180
tccgacgatt	cacacgggtg	ttatggagta	gaatctgttc	ttgtactcct	ggcaaactctc	240
ggagatatct	cttgcctttc	cgcgcctctc	cgtctcogac	tgttctctgt	ccttctctctt	300
ctccgacccc	cgcgcctgat	gtcgtcgtcg	gtggtcgttg	tggtcgttgt	gagtttgttc	360
gtcgttcgtc	ggttgtttac	gataatgata	acagtcctcg	gagatcggat	tctgattttg	420
tttctttgaa	gattagcttc	ttaggagatc	cagaaaatcg	aaaaactagc	ttctcggcga	480
aatatgtgtg	agaagagaaa	gaagtagaaa	tgagagaatt	ggagaaaggt	ataaattgtta	540
cggacaagac	gttatcacatg	ggagggtgctc	gcatttcata	tagtatctgg	gaattagaag	600
ctgagagatc	acgagatcaa	atccctgttg	cttgcaagga	ctctgttgcc	attctctttaa	660
tggttgattt	aaccagtcgt	tgacgcctta	atagtgtcat	tagctgggat	caacaagcta	720
ggaagtcaaa	tcagacggcg	ataccagtta	tggttagaac	caagtttgat	gagttttatct	780
agcttctcat	tgatctccta	tgacaaattg	ctagccaggc	gagaacatat	gcgaaggcctt	840
taaacgcgac	gctcttcttc	tcgagtgcct	catacaacat	aaacgtgaat	aagattcttta	900
agttttgtga	cggcgaagct	cttcgactta	ccatggagcg	tggaacgcaa	tctcacaatc	960
ggagaaccaa	tcacgcagct	ctagaatatg	tattttgata	taataataaa	gaagcgaaatc	1020
ctgaagaatg	cggttttttt	tttttttttt	ttaatcaacg	cgctaaagct	tgctgcgctg	1080
ggaactgacg	gactagtcgt	atttaagcga	aatggagaga	tgaagcgcg	gagatttcgc	1140
ccgcttttct	cc					

(2) INFORMATION FOR SEQ ID NO:126:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 332 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..332

(D) OTHER INFORMATION: / Ceres Seq. ID 1565923

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

Met Ala Gln Ser Cys Leu Lys Ile Val Arg Ile Asn Asn Leu Arg Asn
1 5 10 15
Arg Val Asn Arg Arg Ile Leu Ile Leu Arg Arg Phe Thr Arg Leu Leu
20 25 30
Trp Ser Arg Ile Val Ala Cys Thr Pro Gly Lys Ser Arg Arg Tyr Leu
35 40 45
Leu Leu Ser Arg Ala Leu Pro Ser Pro Thr Val Ser Arg Pro Ser Pro
50 55 60
Ser Pro Ile Pro Ala Val Asp Val Val Val Gly Gly Gly Gly Gly
65 70 75 80
Gly Glu Phe Val Arg Arg Ser Ser Val Val Tyr Asp Asn Asp Asn Ser
85 90 95
His Arg Arg Ser Asp Ser Asp Leu Val Ser Leu Lys Ile Ser Leu Leu
100 105 110
Gly Asp Pro Glu Ile Gly Lys Thr Ser Phe Leu Ala Lys Tyr Val Gly
115 120 125
Glu Glu Lys Glu Val Glu Met Arg Glu Leu Glu Lys Gly Ile Asn Cys
130 135 140
Thr Asp Lys Thr Leu Tyr Met Gly Gly Ala Arg Ile Ser Tyr Ser Ile
145 150 155 160
Trp Glu Leu Glu Ala Glu Arg Ser Arg Asp Gln Ile Pro Val Ala Cys
165 170 175
Lys Asp Ser Val Ala Ile Leu Phe Met Phe Asp Leu Thr Ser Arg Cys
180 185 190
Thr Leu Asn Ser Val Ile Ser Trp Tyr Gln Gln Ala Arg Lys Ser Asn
195 200 205
Gln Thr Ala Ile Pro Val Met Val Gly Thr Lys Phe Asp Glu Phe Ile
210 215 220
Gln Leu Pro Ile Asp Leu Gln Trp Thr Ile Ala Ser Gln Ala Arg Thr
225 230 235 240
Tyr Ala Lys Ala Leu Asn Ala Thr Leu Phe Phe Ser Ser Ala Ser Tyr
245 250 255
Asn Ile Asn Val Asn Lys Ile Phe Lys Phe Cys Asp Gly Glu Ala Leu
260 265 270
Arg Leu Thr Met Asp Gly Gly Thr Gln Ser His Asn Arg Arg Thr Asn
275 280 285
His Arg Leu Leu Glu Tyr Val Phe Val Tyr Asn Ile Lys Glu Ala Asn
290 295 300
Pro Glu Glu Cys Val Phe Phe Phe Phe Phe Phe Asn Ser Ala Ala Lys
305 310 315 320
Ala Cys Arg Arg Gly Thr Asp Arg Thr Ser Arg Ile
325 330

(2) INFORMATION FOR SEQ ID NO:127:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 198 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..198
- (D) OTHER INFORMATION: / Ceres Seq. ID 1565924

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

Met Arg Glu Leu Glu Lys Gly Ile Asn Cys Thr Asp Lys Thr Leu Tyr
1 5 10 15
Met Gly Gly Ala Arg Ile Ser Tyr Ser Ile Trp Glu Leu Glu Ala Glu
20 25 30
Arg Ser Arg Asp Gln Ile Pro Val Ala Cys Lys Asp Ser Val Ala Ile
35 40 45
Leu Phe Met Phe Asp Leu Thr Ser Arg Cys Thr Leu Asn Ser Val Ile

50	55	60	
Ser Trp Tyr Gln Gln	Ala Arg Lys Ser Asn Gln Thr Ala Ile Pro Val		
65	70	75	80
Met Val Gly Thr Lys Phe Asp Glu Phe Ile Gln Leu Pro Ile Asp Leu			
	85	90	95
Gln Trp Thr Thr Ile Ala Ser Gln Ala Arg Thr Tyr Ala Lys Ala Leu Asn			
	100	105	110
Ala Thr Leu Phe Phe Ser Ser Ala Ser Tyr Asn Ile Asn Val Asn Lys			
	115	120	125
Ile Phe Lys Phe Cys Asp Gly Glu Ala Leu Arg Leu Thr Met Asp Gly			
	130	135	140
Gly Thr Gln Ser His Asn Arg Arg Thr Asn His Arg Leu Leu Glu Tyr			
145	150	155	160
Val Phe Val Tyr Asn Ile Lys Glu Ala Asn Pro Glu Glu Cys Val Phe			
	165	170	175
Phe Phe Phe Phe Phe Asn Ser Ala Ala Lys Ala Cys Arg Arg Gly Thr			
	180	185	190
Asp Arg Thr Ser Arg Ile			
	195		

(2) INFORMATION FOR SEQ ID NO:128:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 182 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..182
- (D) OTHER INFORMATION: / Ceres Seq. ID 1565925

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

Met Gly Gly Ala Arg Ile Ser Tyr Ser Ile Trp Glu Leu Glu Ala Glu	
1	5
Arg Ser Arg Asp Gln Ile Pro Val Ala Cys Lys Asp Ser Val Ala Ile	
	20
Leu Phe Met Phe Asp Leu Thr Ser Arg Cys Thr Leu Asn Ser Val Ile	
	35
Ser Trp Tyr Gln Gln Ala Arg Lys Ser Asn Gln Thr Ala Ile Pro Val	
50	55
Met Val Gly Thr Lys Phe Asp Glu Phe Ile Gln Leu Pro Ile Asp Leu	
65	70
Gln Trp Thr Thr Ile Ala Ser Gln Ala Arg Thr Tyr Ala Lys Ala Leu Asn	
	85
Ala Thr Leu Phe Phe Ser Ser Ala Ser Tyr Asn Ile Asn Val Asn Lys	
	100
Ile Phe Lys Phe Cys Asp Gly Glu Ala Leu Arg Leu Thr Met Asp Gly	
	115
Gly Thr Gln Ser His Asn Arg Arg Thr Asn His Arg Leu Leu Glu Tyr	
	130
Val Phe Val Tyr Asn Ile Lys Glu Ala Asn Pro Glu Glu Cys Val Phe	
145	150
Phe Phe Phe Phe Phe Asn Ser Ala Ala Lys Ala Cys Arg Arg Gly Thr	
	165
Asp Arg Thr Ser Arg Ile	
	180

(2) INFORMATION FOR SEQ ID NO:129:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1599 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

(2) INFORMATION FOR SEO ID NO:130:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 368 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

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(ix) FEATURE:
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(A) NAME/KEY: peptide

(B) LOCATION: 1..368

(D) OTHER INFORMATION: / Ceres Seq. ID 1565927

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

Met	Asn	Ser	Thr	5	Ser	Thr	His	Phe	Val	10	Pro	Pro	Arg	Arg	Val	Gly	Ile
1	Tyr	Glu	Pro	Val	His	Gln	Phe	Gly	Met	25	Trp	Gly	Glu	Ser	Phe	Lys	Ser
			20												30		
Asn	Ile	Ser	Asn	Gly	Thr	Met	Asn	Thr	Pro	Asn	His	Ile	Ile	Ile	Pro		
		35					40					45					
Asn	Asn	Gln	Lys	Leu	Asp	Asn	Asn	Val	Ser	Glu	Asp	Thr	Ser	His	Gly		
	50					55					60						
Thr	Ala	Gly	Thr	Pro	His	Met	Phe	Asp	Gln	Glu	Ala	Ser	Thr	Ser	Arg		
65					70					75					80		
His	Pro	Asp	Lys	Ile	Gln	Arg	Arg	Leu	Ala	90	Gln	Asn	Arg	Glu	Ala		
			85												95		
Arg	Lys	Ser	Arg	Leu	Arg	Lys	Lys	Ala	Tyr	105	Val	Gln	Gln	Leu	Glu	Thr	
		100												110			
Ser	Arg	Leu	Lys	Leu	Ile	Gln	Leu	Glu	Gln	Glu	Leu	Asp	Arg	Ala	Arg		
		115					120					125					

```

Gln Gln Gly Phe Tyr Val Gly Asn Gly Ile Asp Thr Asn Ser Leu Gly
   130           135           140
Phe Ser Glu Thr Met Asn Pro Gly Ile Ala Ala Phe Glu Met Glu Tyr
   145           150           155           160
Gly His Trp Val Glu Glu Asn Arg Gln Ile Cys Glu Leu Arg Thr
           165           170           175
Val Leu His Gly His Ile Asn Asp Ile Glu Leu Arg Ser Leu Val Glu
           180           185           190
Asn Ala Met Lys His Tyr Phe Glu Leu Phe Arg Met Lys Ser Ser Ala
           195           200           205
Ala Lys Ala Asp Val Phe Phe Val Met Ser Gly Met Trp Arg Thr Ser
           210           215           220
Ala Glu Arg Phe Phe Leu Trp Ile Gly Gly Phe Arg Pro Ser Asp Leu
   225           230           235           240
Leu Lys Val Leu Leu Pro His Phe Asp Val Leu Thr Asp Gln Gln Leu
           245           250           255
Leu Asp Val Cys Asn Leu Lys Gln Ser Cys Gln Gln Ala Glu Asp Ala
           260           265           270
Leu Thr Gln Gly Met Glu Lys Leu Gln His Thr Leu Ala Asp Cys Val
           275           280           285
Ala Ala Gly Gln Leu Gly Glu Gly Ser Tyr Ile Pro Gln Val Asn Ser
   290           295           300
Ala Met Asp Arg Leu Glu Ala Leu Val Ser Phe Val Asn Gln Ala Asp
   305           310           315           320
His Leu Arg His Glu Thr Leu Gln Gln Met Tyr Arg Ile Leu Thr Thr
           325           330           335
Arg Gln Ala Ala Arg Gly Leu Leu Ala Leu Gly Glu Tyr Phe Gln Arg
           340           345           350
Leu Arg Ala Leu Ser Ser Ser Trp Ala Thr Arg His Arg Glu Pro Thr
           355           360           365

```

(2) INFORMATION FOR SEQ ID NO:131:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 344 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..344
- (D) OTHER INFORMATION: / Ceres Seq. ID 1565928

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:

```

Met Trp Gly Glu Ser Phe Lys Ser Asn Ile Ser Asn Gly Thr Met Asn
   1           5           10           15
Thr Pro Asn His Ile Ile Ile Pro Asn Asn Gln Lys Leu Asp Asn Asn
           20           25           30
Val Ser Glu Asp Thr Ser His Gly Thr Ala Gly Thr Pro His Met Phe
           35           40           45
Asp Gln Glu Ala Ser Thr Ser Arg His Pro Asp Lys Ile Gln Arg Arg
           50           55           60
Leu Ala Gln Asn Arg Glu Ala Ala Arg Lys Ser Arg Leu Arg Lys Lys
           65           70           75           80
Ala Tyr Val Gln Gln Leu Glu Thr Ser Arg Leu Lys Leu Ile Gln Leu
           85           90           95
Glu Gln Glu Leu Asp Arg Ala Arg Gln Gln Gly Phe Tyr Val Gly Asn
           100           105           110
Gly Ile Asp Thr Asn Ser Leu Gly Phe Ser Glu Thr Met Asn Pro Gly
           115           120           125
Ile Ala Ala Phe Glu Met Glu Tyr Gly His Trp Val Glu Glu Asn

```


130 135 140
Arg Gln Ile Cys Glu Leu Arg Thr Val Leu His Gly His Ile Asn Asp
145 150 155 160
Ile Glu Leu Arg Ser Leu Val Glu Asn Ala Met Lys His Tyr Phe Glu
165 170
Leu Phe Arg Met Lys Ser Ser Ala Ala Lys Ala Asp Val Phe Phe Val
180 185 190
Met Ser Gly Met Trp Arg Thr Ser Ala Glu Arg Phe Phe Leu Trp Ile
195 200 205
Gly Gly Phe Arg Pro Ser Asp Leu Leu Lys Val Leu Leu Pro His Phe
210 215 220
Asp Val Leu Thr Asp Gln Gln Leu Leu Asp Val Cys Asn Leu Lys Gln
225 230 235 240
Ser Cys Gln Gln Ala Glu Asp Ala Leu Thr Gln Gly Met Glu Lys Leu
245 250 255
Gln His Thr Leu Ala Asp Cys Val Ala Ala Gly Gln Leu Gly Glu Gly
260 265 270
Ser Tyr Ile Pro Gln Val Asn Ser Ala Met Asp Arg Leu Glu Ala Leu
275 280 285
Val Ser Phe Val Asn Gln Ala Asp His Leu Arg His Glu Thr Leu Gln
290 295 300
Gln Met Tyr Arg Ile Leu Thr Thr Arg Gln Ala Ala Arg Gly Leu Leu
305 310 315 320
Ala Leu Gly Glu Tyr Phe Gln Arg Leu Arg Ala Leu Ser Ser Ser Trp
325 330 335
Ala Thr Arg His Arg Glu Pro Thr
340

(2) INFORMATION FOR SEQ ID NO:132:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 330 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..330
- (D) OTHER INFORMATION: / Ceres Seq. ID 1565929

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

Met Asn Thr Pro Asn His Ile Ile Ile Pro Asn Asn Gln Lys Leu Asp
1 5 10 15
Asn Asn Val Ser Glu Asp Thr Ser His Gly Thr Ala Gly Thr Pro His
20 25 30
Met Phe Asp Gln Glu Ala Ser Thr Ser Arg His Pro Asp Lys Ile Gln
35 40 45
Arg Arg Leu Ala Gln Asn Arg Glu Ala Ala Arg Lys Ser Arg Leu Arg
50 55 60
Lys Lys Ala Tyr Val Gln Gln Leu Glu Thr Ser Arg Leu Lys Leu Ile
65 70 75 80
Gln Leu Glu Gln Glu Leu Asp Arg Ala Arg Gln Gln Gly Phe Tyr Val
85 90 95
Gly Asn Gly Ile Asp Thr Asn Ser Leu Gly Phe Ser Glu Thr Met Asn
100 105 110
Pro Gly Ile Ala Ala Phe Glu Met Glu Tyr Gly His Trp Val Glu Glu
115 120 125
Gln Asn Arg Gln Ile Cys Glu Leu Arg Thr Val Leu His Gly His Ile
130 135 140
Asn Asp Ile Glu Leu Arg Ser Leu Val Glu Asn Ala Met Lys His Tyr
145 150 155 160
Phe Glu Leu Phe Arg Met Lys Ser Ser Ala Ala Lys Ala Asp Val Phe
165 170 175

Phe Val Met Ser Gly Met Trp Arg Thr Ser Ala Glu Arg Phe Phe Leu
180 185 190
Trp Ile Gly Gly Phe Arg Pro Ser Asp Leu Leu Lys Val Leu Leu Pro
195 200 205
His Phe Asp Val Leu Thr Asp Gln Gln Leu Leu Asp Val Cys Asn Leu
210 215 220
Lys Gln Ser Cys Gln Gln Ala Glu Asp Ala Leu Thr Gln Gly Met Glu
225 230 235 240
Lys Leu Gln His Thr Leu Ala Asp Cys Val Ala Ala Gly Gln Leu Gly
245 250 255
Glu Gly Ser Tyr Ile Pro Gln Val Asn Ser Ala Met Asp Arg Leu Glu
260 265 270
Ala Leu Val Ser Phe Val Asn Gln Ala Asp His Leu Arg His Glu Thr
275 280 285
Leu Gln Gln Met Tyr Arg Ile Leu Thr Thr Arg Gln Ala Ala Arg Gly
290 295 300
Leu Leu Ala Leu Gly Glu Tyr Phe Gln Arg Leu Arg Ala Leu Ser Ser
305 310 315 320
Ser Trp Ala Thr Arg His Arg Glu Pro Thr
325 330

(2) INFORMATION FOR SEQ ID NO:133:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1477 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1477

(D) OTHER INFORMATION: / Ceres Seq. ID 1565938

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:

tagttctgctc	ctccgtcaat	ctctctcgcc	gctttatcct	tggtacaaat	cccatcgatc	60
ttttcggaat	cttccctcat	tatgctcagc	caccattaac	agagctccat	tggttcagtt	120
ctccgttcaa	cgattatcgg	aattattcac	aacactatta	gtatcacctg	cgccaacoga	180
ttttgattac	caagcttttgt	gacgacagtc	gtgattaagg	agggttttgt	aaatttcttc	240
gttccgtgtt	gttttcaaa	atggctgctt	tgaaagggtta	tggcttgtgt	tctatggact	300
ctgctcttcc	attccctcgt	cctaagctat	tcaatggcta	taagagaagg	agctcgaaat	360
gggtctctcc	caaaagcagc	gttgtaaccca	atttccatct	cccaatgcgc	agcttggagg	420
ttaaaacagc	gacaaacaca	gacgacatta	aagctctcac	tgtgatcaca	gctatcaaaa	480
cacgctatct	acctgatgga	agattcgacc	ttgaagccta	cgatgactta	gtcaacattc	540
agatacaaaa	cggtgctgaa	ggtgtcatgt	ttggtgttac	aactgtgaag	gacaaactgat	600
gagctgggag	gaacacatta	tgcctatagg	ccataccggt	aactgttttg	gtcgaagcat	660
caaagtcatt	ggaacacgtg	gaagcaattc	gactagagaa	gcaatccacg	cgactgaaca	720
aggattccgc	gttggaatgc	atgctgctct	tcatataaac	ccttactact	gcaagacttc	780
tattgaggga	ctgattgcac	atttccagtc	tgttcttcat	atggggacga	cgattatata	840
caatgtgcct	ggctgaacag	ggcaagatat	acgcctcgtt	gccatcttca	aaactttctca	900
gaatccgaat	ttagctgtgt	tgaaggaaatg	ttgtgggaac	aagcgagctg	aagagtacac	960
tgagaatggg	gttggttgtg	ggagtgaggaa	tgatgatgag	tgtcatgatt	ccagatggga	1020
ttatggagca	acaggagatta	tatcagttac	taktaattta	tgtccggggt	tgatgaggaa	1080
gtgtgatgtt	gaaggttaga	attcatcttt	gaactcaaa	cttctacctt	tgatggcttg	1140
gctgttccac	gaagcaaac	cgattggaat	caacaactgt	ttggtctcag	ttggagtttc	1200
gagggcggtt	tttaggttac	catatgtacc	attgccactg	tctaagaggg	ttgagtttgt	1260
gaaactggtg	aaggagattg	gacgagagca	ttttgtgggt	gagaaagatg	tccaggctct	1320
tgatgatgat	gattttatcc	ttatcggtgc	atattagcat	actttttttt	ttgaattttt	1380
ggttctcttt	tggttggtgt	taatgaagaa	gagatggttc	tatcatttgg	ttttatgtat	1440
ctgatgaatg	aatgaaaaact	caaggaaatga	tttcatc			

(2) INFORMATION FOR SEQ ID NO:134:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 252 amino acids
- (B) TYPE: amino acid

- (C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..252
(D) OTHER INFORMATION: / Ceres Seq. ID 1565939
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:

Met	Ser	Trp	Asp	Glu	His	Ile	Met	Leu	Ile	Gly	His	Thr	Val	Asn	Cys
1				5					10					15	
Phe	Gly	Gly	Ser	Ile	Lys	Val	Ile	Gly	Asn	Thr	Gly	Ser	Asn	Ser	Thr
				20				25					30		
Arg	Glu	Ala	Ile	His	Ala	Thr	Glu	Gln	Gly	Phe	Ala	Val	Gly	Met	His
				35				40				45			
Ala	Ala	Leu	His	Ile	Asn	Pro	Tyr	Tyr	Gly	Lys	Thr	Ser	Ile	Glu	Gly
				50				55				60			
Leu	Ile	Ala	His	Phe	Gln	Ser	Val	Leu	His	Met	Gly	Pro	Thr	Ile	Ile
				65				70				75			80
Tyr	Asn	Val	Pro	Gly	Arg	Thr	Gly	Gln	Asp	Ile	Pro	Pro	Arg	Ala	Ile
				85				90					95		
Phe	Lys	Leu	Ser	Gln	Asn	Pro	Asn	Leu	Ala	Gly	Val	Lys	Glu	Cys	Val
				100				105					110		
Gly	Asn	Lys	Arg	Val	Glu	Glu	Tyr	Thr	Glu	Asn	Gly	Val	Val	Val	Trp
				115				120				125			
Ser	Gly	Asn	Asp	Asp	Glu	Cys	His	Asp	Ser	Arg	Trp	Asp	Tyr	Gly	Ala
				130				135				140			
Thr	Gly	Val	Ile	Ser	Val	Thr	Ser	Asn	Leu	Val	Pro	Gly	Leu	Met	Arg
				145				150				155			160
Lys	Leu	Met	Phe	Glu	Gly	Arg	Asn	Ser	Ser	Leu	Asn	Ser	Lys	Leu	Leu
				165				170					175		
Pro	Leu	Met	Ala	Trp	Leu	Phe	His	Glu	Pro	Asn	Pro	Ile	Gly	Ile	Asn
				180				185					190		
Thr	Ala	Leu	Ala	Gln	Leu	Gly	Val	Ser	Arg	Pro	Val	Phe	Arg	Leu	Pro
				195				200				205			
Tyr	Val	Pro	Leu	Pro	Leu	Ser	Lys	Arg	Leu	Glu	Phe	Val	Lys	Leu	Val
				210				215				220			
Lys	Glu	Ile	Gly	Arg	Glu	His	Phe	Val	Gly	Glu	Lys	Asp	Val	Gln	Ala
				225				230				235			240
Leu	Asp	Asp	Asp	Asp	Phe	Ile	Leu	Ile	Gly	Arg	Tyr				
				245				250							

- (2) INFORMATION FOR SEQ ID NO:135:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 245 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..245
(D) OTHER INFORMATION: / Ceres Seq. ID 1565940
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:

Met	Leu	Ile	Gly	His	Thr	Val	Asn	Cys	Phe	Gly	Gly	Ser	Ile	Lys	Val
1				5					10				15		
Ile	Gly	Asn	Thr	Gly	Ser	Asn	Ser	Thr	Arg	Glu	Ala	Ile	His	Ala	Thr
				20				25					30		
Glu	Gln	Gly	Phe	Ala	Val	Gly	Met	His	Ala	Ala	Leu	His	Ile	Asn	Pro
				35				40				45			
Tyr	Tyr	Gly	Lys	Thr	Ser	Ile	Glu	Gly	Leu	Ile	Ala	His	Phe	Gln	Ser
				50				55				60			
Val	Leu	His	Met	Gly	Pro	Thr	Ile	Ile	Tyr	Asn	Val	Pro	Gly	Arg	Thr

65	70	75	80
Gly Gln Asp Ile	Pro Pro Arg Ala Ile	Phe Lys Leu Ser Gln	Asn Pro
	85	90	95
Asn Leu Ala Gly	Val Lys Glu Cys Val	Gly Asn Lys Arg Val	Glu Glu
	100	105	110
Tyr Thr Glu Asn	Gly Val Val Val Trp Ser	Gly Asn Asp Asp	Glu Cys
	115	120	125
His Asp Ser Arg	Trp Asp Tyr Gly Ala Thr	Gly Val Ile Ser	Val Thr
	130	135	140
Ser Asn Leu Val	Pro Gly Leu Met Arg Lys	Leu Met Phe Glu	Gly Arg
	145	150	155
Asn Ser Ser Leu	Asn Ser Lys Leu Leu Pro	Leu Met Ala Trp	Leu Phe
	165	170	175
His Glu Pro Asn	Pro Ile Gly Ile Asn Thr	Ala Leu Ala Gln	Leu Gly
	180	185	190
Val Ser Arg Pro	Val Phe Arg Leu Pro	Tyr Val Pro Leu	Pro Leu Ser
	195	200	205
Lys Arg Leu Glu	Phe Val Lys Leu Val Lys	Glu Ile Gly Arg	Glu His
	210	215	220
Phe Val Gly Glu	Lys Asp Val Gln Ala Leu	Asp Asp Asp Asp	Phe Ile
	225	230	235
Leu Ile Gly Arg	Tyr		240
	245		

(2) INFORMATION FOR SEQ ID NO:136:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 206 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..206

(D) OTHER INFORMATION: / Ceres Seq. ID 1565941

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:

Met His Ala Ala Leu His Ile Asn Pro Tyr Gly Lys Thr Ser Ile	
1	5 10 15
Glu Gly Leu Ile Ala His Phe Gln Ser Val Leu His Met Gly Pro Thr	
	20 25 30
Ile Ile Tyr Asn Val Pro Gly Arg Thr Gly Gln Asp Ile Pro Pro Arg	
	35 40 45
Ala Ile Phe Lys Leu Ser Gln Asn Pro Asn Leu Ala Gly Val Lys Glu	
	50 55 60
Cys Val Gly Asn Lys Arg Val Glu Glu Tyr Thr Glu Asn Gly Val Val	
	65 70 75 80
Val Trp Ser Gly Asn Asp Asp Glu Cys His Asp Ser Arg Trp Asp Tyr	
	85 90 95
Gly Ala Thr Gly Val Ile Ser Val Thr Ser Asn Leu Val Pro Gly Leu	
	100 105 110
Met Arg Lys Leu Met Phe Glu Gly Arg Asn Ser Ser Leu Asn Ser Lys	
	115 120 125
Leu Leu Pro Leu Met Ala Trp Leu Phe His Glu Pro Asn Pro Ile Gly	
	130 135 140
Ile Asn Thr Ala Leu Ala Gln Leu Gly Val Ser Arg Pro Val Phe Arg	
	145 150 155 160
Leu Pro Tyr Val Pro Leu Pro Leu Ser Lys Arg Leu Glu Phe Val Lys	
	165 170 175
Leu Val Lys Glu Ile Gly Arg Glu His Phe Val Gly Glu Lys Asp Val	
	180 185 190
Gln Ala Leu Asp Asp Asp Asp Phe Ile Leu Ile Gly Arg Tyr	
	195 200 205

(2) INFORMATION FOR SEQ ID NO:137:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 858 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..858
- (D) OTHER INFORMATION: / Ceres Seq. ID 1565946

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:137:

attgaatacc	atatatatat	agatacacag	acatataaac	acacaaatat	tcgtgttttt	60
ttcaaaactgt	gagagaaaaa	gaaagagaga	aagagatggg	agagattggg	tttacagaga	120
agcaagaagc	tttgggtgaag	gaatcgtggg	agatactgaa	acaagacatc	cccaaataca	180
gccttctact	cttctcacag	atactggaga	tagcaccagc	agcaaaaaggc	ttgttctctt	240
tcctaagaga	ctcagatgaa	gtccctcaca	acaatcctaa	actcaaagct	catgctgtta	300
aagtcttcaa	gatgacatgt	gaaacagcta	tacagctgag	ggaggaaagga	aagggtgttag	360
tggctgacac	aaccctccaa	tatttaggct	caattcatct	caaaaagcgcc	gttattgacc	420
ctcacttcga	ggtggtgaaa	gaagctttgc	taaggacatt	gaaagagggg	ttgggggaga	480
aatacaatga	agaagtgga	ggtgcttgg	ctcaagctta	tgatcacttg	gctttagcca	540
tcaagaccga	gatgaacaaa	gaagagtcac	aaaacccctat	tgatcatttg	ggatcgcac	600
acatgaatct	attccacata	catgatacac	atatactgtg	tctgtgtgtg	gtactatggt	660
gcctcttaac	tttctacagt	tcactatttt	aattataaag	aaggatcttg	tgctatcatt	720
agggagatag	gtgatactgt	agttcttctt	gaaattgtta	ttcgtgagaa	atatcatggt	780
ttgaagtatt	tattttcaca	agatggatgt	taacgtgggg	atcattttac	aatcattcta	840
caataatatt	tacttctc					

(2) INFORMATION FOR SEQ ID NO:138:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 158 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..158
- (D) OTHER INFORMATION: / Ceres Seq. ID 1565947

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:

Met	Gly	Glu	Ile	Gly	Phe	Thr	Glu	Lys	Gln	Glu	Ala	Leu	Val	Lys	Glu
1			5						10					15	
Ser	Trp	Glu	Ile	Leu	Lys	Gln	Asp	Ile	Pro	Lys	Tyr	Ser	Leu	His	Phe
			20						25					30	
Phe	Ser	Gln	Ile	Leu	Glu	Ile	Ala	Pro	Ala	Ala	Lys	Gly	Leu	Phe	Ser
			35											40	
Phe	Leu	Arg	Asp	Ser	Asp	Glu	Val	Pro	His	Asn	Asn	Pro	Lys	Leu	Lys
			50											55	
Ala	His	Ala	Val	Lys	Val	Phe	Lys	Met	Thr	Cys	Glu	Thr	Ala	Ile	Gln
			65											70	
Leu	Arg	Glu	Glu	Gly	Lys	Val	Val	Val	Val	Ala	Asp	Thr	Thr	Leu	Gln
			85											90	
Leu	Gly	Ser	Ile	His	Leu	Lys	Ser	Gly	Val	Ile	Asp	Pro	His	Phe	Glu
			100											105	
Val	Val	Lys	Glu	Ala	Leu	Leu	Arg	Thr	Leu	Lys	Glu	Gly	Leu	Gly	Glu
			115											120	
Lys	Tyr	Asn	Glu	Glu	Val	Glu	Gly	Ala	Trp	Ser	Gln	Ala	Tyr	Asp	His
			130											135	
Leu	Ala	Leu	Ala	Ile	Lys	Thr	Glu	Met	Lys	Gln	Glu	Glu	Ser		
			145											150	

(2) INFORMATION FOR SEQ ID NO:139:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 86 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..86
(D) OTHER INFORMATION: / Ceres Seq. ID 1565948
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:139:
Met Thr Cys Glu Thr Ala Ile Gln Leu Arg Glu Glu Gly Lys Val Val
1 5 10 15
Val Ala Asp Thr Thr Leu Gln Tyr Leu Gly Ser Ile His Leu Lys Ser
20 25 30
Gly Val Ile Asp Pro His Phe Glu Val Val Lys Glu Ala Leu Leu Arg
35 40 45
Thr Leu Lys Glu Gly Leu Gly Glu Lys Tyr Asn Glu Glu Val Glu Gly
50 55 60
Ala Trp Ser Gln Ala Tyr Asp His Leu Ala Leu Ala Ile Lys Thr Glu
65 70 75 80
Met Lys Gln Glu Glu Ser
85

(2) INFORMATION FOR SEQ ID NO:140:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1262 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..1262
(D) OTHER INFORMATION: / Ceres Seq. ID 1565957

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:

aaagcaacaa aaacttaacc cattctctct tctttttttg ttctctctctc acaaacacaa 60
caaatatgga atacagctgt gtacagcaga gtagtactac gtcagaatct ctctccatct 120
ctactactcc aaagccgaca acgacaacgg agaagaaact ctcttctcca ccggcgactt 180
cgatcgctct ctacagaatg ggaagcgcgc gaagcagcgt tgttttgat tcagagaacg 240
cgctcgagac cgagtcacga aagcttccgt cgtcgaaata caaaggcgtt gtgcctcagc 300
ctaacggaag atggggagct cagatttacg agaagcatca gcgagtttgg ctccggtactt 360
tcaacgagga agaagaagct cgctctctct acgacatcgc cgtgaggagg ttccgaggcc 420
gcgcgcgcgt cactaaactc aaatctcaag ttgatggaaa cgacgcggaa tcgggttttc 480
ttgacgctca ttctaagct gagatcgtgg atatgttgag gaaacacact tacgcgatg 540
agtttgagca gagtacagcg aagtttgtta accgcgacgg aaaacgctct ggtttggaga 600
cggcgacgta cggaaacgac gctgttttga gagcgcgtga ggttttgttc gagaagactg 660
ttacgcgagc cgagctcggg aagctgaacc gtttagtgat accgaaacaa cacgcggaga 720
acgattttcc gttatcggcg atgcagcagc cgatggggat gaatccGtct ccgacgaaag 780
gcgttttgat taactttgaa gatagaacag ggaaagtgtg ccggttcctgt tacagttact 840
ggaacagcag tcaaaagttac gtgttgacca agggctggag ccggttcctgt aaagagaaga 900
atcttcgacg cgggtgatgtg gtttgttctc agagatcaac ccgaccagac cggcaattgt 960
atatccactg gaaagtcggc tctagtcggc ttcagactgt ggttaggcta ttccgagtc 1020
acattttcaa tgttgagtaac gagaacccaa acgacgtcgc agtagagtgt gttggcaaga 1080
agagatctcg ggaagatgat ttgttttcgt taggggtgtc caagaagcag gcgattatca 1140
acatcttggt acaaatcttt ttttttgggt ttttttctt caattttgtt ctccgttttt 1200
aatattttgt attgaaatg caagtgttaa attaggacaa tacaagaaaa aatgacaact 1260

(2) INFORMATION FOR SEQ ID NO:141:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 382 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:

(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..382

(D) OTHER INFORMATION: / Ceres Seq. ID 1565958

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:141:

Ser	Asn	Lys	Asn	Leu	Thr	His	Phe	Phe	Phe	Phe	Cys	Phe	Ser	Leu
1				5					10				15	
Thr	Asn	Thr	Thr	Asn	Met	Glu	Tyr	Ser	Cys	Val	Asp	Asp	Ser	Thr
			20					25					30	
Thr	Ser	Glu	Ser	Leu	Ser	Ile	Ser	Thr	Thr	Pro	Lys	Pro	Thr	Thr
		35					40					45		
Thr	Glu	Lys	Lys	Leu	Ser	Ser	Pro	Pro	Ala	Thr	Ser	Met	Arg	Leu
	50				55						60			
Arg	Met	Gly	Ser	Gly	Gly	Ser	Ser	Val	Val	Leu	Asp	Ser	Glu	Asn
65				70					75					80
Val	Glu	Thr	Glu	Ser	Arg	Lys	Leu	Pro	Ser	Ser	Lys	Tyr	Lys	Gly
			85						90				95	
Val	Pro	Gln	Pro	Asn	Gly	Arg	Trp	Gly	Ala	Gln	Ile	Tyr	Glu	Lys
		100						105					110	
Gln	Arg	Val	Trp	Leu	Gly	Thr	Phe	Asn	Glu	Glu	Glu	Glu	Ala	Ser
		115						120				125		
Ser	Tyr	Asp	Ile	Ala	Val	Arg	Arg	Phe	Arg	Gly	Arg	Asp	Ala	Val
	130				135						140			
Asn	Phe	Lys	Ser	Gln	Val	Asp	Gly	Asn	Asp	Ala	Glu	Ser	Ala	Phe
145				150					155					160
Asp	Ala	His	Ser	Lys	Ala	Glu	Ile	Val	Asp	Met	Leu	Arg	Lys	His
			165						170				175	
Tyr	Ala	Asp	Glu	Phe	Glu	Gln	Ser	Arg	Arg	Lys	Phe	Val	Asn	Gly
		180						185					190	
Gly	Lys	Arg	Ser	Gly	Leu	Glu	Thr	Ala	Thr	Tyr	Gly	Asn	Asp	Ala
		195					200					205		
Leu	Arg	Ala	Arg	Glu	Val	Leu	Phe	Glu	Lys	Thr	Val	Thr	Pro	Ser
	210				215						220			
Val	Gly	Lys	Leu	Asn	Arg	Leu	Val	Ile	Pro	Lys	Gln	His	Ala	Glu
225				230						235				240
His	Phe	Pro	Leu	Ser	Ala	Met	Thr	Thr	Ala	Met	Gly	Met	Asn	Pro
			245						250				255	
Pro	Thr	Lys	Gly	Val	Leu	Ile	Asn	Leu	Glu	Asp	Arg	Thr	Gly	Lys
		260					265						270	
Trp	Arg	Phe	Arg	Tyr	Ser	Tyr	Trp	Asn	Ser	Ser	Gln	Ser	Tyr	Val
	275						280					285		
Thr	Lys	Gly	Trp	Ser	Arg	Phe	Val	Lys	Glu	Lys	Asn	Leu	Arg	Ala
	290					295					300			
Asp	Val	Val	Cys	Phe	Glu	Arg	Ser	Thr	Gly	Pro	Asp	Arg	Gln	Leu
	305				310					315				320
Ile	His	Trp	Lys	Val	Arg	Ser	Ser	Pro	Val	Gln	Thr	Val	Val	Arg
			325						330				335	
Phe	Gly	Val	Asn	Ile	Phe	Asn	Val	Ser	Asn	Glu	Lys	Pro	Asn	Asp
		340					345						350	
Ala	Val	Glu	Cys	Val	Gly	Lys	Lys	Arg	Ser	Arg	Glu	Asp	Asp	Leu
		355					360					365		
Ser	Leu	Gly	Cys	Ser	Lys	Lys	Gln	Ala	Ile	Ile	Asn	Ile	Leu	
	370					375					380			

(2) INFORMATION FOR SEQ ID NO:142:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 361 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..361

(D) OTHER INFORMATION: / Ceres Seq. ID 1565959

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:

Met	Glu	Tyr	Ser	Cys	Val	Asp	Asp	Ser	Ser	Thr	Thr	Ser	Glu	Ser	Leu
1			5					10					15		
Ser	Ile	Ser	Thr	Thr	Pro	Lys	Pro	Thr	Thr	Thr	Thr	Glu	Lys	Lys	Leu
			20					25					30		
Ser	Ser	Pro	Pro	Ala	Thr	Ser	Met	Arg	Leu	Tyr	Arg	Met	Gly	Ser	Gly
		35					40					45			
Gly	Ser	Ser	Val	Val	Leu	Asp	Ser	Glu	Asn	Gly	Val	Glu	Thr	Glu	Ser
	50					55					60				
Arg	Lys	Leu	Pro	Ser	Ser	Lys	Tyr	Lys	Gly	Val	Val	Pro	Gln	Pro	Asn
	65				70					75				80	
Gly	Arg	Trp	Gly	Ala	Gln	Ile	Tyr	Glu	Lys	His	Gln	Arg	Val	Trp	Leu
			85						90				95		
Gly	Thr	Phe	Asn	Glu	Glu	Glu	Ala	Ala	Ser	Ser	Tyr	Asp	Ile	Ala	
		100					105					110			
Val	Arg	Arg	Phe	Arg	Gly	Arg	Asp	Ala	Val	Thr	Asn	Phe	Lys	Ser	Gln
	115						120					125			
Val	Asp	Gly	Asn	Asp	Ala	Glu	Ser	Ala	Phe	Leu	Asp	Ala	His	Ser	Lys
	130					135					140				
Ala	Glu	Ile	Val	Asp	Met	Leu	Arg	Lys	His	Thr	Tyr	Ala	Asp	Glu	Phe
	145				150					155				160	
Glu	Gln	Ser	Arg	Arg	Lys	Phe	Val	Asn	Gly	Asp	Gly	Lys	Arg	Ser	Gly
				165					170					175	
Leu	Glu	Thr	Ala	Thr	Tyr	Gly	Asn	Asp	Ala	Val	Leu	Arg	Ala	Arg	Glu
		180					185						190		
Val	Leu	Phe	Glu	Lys	Thr	Val	Thr	Pro	Ser	Asp	Val	Gly	Lys	Leu	Asn
	195						200					205			
Arg	Leu	Val	Ile	Pro	Lys	Gln	His	Ala	Glu	Lys	His	Phe	Pro	Leu	Ser
	210					215					220				
Ala	Met	Thr	Thr	Ala	Met	Gly	Met	Asn	Pro	Ser	Pro	Thr	Lys	Gly	Val
	225				230					235				240	
Leu	Ile	Asn	Leu	Glu	Asp	Arg	Thr	Gly	Lys	Val	Trp	Arg	Phe	Arg	Tyr
				245					250					255	
Ser	Tyr	Trp	Asn	Ser	Ser	Gln	Ser	Tyr	Val	Leu	Thr	Lys	Gly	Trp	Ser
		260						265					270		
Arg	Phe	Val	Lys	Glu	Lys	Asn	Leu	Arg	Ala	Gly	Asp	Val	Val	Cys	Phe
	275					280						285			
Glu	Arg	Ser	Thr	Gly	Pro	Asp	Arg	Gln	Leu	Tyr	Ile	His	Trp	Lys	Val
	290					295					300				
Arg	Ser	Ser	Pro	Val	Gln	Thr	Val	Val	Arg	Leu	Phe	Gly	Val	Asn	Ile
	305				310				315					320	
Phe	Asn	Val	Ser	Asn	Glu	Lys	Pro	Asn	Asp	Val	Ala	Val	Glu	Cys	Val
				325					330					335	
Gly	Lys	Lys	Arg	Ser	Arg	Glu	Asp	Asp	Leu	Phe	Ser	Leu	Gly	Cys	Ser
			340				345						350		
Lys	Lys	Gln	Ala	Ile	Ile	Asn	Ile	Leu							
		355				360									

(2) INFORMATION FOR SEQ ID NO:143:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 322 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..322

(D) OTHER INFORMATION: / Ceres Seq. ID 1565960

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:143:

```
Met Arg Leu Tyr Arg Met Gly Ser Gly Gly Ser Ser Val Val Leu Asp
1      5      10      15
Ser Glu Asn Gly Val Glu Thr Glu Ser Arg Lys Leu Pro Ser Ser Lys
20      25      30
Tyr Lys Gly Val Val Pro Gln Pro Asn Gly Arg Trp Gly Ala Gln Ile
35      40      45
Tyr Glu Lys His Gln Arg Val Trp Leu Gly Thr Phe Asn Glu Glu Glu
50      55      60
Glu Ala Ala Ser Ser Tyr Asp Ile Ala Val Arg Arg Phe Arg Gly Arg
65      70      75      80
Asp Ala Val Thr Asn Phe Lys Ser Gln Val Asp Gly Asn Asp Ala Glu
85      90      95
Ser Ala Phe Leu Asp Ala His Ser Lys Ala Glu Ile Val Asp Met Leu
100      105      110
Arg Lys His Thr Tyr Ala Asp Glu Phe Glu Gln Ser Arg Arg Lys Phe
115      120      125
Val Asn Gly Asp Gly Lys Arg Ser Gly Leu Glu Thr Ala Thr Tyr Gly
130      135      140
Asn Asp Ala Val Leu Arg Ala Arg Glu Val Leu Phe Glu Lys Thr Val
145      150      155      160
Thr Pro Ser Asp Val Gly Lys Leu Asn Arg Leu Val Ile Pro Lys Gln
165      170      175
His Ala Glu Lys His Phe Pro Leu Ser Ala Met Thr Thr Ala Met Gly
180      185      190
Met Asn Pro Ser Pro Thr Lys Gly Val Leu Ile Asn Leu Glu Asp Arg
195      200      205
Thr Gly Lys Val Trp Arg Phe Arg Tyr Ser Tyr Trp Asn Ser Ser Gln
210      215      220
Ser Tyr Val Leu Thr Lys Gly Trp Ser Arg Phe Val Lys Glu Lys Asn
225      230      235      240
Leu Arg Ala Gly Asp Val Val Cys Phe Glu Arg Ser Thr Gly Pro Asp
245      250      255
Arg Gln Leu Tyr Ile His Trp Lys Val Arg Ser Ser Pro Val Gln Thr
260      265      270
Val Val Arg Leu Phe Gly Val Asn Ile Phe Asn Val Ser Asn Glu Lys
275      280      285
Pro Asn Asp Val Ala Val Glu Cys Val Gly Lys Lys Arg Ser Arg Glu
290      295      300
Asp Asp Leu Phe Ser Leu Gly Cys Ser Lys Lys Gln Ala Ile Ile Asn
305      310      315      320
Ile Leu
```

(2) INFORMATION FOR SEQ ID NO:144:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1351 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1351

(D) OTHER INFORMATION: / Ceres Seq. ID 1565965

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:

```
aactggtataa ccctaagaat cctccgcaat ttccgaattt tgtgaaggag ccgccggcta      60
aatttgatgg cagaccacaag ttccggagatc gtcaatgctc tgtcgtcgga gatggaagct      120
gtttccggtt catcaactca ggcattctct tcgtccgatg gattccagat gatgtaagaa      180
gttgagaaga gatacaaaat tgtaggagt atcggtagg aatgtatata agaggaagag      240
```

ctaagaatc	ttcttgc	taa	gaagcgt	gct	cgcattt	gct	acgacg	ggtt	tgaacat	caa	300
ggaagaatgc	acattgct	gca	ggagtgat	g	aaagtcat	ca	atgtga	acaa	aatga	acttca	360
ctcgggttgc	gagtgaa	gat	ttggatt	Tgc	tgattgg	ttt	gctcag	ttga	acaacaaa	aat	420
gggtggtgac	ttgaagaaa	aa	tcagagtg	ggt	tggaagaa	ta	tttcaaga	ga	tatgga	aggc	480
tgctgggatg	gataatg	aca	aagtagag	tt	ttgtgg	tgc	tccgaaga	aaa	ttaat	tctaa	540
ggcagataag	tattggc	ctc	ttgtgat	gga	cattgct	cgc	aaaaaca	agc	tcctaga	aat	600
cttaagggtg	gtgcagat	ta	tgggacg	tag	tgagact	gat	gaactga	gtg	ctgccag	act	660
cctttacc	tgcatg	caat	gtgcagat	at	ttttt	cctt	gaggctg	ata	ttggcag	ct	720
tggtgat	gat	caaa	gaaa	g	taa	Catgtgc	tagcgaga	ga	at	actgtgat	780
ggaaaaacaa	accgata	atc	ttgtcac	acc	atatg	cttcc	tggtctc	caa	caaggaca	ag	840
aaaaagatgc	caaaagtg	at	ccattat	ctg	ctatct	ttat	ggaagat	gaa	gaggctga	g	900
ttaatgtgaa	gatcaaga	aaa	gcttact	gcc	ctccaaa	agt	cgtgaagg	gc	aatcat	gcc	960
tcgaatacat	caaatacat	c	aaatacat	ca	ttctacc	atg	ggttgat	gag	ttcaac	agt	1020
agagaaatga	agaatat	ggc	ggtaa	caaga	cctacaaa	g	ctttgaag	ac	attgct	gtg	1080
actatgagag	cggcgag	ttg	caccctg	gcg	atctaaa	gaa	aggcctg	atg	aacgcg	ttga	1140
ataagatttt	gcaacct	gtt	cgtgat	catt	tcaaaa	caga	cgcacg	cgcg	aagaat	ctac	1200
tcaaacagat	caaggct	tac	agagtc	acca	gataaaa	ta	gagagc	caga	atgtgt	ctatt	1260
gaaagctt	ctctact	tta	tgaact	t	tattacca	aaa	aacacact	gt	aaaact	ctctg	1320
gattttgtt	atttgggt	at	atcagat	gct	c						

(2) INFORMATION FOR SEQ ID NO:145:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 140 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..140

(D) OTHER INFORMATION: / Ceres Seq. ID 1565966

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:145:

Met	Leu	Pro	Gly	Leu	Gln	Gln	Gly	Gln	Lys	Met	Ser	Lys	Ser	Asp
1			5					10				15		
Pro	Leu	Ser	Ala	Ile	Phe	Met	Glu	Asp	Glu	Glu	Ala	Glu	Val	Asn
			20					25				30		
Lys	Ile	Lys	Lys	Ala	Tyr	Cys	Pro	Pro	Lys	Val	Val	Lys	Gly	Asn
			35				40					45		
Cys	Leu	Glu	Tyr	Ile	Lys	Tyr	Ile	Lys	Tyr	Ile	Ile	Leu	Pro	Trp
			50				55				60			
Asp	Glu	Phe	Thr	Val	Glu	Arg	Asn	Glu	Glu	Tyr	Gly	Gly	Asn	Lys
			65				70				75			80
Tyr	Lys	Ser	Phe	Glu	Asp	Ile	Ala	Ala	Asp	Tyr	Glu	Ser	Gly	Glu
			85				90				95			
His	Pro	Gly	Asp	Leu	Lys	Lys	Gly	Leu	Met	Asn	Ala	Leu	Asn	Lys
			100				105					110		
Leu	Gln	Pro	Val	Arg	Asp	His	Phe	Lys	Thr	Asp	Ala	Arg	Ala	Lys
			115				120					125		
Leu	Leu	Lys	Gln	Ile	Lys	Ala	Tyr	Arg	Val	Thr	Arg			
			130				135				140			

(2) INFORMATION FOR SEQ ID NO:146:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..129

(D) OTHER INFORMATION: / Ceres Seq. ID 1565967

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:146:

```

Met Ser Lys Ser Asp Pro Leu Ser Ala Ile Phe Met Glu Asp Glu Glu
1          5          10          15
Ala Glu Val Asn Val Lys Ile Lys Lys Ala Tyr Cys Pro Pro Lys Val
20          25          30
Val Lys Gly Asn Pro Cys Leu Glu Tyr Ile Lys Tyr Ile
35          40          45
Ile Leu Pro Trp Phe Asp Glu Phe Thr Val Glu Arg Asn Glu Glu Tyr
50          55          60
Gly Gly Asn Lys Thr Tyr Lys Ser Phe Glu Asp Ile Ala Ala Asp Tyr
65          70          75          80
Glu Ser Gly Glu Leu His Pro Gly Asp Leu Lys Lys Gly Leu Met Asn
85          90          95
Ala Leu Asn Lys Ile Leu Gln Pro Val Arg Asp His Phe Lys Thr Asp
100          105          110
Ala Arg Ala Lys Asn Leu Leu Lys Gln Ile Lys Ala Tyr Arg Val Thr
115          120          125
Arg

```

(2) INFORMATION FOR SEQ ID NO:147:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 118 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..118
- (D) OTHER INFORMATION: / Ceres Seq. ID 1565968

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:147:

```

Met Glu Asp Glu Glu Ala Glu Val Asn Val Lys Ile Lys Lys Ala Tyr
1          5          10          15
Cys Pro Pro Lys Val Val Lys Gly Asn Pro Cys Leu Glu Tyr Ile Lys
20          25          30
Tyr Ile Lys Tyr Ile Ile Leu Pro Trp Phe Asp Glu Phe Thr Val Glu
35          40          45
Arg Asn Glu Glu Tyr Gly Gly Asn Lys Thr Tyr Lys Ser Phe Glu Asp
50          55          60
Ile Ala Ala Asp Tyr Glu Ser Gly Glu Leu His Pro Gly Asp Leu Lys
65          70          75          80
Lys Gly Leu Met Asn Ala Leu Asn Lys Ile Leu Gln Pro Val Arg Asp
85          90          95
His Phe Lys Thr Asp Ala Arg Ala Lys Asn Leu Leu Lys Gln Ile Lys
100          105          110
Ala Tyr Arg Val Thr Arg
115

```

(2) INFORMATION FOR SEQ ID NO:148:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1164 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1164
- (D) OTHER INFORMATION: / Ceres Seq. ID 1565973

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:148:

```

aattagctca aggagaatca aaAgcgtogt ctcttggtcC ttccgctgcc aacaaaatgg      60
agctgtcgctc tgcgtccgcc atattaagcc actcctcctc cgccgctcag ctctctcagac      120
ctaagctcgg gtttattgat tgcgttcctc gtcgagcgat gatgttttct tctccttctt      180

```

ctctcgcttcc	tcgatttttt	cggatggaat	ctcaatctca	gcttcgccaa	tctatctctt	240
gcctcgtcttc	ttctctctct	ttctatggcat	taggtagaat	tgagagaagta	aagagagtaa	300
caaaaggaaac	gaatgttttca	gtgaagatta	atttgatgg	tactggagtt	gcagatagtt	360
ctagtggaaat	tcctttctct	gaccatattgt	tagatcaact	tgcttcgcgt	ggcttgtttg	420
atgtgcacgt	tagagctact	gggtgatgttc	acattgatga	tcatacact	aatgaagata	480
tagctctttgc	cattggaaact	gctctatttaa	aggctctttg	tgagcgtaaaa	gggattaacc	540
gggtttggtga	cttcacagact	cctctagatg	aagcgcttat	acatgtttcc	ttggacttgt	600
ctggctgcacc	atatctttggt	tacaacttgg	agataccaa	tcagagagtt	ggaacatagt	660
atactcagtt	gggtgagcac	tttttccagt	cattggtgaa	tactctcgtt	atgactcttc	720
acatccggca	gctcgtctgt	gaaaactctc	atcacataat	agagggcagc	tttaaggcgt	780
ttgcacagc	tctacagcaa	gcaacagaga	ctgacCacg	ccgtggtggg	acaataccaa	840
gttcaaaagg	agctcttatca	cgtctctttaa	agctaataca	acacacaaga	cagttccocag	900
attcacactt	catcgtcgag	ttcatgagcc	atcgtcaatt	ctcttatggt	accaaatgcc	960
aagcctgttg	gatcttctgt	ttccattcca	ttacagaagc	acaaaagcga	aaatgtgaaa	1020
atagattaga	gatcacacag	ttcagaagat	cataggctca	tctttatatt	aactcgttgt	1080
tgacagtggt	attaaacctc	ttaccattgc	tgtatcatca	tcaactgaga	acttactgtg	1140
agttgaagtg	actgttaatt	gctc				

(2) INFORMATION FOR SEQ ID NO:149:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 288 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..288

(D) OTHER INFORMATION: / Ceres Seq. ID 1565974

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:149:

Leu	Ala	Gln	Gly	Glu	Ser	Lys	Ala	Ser	Ser	Leu	Val	Pro	Ser	Ala	Ala
1		5		10		15		20		25		30		35	
Asn	Lys	Met	Glu	Ser	Ser	Ala	Ser	Ala	Ile	Leu	Ser	His	Ser	Ser	
		20		25		30		35		40		45		50	
Ser	Ala	Ala	Gln	Leu	Leu	Arg	Pro	Lys	Leu	Gly	Phe	Ile	Asp	Leu	Leu
		35		40		45		50		55		60		65	
Pro	Arg	Arg	Ala	Met	Ile	Val	Ser	Ser	Pro	Ser	Ser	Ser	Leu	Pro	Arg
		50		55		60		65		70		75		80	
Phe	Leu	Arg	Met	Glu	Ser	Gln	Ser	Gln	Leu	Arg	Gln	Ser	Ile	Ser	Cys
65		70		75		80		85		90		95		100	
Ser	Ala	Ser	Ser	Ser	Ser	Met	Ala	Leu	Gly	Arg	Ile	Gly	Glu	Val	
		85		90		95		100		105		110		115	
Lys	Arg	Val	Thr	Lys	Glu	Thr	Asn	Val	Ser	Val	Lys	Ile	Asn	Leu	Asp
		100		105		110		115		120		125		130	
Gly	Thr	Gly	Val	Ala	Asp	Ser	Ser	Ser	Gly	Ile	Pro	Phe	Leu	Asp	His
		115		120		125		130		135		140		145	
Met	Leu	Asp	Gln	Leu	Ala	Ser	His	Gly	Leu	Phe	Asp	Val	His	Val	Arg
		130		135		140		145		150		155		160	
Ala	Thr	Gly	Asp	Val	His	Ile	Asp	Asp	His	His	Thr	Asn	Glu	Asp	Ile
145		150		155		160		165		170		175		180	
Ala	Leu	Ala	Ile	Gly	Thr	Ala	Leu	Leu	Lys	Ala	Leu	Gly	Glu	Arg	Lys
		165		170		175		180		185		190		195	
Gly	Ile	Asn	Arg	Phe	Gly	Asp	Phe	Thr	Ala	Pro	Leu	Asp	Glu	Ala	Leu
		180		185		190		195		200		205		210	
Ile	His	Val	Ser	Leu	Asp	Leu	Ser	Gly	Arg	Pro	Tyr	Leu	Gly	Tyr	Asn
		195		200		205		210		215		220		225	
Leu	Glu	Ile	Pro	Thr	Gln	Arg	Val	Gly	Thr	Tyr	Asp	Thr	Gln	Leu	Val
		210		215		220		225		230		235		240	
Glu	His	Phe	Phe	Gln	Ser	Leu	Val	Asn	Thr	Ser	Gly	Met	Thr	Leu	His
225		230		235		240		245		250		255		260	
Ile	Arg	Gln	Leu	Ala	Gly	Glu	Asn	Ser	His	His	Ile	Ile	Glu	Ala	Thr
		245		250		255		260		265		270		275	

Phe	Lys	Ala	Phe	Ala	Arg	Ala	Leu	Arg	Gln	Ala	Thr	Glu	Thr	Asp	Pro	
		260						265					270			
Arg	Arg	Gly	Gly	Thr	Ile	Pro	Ser	Ser	Lys	Gly	Val	Leu	Ser	Arg	Ser	
		275					280					285				

(2) INFORMATION FOR SEQ ID NO:150:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 270 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..270

(D) OTHER INFORMATION: / Ceres Seq. ID 1565975

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:150:

Met	Glu	Leu	Ser	Ser	Ala	Ser	Ala	Ile	Leu	Ser	His	Ser	Ser	Ser	Ala	
1			5					10						15		
Ala	Gln	Leu	Leu	Arg	Pro	Lys	Leu	Gly	Phe	Ile	Asp	Leu	Leu	Pro	Arg	
		20						25					30			
Arg	Ala	Met	Ile	Val	Ser	Ser	Pro	Ser	Ser	Ser	Leu	Pro	Arg	Phe	Leu	
		35					40				45					
Arg	Met	Glu	Ser	Gln	Ser	Gln	Leu	Arg	Gln	Ser	Ile	Ser	Cys	Ser	Ala	
		50				55					60					
Ser	Ser	Ser	Ser	Ser	Met	Ala	Leu	Gly	Arg	Ile	Gly	Glu	Val	Lys	Arg	
65					70				75					80		
Val	Thr	Lys	Glu	Thr	Asn	Val	Ser	Val	Lys	Ile	Asn	Leu	Asp	Gly	Thr	
				85					90				95			
Gly	Val	Ala	Asp	Ser	Ser	Ser	Gly	Ile	Pro	Phe	Leu	Asp	His	Met	Leu	
			100						105				110			
Asp	Gln	Leu	Ala	Ser	His	Gly	Leu	Phe	Asp	Val	His	Val	Arg	Ala	Thr	
		115					120					125				
Gly	Asp	Val	His	Ile	Asp	Asp	His	His	Thr	Asn	Glu	Asp	Ile	Ala	Leu	
		130				135					140					
Ala	Ile	Gly	Thr	Ala	Leu	Leu	Lys	Ala	Leu	Gly	Glu	Arg	Lys	Gly	Ile	
145				150					155					160		
Asn	Arg	Phe	Gly	Asp	Phe	Thr	Ala	Pro	Leu	Asp	Glu	Ala	Leu	Ile	His	
			165						170				175			
Val	Ser	Leu	Asp	Leu	Ser	Gly	Arg	Pro	Tyr	Leu	Gly	Tyr	Asn	Leu	Glu	
		180					185						190			
Ile	Pro	Thr	Gln	Arg	Val	Gly	Thr	Tyr	Asp	Thr	Gln	Leu	Val	Glu	His	
		195					200					205				
Phe	Phe	Gln	Ser	Leu	Val	Asn	Thr	Ser	Gly	Met	Thr	Leu	His	Ile	Arg	
		210				215					220					
Gln	Leu	Ala	Gly	Glu	Asn	Ser	His	His	Ile	Ile	Glu	Ala	Thr	Phe	Lys	
225					230					235					240	
Ala	Phe	Ala	Arg	Ala	Leu	Arg	Gln	Ala	Thr	Glu	Thr	Asp	Pro	Arg	Arg	
			245						250					255		
Gly	Gly	Thr	Ile	Pro	Ser	Ser	Lys	Gly	Val	Leu	Ser	Arg	Ser			
		260					265						270			

(2) INFORMATION FOR SEQ ID NO:151:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 236 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..236

(D) OTHER INFORMATION: / Ceres Seq. ID 1565976

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:151:

Met	Ile	Val	Ser	Ser	Pro	Ser	Ser	Ser	Leu	Pro	Arg	Phe	Leu	Arg	Met
1			5					10					15		
Glu	Ser	Gln	Ser	Gln	Leu	Arg	Gln	Ser	Ile	Ser	Cys	Ser	Ala	Ser	Ser
			20					25					30		
Ser	Ser	Ser	Met	Ala	Leu	Gly	Arg	Ile	Gly	Glu	Val	Lys	Arg	Val	Thr
			35				40					45			
Lys	Glu	Thr	Asn	Val	Ser	Val	Lys	Ile	Asn	Leu	Asp	Gly	Thr	Gly	Val
			50				55				60				
Ala	Asp	Ser	Ser	Ser	Gly	Ile	Pro	Phe	Leu	Asp	His	Met	Leu	Asp	Gln
65					70				75				80		
Leu	Ala	Ser	His	Gly	Leu	Phe	Asp	Val	His	Val	Arg	Ala	Thr	Gly	Asp
			85					90					95		
Val	His	Ile	Asp	Asp	His	His	Thr	Asn	Glu	Asp	Ile	Ala	Leu	Ala	Ile
			100					105					110		
Gly	Thr	Ala	Leu	Leu	Lys	Ala	Leu	Gly	Glu	Arg	Lys	Gly	Ile	Asn	Arg
			115				120					125			
Phe	Gly	Asp	Phe	Thr	Ala	Pro	Leu	Asp	Glu	Ala	Leu	Ile	His	Val	Ser
			130				135				140				
Leu	Asp	Leu	Ser	Gly	Arg	Pro	Tyr	Leu	Gly	Tyr	Asn	Leu	Glu	Ile	Pro
145					150				155						
Thr	Gln	Arg	Val	Gly	Thr	Tyr	Asp	Thr	Gln	Leu	Val	Glu	His	Phe	Phe
			165					170					175		
Gln	Ser	Leu	Val	Asn	Thr	Ser	Gly	Met	Thr	Leu	His	Ile	Arg	Gln	Leu
			180					185					190		
Ala	Gly	Glu	Asn	Ser	His	His	Ile	Ile	Glu	Ala	Thr	Phe	Lys	Ala	Phe
			195				200					205			
Ala	Arg	Ala	Leu	Arg	Gln	Ala	Thr	Glu	Thr	Asp	Pro	Arg	Arg	Gly	Gly
			210				215				220				
Thr	Ile	Pro	Ser	Ser	Lys	Gly	Val	Leu	Ser	Arg	Ser				
225					230					235					

(2) INFORMATION FOR SEQ ID NO:152:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1820 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1820

(D) OTHER INFORMATION: / Ceres Seq. ID 1565981

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:152:

acaatcattt	gattatttcc	tctctccgt	atctgtgtct	ctctctctct	gatcttttag	60
tggtcttgct	ttgtcgcttc	aacgcttaag	tttggaattg	tgtagctctg	cataatcatg	120
gcgaggaaga	tgcttgttga	tggtgagatt	gataaggttg	cgctgatgat	agccaacgcg	180
acgcactatg	attttgattt	gtttgtcatc	ggtgccggga	gtggcgtggt	tcgtgctgct	240
agggttttcg	gttaatcatg	cgctaagggt	ggtatttttg	agcttcacatt	tcacctatt	300
agcgtctagg	agattggagg	cgttggtgga	acctgtgtta	tcctgtggtg	tggtctctaaa	360
aagattctcg	tctatggagc	tacttacggt	ggtgaacctg	aggatgctaa	aaattatggg	420
tggaataata	atgagaaagt	cgacttcaca	tgggaagaagc	ttttgcaaaa	gaagactgat	480
gagataactga	gactgaataa	tatctacaag	cggttatgtg	caaatgctgc	ggtgaatttg	540
tatgaagctg	aaggaagagt	agttggtccc	aacgaagtgg	aggtagagca	atgatagggc	600
acaaaaataa	gtttataccg	aaagcacata	ttgattgcca	ctggcagctg	ggcgcaaaa	660
cctaattatc	ctggacatga	ggtgcttatt	acatctgatg	aagctttgag	cttggaaaga	720
tttcccaagg	gtgctatagt	gcttggagga	gggtatatgt	ctgtggagtt	tgcatcaata	780
tggtgtggaa	tggtgtctac	tgtagattta	ttcttcagga	aggaacttcc	cgtaaggggt	840
ttttagtacg	aaatgagggc	actagttgct	agaaactctg	aaggaagggg	cgttaatctg	900
catccacaaa	caagtttgac	tcagtttgaca	aaaacagacc	aggggatcaa	atgcatactg	960

tcccatgggg	aggaattcgt	ggcagatgtc	gtccatattg	ctactggcag	aagtccta	1020
acccaaaagt	tgaatttaga	agctgttggt	gttgaaactg	atcaggctgg	agctgtgaag	1080
gttgacgagt	attcacgaac	taataatact	agcatatggg	ctgtaggaga	tgcacaaac	1140
cgaattaacc	ttacacactg	tgcgttaaat	gaggccacct	gttttgcgaa	cactgtcttt	1200
gggtgaaagc	ctactaaagc	agaatacagc	aatgtgcgct	gtgctgtatt	ttgcatacca	1260
ccactagctg	tagtgggtct	cagcgaagaa	gaagcagtag	aacaagcaac	cggtgataatt	1320
ctgggtcttca	cctcaggctt	taatccaatg	aagaacacca	ttcttggacg	ccaggaaaaag	1380
acattgatga	agctaaatag	tgatgagaag	agtgataaag	ttattggagc	atccatgtgc	1440
ggctctgatg	cagctgagat	catgcagggg	attgcaattg	cgctcaagtg	tggagcaacc	1500
aaagcacaa	ttgatagcac	ggbtsggatG	CGCacatcca	tcttctgcag	aggaattttgt	1560
gacaattgcgc	agtgtgacca	gacgcattgc	ccacaaaccc	aaaccttaaga	caaattctatg	1620
aaocccaaaa	tataaagagc	tatatagcat	gaaaactcgg	tacacttagt	ttgatcaaaag	1680
agtcagacaa	cgatgagttt	aatcatactc	gtgtcccaat	aaaggatttg	taatttttgt	1740
ttgtttgtat	gatgtcttct	tcttacttta	cttgagaaaa	catcaagggt	tcttctctta	1800
ttgcttagtg	gaactttatt					

(2) INFORMATION FOR SEQ ID NO:153:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 496 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..496

(D) OTHER INFORMATION: / Ceres Seq. ID 1565982

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:153:

Met	Ala	Arg	Lys	Met	Leu	Val	Asp	Gly	Glu	Ile	Asp	Lys	Val	Ala	Ala
1				5					10					15	
Asp	Glu	Ala	Asn	Ala	Thr	His	Tyr	Asp	Phe	Asp	Leu	Phe	Val	Ile	Gly
			20					25					30		
Ala	Gly	Ser	Gly	Gly	Val	Arg	Ala	Arg	Phe	Ser	Ala	Asn	His	Gly	
			35				40					45			
Ala	Lys	Val	Gly	Ile	Cys	Glu	Leu	Pro	Phe	His	Pro	Ile	Ser	Ser	Glu
			50			55					60				
Glu	Ile	Gly	Gly	Val	Gly	Thr	Cys	Val	Ile	Arg	Gly	Cys	Val	Pro	
65				70				75					80		
Lys	Lys	Ile	Leu	Val	Tyr	Gly	Ala	Thr	Tyr	Gly	Gly	Glu	Leu	Glu	Asp
			85					90					95		
Ala	Lys	Asn	Tyr	Gly	Trp	Glu	Ile	Asn	Glu	Lys	Val	Asp	Phe	Thr	Trp
			100					105					110		
Lys	Lys	Leu	Leu	Gln	Lys	Lys	Thr	Asp	Glu	Ile	Leu	Arg	Leu	Asn	Asn
			115				120					125			
Ile	Tyr	Lys	Arg	Leu	Leu	Ala	Asn	Ala	Ala	Val	Lys	Leu	Tyr	Glu	Gly
			130			135						140			
Glu	Gly	Arg	Val	Val	Gly	Pro	Asn	Glu	Val	Glu	Val	Arg	Gln	Ile	Asp
145				150					155					160	
Gly	Thr	Lys	Ile	Ser	Tyr	Thr	Ala	Lys	His	Ile	Leu	Ile	Ala	Thr	Gly
			165					170					175		
Ser	Arg	Ala	Gln	Lys	Pro	Asn	Ile	Pro	Gly	His	Glu	Leu	Ala	Ile	Thr
			180				185						190		
Ser	Asp	Glu	Ala	Leu	Ser	Leu	Glu	Glu	Phe	Pro	Lys	Arg	Ala	Ile	Val
			195				200					205			
Leu	Gly	Gly	Gly	Tyr	Ile	Ala	Val	Glu	Phe	Ala	Ser	Ile	Trp	Arg	Gly
			210			215						220			
Met	Gly	Ala	Thr	Val	Asp	Leu	Phe	Phe	Arg	Lys	Glu	Leu	Pro	Leu	Arg
225				230					235					240	
Gly	Phe	Asp	Asp	Glu	Met	Arg	Ala	Leu	Val	Ala	Arg	Asn	Leu	Glu	Gly
			245					250					255		
Arg	Gly	Val	Asn	Leu	His	Pro	Gln	Thr	Ser	Leu	Thr	Gln	Leu	Thr	Lys
			260				265						270		

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Thr Asp Gln Gly Ile Lys Val Ile Ser Ser His Gly Glu Glu Phe Val
275 280 285
Ala Asp Val Val Leu Phe Ala Thr Gly Arg Ser Pro Asn Thr Lys Arg
290 295 300
Leu Asn Leu Glu Ala Val Gly Val Glu Leu Asp Gln Ala Gly Ala Val
305 310 315 320
Lys Val Asp Glu Tyr Ser Arg Thr Asn Ile Pro Ser Ile Trp Ala Val
325 330 335
Gly Asp Ala Thr Asn Arg Ile Asn Leu Thr Pro Val Ala Leu Met Glu
340 345 350
Ala Thr Cys Phe Ala Asn Thr Ala Phe Gly Gly Lys Pro Thr Lys Ala
355 360 365
Glu Tyr Ser Asn Val Ala Cys Ala Val Phe Cys Ile Pro Pro Leu Ala
370 375 380
Val Val Gly Leu Ser Glu Glu Glu Ala Val Glu Gln Ala Thr Gly Asp
385 390 395 400
Ile Leu Val Phe Thr Thr Ser Gly Phe Asn Pro Met Lys Asn Thr Ile Ser
405 410 415
Gly Arg Gln Glu Lys Thr Leu Met Lys Leu Ile Val Asp Glu Lys Ser
420 425 430
Asp Lys Val Ile Gly Ala Ser Met Cys Gly Pro Asp Ala Ala Glu Ile
435 440 445
Met Gln Gly Ile Ala Ile Ala Leu Lys Cys Gly Ala Thr Lys Ala Gln
450 455 460
Phe Asp Ser Thr Xaa Xaa Met Arg Thr Ser Ile Phe Cys Arg Gly Ile
465 470 475 480
Cys Asp Asn Ala Gln Cys Asp Gln Thr His Cys Pro Gln Thr Gln Thr
485 490 495

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(2) INFORMATION FOR SEQ ID NO:154:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 492 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..492
- (D) OTHER INFORMATION: / Ceres Seq. ID 1565983

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:154:

```

Met Leu Val Asp Gly Glu Ile Asp Lys Val Ala Ala Asp Glu Ala Asn
1 5 10 15
Ala Thr His Tyr Asp Phe Asp Leu Phe Val Ile Gly Ala Gly Ser Gly
20 25 30
Gly Val Arg Ala Ala Arg Phe Ser Ala Asn His Gly Ala Lys Val Gly
35 40 45
Ile Cys Glu Leu Pro Phe His Pro Ile Ser Ser Glu Glu Ile Gly Gly
50 55 60
Val Gly Gly Thr Cys Val Ile Arg Gly Cys Val Pro Lys Lys Ile Leu
65 70 75 80
Val Tyr Gly Ala Thr Tyr Gly Gly Glu Leu Glu Asp Ala Lys Asn Tyr
85 90 95
Gly Trp Glu Ile Asn Glu Lys Val Asp Phe Thr Trp Lys Lys Leu Leu
100 105 110
Gln Lys Lys Thr Asp Glu Ile Leu Arg Leu Asn Asn Ile Tyr Lys Arg
115 120 125
Leu Leu Ala Asn Ala Ala Val Lys Leu Tyr Glu Gly Glu Gly Arg Val
130 135 140
Val Gly Pro Asn Glu Val Glu Val Arg Gln Ile Asp Gly Thr Lys Ile

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145 150 155 160
Ser Tyr Thr Ala Lys His Ile Leu Ile Ala Thr Gly Ser Arg Ala Gln
165 170 175
Lys Pro Asn Ile Pro Gly His Glu Leu Ala Ile Thr Ser Asp Glu Ala
180 185 190
Leu Ser Leu Glu Glu Phe Pro Lys Arg Ala Ile Val Leu Gly Gly Gly
195 200 205
Tyr Ile Ala Val Glu Phe Ala Ser Ile Trp Arg Gly Met Gly Ala Thr
210 215 220
Val Asp Leu Phe Phe Arg Lys Glu Leu Pro Leu Arg Gly Phe Asp Asp
225 230 235 240
Glu Met Arg Ala Leu Val Ala Arg Asn Leu Glu Gly Arg Gly Val Asn
245 250 255
Leu His Pro Gln Thr Ser Leu Thr Gln Leu Thr Lys Thr Asp Gln Gly
260 265 270
Ile Lys Val Ile Ser Ser His Gly Glu Glu Phe Val Ala Asp Val Val
275 280 285
Leu Phe Ala Thr Gly Arg Ser Pro Asn Thr Lys Arg Leu Asn Leu Glu
290 295 300
Ala Val Gly Val Glu Leu Asp Gln Ala Gly Ala Val Lys Val Asp Glu
305 310 315 320
Tyr Ser Arg Thr Asn Ile Pro Ser Ile Trp Ala Val Gly Asp Ala Thr
325 330 335
Asn Arg Ile Asn Leu Thr Pro Val Ala Leu Met Glu Ala Thr Cys Phe
340 345 350
Ala Asn Thr Ala Phe Gly Gly Lys Pro Thr Lys Ala Glu Tyr Ser Asn
355 360 365
Val Ala Cys Ala Val Phe Cys Ile Pro Pro Leu Ala Val Val Gly Leu
370 375 380
Ser Glu Glu Glu Ala Val Glu Gln Ala Thr Gly Asp Ile Leu Val Phe
385 390 395 400
Thr Ser Gly Phe Asn Pro Met Lys Asn Thr Thr Ile Ser Gly Arg Gln Glu
405 410 415
Lys Thr Leu Met Lys Leu Ile Val Asp Glu Lys Ser Asp Lys Val Ile
420 425 430
Gly Ala Ser Met Cys Gly Pro Asp Ala Ala Glu Ile Met Gln Gly Ile
435 440 445
Ala Ile Ala Leu Lys Cys Gly Ala Thr Lys Ala Gln Phe Asp Ser Thr
450 455 460
Xaa Xaa Met Arg Thr Ser Ile Phe Cys Arg Gly Ile Cys Asp Asn Ala
465 470 475 480
Gln Cys Asp Gln Thr His Cys Pro Gln Thr Gln Thr
485 490

(2) INFORMATION FOR SEQ ID NO:155:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 272 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..272

(D) OTHER INFORMATION: / Ceres Seq. ID 1565984

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:155:

Met Gly Ala Thr Val Asp Leu Phe Phe Arg Lys Glu Leu Pro Leu Arg
1 5 10 15
Gly Phe Asp Asp Glu Met Arg Ala Leu Val Ala Arg Asn Leu Glu Gly
20 25 30
Arg Gly Val Asn Leu His Pro Gln Thr Ser Leu Thr Gln Leu Thr Lys
35 40 45

Thr	Asp	Gln	Gly	Ile	Lys	Val	Ile	Ser	Ser	His	Gly	Glu	Glu	Phe	Val
50					55						60				
Ala	Asp	Val	Val	Leu	Phe	Ala	Thr	Gly	Arg	Ser	Pro	Asn	Thr	Lys	Arg
65					70					75				80	
Leu	Asn	Leu	Glu	Ala	Val	Gly	Val	Glu	Leu	Asp	Gln	Ala	Gly	Ala	Val
				85					90					95	
Lys	Val	Asp	Glu	Tyr	Ser	Arg	Thr	Asn	Ile	Pro	Ser	Ile	Trp	Ala	Val
				100				105					110		
Gly	Asp	Ala	Thr	Asn	Arg	Ile	Asn	Leu	Thr	Pro	Val	Ala	Leu	Met	Glu
		115					120					125			
Ala	Thr	Cys	Phe	Ala	Asn	Thr	Ala	Phe	Gly	Gly	Lys	Pro	Thr	Lys	Ala
		130				135					140				
Glu	Tyr	Ser	Asn	Val	Ala	Cys	Ala	Val	Phe	Cys	Ile	Pro	Pro	Leu	Ala
145					150					155				160	
Val	Val	Gly	Leu	Ser	Glu	Glu	Glu	Ala	Val	Glu	Gln	Ala	Thr	Gly	Asp
				165					170					175	
Ile	Leu	Val	Phe	Thr	Ser	Gly	Phe	Asn	Pro	Met	Lys	Asn	Thr	Ile	Ser
				180				185					190		
Gly	Arg	Gln	Glu	Lys	Thr	Leu	Met	Lys	Leu	Ile	Val	Asp	Glu	Lys	Ser
		195					200					205			
Asp	Lys	Val	Ile	Gly	Ala	Ser	Met	Cys	Gly	Pro	Asp	Ala	Ala	Glu	Ile
		210				215					220				
Met	Gln	Gly	Ile	Ala	Ile	Ala	Leu	Lys	Cys	Gly	Ala	Thr	Lys	Ala	Gln
225					230					235				240	
Phe	Asp	Ser	Thr	Xaa	Xaa	Met	Arg	Thr	Ser	Ile	Phe	Cys	Arg	Gly	Ile
				245					250					255	
Cys	Asp	Asn	Ala	Gln	Cys	Asp	Gln	Thr	His	Cys	Pro	Gln	Thr	Gln	Thr
				260				265						270	

(2) INFORMATION FOR SEQ ID NO:156:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1312 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1312

(D) OTHER INFORMATION: / Ceres Seq. ID 1566011

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:156:

tccctgaagc	gtctctttct	tcctctgccc	ttctgttttt	ttgttttctg	cgtctctctc	60
tcccgctctg	aaaaaatcgc	agaatccgtc	atgtctctcc	gcgtaaatcc	aactggctcc	120
gcgcgcagcg	cacccggaggt	tgacaagatg	ttctttctgt	accagtgcaa	caaacacgct	180
acaactctcaa	ttctctctac	cgctgatcct	ttttgtccaa	ttgttaacca	agggtttctt	240
gaagaatcag	aagaccctaa	ccctaataca	tcctccaatt	tcaaccctaa	ctctctctgat	300
tcctttttcc	ccatggccga	tcctttctcc	accttgctcc	cgctcatatt	cggtctctcc	360
gctgcgcctc	cttccggcat	ggacttcatg	agcttattcg	gtccttcgat	gcaaccacag	420
gctcgttcca	ctcagcagaa	tcctcagttc	gacgcgtttg	atcgcgtttc	gtttcttcag	480
aatcatctcc	agactttgcg	atctagcggg	acgcactttg	agttcgtgat	cgagaatcat	540
ccttgatcgc	caggttaatg	tatgcctggg	aatttcgggt	attactctct	tggtccaggt	600
cttgagcagt	tgattcagca	actagctgag	aatgatccca	atcgtttacg	aactcctcct	660
gcttcccaat	ccgccattga	tgctcttctc	actgttaagg	taacgaagga	tatgttgaaa	720
tccgagatga	accaatcgcc	ggtgtgtatg	gatgagtttg	aggatgtagg	cgatgttaag	780
catagtcctt	gtaagcacgt	ctttcatcag	gactgtttgc	tccttgggct	ggagttgcgt	840
aattcgtgtc	ctgttttgtc	attccaggtg	Cctacgggat	attcctgatta	tgagaacagg	900
agtcacggaa	gtcagggggc	tggtgatgga	cgaggatcgg	ttgaggggtc	cgagacggcg	960
aggttttaga	tacaactctc	ttggccgttc	aggagacaa	atggctctcg	ttcaggctcg	1020
ggagcacctg	gtgctggtgg	aggttaattc	gagacacagg	gtgaagattt	ggatggagaa	1080
tgtgttggtc	agtcattgct	tggaactcgg	atcagaagga	tatctatccc	aagtctccca	1140

(2) INFORMATION FOR SEQ ID NO:157:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 358 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ix) FEATURE:

(B) LOCATION: 1..358

SEQUENCE DESCRIPTION: SEO ID NO:157:

[illegible]

(2) INFORMATION FOR SEQ ID NO:158:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 328 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..328
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1566013

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:158:

Met	Ser	Ser	Gly	Val	Asn	Ser	Thr	Gly	Ser	Ala	Ala	Ala	Ala	Pro	Glu
1				5				10						15	
Val	Asp	Lys	Met	Phe	Phe	Cys	Tyr	Gln	Cys	Asn	Gln	Thr	Val	Thr	Ile
		20						25					30		
Ser	Ile	Ser	Ser	Ser	Ala	Asp	Pro	Phe	Cys	Pro	Ile	Cys	Asn	Gln	Gly
		35					40					45			
Phe	Leu	Glu	Glu	Tyr	Glu	Asp	Pro	Asn	Pro	Asn	Gln	Ser	Leu	Asn	Phe
		50				55					60				
Asn	Pro	Asn	Ser	Ser	Asp	Ser	Phe	Phe	Pro	Met	Ala	Asp	Pro	Phe	Ser
				70						75				80	
Thr	Leu	Leu	Pro	Leu	Ile	Phe	Gly	Ser	Ser	Ala	Ala	Ala	Pro	Ser	Gly
			85					90						95	
Met	Asp	Phe	Met	Ser	Leu	Phe	Gly	Pro	Ser	Met	Gln	Pro	Gln	Ala	Arg
			100					105					110		
Ser	Thr	Gln	Gln	Asn	Pro	Gln	Ser	Asp	Ala	Phe	Asp	Pro	Phe	Thr	Phe
			115					120					125		
Leu	Gln	Asn	His	Leu	Gln	Thr	Leu	Arg	Ser	Ser	Gly	Thr	His	Phe	Glu
			130				135				140				
Phe	Val	Ile	Glu	Asn	His	Pro	Ser	Asp	Pro	Gly	Asn	Arg	Met	Pro	Gly
			145				150				155			160	
Asn	Phe	Gly	Asp	Tyr	Phe	Phe	Gly	Pro	Gly	Leu	Glu	Gln	Leu	Ile	Gln
			165						170					175	
Gln	Leu	Ala	Glu	Asn	Asp	Pro	Asn	Arg	Tyr	Gly	Thr	Pro	Pro	Ala	Ser
			180					185					190		
Lys	Ser	Ala	Ile	Asp	Ala	Leu	Pro	Thr	Val	Lys	Val	Thr	Lys	Asp	Met
			195				200					205			
Leu	Lys	Ser	Glu	Met	Asn	Gln	Cys	Ala	Val	Cys	Met	Asp	Glu	Phe	Glu
			210				215				220				
Asp	Gly	Ser	Asp	Val	Lys	Gln	Met	Pro	Cys	Lys	His	Val	Phe	His	Gln
			225			230				235				240	
Asp	Cys	Leu	Leu	Pro	Trp	Leu	Glu	Leu	His	Asn	Ser	Cys	Pro	Val	Cys
			245					250						255	
Arg	Phe	Glu	Leu	Pro	Thr	Asp	Asp	Pro	Asp	Tyr	Glu	Asn	Arg	Ser	Gln
			260				265						270		
Gly	Ser	Gln	Gly	Ser	Gly	Asp	Gly	Arg	Gly	Ser	Val	Glu	Gly	Gln	Gln
			275				280					285			
Thr	Pro	Arg	Phe	Ser	Ile	Gln	Leu	Pro	Trp	Pro	Phe	Arg	Arg	Gln	Asp
			290				295				300				
Gly	Ser	Gly	Ser	Gly	Ser	Gly	Ala	Pro	Gly	Ala	Gly	Gly	Gly	Asn	Leu
			305			310				315					320
Glu	Thr	Arg	Gly	Glu	Asp	Leu	Asp								
						325									

(2) INFORMATION FOR SEQ ID NO:159:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 309 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..309

(D) OTHER INFORMATION: / Ceres Seq. ID 1566014

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:159:

Met	Phe	Phe	Cys	Tyr	Gln	Cys	Asn	Gln	Thr	Val	Thr	Ile	Ser	Ile	Ser
1			5					10					15		
Ser	Ser	Ala	Asp	Pro	Phe	Cys	Pro	Ile	Cys	Asn	Gln	Gly	Phe	Leu	Glu
		20						25				30			
Glu	Tyr	Glu	Asp	Pro	Asn	Pro	Asn	Gln	Ser	Leu	Asn	Phe	Asn	Pro	Asn
	35					40					45				
Ser	Ser	Asp	Ser	Phe	Phe	Pro	Met	Ala	Asp	Pro	Phe	Ser	Thr	Leu	Leu
	50				55						60				
Pro	Leu	Ile	Phe	Gly	Ser	Ser	Ala	Ala	Ala	Pro	Ser	Gly	Met	Asp	Phe
65				70					75					80	
Met	Ser	Leu	Phe	Gly	Pro	Ser	Met	Gln	Pro	Gln	Ala	Arg	Ser	Thr	Gln
			85					90					95		
Gln	Asn	Pro	Gln	Ser	Asp	Ala	Phe	Asp	Pro	Phe	Thr	Phe	Leu	Gln	Asn
		100						105					110		
His	Leu	Gln	Thr	Leu	Arg	Ser	Ser	Gly	Thr	His	Phe	Glu	Phe	Val	Ile
	115					120						125			
Glu	Asn	His	Pro	Ser	Asp	Pro	Gly	Asn	Arg	Met	Pro	Gly	Asn	Phe	Gly
	130				135						140				
Asp	Tyr	Phe	Phe	Gly	Pro	Gly	Leu	Glu	Gln	Leu	Ile	Gln	Gln	Leu	Ala
145				150					155					160	
Glu	Asn	Asp	Pro	Asn	Arg	Tyr	Gly	Thr	Pro	Pro	Ala	Ser	Lys	Ser	Ala
			165						170					175	
Ile	Asp	Ala	Leu	Pro	Thr	Val	Lys	Val	Thr	Lys	Asp	Met	Leu	Lys	Ser
		180						185					190		
Glu	Met	Asn	Gln	Cys	Ala	Val	Cys	Met	Asp	Glu	Phe	Glu	Asp	Gly	Ser
		195						200					205		
Asp	Val	Lys	Gln	Met	Pro	Cys	Lys	His	Val	Phe	His	Gln	Asp	Cys	Leu
	210					215						220			
Leu	Pro	Trp	Leu	Glu	Leu	His	Asn	Ser	Cys	Pro	Val	Cys	Arg	Phe	Glu
225					230					235				240	
Leu	Pro	Thr	Asp	Asp	Pro	Asp	Tyr	Glu	Asn	Arg	Ser	Gln	Gly	Ser	Gln
			245						250					255	
Gly	Ser	Gly	Asp	Gly	Arg	Gly	Ser	Val	Glu	Gly	Gln	Gln	Thr	Pro	Arg
		260						265					270		
Phe	Ser	Ile	Gln	Leu	Pro	Trp	Pro	Phe	Arg	Arg	Gln	Asp	Gly	Ser	Gly
		275					280						285		
Ser	Gly	Ser	Gly	Ala	Pro	Gly	Ala	Gly	Gly	Gly	Asn	Leu	Glu	Thr	Arg
	290					295					300				
Gly	Glu	Asp	Leu	Asp											
305															

(2) INFORMATION FOR SEQ ID NO:160:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 766 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..766

(D) OTHER INFORMATION: / Ceres Seq. ID 1566024

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:160:

acgtgtcctc	agcttgaaca	gataattctg	cgactcttga	gaaaggaaga	cgaaggaagg	60
agaatagttag	aagaagaaga	aaggagagtg	cttgatgatat	ctacgtagaaa	ggaagatggc	120
cttatctcaaa	gtgtctcgct	ctctcgcctt	ttctcttccc	aattctcggtg	ccctaagagc	180
agccacaatc	acaaacccaa	cttctacatg	tcgggtttcat	gttccgcaac	ttgctggaat	240

ccgatccacc ttgccttctg gttctcctct cttgccattg aagttgagta tgacccgtag 300
aggaggaaac agagcagcat cagtttccat aagaagttag caaagtacag aaggaagcag 360
tggtttgat atatggttg gtcgtggcgc catggttggt ttgocagttg ccattactgt 420
tgaaatttcc actggaanaa gacttcttga gaattttgga gtacgaagtc cattgCctac 480
ggttgcttta gctgttacag cattgggttg ggttctagct gcgggtttca tcttccaatc 540
ttcttctaaa aactgatcaa caagaatctt gtttgtagt ctgccgagga tcatttttctt 600
gtattaagaa tcttgatata tatatcactg taacttctac atccatcagt ggaaaaaatc 660
ttacattctt agtttttttt ggcaacatac atgatctata catgtctttt ggccaaatct 720
tatttttgta tttttaaaac atgatctata acatgtatta agtttg

(2) INFORMATION FOR SEQ ID NO:161:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 146 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..146

(D) OTHER INFORMATION: / Ceres Seq. ID 1566025

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:161:

Met Ala Leu Ser Gln Val Ser Ala Ser Leu Ala Phe Ser Leu Pro Asn
1 5 10 15
Ser Gly Ala Leu Lys Leu Ala Thr Ile Thr Asn Pro Thr Ser Thr Cys
20 25 30
Arg Val His Val Pro Gln Leu Ala Gly Ile Arg Ser Thr Phe Ala Ser
35 40 45
Gly Ser Pro Leu Leu Pro Leu Lys Leu Ser Met Thr Arg Arg Gly Gly
50 55 60
Asn Arg Ala Ala Ser Val Ser Ile Arg Ser Glu Gln Ser Thr Glu Gly
65 70 75 80
Ser Ser Gly Leu Asp Ile Trp Leu Gly Arg Gly Ala Met Val Gly Phe
85 90 95
Ala Val Ala Ile Thr Val Glu Ile Ser Thr Gly Lys Gly Leu Leu Glu
100 105 110
Asn Phe Gly Val Ala Ser Pro Leu Pro Thr Val Ala Leu Ala Val Thr
115 120 125
Ala Leu Val Gly Val Leu Ala Ala Val Phe Ile Phe Gln Ser Ser Ser
130 135 140
Lys Asn
145

(2) INFORMATION FOR SEQ ID NO:162:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 88 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..88

(D) OTHER INFORMATION: / Ceres Seq. ID 1566026

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:162:

Met Thr Arg Arg Gly Gly Asn Arg Ala Ala Ser Val Ser Ile Arg Ser
1 5 10 15
Glu Gln Ser Thr Glu Gly Ser Ser Gly Leu Asp Ile Trp Leu Gly Arg
20 25 30
Gly Ala Met Val Gly Phe Ala Val Ala Ile Thr Val Glu Ile Ser Thr
35 40 45
Gly Lys Gly Leu Leu Glu Asn Phe Gly Val Ala Ser Pro Leu Pro Thr
50 55 60

Val Ala Leu Ala Val Thr Ala Leu Val Gly Val Leu Ala Ala Val Phe
65 70 75 80
Ile Phe Gln Ser Ser Ser Lys Asn
95

(2) INFORMATION FOR SEQ ID NO:163:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1610 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1610

(D) OTHER INFORMATION: / Ceres Seq. ID 1566031

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:163:

```
tctcttttct ttcactctct gttttgttct ttatgcctcg agaattgatg tggattttttc    60
atatattcagt taactcttagc taattgactt gaaattcaat gaaaagattc aatttttgggt    120
ttaattaaagc aagttgtgag atagatgaac gaatttgttg accaattgcg ttttacaggga    180
tacggttgggt gctctatgaa gtcttataga ttatctgaac ttagtctctc ccaagttgat    240
agtttgaagt cagccctcgc cattgacctc tcttctattt tcgccactgt gaacccgatt    300
atcgatgctg ttcgtagcaa tggggataat gctgtcaaag aatacactga aagatttgac    360
aaagtccagc tgaataaagt tgtggaagat atgtctgagc ttctgtgtcc tgagctcgat    420
tcacaatgtca aagaagcggt tgcgtgtgag tatgacaaca tatatgcgtt tcaactgacc    480
caaaaagtc aa ctgagaaaag cggttgagaat atgaaaaggtg tcagatgtaa aaggggtgca    540
agatctattg gcctcttagg tcTtTaWkt gcctgggtgga acagctgttt tgccatcaac    600
ggcctttgatg ctgtctattc ctgctcaaat tgctggatgt aaaaacagttg ttcttgcaac    660
tcacccaagt aagatggaaa gcatttgtaa ggaaggttctg tattgcgcca agagggctgg    720
tgtaactcac atactcaaa gctgggtgagc gcaggctata gctgccatgg cctgggggag    780
agatctcttg ccaaaagttg agaagatttt tggctcctggg aaccagtatg tcacagctgc    840
taagatgatt ctccaaaaca gcgaggcaat ggtctcaatc gatatgcctg ctggtccttc    900
agaagtctca gttattgtcg actgaacatgc tagtccagtt tacattgcag cagactactc    960
ttctcaggcg gagcatggtc cagatagtc aagtgttctt gtatgtgtgg gcgagtagtg    1020
agatctcaac gccatcgaag aagaaattgc caagcagtg aaaagccttc ctagaggaga    1080
gtttgtctca aagcactaaa gtcacagttt cacagtggtt gctcgagata tgattgaggc    1140
aatatctttc tcaaatctat atgcacccga acatttgatc atcaatgtca aagacgctga    1200
gaaatggggg ggactgatt agaacgcagg ctcggttttc ataggacat ggaactccaga    1260
gagtggtggg gattatgcga gcgggacaaa ccacgttctt ccaacatagc gatatgcagg    1320
aatgtacagt ggcgtctctc tcgactcttt cctaaaagttc atgactgtac aatctttgac    1380
agaggaaaggt ctgagaaaac tcggccctta ttagcaaac atggctgaaa tcgaaggttt    1440
agatgcacac aagagagccg ttactctcag actcaaggt atcgaagcca aacagcttgc    1500
ataatccaat tgagatttat attcagacaa aagagcgcaa aattcttttt gtattgtatg    1560
aacatatttg gtttctcgag attggaatac aataaaataa gagatgttgg
```

(2) INFORMATION FOR SEQ ID NO:164:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 298 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..298

(D) OTHER INFORMATION: / Ceres Seq. ID 1566032

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:164:

```
Met Leu Ala Ile Pro Ala Gln Ile Ala Gly Cys Lys Thr Val Leu
1 5 10 15
Ala Thr Pro Pro Ser Lys Asp Gly Ser Ile Cys Lys Glu Val Leu Tyr
20 25 30
Cys Ala Lys Arg Ala Gly Val Thr His Ile Leu Lys Ala Gly Gly Ala
35 40 45
```

Gln Ala Ile Ala Ala Met Ala Trp Gly Thr Asp Ser Cys Pro Lys Val
50 55 60
Glu Lys Ile Phe Gly Pro Gly Asn Gln Tyr Val Thr Ala Ala Lys Met
65 70 75 80
Ile Leu Gln Asn Ser Glu Ala Met Val Ser Ile Asp Met Pro Ala Gly
85 90 95
Pro Ser Glu Val Leu Val Ile Ala Asp Glu His Ala Ser Pro Val Tyr
100 105 110
Ile Ala Ala Asp Leu Leu Ser Gln Ala Glu His Gly Pro Asp Ser Gln
115 120 125
Val Val Leu Val Val Val Gly Asp Ser Val Asp Leu Asn Ala Ile Glu
130 135 140
Glu Glu Ile Ala Lys Gln Cys Lys Ser Leu Pro Arg Gly Glu Phe Ala
145 150 155 160
Ser Lys Ala Leu Ser His Ser Phe Thr Val Phe Ala Arg Asp Met Ile
165 170 175
Glu Ala Ile Ser Phe Ser Asn Leu Tyr Ala Pro Glu His Leu Ile Ile
180 185 190
Asn Val Lys Asp Ala Glu Lys Trp Glu Gly Leu Ile Glu Asn Ala Gly
195 200 205
Ser Val Phe Ile Gly Pro Trp Thr Pro Glu Ser Val Gly Asp Tyr Ala
210 215 220
Ser Gly Thr Asn His Val Leu Pro Thr Tyr Gly Tyr Ala Arg Met Tyr
225 230 235 240
Ser Gly Val Ser Leu Asp Ser Phe Leu Lys Phe Met Thr Val Gln Ser
245 250 255
Leu Thr Glu Glu Gly Leu Arg Asn Leu Gly Pro Tyr Val Ala Thr Met
260 265 270
Ala Glu Ile Glu Gly Leu Asp Ala His Lys Arg Ala Val Thr Leu Arg
275 280 285
Leu Lys Asp Ile Glu Ala Lys Gln Leu Ala
290 295

(2) INFORMATION FOR SEQ ID NO:165:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 245 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..245
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566033

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:165:

Met Ala Trp Gly Thr Asp Ser Cys Pro Lys Val Glu Lys Ile Phe Gly
1 5 10 15
Pro Gly Asn Gln Tyr Val Thr Ala Ala Lys Met Ile Leu Gln Asn Ser
20 25 30
Glu Ala Met Val Ser Ile Asp Met Pro Ala Gly Pro Ser Glu Val Leu
35 40 45
Val Ile Ala Asp Glu His Ala Ser Pro Val Tyr Ile Ala Ala Asp Leu
50 55 60
Leu Ser Gln Ala Glu His Gly Pro Asp Ser Gln Val Val Leu Val Val
65 70 75 80
Val Gly Asp Ser Val Asp Leu Asn Ala Ile Glu Glu Glu Ile Ala Lys
85 90 95
Gln Cys Lys Ser Leu Pro Arg Gly Glu Phe Ala Ser Lys Ala Leu Ser
100 105 110
His Ser Phe Thr Val Phe Ala Arg Asp Met Ile Glu Ala Ile Ser Phe
115 120 125
Ser Asn Leu Tyr Ala Pro Glu His Leu Ile Ile Asn Val Lys Asp Ala

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 472 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..472

(D) OTHER INFORMATION: / Ceres Seq. ID 1566045

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:167:

aattcatttc	ataatcatatc	acctctctac	atttgttact	actttctctt	aacttgtttt	60
caaaagagaaa	tcacaatcta	tctgttccaa	gatgagtc	tacagccaaa	accaatcttc	120
aggagcttat	cctacgccgc	cagtgtctac	cgcccttac	gtggcaccgc	caccgctagg	180
ttaccaacag	aacgacacaa	gtcatgccac	ggtggcaacg	gtggagacaa	agtccaaggg	240
tgatggattc	ttaaaaggct	gtcttgcggc	catgtgtgtg	tgttgtgtcc	tcgacgcgat	300
cttctgaaga	cttagatggg	ttattttgat	tatctttgta	ttttgtttta	ccaaaatgat	360
ctgactaggt	ttatgacatt	tggtacttct	atttgttaat	tcatttctat	atcaactctt	420
ctWttKgc	at	tgtgtaatt	tataaattck	taatatatcg	ttgttttct	ct

(2) INFORMATION FOR SEQ ID NO:168:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 80 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..80

(D) OTHER INFORMATION: / Ceres Seq. ID 1566046

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:168:

Asn	Ser	Phe	His	Asn	His	Thr	Pro	Leu	Tyr	Ile	Cys	Tyr	Tyr	Phe	Leu
1			5					10						15	
Leu	Thr	Cys	Phe	Gln	Arg	Glu	Ile	Thr	Ile	Tyr	Leu	Phe	Gln	Asp	Glu
			20					25					30		
Ser	Ile	Gln	Pro	Lys	Pro	Ile	Phe	Arg	Ser	Leu	Ser	Tyr	Ala	Ala	Ser
			35				40					45			
Val	Tyr	Arg	Pro	Leu	Arg	Gly	Thr	Ala	Thr	Ala	Arg	Leu	Pro	Asn	Glu
			50				55				60				
Arg	His	Lys	Ser	Cys	His	Gly	Gly	Asn	Gly	Gly	Asp	Lys	Val	Gln	Gly
65					70				75					80	

(2) INFORMATION FOR SEQ ID NO:169:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 71 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..71

(D) OTHER INFORMATION: / Ceres Seq. ID 1566047

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:169:

Met	Ser	Gln	Tyr	Ser	Gln	Asn	Gln	Ser	Ser	Gly	Ala	Tyr	Pro	Thr	Pro
1			5					10						15	
Pro	Val	Ser	Thr	Gly	Pro	Tyr	Val	Ala	Pro	Pro	Pro	Leu	Gly	Tyr	Pro
			20					25					30		
Thr	Asn	Asp	Thr	Ser	His	Ala	Thr	Val	Ala	Thr	Val	Glu	Thr	Lys	Ser
			35				40					45			
Lys	Gly	Asp	Gly	Phe	Leu	Lys	Gly	Cys	Leu	Ala	Ala	Met	Cys	Cys	Cys
			50				55				60				
Cys	Val	Leu	Asp	Ala	Cys	Phe									
65					70										

(2) INFORMATION FOR SEQ ID NO:170:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1268 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1268

(D) OTHER INFORMATION: / Ceres Seq. ID 1566048

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:170:

taggaagat	gatccaagc	tgcgcgctt	agctcagact	aaagttgaaa	accgtgacga	60
aGttagagct	gatcatcgc	gtattagaca	ggctgagatt	atatctacgg	aagaagaaga	120
atcgaggaat	caagagaata	gagacgagga	tgatgatgaa	gatgccttgg	aagaagaaga	180
aagaagaatt	aaggagaaga	atcttagact	agcacaagag	gaggtgcttt	tacttccctt	240
agaagaagaa	gatgagatac	aagaggaaga	agaggaggag	gaggagctcg	agtacgagac	300
tgattcggaa	gatgatatgc	ctggtattgc	cttgattaa	cctgtttttg	taccgaaagc	360
tgagagagat	acaattgcag	agcagagagag	gcttgaggct	gaagaagaag	ctcttgagga	420
attagcaaat	agaaaaattg	agcaaaagaa	aatagagaca	aagcaaat	tggttgagga	480
agttaggaaa	gatgaagaga	tacggaagaa	catactattg	gaggaagcta	atattggaga	540
tgttggaact	gatgacgaac	tcaatgaagc	tgaggagtat	gaagtttgga	agacaagaga	600
gattggttag	atcaagagag	aaagagatgc	aagggaagct	atgctgagag	agagggaaaga	660
aatagagaag	ttgagggaata	tgacagagca	ggagaggaga	gattgggaga	ggaagaatacc	720
gaaacctctt	tcagctcaac	cgaaaaagaa	atggaaactt	atgcagaaat	attaccataa	780
gggtgccttc	tccagcgag	atcctgatga	tgaggcaggt	tctgctggaa	cagatggat	840
atttcagcgc	gacttctctg	ctccaaccgg	agaagatagg	ttggacaaat	cgattctccc	900
caaatgtatg	caagctcaagc	actttggtcg	tagtggaaga	actaatgata	ctcaccttgt	960
caatgaagac	acaacagatt	ggagtaaccc	gtggacttcc	aatgatcttc	tacgtgaaaa	1020
atacaacaag	aaaatggcag	gcattggatgc	tccaatcgca	aaaccaaag	ggagcaagaa	1080
gatgaagaat	tgaggagact	aaacccgacc	aacatttact	ttgtttgttt	ttaaaatcca	1140
atgatgcagc	agtggttatgt	ggtagtataa	aaacatcgta	acatcttact	cagttatgtc	1200
tctgagtctc	ctaaatccta	gtaattaaaa	atttgtctca	aaagaatgaa	gacctaacat	1260
aattcatt						

(2) INFORMATION FOR SEQ ID NO:171:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 366 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..366

(D) OTHER INFORMATION: / Ceres Seq. ID 1566049

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:171:

Arg	Lys	Asp	Asp	Pro	Arg	Leu	Arg	Arg	Leu	Ala	Gln	Thr	Lys	Val	Glu
1		5							10					15	
Asn	Arg	Asp	Glu	Val	Arg	Ala	Asp	His	Arg	Arg	Ile	Arg	Gln	Ala	Glu
		20						25					30		
Ile	Ile	Ser	Thr	Glu	Glu	Glu	Glu	Ser	Arg	Asn	Gln	Glu	Asn	Arg	Asp
		35					40					45			
Glu	Asp	Asp	Asp	Glu	Asp	Ala	Leu	Glu	Glu	Arg	Arg	Arg	Arg	Ile	Lys
		50				55						60			
Glu	Lys	Asn	Leu	Arg	Leu	Ala	Gln	Glu	Glu	Ala	Ala	Leu	Leu	Pro	Leu
		65				70				75				80	
Glu	Glu	Glu	Asp	Glu	Ile	Gln	Glu	Glu	Glu	Glu	Glu	Glu	Glu	Glu	Ser
			85						90					95	
Glu	Tyr	Glu	Thr	Asp	Ser	Glu	Asp	Asp	Met	Pro	Gly	Ile	Ala	Leu	Ile
			100					105					110		
Lys	Ser	Val	Phe	Val	Pro	Lys	Ala	Glu	Arg	Asp	Thr	Ile	Ala	Glu	Arg
		115						120						125	

Glu Arg Leu Glu Ala Glu Glu Glu Ala Leu Glu Glu Leu Ala Lys Arg
130 135 140
Lys Leu Glu Gln Arg Lys Ile Glu Thr Lys Gln Ile Val Val Glu Glu
145 150 155 160
Val Arg Lys Asp Glu Glu Ile Arg Lys Asn Ile Leu Leu Glu Glu Ala
165 170 175
Asn Ile Gly Asp Val Glu Thr Asp Asp Glu Leu Asn Glu Ala Glu Glu
180 185 190
Tyr Glu Val Trp Lys Thr Arg Glu Ile Gly Arg Ile Lys Arg Glu Arg
195 200 205
Asp Ala Arg Glu Ala Met Leu Arg Glu Arg Glu Glu Ile Glu Lys Leu
210 215 220
Arg Asn Met Thr Glu Gln Glu Arg Arg Asp Trp Glu Arg Lys Asn Pro
225 230 235 240
Lys Pro Ser Ser Ala Gln Pro Lys Lys Lys Asn Phe Met Gln Lys
245 250 255
Tyr Tyr His Lys Lys Gly Ala Phe Phe Gln Ala Asp Pro Asp Asp Glu Ala
260 265 270
Gly Ser Ala Gly Thr Asp Gly Ile Phe Gln Arg Asp Phe Ser Ala Pro
275 280 285
Thr Gly Glu Asp Arg Leu Asp Lys Ser Ile Leu Pro Lys Val Met Gln
290 295 300
Val Lys His Phe Gly Arg Ser Gly Arg Thr Lys Trp Thr His Leu Val
305 310 315 320
Asn Glu Asp Thr Thr Asp Trp Ser Asn Pro Trp Thr Ser Asn Asp Pro
325 330 335
Leu Arg Glu Lys Tyr Asn Lys Lys Met Ala Gly Met Asp Ala Pro Ile
340 345 350
Ala Lys Pro Lys Gly Ser Lys Lys Met Lys Asp Trp Glu Thr
355 360 365

(2) INFORMATION FOR SEQ ID NO:172:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 261 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide
(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..261
(D) OTHER INFORMATION: / Ceres Seq. ID 1566050

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:172:

Met Pro Gly Ile Ala Leu Ile Lys Pro Val Phe Val Pro Lys Ala Glu
1 5 10 15
Arg Asp Thr Ile Ala Glu Arg Glu Arg Leu Glu Ala Glu Glu Ala
20 25 30
Leu Glu Glu Leu Ala Lys Arg Lys Leu Glu Gln Arg Lys Ile Glu Thr
35 40 45
Lys Gln Ile Val Val Glu Glu Val Arg Lys Asp Glu Glu Ile Arg Lys
50 55 60
Asn Ile Leu Leu Glu Glu Ala Asn Ile Gly Asp Val Glu Thr Asp Asp
65 70 75 80
Glu Leu Asn Glu Ala Glu Glu Tyr Glu Val Trp Lys Thr Arg Glu Ile
85 90 95
Gly Arg Ile Lys Arg Glu Arg Asp Ala Arg Glu Ala Met Leu Arg Glu
100 105 110
Arg Glu Glu Ile Glu Lys Leu Arg Asn Met Thr Glu Gln Glu Arg Arg
115 120 125
Asp Trp Glu Arg Lys Asn Pro Lys Pro Ser Ser Ala Gln Pro Lys Lys
130 135 140
Lys Trp Asn Phe Met Gln Lys Tyr Tyr His Lys Gly Ala Phe Phe Gln

145	150	155	160
Ala Asp Pro Asp	Asp Glu Ala Gly	Ser Ala Gly Thr	Asp Gly Ile Phe
	165	170	175
Gln Arg Asp Phe	Ser Ala Pro Thr	Gly Glu Asp Arg	Leu Asp Lys Ser
	180	185	190
Ile Leu Pro Lys	Val Met Gln Val	Lys His Phe Gly	Arg Ser Gly Arg
	195	200	205
Thr Lys Trp Thr	His Leu Val Asn	Glu Asp Thr Thr	Asp Trp Ser Asn
	210	215	220
Pro Trp Thr Ser	Asn Asp Pro Leu	Arg Glu Lys Tyr	Asn Lys Lys Met
	225	230	235
Ala Gly Met Asp	Ala Pro Ile Ala	Lys Pro Lys Gly	Ser Lys Lys Met
	240	245	250
Lys Asp Trp Glu	Thr		
	260		

(2) INFORMATION FOR SEQ ID NO:173:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1018 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1018

(D) OTHER INFORMATION: / Ceres Seq. ID 1566062

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:173:

gaccatcgac	catcgctcgtc	tctcgcgagc	tcagttgaaa	gatgttaacg	gctgatatac	60
caccaaatca	gtcaatctac	ataaaacata	tcaatgagaa	gatcaagaaa	gaagagctga	120
agaggtctct	tactgtgttg	ttctctcagt	ttggaagatt	acttgatgtg	gttgcgttaa	180
agactcctaa	gtctcgggga	caagcatggg	ttgtttttac	tgaagtcacc	gctgctagca	240
acgctgtccg	tcagatgcag	aactttcctt	tctatgataa	gcctatgcgg	atacaatag	300
caaaatcaaa	gtcagattat	gttactaaag	cgaagggcto	ttttgttcca	aaagaaaaga	360
agatgaagca	agCaagagaa	agttgaaagg	aagcgacatg	ctgaagaaac	tcaacaacca	420
agcatgccta	atggcgcaac	tactcagaac	ggaatgcctg	tgccaatttc	tctttctcgc	480
atcatcccaa	caatacaata	ttatcttctg	acagacgtca	ttatcgcaac	ttagtctgtg	540
aatttctgtt	tcttaatacc	cgtctctgtg	atttccacgc	ctcctttcca	gccgagtggtg	600
caagacacga	tgcacacaaa	caacatactc	ttcattcata	atcttcccat	tgagacgaat	660
agtatgatgc	ttcagctcgt	ctttgagcaa	taccacggat	tcaaaagagat	aagaatgatc	720
gaagcaaaac	ccggaattgc	gtttgtggag	tatgaagacg	atgttcagtc	ttccatggcc	780
atgcaggtct	tccagggttt	caagatcact	ccgcagaatc	caatggctgt	ctcttttgc	840
aaagaagtga	aaccagagtt	ttgttatgcg	gatgaatggt	aatgatatac	taattagtag	900
ctgtttaaaa	gcaaacctgc	ttattttatt	tggttcgttt	ccgattagtg	gtgtgaatga	960
ccccgaagct	ttagaccaga	atgtaatgag	atcgaagaat	tgagagtgat	ttggttgg	

(2) INFORMATION FOR SEQ ID NO:174:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 114 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..114

(D) OTHER INFORMATION: / Ceres Seq. ID 1566063

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:174:

Met Thr Ala Asp	Ile Pro Pro	Asn Gln Ser	Ile Tyr Ile	Lys His
1	5	10	15	
Ile Asn Gln Lys	Ile Lys Lys	Glu Glu Leu	Lys Arg Ser	Leu Tyr Cys
	20	25	30	
Leu Phe Ser Gln	Phe Gly Arg	Leu Leu	Asp Val Val	Ala Leu Lys Thr

	35				40					45					
Pro	Lys	Leu	Arg	Gly	Gln	Ala	Trp	Val	Val	Phe	Thr	Glu	Val	Thr	Ala
	50					55					60				
Ala	Ser	Asn	Ala	Val	Arg	Gln	Met	Gln	Asn	Phe	Pro	Phe	Tyr	Asp	Lys
65					70					75					80
Pro	Met	Arg	Ile	Gln	Tyr	Ala	Lys	Ser	Lys	Ser	Asp	Tyr	Val	Thr	Lys
				85					90					95	
Ala	Glu	Gly	Ser	Phe	Val	Pro	Lys	Glu	Lys	Lys	Met	Lys	Gln	Ala	Arg
			100					105						110	
Glu	Ser														

(2) INFORMATION FOR SEQ ID NO:175:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 83 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..83
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566064

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:175:

Met	Lys	Thr	Met	Phe	Ser	Leu	Pro	Trp	Pro	Cys	Arg	Leu	Phe	Arg	Val
1				5					10				15		
Ser	Arg	Ser	Leu	Arg	Arg	Ile	Gln	Trp	Ser	Ser	Leu	Leu	Pro	Arg	Ser
			20					25					30		
Glu	Asn	Gln	Ser	Phe	Val	Met	Arg	Met	Asn	Gly	Asn	Asp	Ile	Leu	Ile
			35				40				45				
Ser	Ser	Cys	Leu	Lys	Ala	Asn	Cys	Leu	Ile	Leu	Phe	Gly	Ser	Phe	Pro
	50					55				60					
Ile	Ser	Gly	Val	Asn	Asp	Pro	Glu	Ala	Leu	Asp	Gln	Asn	Val	Met	Arg
65				70						75				80	
Ser	Lys	Asn													

(2) INFORMATION FOR SEQ ID NO:176:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 80 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..80
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566065

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:176:

Met	Phe	Ser	Leu	Pro	Trp	Pro	Cys	Arg	Leu	Phe	Arg	Val	Ser	Arg	Ser
1				5					10				15		
Leu	Arg	Arg	Ile	Gln	Trp	Ser	Ser	Leu	Leu	Pro	Arg	Ser	Glu	Asn	Gln
			20					25					30		
Ser	Phe	Val	Met	Arg	Met	Asn	Gly	Asn	Asp	Ile	Leu	Ile	Ser	Ser	Cys
			35				40					45			
Leu	Lys	Ala	Asn	Cys	Leu	Ile	Leu	Phe	Gly	Ser	Phe	Pro	Ile	Ser	Gly
	50					55				60					
Val	Asn	Asp	Pro	Glu	Ala	Leu	Asp	Gln	Asn	Val	Met	Arg	Ser	Lys	Asn
65				70						75				80	

(2) INFORMATION FOR SEQ ID NO:177:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 842 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..842

(D) OTHER INFORMATION: / Ceres Seq. ID 1566100

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:177:

ctacgattag	tttaattctct	cagtcacccg	gagagtgttaa	aaacagcgag	aaaatcgacg	60
tcgttogatc	gcgcactgcg	agcgaaagaag	aagatggctg	aagaagaagt	tgactacgta	120
ttcaagggtt	ttttgaacgg	agattcagcg	gttgggaagt	cacagctacg	ggctcggttc	180
caaaagagacg	aattcagtat	ggattccaaa	gccacaattc	ggtgtcgatt	tcaatactcg	240
aacgcctcgtt	attgacgata	agaacatcaa	agctcagatc	tgggacatcg	caggccagaa	300
acgcacacaga	gctattacat	aagcctacta	caaaggtgct	gttggtgcaa	tgtagtttta	360
cgatatgaca	atacgtgaag	gctttgagca	cattcctcag	tggttgggaag	aactacgagt	420
gcacgcggat	aagaacattg	tcatcatctt	gattggtaac	aagacggatt	tagaagaacca	480
gagatcggtt	cctgtggaag	atgccaaagga	atttcagag	aaggaagggc	ttttttcct	540
tgagacttcv	Gaactaaact	ccacaaatgt	cgagaactct	tcaAcactc	tcttgactga	600
gatcttcaac	aaggtgaaca	agaagaatct	cgtaagacc	accgtgtctt	gcagctcaca	660
agtcagtcct	ctaagaccac	cgtgtgttgc	agctcaamta	gtcagtcctc	tcgatttggt	720
ccattacagt	ttagaatgaa	ataaaccatt	tcataactt	caaaaatatt	gtttatattt	780
ggtttttaga	tagtgagttt	tgtgtagtgt	acgttgattt	ttagaacaaa	atctttcatt	840
tt						

(2) INFORMATION FOR SEQ ID NO:178:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 116 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..116

(D) OTHER INFORMATION: / Ceres Seq. ID 1566101

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:178:

Met	Leu	Val	Tyr	Asp	Met	Thr	Ile	Arg	Glu	Ser	Phe	Glu	His	Ile	Pro
1			5					10					15		
Gln	Trp	Leu	Glu	Glu	Leu	Arg	Val	His	Ala	Asp	Lys	Asn	Ile	Val	Ile
			20					25					30		
Ile	Leu	Ile	Gly	Asn	Lys	Thr	Asp	Leu	Glu	Asn	Gln	Arg	Ser	Val	Pro
			35				40					45			
Val	Glu	Asp	Ala	Lys	Glu	Phe	Ala	Glu	Lys	Glu	Gly	Leu	Phe	Phe	Leu
			50				55				60				
Glu	Thr	Xaa	Ala	Leu	Asn	Ser	Thr	Asn	Val	Glu	Asn	Ser	Phe	Asn	Thr
					70				75					80	
Leu	Leu	Thr	Glu	Ile	Phe	Asn	Lys	Val	Asn	Lys	Lys	Asn	Leu	Ala	Lys
					85				90				95		
Thr	Thr	Val	Ser	Cys	Ser	Ser	Gln	Val	Ser	Leu	Leu	Arg	Pro	Pro	Cys
			100				105						110		
Val	Ala	Ala	Xaa												
			115												

(2) INFORMATION FOR SEQ ID NO:179:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 111 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1..111
(D) OTHER INFORMATION: / Ceres Seq. ID 1566102

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:179:

```
Met Thr Ile Arg Glu Ser Phe Glu His Ile Pro Gln Trp Leu Glu Glu
1      5      10      15
Leu Arg Val His Ala Asp Lys Asn Ile Val Ile Ile Leu Ile Gly Asn
20      25      30
Lys Thr Asp Leu Glu Asn Gln Arg Ser Val Pro Val Glu Asp Ala Lys
35      40      45
Glu Phe Ala Glu Lys Glu Gly Leu Phe Phe Leu Glu Thr Xaa Ala Leu
50      55      60
Asn Ser Thr Asn Val Glu Asn Ser Phe Asn Thr Leu Leu Thr Glu Ile
65      70      75
Phe Asn Lys Val Asn Lys Lys Asn Leu Ala Lys Thr Thr Val Ser Cys
85      90      95
Ser Ser Gln Val Ser Leu Leu Arg Pro Pro Cys Val Ala Ala Xaa
100     105     110
```

(2) INFORMATION FOR SEQ ID NO:180:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 579 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -
(B) LOCATION: 1..579
(D) OTHER INFORMATION: / Ceres Seq. ID 1566103

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:180:

```
gcgtagtaca aaaaacaatct tgataaaatag ataaataaac atctttctat tcgtaaggac      60
gacaaagaatc tctcaggttc tgtagaattg tcagaatcat ttctaaggg aggtaaaaag      120
ggatcagttac cggagcaaaa cacagagaag cttctctggc agtcaagcga cgtcgctgat      180
agcgtgtact ccaagttcgc gtgttgctcg tggagggtcc ttacgaggc tcgcgcgaag      240
ttgtacgcgc tgggacattc tgatcgtcgg aaactttact tctccatcaa gatgggaatt      300
gctttggcac tctgttcttt cgtcatcttt ctcaaagaac cgtctcaaga tgctagtaaa      360
ttcgcagttt gggcgattct caccgtcggt ctcatcttgc agtattacgt cggagcaact      420
ttgggtaaag gattcaatag agcattagcg acaatgttag tcggaggact tgctctcgcc      480
gtcgcgcagC tctctgtttt agcaggagag tttgaagaag tcatcatcgt aatctgcata      540
ttccttgtag gKttttTggt gctagtatt tgaaActat
```

(2) INFORMATION FOR SEQ ID NO:181:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 155 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1..155
(D) OTHER INFORMATION: / Ceres Seq. ID 1566104

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:181:

```
Met Gly Gly Lys Met Gly Ser Val Pro Glu Gln Asn Thr Glu Lys Leu
1      5      10      15
Leu Trp Gln Ser Ser Asp Val Ala Asp Ser Arg Asp Ser Lys Phe Arg
20      25      30
Cys Cys Ser Trp Arg Ala Leu Tyr Glu Ala Pro Ala Lys Leu Tyr Ala
35      40      45
Leu Gly His Ser Asp Arg Arg Lys Leu Tyr Phe Ser Ile Lys Met Gly
50      55      60
Ile Ala Leu Ala Leu Cys Ser Phe Val Ile Phe Leu Lys Glu Pro Leu
```


65 70 75 80
Gln Asp Ala Ser Lys Phe Ala Val Trp Ala Ile Leu Thr Val Val Leu
85 90 95
Ile Phe Glu Tyr Tyr Val Gly Ala Thr Leu Val Lys Gly Phe Asn Arg
100 105 110
Ala Leu Gly Thr Met Leu Ala Gly Gly Leu Ala Leu Gly Val Ala Gln
115 120 125
Leu Ser Val Leu Ala Gly Glu Phe Glu Glu Val Ile Ile Val Ile Cys
130 135 140
Ile Phe Leu Ala Xaa Phe Leu Val Leu Val Ile
145 150 155

(2) INFORMATION FOR SEQ ID NO:182:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 151 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..151

(D) OTHER INFORMATION: / Ceres Seq. ID 1566105

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:182:

Met Gly Ser Val Pro Glu Gln Asn Thr Glu Lys Leu Leu Trp Gln Ser
1 5 10 15
Ser Asp Val Ala Asp Ser Arg Asp Ser Lys Phe Arg Cys Cys Ser Trp
20 25 30
Arg Ala Leu Tyr Glu Ala Pro Ala Lys Leu Tyr Ala Leu Gly His Ser
35 40 45
Asp Arg Arg Lys Leu Tyr Phe Ser Ile Lys Met Gly Ile Ala Leu Ala
50 55 60
Leu Cys Ser Phe Val Ile Phe Leu Lys Glu Pro Leu Gln Asp Ala Ser
65 70 75 80
Lys Phe Ala Val Trp Ala Ile Leu Thr Val Leu Ile Phe Glu Tyr
85 90 95
Tyr Val Gly Ala Thr Leu Val Lys Gly Phe Asn Arg Ala Leu Gly Thr
100 105 110
Met Leu Ala Gly Gly Leu Ala Leu Gly Val Ala Gln Leu Ser Val Leu
115 120 125
Ala Gly Glu Phe Glu Glu Val Ile Ile Val Ile Cys Ile Phe Leu Ala
130 135 140
Xaa Phe Leu Val Leu Val Ile
145 150

(2) INFORMATION FOR SEQ ID NO:183:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 93 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..93

(D) OTHER INFORMATION: / Ceres Seq. ID 1566106

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:183:

Met Gly Ile Ala Leu Ala Leu Cys Ser Phe Val Ile Phe Leu Lys Glu
1 5 10 15
Pro Leu Gln Asp Ala Ser Lys Phe Ala Val Trp Ala Ile Leu Thr Val
20 25 30
Val Leu Ile Phe Glu Tyr Tyr Val Gly Ala Thr Leu Val Lys Gly Phe
35 40 45

Asn Arg Ala Leu Gly Thr Met Leu Ala Gly Gly Leu Ala Leu Gly Val
50 55 60
Ala Gln Leu Ser Val Leu Ala Gly Glu Phe Glu Val Ile Ile Val
65 70 75 80
Ile Cys Ile Phe Leu Ala Xaa Phe Leu Val Leu Val Ile
85 90

(2) INFORMATION FOR SEQ ID NO:184:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 939 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..939
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566115

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:184:

ctatctctca	tcacacatctt	agttcatgtt	cgagtttctc	tgcttcaatt	acaaagaatg	60
gctgcttcaa	gtgctgtcac	cgcaaaactac	gtctccaagc	cacctccatt	cgcactggat	120
gctttggagc	cgcatatgag	caaacaaact	ctggagtttc	actggggaaa	acatcacaga	180
gcttacgttg	acaaacctcaa	gaaacaggtt	cttggaaaccg	agcttgaagg	caagccctta	240
gagcacatta	tcacacagcac	ttacaacaat	ggtgatcttc	tccttgcttt	caacaacgct	300
gctcaggcgt	ggaaccacga	gttctcttgg	gagtcaatga	aaccagggtg	tggaggaaaa	360
ccatcaggag	agcttcttgc	tttgcttgaa	agagatttca	cttcttatga	gaagttctat	420
gaagagttca	atgctgtctg	agccactcag	tttgagctgt	gctgggcctg	gcttgcttat	480
tcaaatgaaa	aactcaaatg	agtgaatact	cccaatgctg	tgaatccctt	tgtgctctgc	540
tttttccca	ttgctttacca	ttgatgtctg	ggagcatgct	tactaccttg	acttccagaa	600
ccgaagacca	gattacataa	agacattcat	gaccaatctt	gtgtcttggt	aagctgttaag	660
tgccagactt	gaggccgcga	aggctgtctc	tgcttaagca	aattttctga	caatttgact	720
tcagtgacag	tgagttctgc	atcaccgaag	tctcttataa	aattattgtc	gctgtaataa	780
ggacacagct	ctcttgttgt	gtatgtgtca	cagagtttct	cattttgctt	gtgtaatgaa	840
caattaaaca	tgctcttttc	tgagtggtgt	tgcgttttgt	gtgtgtcaag	tttttcatcg	900
ttctctttat	taaaactcaa	ttggcaccta	ccatcagtg			

(2) INFORMATION FOR SEQ ID NO:185:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 187 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..187
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566116

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:185:

Leu Ser Leu Ile His Ile Leu Val His Val Arg Val Ser Leu Leu Gln	
1 5 10 15	
Leu Gln Arg Met Ala Ala Ser Ser Ala Val Thr Ala Asn Tyr Val Leu	
20 25 30	
Lys Pro Pro Pro Phe Ala Leu Asp Ala Leu Glu Pro His Met Ser Lys	
35 40 45	
Gln Thr Leu Glu Phe His Trp Gly Lys His His Arg Ala Tyr Val Asp	
50 55 60	
Asn Leu Lys Lys Gln Val Leu Gly Thr Glu Leu Glu Gly Lys Pro Leu	
65 70 75 80	
Glu His Ile Ile His Ser Thr Tyr Asn Asn Gly Asp Leu Leu Pro Ala	
85 90 95	
Phe Asn Asn Ala Ala Gln Ala Trp Asn His Glu Phe Phe Trp Glu Ser	
100 105 110	
Met Lys Pro Gly Gly Gly Lys Pro Ser Gly Glu Leu Leu Ala Leu	

Met	Ser	Lys	Gln	Thr	Leu	Glu	Phe	His	Trp	Gly	Lys	His	His	Arg	Ala
1			5						10					15	
Tyr	Val	Asp	Asn	Leu	Lys	Lys	Gln	Val	Leu	Gly	Thr	Glu	Leu	Glu	Gly
			20					25						30	
Lys	Pro	Leu	Glu	His	Ile	Ile	His	Ser	Thr	Tyr	Asn	Asn	Gly	Asp	Leu
		35					40					45			

```

Leu Pro Ala Phe Asn Asn Ala Ala Gln Ala Trp Asn His Glu Phe Phe
50 55 60
Trp Glu Ser Met Lys Pro Gly Gly Gly Lys Pro Ser Gly Glu Leu
65 70 75 80
Leu Ala Leu Leu Glu Arg Asp Phe Thr Ser Tyr Glu Lys Phe Tyr Glu
85 90 95
Glu Phe Asn Ala Ala Ala Thr Gln Phe Gly Ala Gly Trp Ala Trp
100 105 110
Leu Ala Tyr Ser Asn Glu Lys Leu Lys Val Val Lys Thr Pro Asn Ala
115 120 125
Val Asn Pro Leu Val Leu Gly Ser Phe Pro Ile Ala Tyr His
130 135 140

```

(2) INFORMATION FOR SEQ ID NO:188:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1217 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1217
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566127

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:188:

```

ctcgaaacttg tttttggttc atctctcaaaa accaaaaatca ctaaagaggga gaagattgct 60
aaagtttgat aaaaacttcc aaaaatcaatg gctgatagga tcaaaggtcc atggagtctc 120
gaagaagacg acgagcttcg taggcttggt gttaaatacg gtccaagaaa ctggacagtg 180
attaqcaaat ctattcccg tagatcgggg aatatcgtgc gttacggtg gtgcaaccag 240
ctttcgccgc aagttgagca toggccgttt tcgctgaggg aagacgagac gatcgacagt 300
gctcacgctc agttcggtta taaatggggc acgattgctc gtcttctcaa cggctgtagc 360
gacacgcgcg tgaagaatca ctggaactcg acgctcaaga ggaatgcggc cgtttacgac 420
catcgggggtt acgattggtt ggaggatcat cgcccggtta agagatcgtt gaagtgcggga 480
tctccacctg ttgttactgg gctttacatg agcccaggaa gcccaactgg atctgatgtc 540
agtgattcaa gtactatccc gatattacct tccgttgagc ttttcaagcc tgtgcctaga 600
cctgggtgctg wtgtgctacc gcytctctatc gaaacgtcgt ctcttctccga tgatccaccg 660
aMttcgttaa gctttgcact tctcgttgcc gacgtaagcg aggagtcaaa ccgtagccac 720
gagtcaacga atatcaacaa caccacttgc agccgccaca accacaacaa tacggtgtgc 780
tttatgccct ttagtggtgg gtttagaggt gcgattgagg aatgggggaa gtcttttccc 840
ggtaacggag gcgagtttat gcggttggtg caagagatga ttaaggcgga agtgaggagt 900
tatactgcagc agatgcaacg gaacaatggt gcgcgattcg tcggaggatt cattgataat 960
ggcatgattc cgatgctca aattggagtt gggagaatcg agtagacaaa gtaggagatt 1020
taggaaactg tttaaattgg aagaagaagaa aatgctctgc ttttttctc ctttgattat 1080
ggcttaagaa ttttgggttt taaggaaatg tataagggaa atcagtgtaa caaagctcga 1140
gagctggggga cgtagtgaac aagacgaaga tcaaaattct cttaagctat tcaggaaaat 1200
aaaataaatt tttattt

```

(2) INFORMATION FOR SEQ ID NO:189:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 305 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..305
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566128

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:189:

```

Met Ala Asp Arg Ile Lys Gly Pro Trp Ser Pro Glu Glu Asp Glu Gln
1 5 10 15
Leu Arg Arg Leu Val Val Lys Tyr Gly Pro Arg Asn Trp Thr Val Ile
20 25 30

```

```

Ser Lys Ser Ile Pro Gly Arg Ser Gly Lys Ser Cys Arg Leu Arg Trp
      35              40              45
Cys Asn Gln Leu Ser Pro Gln Val Glu His Arg Pro Phe Ser Ala Glu
      50              55              60
Glu Asp Glu Thr Ile Ala Arg Ala His Ala Gln Phe Gly Asn Lys Trp
      65              70              75
Ala Thr Ile Ala Arg Leu Leu Asn Gly Arg Thr Asp Asn Ala Val Lys
      85              90              95
Asn His Trp Asn Ser Thr Leu Lys Arg Lys Cys Gly Gly Tyr Asp His
      100             105             110
Arg Gly Tyr Asp Gly Ser Glu Asp His Arg Pro Val Lys Arg Ser Val
      115             120             125
Ser Ala Gly Ser Pro Pro Val Val Thr Gly Leu Tyr Met Ser Pro Gly
      130             135             140
Ser Pro Thr Gly Ser Asp Val Ser Asp Ser Ser Thr Ile Pro Ile Leu
      145             150             155
Pro Ser Val Glu Leu Phe Lys Pro Val Pro Arg Pro Gly Ala Xaa Val
      165             170             175
Leu Pro Xaa Pro Ile Glu Thr Ser Ser Ser Ser Asp Asp Pro Pro Xaa
      180             185             190
Ser Leu Ser Leu Ser Leu Pro Gly Ala Asp Val Ser Glu Glu Ser Asn
      195             200             205
Arg Ser His Glu Ser Thr Asn Ile Asn Asn Thr Thr Ser Ser Arg His
      210             215             220
Asn His Asn Asn Thr Val Ser Phe Met Pro Phe Ser Gly Gly Phe Arg
      225             230             235
Gly Ala Ile Glu Glu Met Gly Lys Ser Phe Pro Gly Asn Gly Gly Glu
      245             250             255
Phe Met Ala Val Val Gln Glu Met Ile Lys Ala Glu Val Arg Ser Tyr
      260             265             270
Met Thr Glu Met Gln Arg Asn Asn Gly Gly Gly Phe Val Gly Gly Phe
      275             280             285
Ile Asp Asn Gly Met Ile Pro Met Ser Gln Ile Gly Val Gly Arg Ile
      290             295             300
Glu
305

```

(2) INFORMATION FOR SEQ ID NO:190:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 165 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..165
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566129

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:190:

```

Met Ser Pro Gly Ser Pro Thr Gly Ser Asp Val Ser Asp Ser Ser Thr
1      5      10      15
Ile Pro Ile Leu Pro Ser Val Glu Leu Phe Lys Pro Val Pro Arg Pro
      20      25      30
Gly Ala Xaa Val Leu Pro Xaa Pro Ile Glu Thr Ser Ser Ser Asp
      35      40      45
Asp Pro Pro Xaa Ser Leu Ser Leu Ser Leu Pro Gly Ala Asp Val Ser
      50      55      60
Glu Glu Ser Asn Arg Ser His Glu Ser Thr Asn Ile Asn Asn Thr Thr
      65      70      75
Ser Ser Arg His Asn His Asn Asn Thr Val Ser Phe Met Pro Phe Ser
      85      90      95
Gly Gly Phe Arg Gly Ala Ile Glu Glu Met Gly Lys Ser Phe Pro Gly

```

Asn	Gly	Gly	Glu	Phe	Met	Ala	Val	Val	Gln	Glu	Met	Ile	Lys	Ala	Glu
115							120						125		
Val	Arg	Ser	Tyr	Met	Thr	Glu	Met	Gln	Arg	Asn	Asn	Gly	Gly	Gly	Phe
130							135					140			
Val	Gly	Gly	Phe	Ile	Asp	Asn	Gly	Met	Ile	Pro	Met	Ser	Gln	Ile	Gly
145						150				155				160	
Val	Gly	Arg	Ile	Glu											

(2) INFORMATION FOR SEQ ID NO:191:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 702 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..702
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566130

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:191:

aaaaactcgct	ctccgggtgat	cgctctttcgg	tcagattctt	ataagcgtgc	ttgattttca	60
aatcaagttt	gtttctttat	ctccagagtt	tatcatctct	tatgtgactg	tgttaaaatg	120
aattttcttaa	actcagctgc	atccatttgc	agaagagtta	gtctgaggga	actcatcatc	180
gaggttctctg	cttatactgg	cagcagcatt	tccgatgggt	cttcaagtgg	gttgagtttg	240
gtcttggaagc	gttgggctac	taagaaaaacc	gctggttcta	caaagaacgg	tcgtgactct	300
aatcccaagt	tcttctgtgt	taagaaatct	ggaggagaga	gtgtgatacc	tggaaacatc	360
atagttctgt	aacgtggaac	tcggtttcat	cctggagact	atgtcgggat	tggtaaggac	420
cataactctgt	ttgcactgaa	ggaaggacga	gtcagggttc	agaaaaacaa	gattacagga	480
cgcaaatgga	ttcatgttga	tccaataggt	ggtcatgttc	ttcacccat	ctacacaaaa	540
gcgcagctgt	caaaatcgac	taagttgaac	acagcttcat	agcaaaactg	acaatctaaa	600
cgtgtctctg	tttcttcttt	tagattatat	gatctctcvt	agtaaaaagt	gatggtatct	660
tagaatctca	acactcattt	caataacagc	tgctgttttg	tt		

(2) INFORMATION FOR SEQ ID NO:192:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 154 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..154
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566131

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:192:

Met	Asn	Phe	Leu	Asn	Ser	Ala	Ala	Ser	Ile	Cys	Arg	Arg	Val	Ser	Leu
1			5						10				15		
Arg	Glu	Leu	Ile	Thr	Glu	Val	Pro	Ala	Tyr	Thr	Gly	Ser	Ser	Ile	Ser
		20					25				30				
Asp	Gly	Ser	Ser	Ser	Gly	Leu	Ser	Leu	Val	Leu	Lys	Arg	Trp	Ala	Thr
		35				40					45				
Lys	Lys	Thr	Ala	Gly	Ser	Thr	Lys	Asn	Gly	Arg	Asp	Ser	Asn	Pro	Lys
		50				55					60				
Phe	Leu	Gly	Val	Lys	Lys	Phe	Gly	Gly	Glu	Ser	Val	Ile	Pro	Gly	Asn
		65				70					75			80	
Ile	Ile	Val	Arg	Gln	Arg	Gly	Thr	Arg	Phe	His	Pro	Gly	Asp	Tyr	Val
			85						90					95	
Gly	Ile	Gly	Lys	Asp	His	Thr	Leu	Phe	Ala	Leu	Lys	Glu	Gly	Arg	Val
			100						105				110		
Arg	Phe	Glu	Lys	Ser	Lys	Ile	Thr	Gly	Arg	Lys	Trp	Ile	His	Val	Asp
		115							120						

Pro Ile Gly Gly His Val Leu His Pro Ile Tyr Thr Lys Ala Ala Ala
130 135 140
Ala Lys Ser Thr Lys Leu Asn Thr Ala Ser
145 150

(2) INFORMATION FOR SEQ ID NO:193:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1239 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1239

(D) OTHER INFORMATION: / Ceres Seq. ID 1566132

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:193:

atcgagtgtc	tcgccagct	tcttcagctc	tcaccacata	atattaataa	aaagcatttt	60
ctctctttga	ttgcttcaga	ttcgctcagc	cactctttcc	ttctccagaag	aaaccctaga	120
catctcattc	caaaaatgtt	cagatctatg	ctcgctccga	cttctgcctc	cgcggaagCag	180
cggtgatccc	gcggtagctt	ctctctccgt	tcgctccccc	agcgtaaaat	cgccatctct	240
ggtgcgcgct	tggaattgg	tcagcctctt	gctctctcca	tgaagcttaa	tcctcttggt	300
ttctctctct	ccctctacga	tatcgctaac	actcccggag	ttgctgtgta	gtcggtgtac	360
atcaacacca	gatctgaggt	tggtggatac	atgggctgat	ataacttggt	caagctctca	420
gaaggagctg	attctgctta	cattccaagt	ggtgtgccaa	ggaagccttg	tatgaccctg	480
gacgatcttt	tcacatttaa	tgctggaaat	gtcaagaacc	ttgcaactgc	catcgcccaag	540
tactgcccac	attgcgttat	taatatgata	agcaaccctg	tgaactctac	tggtccaatt	600
cgagctgaga	tatttaagaa	ggctgggtat	tacgatgaaa	agaaaattgt	tggtgttaac	660
actcttgacg	tcgtcagggc	caggactttc	tatgctggaa	agggcaaatg	cccagttgtca	720
gaagttaatg	ttccgggtga	tggtgggtcat	gctgggggta	ctattctccc	ttctctctct	780
cagggaactc	ctcaagccaa	cttgtcaagt	gacatactta	ccgcccttac	taagcgtacc	840
caagatggag	gtcagagaagt	cgtggaggca	aaagcaggaa	aaggttcacg	tacattgttc	900
atggcctatg	cgcgagcatt	gttcgctgat	gcattgctga	aaggactcaa	cggtgttcca	960
gatgtcatag	aatgctcata	cgtgcaatct	acaatcacgc	agcttctctt	ctttgcctcg	1020
aagggtgaggt	tggggaagaa	tggtgtggag	gaggttcttg	actttgggac	actctcaagc	1080
tttgagaagg	aagccttgga	agcattgaag	ccagaactca	agctctccat	agaaaaggga	1140
gtcaagtttg	ccaaccagtg	attaaaccga	gtttactcgg	taatttttcc	aattttkccag	1200
ctagagttgc	ccactctctc	ttcatcgggt	tgatatcaat			

(2) INFORMATION FOR SEQ ID NO:194:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 386 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..386

(D) OTHER INFORMATION: / Ceres Seq. ID 1566133

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:194:

Ile	Glu	Cys	Leu	Ala	Gln	Leu	Leu	Gln	Ser	Pro	His	Asn	Ile	Asn
1		5						10					15	
Lys	Lys	His	Phe	Leu	Leu	Ser	Ile	Ala	Ser	Asp	Ser	Ser	Ala	His
		20						25					30	
Phe	Leu	Ser	Arg	Arg	Asn	Pro	Arg	His	Leu	Ile	Ala	Lys	Met	Phe
		35						40					45	
Ser	Met	Leu	Val	Arg	Ser	Ser	Ala	Ser	Ala	Lys	Gln	Ala	Ala	Ile
		50						55					60	
Arg	Ser	Phe	Ser	Ser	Gly	Ser	Val	Pro	Glu	Arg	Lys	Val	Ala	Ile
		65						70					75	
Gly	Ala	Ala	Gly	Gly	Ile	Gly	Gln	Pro	Leu	Ala	Leu	Leu	Met	Lys
		85						90					95	

Asn Pro Leu Val Ser Ser Leu Ser Leu Tyr Asp Ile Ala Asn Thr Pro
100 105 110
Gly Val Ala Ala Asp Val Gly His Ile Asn Thr Arg Ser Glu Val Val
115 120 125
Gly Tyr Met Gly Asp Asp Asn Leu Ala Lys Ala Leu Glu Gly Ala Asp
130 135 140
Leu Val Ile Ile Pro Ala Gly Val Pro Arg Lys Pro Gly Met Thr Arg
145 150 155 160
Asp Asp Leu Phe Asn Ile Asn Ala Gly Ile Val Lys Asn Leu Cys Thr
165 170 175
Ala Ile Ala Lys Tyr Cys Pro His Ala Leu Ile Asn Met Ile Ser Asn
180 185 190
Pro Val Asn Ser Thr Val Pro Ile Ala Ala Glu Ile Phe Lys Lys Ala
195 200 205
Gly Met Tyr Asp Glu Lys Lys Leu Phe Gly Val Thr Thr Leu Asp Val
210 215 220
Val Arg Ala Arg Thr Phe Tyr Ala Gly Lys Ala Asn Val Pro Val Ala
225 230 235 240
Glu Val Asn Val Pro Val Ile Gly Gly His Ala Gly Val Thr Ile Leu
245 250 255
Pro Leu Phe Ser Gln Ala Thr Pro Gln Ala Asn Leu Ser Ser Asp Ile
260 265 270
Leu Thr Ala Leu Thr Lys Arg Thr Gln Asp Gly Gly Thr Glu Val Val
275 280 285
Glu Ala Lys Ala Gly Lys Gly Ser Ala Thr Leu Ser Met Ala Tyr Ala
290 295 300
Gly Ala Leu Phe Ala Asp Ala Cys Leu Lys Gly Leu Asn Gly Val Pro
305 310 315 320
Asp Val Ile Glu Cys Ser Tyr Val Gln Ser Thr Thr Ile Thr Glu Leu Pro
325 330 335
Phe Phe Ala Ser Lys Val Arg Leu Gly Lys Asn Gly Val Glu Glu Val
340 345 350
Leu Asp Leu Gly Pro Leu Ser Asp Phe Glu Lys Glu Gly Leu Glu Ala
355 360 365
Leu Lys Pro Glu Leu Lys Ser Ser Ile Glu Lys Gly Val Lys Phe Ala
370 375 380
Asn Gln
385

(2) INFORMATION FOR SEQ ID NO:195:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 341 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..341

(D) OTHER INFORMATION: / Ceres Seq. ID 1566134

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:195:

Met Phe Arg Ser Met Leu Val Arg Ser Ser Ala Ser Ala Lys Gln Ala
1 5 10 15
Ala Ile Arg Arg Ser Phe Ser Ser Gly Ser Val Pro Glu Arg Lys Val
20 25 30
Ala Ile Leu Gly Ala Ala Gly Gly Ile Gly Gln Pro Leu Ala Leu Leu
35 40 45
Met Lys Leu Asn Pro Leu Val Ser Ser Leu Ser Leu Tyr Asp Ile Ala
50 55 60
Asn Thr Pro Gly Val Ala Ala Asp Val Gly His Ile Asn Thr Arg Ser
65 70 75 80
Glu Val Val Gly Tyr Met Gly Asp Asp Asn Leu Ala Lys Ala Leu Glu

[illegible]

(i) SEQUENCE CHARACTERISTICS:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 337 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..33

(D) OTHER INFORMATION: / Ceres Seq. ID 1566135

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:196:

Met	Leu	Val	Arg	Ser	Ser	Ala	Ser	Ala	Lys	Gln	Ala	Ala	Ile	Arg	Arg
1				5					10					15	
Ser	Phe	Ser	Ser	Gly	Ser	Val	Pro	Glu	Arg	Lys	Val	Ala	Ile	Leu	Gly
				20				25					30		
Ala	Ala	Gly	Gly	Ile	Gly	Gln	Pro	Leu	Ala	Leu	Leu	Met	Lys	Leu	Asn
		35					40					45			
Pro	Leu	Val	Ser	Ser	Leu	Ser	Leu	Tyr	Asp	Ile	Ala	Asn	Thr	Pro	Gly
	50					55					60				
Val	Ala	Ala	Asp	Val	Gly	His	Ile	Asn	Thr	Arg	Ser	Glu	Val	Val	Gly
65					70					75					80
Tyr	Met	Gly	Asp	Asp	Asn	Leu	Ala	Lys	Ala	Leu	Glu	Gly	Ala	Asp	Leu
				85				90						95	
Val	Ile	Ile	Pro	Ala	Gly	Val	Pro	Arg	Lys	Pro	Gly	Met	Thr	Arg	Asp
			100					105					110		
Asp	Leu	Phe	Asn	Ile	Asn	Ala	Gly	Ile	Val	Lys	Asn	Leu	Cys	Thr	Ala
		115				120						125			

Ile Ala Lys Tyr Cys Pro His Ala Leu Ile Asn Met Ile Ser Asn Pro
130 135 140
Val Asn Ser Thr Val Pro Ile Ala Ala Glu Ile Phe Lys Lys Ala Gly
145 150 155 160
Met Tyr Asp Glu Lys Lys Leu Phe Gly Val Thr Thr Leu Asp Val Val
165 170 175
Arg Ala Arg Thr Phe Tyr Ala Gly Lys Ala Asn Val Pro Val Ala Glu
180 185 190
Val Asn Val Pro Val Ile Gly Gly His Ala Gly Val Thr Ile Leu Pro
195 200 205
Leu Phe Ser Gln Ala Thr Pro Gln Ala Asn Leu Ser Ser Asp Ile Leu
210 215 220
Thr Ala Leu Thr Lys Arg Thr Gln Asp Gly Gly Thr Glu Val Val Glu
225 230 235 240
Ala Lys Ala Gly Lys Gly Ser Ala Thr Leu Ser Met Ala Tyr Ala Gly
245 250 255
Ala Leu Phe Ala Asp Ala Cys Leu Lys Gly Leu Asn Gly Val Pro Asp
260 265 270
Val Ile Glu Cys Ser Tyr Val Gln Ser Thr Ile Thr Glu Leu Pro Phe
275 280 285
Phe Ala Ser Lys Val Arg Leu Gly Lys Asn Gly Val Glu Glu Val Leu
290 295 300
Asp Leu Gly Pro Leu Ser Asp Phe Glu Lys Glu Gly Leu Glu Ala Leu
305 310 315 320
Lys Pro Glu Leu Lys Ser Ser Ile Glu Lys Gly Val Lys Phe Ala Asn
325 330 335
Gln

(2) INFORMATION FOR SEQ ID NO:197:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1844 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1844

(D) OTHER INFORMATION: / Ceres Seq. ID 1566150

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:197:

ttcaatctca	ttaaagagaa	aagaaacgat	tagagaaaga	gaagagggta	gagactttctt	60
ttctttgttt	ctgtagaggc	tcttcttctt	cttctctgtc	tctgtctctg	tctctgtctc	120
ctgttaactc	tctgtgtctc	ccacaaattt	gtctctccct	tctctctcgc	actccacaaa	180
ttttgagctt	ctttttttga	agttcttgag	aacaagtga	agagctta	atccacaaga	240
ctctgtttc	tttcttaaat	ggctaaagt	tattggcctt	atttcgatcc	tgaatatgat	300
aacttgagct	ccagaatcaa	tctccaagt	gtttctatag	ataaacctag	ctgcaaaaga	360
tgcaactctg	tcaaggtgga	cagtatgaac	aaacctggaa	tactacttga	agttgtgcga	420
gtcctaaccg	atctcgatct	cactatcact	aaagcttata	tctcttctga	tggtggatgg	480
ttcatggacg	tattccatgt	caccgatcaa	caaggaaaca	aggttactga	tagcaaaaacc	540
atcgattaca	tcgagaaggt	gttaggacca	aagggtcatg	cttcggcttc	acaaaacact	600
tgccctggta	aaagagtgcg	gttcCattca	ttaggcgacc	acacatcgat	agagattatt	660
gtcctgagtc	gtcctggcct	ctgtctggag	gtttcagccg	tactagcaga	ctctcaacatt	720
aatgtgggtg	cagctgaagc	atggactcac	aaccgtagga	ttgcgtgtgt	ctcttatgtg	780
aatgacaatg	caactcttag	agccgttgat	gatccagaaa	gattgtcttc	catggaagaa	840
cagcttaaca	atgtgctgcg	tgggtgcgaa	gaacaagatg	agaaatttgc	tcggacgagt	900
ctctccattg	ggctgactca	cgttgataga	aggcttcac	agatgttttt	cgctgataga	960
gactacgaag	cagtgactaa	gcttgatgat	tctgcttctt	gcggatttga	gcccaaaatc	1020
acggttgagc	attgtgaaga	gaaaggttac	tccgtgataa	acgtgagctg	cgagatgcga	1080
ccaaagctca	tgtttgacat	tgtatgcacg	cttaccggata	tgaataacat	tggttttcac	1140
gccacgattt	catcaagcgg	ctctcatgct	tctcaggagt	atttcacag	acacaagac	1200
ggttgcactc	ttgacacaga	aggagagaaa	gagagagdtg	tcaaatgtct	agaagctgcga	1260

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atccatagac gagtcagcga ggggttgagt ttggagctct gcgcaaagga cacagattgga 1320
ttactgtcgg aagtgacaag gattctgaga gagcacgggc tatcagtgct gagagctgggt 1380
gtgacaacag tagggagaaca agccgtcaac gttttctatg tgaaagatgc ttcagggaat 1440
ccagtggtatg tgaagacgat tgaggcggtta cgccggagaga ttggacacag tatgatgatt 1500
gacttcaaga ataaagttcc gagcagaaaaa tggaaagaag aaggtaacag cggaaacagga 1560
ggaggatggg ccaaaaccag tttcttcttt gggaatttgc ttgagaagtt actgccttga 1620
gagaaaaagt aactatgtgt ggataaaacg tactgtataaa tgtgtattat gtagatcata 1680
gagggcctta gtgtgatgta tgactttgtc agggattttg gtggtttgoc cgaagtcaaa 1740
ccgaacaaaa actggttttc ggttacttta gactttagtc atagtataat gaacatgtct 1800
ataaatgaat aatatgcaac tcttccaatt ggtaggcttg cttt

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(2) INFORMATION FOR SEQ ID NO:198:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 453 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..453

(D) OTHER INFORMATION: / Ceres Seq. ID 1566151

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:198:

```

Met Ala Lys Val Tyr Trp Pro Tyr Phe Asp Pro Glu Tyr Glu Asn Leu
1      5      10      15
Ser Ser Arg Ile Asn Pro Pro Ser Val Ser Ile Asp Asn Thr Ser Cys
20     25     30
Lys Glu Cys Thr Leu Val Lys Val Asp Ser Met Asn Lys Pro Gly Ile
35     40     45
Leu Leu Glu Val Val Gln Val Leu Thr Asp Leu Asp Leu Thr Ile Thr
50     55     60
Lys Ala Tyr Ile Ser Ser Asp Gly Gly Trp Phe Met Asp Val Phe His
65     70     75     80
Val Thr Asp Gln Gln Gly Asn Lys Val Thr Asp Ser Lys Thr Ile Asp
85     90     95
Tyr Ile Glu Lys Val Leu Gly Pro Lys Gly His Ala Ser Ala Ser Gln
100    105    110
Asn Thr Trp Pro Gly Lys Arg Val Gly Val His Ser Leu Gly Asp His
115    120    125
Thr Ser Ile Glu Ile Ile Ala Arg Asp Arg Pro Gly Leu Leu Ser Glu
130    135    140
Val Ser Ala Val Leu Ala Asp Leu Asn Ile Asn Val Val Ala Ala Glu
145    150    155    160
Ala Trp Thr His Asn Arg Arg Ile Ala Cys Val Leu Tyr Val Asn Asp
165    170    175
Asn Ala Thr Ser Arg Ala Val Asp Asp Pro Glu Arg Leu Ser Ser Met
180    185    190
Glu Glu Gln Leu Asn Asn Val Leu Arg Gly Cys Glu Glu Gln Asp Glu
195    200    205
Lys Phe Ala Arg Thr Ser Leu Ser Ile Gly Ser Thr His Val Asp Arg
210    215    220
Arg Leu His Gln Met Thr Phe Ala Asp Arg Asp Tyr Glu Ala Val Thr
225    230    235    240
Lys Leu Asp Asp Ser Ala Ser Cys Gly Phe Glu Pro Lys Ile Thr Val
245    250    255
Glu His Cys Glu Glu Lys Gly Tyr Ser Val Ile Asn Val Ser Cys Glu
260    265    270
Asp Arg Pro Lys Leu Met Phe Asp Ile Val Cys Thr Leu Thr Asp Met
275    280    285
Gln Tyr Ile Val Phe His Ala Thr Ile Ser Ser Ser Gly Ser His Ala
290    295    300
Ser Gln Glu Tyr Phe Ile Arg His Lys Asp Gly Cys Thr Leu Asp Thr

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305		310		315		320
Glu Gly	Glu Lys	Glu Arg	Xaa Val	Lys Cys	Leu Glu	Ala Ala
	325			330		Ile His
Arg Arg	Val Ser	Glu Gly	Trp Ser	Leu Glu	Leu Cys	Ala Lys
	340			345		350
Val Gly	Leu Leu	Ser Glu	Val Thr	Arg Ile	Leu Arg	Glu His
	355			360		365
Ser Val	Ser Arg	Ala Gly	Val Thr	Thr Val	Gly Glu	Gln Ala
	370			375		380
Val Phe	Tyr Val	Lys Asp	Ala Ser	Gly Asn	Pro Val	Asp Val
	385			390		395
Ile Glu	Ala Leu	Arg Gly	Glu Ile	Gly His	Ser Met	Met Ile
	405			410		415
Lys Asn	Lys Val	Pro Ser	Arg Lys	Trp Lys	Glu Glu	Gly Gln
	420			425		430
Thr Gly	Gly Gly	Trp Ala	Lys Thr	Ser Phe	Phe Phe	Phe Gly
	435			440		445
Glu Lys	Leu Leu	Pro				
	450					

(2) INFORMATION FOR SEQ ID NO:199:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 411 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..411

(D) OTHER INFORMATION: / Ceres Seq. ID 1566152

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:199:

Met Asn	Lys Pro	Gly Ile	Leu Leu	Glu Val	Val Gln	Val Leu	Thr Asp
1	5			10		15	
Leu Asp	Leu Thr	Ile Thr	Lys Ala	Tyr Ile	Ser Ser	Asp Gly	Trp
	20			25		30	
Phe Met	Asp Val	Phe His	Val Thr	Asp Gln	Gln Gly	Asn Lys	Val Thr
	35			40		45	
Asp Ser	Lys Thr	Ile Asp	Tyr Ile	Glu Lys	Val Leu	Gly Pro	Lys Gly
	50			55		60	
His Ala	Ser Ala	Ser Gln	Asn Thr	Trp Pro	Gly Lys	Arg Val	Gly Val
	65			70		75	
His Ser	Leu Gly	Asp His	Thr Ser	Ile Glu	Ile Ile	Ala Arg	Asp Arg
	85			90		95	
Pro Gly	Leu Leu	Ser Glu	Val Ser	Ala Val	Leu Ala	Asp Leu	Asn Ile
	100			105		110	
Asn Val	Val Ala	Ala Glu	Ala Trp	Thr His	Asn Arg	Arg Ile	Ala Cys
	115			120		125	
Val Leu	Tyr Val	Asn Asp	Asn Ala	Thr Ser	Arg Ala	Val Asp	Asp Pro
	130			135		140	
Glu Arg	Leu Ser	Ser Met	Glu Glu	Gln Leu	Asn Asn	Val Leu	Arg Gly
	145			150		155	
Cys Glu	Glu Gln	Asp Glu	Lys Phe	Ala Arg	Thr Ser	Leu Ser	Ile Gly
	165			170		175	
Ser Thr	His Val	Asp Arg	Arg Leu	His Gln	Met Phe	Phe Ala	Asp Arg
	180			185		190	
Asp Tyr	Glu Ala	Val Thr	Lys Leu	Asp Asp	Ser Ala	Ser Cys	Gly Phe
	195			200		205	
Glu Pro	Lys Ile	Thr Val	Glu His	Cys Glu	Glu Lys	Gly Tyr	Ser Val
	210			215		220	
Ile Asn	Val Ser	Cys Glu	Asp Arg	Pro Lys	Leu Met	Phe Asp	Ile Val
	225			230		235	
							240

Cys	Thr	Leu	Thr	Asp	Met	Gln	Tyr	Ile	Val	Phe	His	Ala	Thr	Ile	Ser	
				245					250					255		
Ser	Ser	Gly	Ser	His	Ala	Ser	Gln	Glu	Tyr	Phe	Ile	Arg	His	Lys	Asp	
				260				265					270			
Gly	Cys	Thr	Leu	Asp	Thr	Glu	Gly	Glu	Lys	Glu	Arg	Xaa	Val	Lys	Cys	
				275				280				285				
Leu	Glu	Ala	Ala	Ile	His	Arg	Arg	Val	Ser	Glu	Gly	Trp	Ser	Leu	Glu	
				290				295				300				
Leu	Cys	Ala	Lys	Asp	Arg	Val	Gly	Leu	Leu	Ser	Glu	Val	Thr	Arg	Ile	
				305				310				315			320	
Leu	Arg	Glu	His	Gly	Leu	Ser	Val	Ser	Arg	Ala	Gly	Val	Thr	Thr	Val	
				325				330						335		
Gly	Glu	Gln	Ala	Val	Asn	Val	Phe	Tyr	Val	Lys	Asp	Ala	Ser	Gly	Asn	
				340				345					350			
Pro	Val	Asp	Val	Lys	Thr	Ile	Glu	Ala	Leu	Arg	Gly	Glu	Ile	Gly	His	
				355				360				365				
Ser	Met	Met	Ile	Asp	Phe	Lys	Asn	Lys	Val	Pro	Ser	Arg	Lys	Trp	Lys	
				370				375				380				
Glu	Glu	Gly	Gln	Ala	Gly	Thr	Gly	Gly	Gly	Trp	Ala	Lys	Thr	Ser	Phe	
				385				390				395			400	
Phe	Phe	Gly	Asn	Leu	Leu	Glu	Lys	Leu	Leu	Pro						
				405				410								

(2) INFORMATION FOR SEQ ID NO:200:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 378 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..378

(D) OTHER INFORMATION: / Ceres Seq. ID 1566153

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:200:

Met	Asp	Val	Phe	His	Val	Thr	Asp	Gln	Gln	Gly	Asn	Lys	Val	Thr	Asp	
1				5					10					15		
Ser	Lys	Thr	Ile	Asp	Tyr	Ile	Glu	Lys	Val	Leu	Gly	Pro	Lys	Gly	His	
				20				25					30			
Ala	Ser	Ala	Ser	Gln	Asn	Thr	Trp	Pro	Gly	Lys	Arg	Val	Gly	Val	His	
				35				40				45				
Ser	Leu	Gly	Asp	His	Thr	Ser	Ile	Glu	Ile	Ala	Arg	Asp	Arg	Pro		
				50				55				60				
Gly	Leu	Leu	Ser	Glu	Val	Ser	Ala	Val	Leu	Ala	Asp	Leu	Asn	Ile	Asn	
				65				70				75			80	
Val	Val	Ala	Ala	Glu	Ala	Trp	Thr	His	Asn	Arg	Arg	Ile	Ala	Cys	Val	
				85				90						95		
Leu	Tyr	Val	Asn	Asp	Asn	Ala	Thr	Ser	Arg	Ala	Val	Asp	Asp	Pro	Glu	
				100				105					110			
Arg	Leu	Ser	Ser	Met	Glu	Glu	Gln	Leu	Asn	Asn	Val	Leu	Arg	Gly	Cys	
				115				120					125			
Glu	Glu	Gln	Asp	Glu	Lys	Phe	Ala	Arg	Thr	Ser	Leu	Ser	Ile	Gly	Ser	
				130				135				140				
Thr	His	Val	Asp	Arg	Arg	Leu	His	Gln	Met	Phe	Phe	Ala	Asp	Arg	Asp	
				145				150				155			160	
Tyr	Glu	Ala	Val	Thr	Lys	Leu	Asp	Asp	Ser	Ala	Ser	Cys	Gly	Phe	Glu	
				165				170						175		
Pro	Lys	Ile	Thr	Val	Glu	His	Cys	Glu	Glu	Lys	Gly	Tyr	Ser	Val	Ile	
				180				185					190			
Asn	Val	Ser	Cys	Glu	Asp	Arg	Pro	Lys	Leu	Met	Phe	Asp	Ile	Val	Cys	
				195				200				205				
Thr	Leu	Thr	Asp	Met	Gln	Tyr	Ile	Val	Phe	His	Ala	Thr	Ile	Ser	Ser	

210	215	220
Ser Gly Ser His Ala	Ser Gln Glu Tyr Phe	Ile Arg His Lys Asp Gly
225	230	235
Cys Thr Leu Asp Thr	Glu Gly Glu Lys Glu Arg	Xaa Val Lys Cys Leu
240	245	250
Glu Ala Ala Ile His	Arg Arg Val Ser Glu Gly	Trp Ser Leu Glu Leu
255	260	265
Cys Ala Lys Asp Arg	Val Gly Leu Leu Ser Glu	Val Thr Arg Ile Leu
270	275	280
Arg Glu His Gly Leu	Ser Val Ser Arg Ala Gly	Val Thr Thr Val Gly
285	290	295
Glu Gln Ala Val Asn	Val Phe Tyr Val Lys Asp	Ala Ser Gly Asn Pro
300	305	310
Val Asp Val Lys Thr	Ile Glu Ala Leu Arg	Gly Glu Ile Gly His Ser
315	320	325
Met Met Ile Asp Phe	Lys Asn Lys Val Pro	Ser Arg Lys Trp Lys Glu
330	335	340
Glu Gly Gln Ala Gly	Thr Gly Gly Trp Ala	Lys Thr Ser Phe Phe
345	350	355
Phe Gly Asn Leu Leu	Glu Lys Leu Leu Pro	
360	365	

(2) INFORMATION FOR SEQ ID NO:201:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 676 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..676
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566154

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:201:

acataagtcct	ctctctttaca	ttttgaaacc	ctaattttctc	aaaaaaaaatg	tctgaagttg	60
agtaccgggtg	ctttgtcggc	ggccttgcct	gggccaccaca	tgatgaagat	cttcaaaagga	120
cgttctcaca	gttcggcgac	gttatcgatt	ctaagatcat	taacgaccgc	gagagtggaa	180
gatcaagggg	attcggattc	gtcaccttca	aggacgagaa	agccatgagg	gatgcgattg	240
aagagatgaa	cggtaaaagag	ctcgatggac	gtgtcatcac	cgtgaacgag	gctcagtcga	300
gaggtagcgg	cggtggcggc	ggatactcag	gaggaggcgg	tggtggttac	gagagacgta	360
cgaggaggtta	cggatctggt	ggargcgggt	gtggccgagg	atacgggtgt	ggtggacgcc	420
gtgagggagg	tggctacgga	ggcgggtgat	gtggaagtta	cgccggcggt	ggtggcggtg	480
ggtaatacaaa	gatagagttg	tttgcgtgct	gctgctctgt	ttttggttta	gatttgggat	540
ttgtgtcacc	actctctggt	tggttatcgt	tcgttkggtt	tacttttttg	atgaaacagt	600
ttcgttttaag	tcttctttgt	ctggatcgaa	atgttaattc	gcgtgttgtt	tactaaattt	660
ataacgtttc	cttttc					

(2) INFORMATION FOR SEQ ID NO:202:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 145 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..145
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566155

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:202:

Met Ser Glu Val Glu Tyr Arg Cys Phe Val Gly Gly Leu Ala Trp Ala	
1	15
Thr Asn Asp Glu Asp Leu Gln Arg Thr Phe Ser Gln Phe Gly Asp Val	
20	30

```

Ile Asp Ser Lys Ile Ile Asn Asp Arg Glu Ser Gly Arg Ser Arg Gly
    35          40          45
Phe Gly Phe Val Thr Phe Lys Asp Glu Lys Ala Met Arg Asp Ala Ile
    50          55          60
Glu Glu Met Asn Gly Lys Glu Leu Asp Gly Arg Val Ile Thr Val Asn
    65          70          75          80
Glu Ala Gln Ser Arg Gly Ser Gly Gly Gly Tyr Ser Gly Gly
    85          90          95
Gly Gly Gly Gly Tyr Glu Arg Arg Ser Gly Gly Tyr Gly Ser Gly Gly
    100          105          110
Xaa Gly Gly Gly Arg Gly Tyr Gly Gly Gly Arg Arg Glu Gly Gly
    115          120          125
Gly Tyr Gly Gly Gly Asp Gly Gly Ser Tyr Gly Gly Gly Gly Gly
    130          135          140

```

Trp
145

(2) INFORMATION FOR SEQ ID NO:203:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 86 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..86
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566156

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:203:

```

Met Arg Asp Ala Ile Glu Glu Met Asn Gly Lys Glu Leu Asp Gly Arg
1          5          10          15
Val Ile Thr Val Asn Glu Ala Gln Ser Arg Gly Ser Gly Gly Gly Gly
    20          25          30
Gly Tyr Ser Gly Gly Gly Gly Gly Gly Tyr Glu Arg Arg Ser Gly Gly
    35          40          45
Tyr Gly Ser Gly Gly Xaa Gly Gly Gly Arg Gly Tyr Gly Gly Gly Gly
    50          55          60
Arg Arg Glu Gly Gly Gly Tyr Gly Gly Gly Asp Gly Gly Ser Tyr Gly
    65          70          75          80
Gly Gly Gly Gly Gly Trp
    85

```

(2) INFORMATION FOR SEQ ID NO:204:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 79 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..79
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566157

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:204:

```

Met Asn Gly Lys Glu Leu Asp Gly Arg Val Ile Thr Val Asn Glu Ala
1          5          10          15
Gln Ser Arg Gly Ser Gly Gly Gly Gly Gly Tyr Ser Gly Gly Gly Gly
    20          25          30
Gly Gly Tyr Glu Arg Arg Ser Gly Gly Tyr Gly Ser Gly Gly Xaa Gly
    35          40          45
Gly Gly Arg Gly Tyr Gly Gly Gly Gly Arg Arg Glu Gly Gly Gly Tyr
    50          55          60
Gly Gly Gly Asp Gly Gly Ser Tyr Gly Gly Gly Gly Gly Trp

```

65

70

75

(2) INFORMATION FOR SEQ ID NO:205:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1415 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1415
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566170

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:205:

atgttcacatg	tgaattgttt	agttgggttt	aattctctttt	taagacaaca	tataatgtca	60
atgttatgta	cgtttttctt	gtttctctta	aacacttctt	ttgcgtttgc	attttgcgatt	120
cctaaaccgc	caatagtaag	gagactatca	acgacagtga	catcaaatcc	aacagcgctct	180
ctttgtctcg	ccaatggaaa	tccaatcgat	gagtgttgga	gatgcgacga	aaactggaag	240
gacaaccgca	aaaacctcgc	ggattgcgcg	gttggtattcg	gacgcgactc	aattggcggt	300
agagccgggg	agttctacac	gggtgactgat	tcaggagacg	acaatcctct	aaatccaact	360
ccaggtagcat	tacggtagcg	tcgcgacaca	gatcaaacctc	tatggatcat	ttttgatgca	420
gacatggttaa	tacaactaaa	acaagatctt	caagtagctt	catacaaaaac	cattgatgggt	480
agaggaaata	acgtacaatat	agcttatgga	cgtgtgttaa	ctttatataa	agtttagtaac	540
attattataa	acaattctta	tattcacgat	tgtgttcccg	cgaaacggaa	tgctttatcg	600
tcgttgggag	gatactcgga	tggaagtga	atacgatat	tcgagtcctg	agatattttg	660
attgatcatt	gtacgttaga	gaaatgttac	gatgggctta	ttgatgcggt	gaatggatcc	720
acggatataa	cgattttcgga	tagttacatg	ttgaatcata	atgaagtcat	gcttttggtgc	780
catagtgtat	agttattccg	tgatcgggat	atgcgagtta	cgatgcgctt	taactatttt	840
gggtgaaggac	ttgtccaagg	aattgccaaag	tgtaggcatg	gatattttca	catagtgaat	900
aaacatttata	gagactggaa	gatgtatgct	attgtgtgaa	gtgctaattcc	aacgatcttt	960
agccaaggaa	atgtttttac	agcttccaat	aatacgttca	ccaaggaggt	tacaagcgaa	1020
gagagtgacg	atggagacaga	agaatggaag	gaatggaaact	ggaatcaaga	aggagacgaa	1080
atggtttaaag	gagcttttct	tacaccgtca	gggaagagag	attctccgag	Ctaacgcaaa	1140
ttttcgagta	tggttagctcg	accagcttca	cttctcaaga	ccacacatcc	atcagtaggt	1200
gtttcttagt	gcgaaattga	ccaagcttgt	taaaaacaca	aacataagct	tgtgaccaaa	1260
tctagtgttt	gtccttcttt	ttcttttttg	ctcttctact	tggtgtggtt	atgtgttatcg	1320
taaatagtag	ttgtactgaa	tgtgatgatg	atcatagacc	caaaacaaca	ttgttcatgt	1380
tcaatttctt	taccaaaaaa	ttctttttac	gagtc			

(2) INFORMATION FOR SEQ ID NO:206:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 410 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..410
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566171

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:206:

Met	Phe	Ile	Val	Lys	Leu	Leu	Val	Gly	Phe	Asn	Leu	Phe	Leu	Arg	Gln
1				5				10						15	
His	Ile	Met	Ser	Ile	Val	Cys	Thr	Phe	Phe	Leu	Phe	Leu	Leu	Asn	Thr
				20				25						30	
Ser	Phe	Ala	Phe	Ala	Phe	Ala	Ile	Pro	Lys	Pro	Pro	Ile	Val	Arg	Arg
				35				40						45	
Leu	Ser	Thr	Thr	Val	Thr	Ser	Asn	Ser	Thr	Ala	Ser	Ser	Cys	Ser	Ala
				50				55						60	
Asn	Gly	Asn	Pro	Ile	Asp	Glu	Cys	Trp	Arg	Cys	Asp	Glu	Asn	Trp	Lys
65				70				75						80	
Asp	Asn	Arg	Lys	Asn	Leu	Ala	Asp	Cys	Ala	Val	Gly	Phe	Gly	Arg	Asp
				85				90						95	

Ser Ile Gly Gly Arg Ala Gly Glu Phe Tyr Thr Val Thr Asp Ser Gly
100 105 110
Asp Asp Asn Pro Leu Asn Pro Thr Pro Gly Thr Leu Arg Tyr Ala Ala
115 120 125
Thr Gln Asp Gln Pro Leu Trp Ile Ile Phe Asp Arg Asp Met Val Ile
130 135 140
Gln Leu Lys Gln Asp Leu Gln Val Ala Ser Tyr Lys Thr Ile Asp Gly
145 150 155 160
Arg Gly Asn Asn Val Gln Ile Ala Tyr Gly Pro Cys Leu Thr Leu Tyr
165 170 175
Lys Val Ser Asn Ile Ile Ile Asn Asn Leu Tyr Ile His Asp Cys Val
180 185 190
Pro Ala Lys Arg Asn Ala Leu Ser Ser Leu Gly Gly Tyr Ser Asp Gly
195 200 205
Asp Gly Ile Ser Ile Phe Glu Ser Arg Asp Ile Trp Ile Asp His Cys
210 215 220
Thr Leu Glu Lys Cys Tyr Asp Gly Leu Ile Asp Ala Val Asn Gly Ser
225 230 235 240
Thr Asp Ile Thr Ile Ser Asn Ser Tyr Met Leu Asn His Asn Glu Val
245 250 255
Met Leu Leu Gly His Ser Asp Glu Tyr Ser Gly Asp Arg Asp Met Arg
260 265 270
Val Thr Ile Ala Phe Asn Tyr Phe Gly Glu Gly Leu Val Gln Arg Met
275 280 285
Pro Arg Cys Arg His Gly Tyr Phe His Ile Val Asn Asn Ile Tyr Arg
290 295 300
Asp Trp Lys Met Tyr Ala Ile Gly Gly Ser Ala Asn Pro Thr Ile Phe
305 310 315 320
Ser Gln Gly Asn Val Phe Ile Ala Ser Asn Asn Gln Phe Thr Lys Glu
325 330 335
Val Thr Lys Arg Glu Ser Ala Asp Gly Asp Glu Glu Trp Lys Glu Trp
340 345 350
Asn Trp Lys Ser Glu Gly Asp Glu Met Val Asn Gly Ala Phe Phe Thr
355 360 365
Pro Ser Gly Lys Glu Asp Ser Pro Ser Tyr Ala Lys Phe Ser Ser Met
370 375 380
Val Ala Arg Pro Ala Ser Leu Leu Lys Thr Thr His Pro Ser Val Gly
385 390 395 400
Val Leu Ser Cys Glu Ile Asp Gln Ala Cys
405 410

(2) INFORMATION FOR SEQ ID NO:207:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 392 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..392

(D) OTHER INFORMATION: / Ceres Seq. ID 1566173

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:207:

Met Ser Ile Val Cys Thr Phe Phe Leu Phe Leu Leu Asn Thr Ser Phe
1 5 10 15
Ala Phe Ala Phe Ala Ile Pro Lys Pro Pro Ile Val Arg Arg Leu Ser
20 25 30
Thr Thr Val Thr Ser Asn Ser Thr Ala Ser Ser Cys Ser Ala Asn Gly
35 40 45
Asn Pro Ile Asp Glu Cys Trp Arg Cys Asp Glu Asn Trp Lys Asp Asn
50 55 60
Arg Lys Asn Leu Ala Asp Cys Ala Val Gly Phe Gly Arg Asp Ser Ile

65 70 75 80
Gly Gly Arg Ala Gly Glu Phe Tyr Thr Val Thr Asp Ser Gly Asp Asp
85 90 95
Asn Pro Leu Asn Pro Thr Pro Gly Thr Leu Arg Tyr Ala Ala Thr Gln
100 105 110
Asp Gln Pro Leu Trp Ile Ile Phe Asp Arg Asp Met Val Ile Gln Leu
115 120 125
Lys Gln Asp Leu Gln Val Ala Ser Tyr Lys Thr Ile Asp Gly Arg Gly
130 135 140
Asn Asn Val Gln Ile Ala Tyr Gly Pro Cys Leu Thr Leu Tyr Lys Val
145 150 155 160
Ser Asn Ile Ile Ile Asn Asn Leu Tyr Ile His Asp Cys Val Pro Ala
165 170 175
Lys Arg Asn Ala Leu Ser Ser Leu Gly Tyr Ser Asp Gly Asp Gly
180 185 190
Ile Ser Ile Phe Glu Ser Arg Asp Ile Trp Ile Asp His Cys Thr Leu
195 200 205
Glu Lys Cys Tyr Asp Gly Leu Ile Asp Ala Val Asn Gly Ser Thr Asp
210 215 220
Ile Thr Ile Ser Asn Ser Tyr Met Leu Asn His Asn Glu Val Met Leu
225 230 235 240
Leu Gly His Ser Asp Glu Tyr Ser Gly Asp Arg Asp Met Arg Val Thr
245 250 255
Ile Ala Phe Asn Tyr Phe Gly Glu Gly Leu Val Gln Arg Met Pro Arg
260 265 270
Cys Arg His Gly Tyr Phe His Ile Val Asn Asn Ile Tyr Arg Asp Trp
275 280 285
Lys Met Tyr Ala Ile Gly Gly Ser Ala Asn Pro Thr Ile Phe Ser Gln
290 295 300
Gly Asn Val Phe Ile Ala Ser Asn Asn Gln Phe Thr Lys Glu Val Thr
305 310 315 320
Lys Arg Glu Ser Ala Asp Gly Asp Glu Glu Trp Lys Glu Trp Asn Trp
325 330 335
Lys Ser Glu Gly Asp Glu Met Val Asn Gly Ala Phe Phe Thr Pro Ser
340 345 350
Gly Lys Glu Asp Ser Pro Ser Tyr Ala Lys Phe Ser Ser Met Val Ala
355 360 365
Arg Pro Ala Ser Leu Leu Lys Thr Thr His Pro Ser Val Gly Val Leu
370 375 380
Ser Cys Glu Ile Asp Gln Ala Cys
385 390

(2) INFORMATION FOR SEQ ID NO:208:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 731 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..731

(D) OTHER INFORMATION: / Ceres Seq. ID 1566181

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:208:

agtttttgtt	tgttttgggt	gttgcgagtt	gttgactata	aaacctcttc	cacttggttc	60
ttcaacttca	ctgtttctca	tctcttggtc	ttctccgctc	ccttcaatct	cactccggtc	120
tctctacgat	tcattcggtt	tatggtcttc	attgctgctt	ctgcctctat	ttcccttcaa	180
gctcgtcttc	gcccaactgc	gatcgcgggt	aggcaagtta	aaagcttttg	caatggaaga	240
agaagcagtc	tttcttttaa	ttctccgcag	cttctctacc	gcttgactgt	ttcctgcgct	300
gcaaaacctg	agacagtgga	caaggtgtgt	gcagttgtca	gaaagcaact	ctcaactaaa	360
gaggctgacg	aaattactgc	tgccaccaaa	tttgctgcac	ttggtgctga	ttcccttgat	420
acggtggaga	ttgtgatggg	actagaggaa	gagttcggga	ttgaaatggc	ggaggagaaa	480

gcacagtcac tcgccacagt tgagcaagca Gctgcgcgtca ttgaggagct cttgtttgaa 540
aaggccaagt agaatacttt tattacatta gcaaaaacga aaaaaatcaa aaccccaaac 600
actactttat tgtttcggtta gctagagagc aattgtgtct gttgaaagat tttagttat 660
tttggggaaa ttattacaag gcttgtatct gactttttatc tttcttctaa aacattttac 720
tttcagctc c

(2) INFORMATION FOR SEQ ID NO:209:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 183 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..183
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566182

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:209:

Ser Phe Cys Leu Phe Trp Leu Leu Arg Val Cys Asp Tyr Lys Thr Ser
1 5 10 15
Pro Thr Trp Phe Phe Thr Leu Thr Val Ser His Leu Phe Val Phe Ser
20 25 30
Ala Ser Phe Asn Leu Thr Pro Ile Ser Leu Arg Phe Ile Arg Ser Met
35 40 45
Ala Ser Ile Ala Ala Ser Ala Ser Ile Ser Leu Gln Ala Arg Pro Arg
50 55 60
Gln Leu Ala Ile Ala Ala Arg Gln Val Lys Ser Phe Ser Asn Gly Arg
65 70 75 80
Arg Ser Ser Leu Ser Phe Asn Leu Arg Gln Leu Pro Thr Arg Leu Thr
85 90 95
Val Ser Cys Ala Ala Lys Pro Glu Thr Val Asp Lys Val Cys Ala Val
100 105 110
Val Arg Lys Gln Leu Ser Leu Lys Glu Ala Asp Glu Ile Thr Ala Ala
115 120 125
Thr Lys Phe Ala Ala Leu Gly Ala Asp Ser Leu Asp Thr Val Glu Ile
130 135 140
Val Met Gly Leu Glu Glu Glu Phe Gly Ile Glu Met Ala Glu Glu Lys
145 150 155 160
Ala Gln Ser Ile Ala Thr Val Glu Gln Ala Ala Ala Leu Ile Glu Glu
165 170 175
Leu Leu Phe Glu Lys Ala Lys
180

(2) INFORMATION FOR SEQ ID NO:210:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 94 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..94
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566183

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:210:

Val Phe Val Cys Phe Gly Cys Cys Glu Phe Val Thr Ile Lys Pro Leu
1 5 10 15
Pro Leu Gly Ser Ser Leu Ser Leu Phe Leu Ile Ser Ser Ser Ser Pro
20 25 30
Pro Pro Ser Ile Ser Leu Arg Ser Leu Tyr Asp Ser Phe Val Leu Trp
35 40 45
Leu Pro Leu Leu Leu Leu Leu Phe Pro Phe Lys Leu Val Leu Ala
50 55 60

Asn Trp Arg Ser Arg Leu Gly Lys Leu Lys Ala Leu Ala Met Glu Glu
65 70 75 80
Glu Ala Val Phe Leu Leu Ile Ser Ala Ser Phe Leu Pro Ala
85 90

(2) INFORMATION FOR SEQ ID NO:211:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 136 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..136
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566184

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:211:

Met Ala Ser Ile Ala Ala Ser Ala Ser Ile Ser Leu Gln Ala Arg Pro
1 5 10 15
Arg Gln Leu Ala Ile Ala Ala Arg Gln Val Lys Ser Phe Ser Asn Gly
20 25 30
Arg Arg Ser Ser Leu Ser Phe Asn Leu Arg Gln Leu Pro Thr Arg Leu
35 40 45
Thr Val Ser Cys Ala Ala Lys Pro Glu Thr Val Asp Lys Val Cys Ala
50 55 60
Val Val Arg Lys Gln Leu Ser Leu Lys Glu Ala Asp Glu Ile Thr Ala
65 70 75 80
Ala Thr Lys Phe Ala Ala Leu Gly Ala Asp Ser Leu Asp Thr Val Glu
85 90 95
Ile Val Met Gly Leu Glu Glu Glu Phe Gly Ile Glu Met Ala Glu Glu
100 105 110
Lys Ala Gln Ser Ile Ala Thr Val Glu Gln Ala Ala Ala Leu Ile Glu
115 120 125
Glu Leu Leu Phe Glu Lys Ala Lys
130 135

(2) INFORMATION FOR SEQ ID NO:212:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1158 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1158
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566185

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:212:

gaagaaacaaa cacaaaaaatg gcgacgggtac cattgtttcac ccagttttccc tgcaaaacccc 60
taaattccaag ctcatcaaac actaaacac aatcgaaatc tccgatctcta ctaccgatta 120
actcaataaaa tcgatcggag attggagtct ctgttcatcg gccagatttc aaaatcccgag 180
cgacggacat cgacgacgaa tgggggtcaag atggagtggg gagagtattt gcctcatctt 240
caaccgtatc ggtagcagat aaagcaatcg aatccgtgga ggagacggag aggcataaaga 300
gatcactagc ggattcggtt tacggaacag atcgaggttt aagcgtatcg agtgatacga 360
gagctgagat cagcgagctc atcacacagc tcgagttctaa gaacccctact ccagctctcta 420
acgaagctct gtttctctc aacggcaaat ggatcctcgc ctacacgtcg ttctgtggggt 480
tgttccatt gctctcacga agaattgaac cgttggttaa agtggatgat atctcacaaa 540
ccattgattc cgatagcttc accgttcaaa actctgtccg gttcgtcgtt ccgtttttcca 600
caacgtcgtt tagcaccaac gctaagtttg aaatccgaag tctataaacgt gtccagatta 660
agttcgagca aggtgttata ggRactcttc agctaaccga ttcgattgaa ataccggaat 720
ccgtggaggt tcttggtcgc aaaaatcgatc tcaatcccat taaaggttta ctatcatcat 780
tccaagacac tgcttcttca gtggctagaa ccaatttcaaa ccaaccacca ttgaagtttt 840
ctctgcctag tgacaacacg cagtctgtgc tgcacaaac ttatctcgac aagacCttc 900

ggatctcgag aggcgatggt ggaagcgtct atgtgctcat caaagaagga agctctctct 960
taaaccctta aatcatcata actctcatca catccatagt aacatatata caagtatatga 1020
cccatctgtc tatgtttact agtgttgtaa ctgtttatata gctctttac ctgttgagaga 1080
gttataaact tataatggat gttactcttg gtatactgta ctacaataca tatacataac 1140
tacatacttg aacaggcc

(2) INFORMATION FOR SEQ ID NO:213:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 322 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..322
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566186

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:213:

Arg	Thr	Asn	Thr	Lys	Met	Ala	Thr	Val	Pro	Leu	Phe	Thr	Gln	Phe	Pro
1			5						10				15		
Cys	Lys	Thr	Leu	Asn	Pro	Ser	Ser	Ser	Asn	Thr	Lys	His	Gln	Ser	Lys
			20					25					30		
Ser	Pro	Ile	Leu	Leu	Pro	Ile	Asn	Ser	Ile	Asn	Arg	Ser	Glu	Ile	Gly
		35					40				45				
Val	Ser	Val	His	Arg	Pro	Asp	Phe	Lys	Ile	Arg	Ala	Thr	Asp	Ile	Asp
		50				55					60				
Asp	Glu	Trp	Gly	Gln	Asp	Gly	Val	Glu	Arg	Val	Phe	Ala	Ser	Ser	Ser
		65			70				75				80		
Thr	Val	Ser	Val	Ala	Asp	Lys	Ala	Ile	Glu	Ser	Val	Glu	Glu	Thr	Glu
			85						90				95		
Arg	Leu	Lys	Arg	Ser	Leu	Ala	Asp	Ser	Leu	Tyr	Gly	Thr	Asp	Arg	Gly
			100					105					110		
Leu	Ser	Val	Ser	Ser	Asp	Thr	Arg	Ala	Glu	Ile	Ser	Glu	Leu	Ile	Thr
		115						120				125			
Gln	Leu	Glu	Ser	Lys	Asn	Pro	Thr	Pro	Ala	Pro	Asn	Glu	Ala	Leu	Phe
		130				135					140				
Leu	Leu	Asn	Gly	Lys	Trp	Ile	Leu	Ala	Tyr	Thr	Ser	Phe	Val	Gly	Leu
		145			150					155				160	
Phe	Pro	Leu	Leu	Ser	Arg	Arg	Ile	Glu	Pro	Leu	Val	Lys	Val	Asp	Glu
			165						170					175	
Ile	Ser	Gln	Thr	Ile	Asp	Ser	Asp	Ser	Phe	Thr	Val	Gln	Asn	Ser	Val
			180					185					190		
Arg	Phe	Ala	Gly	Pro	Phe	Ser	Thr	Thr	Ser	Phe	Ser	Thr	Asn	Ala	Lys
		195						200				205			
Phe	Glu	Ile	Arg	Ser	Pro	Lys	Arg	Val	Gln	Ile	Lys	Phe	Glu	Gln	Gly
		210				215					220				
Val	Ile	Xaa	Thr	Pro	Gln	Leu	Thr	Asp	Ser	Ile	Glu	Ile	Pro	Glu	Ser
		225			230					235				240	
Val	Glu	Val	Leu	Gly	Gln	Lys	Ile	Asp	Leu	Asn	Pro	Ile	Lys	Gly	Leu
			245						250				255		
Leu	Thr	Ser	Val	Gln	Asp	Thr	Ala	Ser	Ser	Val	Ala	Arg	Thr	Ile	Ser
			260					265				270			
Asn	Gln	Pro	Pro	Leu	Lys	Phe	Ser	Leu	Pro	Ser	Asp	Asn	Thr	Gln	Ser
		275					280					285			
Trp	Leu	Leu	Thr	Thr	Tyr	Leu	Asp	Lys	Asp	Leu	Arg	Ile	Ser	Arg	Gly
		290				295					300				
Asp	Gly	Gly	Ser	Val	Tyr	Val	Leu	Ile	Lys	Glu	Gly	Ser	Ser	Leu	Leu
		305			310					315				320	
Asn	Pro														

(2) INFORMATION FOR SEQ ID NO:214:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 317 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..317
(D) OTHER INFORMATION: / Ceres Seq. ID 1566187
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:214:
Met Ala Thr Val Pro Leu Phe Thr Gln Phe Pro Cys Lys Thr Leu Asn
1 5 10 15
Pro Ser Ser Ser Asn Thr Lys His Gln Ser Lys Ser Pro Ile Leu Leu
20 25 30
Pro Ile Asn Ser Ile Asn Arg Ser Glu Ile Gly Val Ser Val His Arg
35 40 45
Pro Asp Phe Lys Ile Arg Ala Thr Asp Ile Asp Asp Glu Trp Gly Gln
50 55 60
Asp Gly Val Glu Arg Val Phe Ala Ser Ser Ser Thr Val Ser Val Ala
65 70 75 80
Asp Lys Ala Ile Glu Ser Val Glu Glu Thr Glu Arg Leu Lys Arg Ser
85 90 95
Leu Ala Asp Ser Leu Tyr Gly Thr Asp Arg Gly Leu Ser Val Ser Ser
100 105 110
Asp Thr Arg Ala Glu Ile Ser Glu Leu Ile Thr Gln Leu Glu Ser Lys
115 120 125
Asn Pro Thr Pro Ala Pro Asn Glu Ala Leu Phe Leu Leu Asn Gly Lys
130 135 140
Trp Ile Leu Ala Tyr Thr Ser Phe Val Gly Leu Phe Pro Leu Leu Ser
145 150 155 160
Arg Arg Ile Glu Pro Leu Val Lys Val Asp Glu Ile Ser Gln Thr Ile
165 170 175
Asp Ser Asp Ser Phe Thr Val Gln Asn Ser Val Arg Phe Ala Gly Pro
180 185 190
Phe Ser Thr Thr Ser Phe Ser Thr Asn Ala Lys Phe Glu Ile Arg Ser
195 200 205
Pro Lys Arg Val Gln Ile Lys Phe Glu Gln Gly Val Ile Xaa Thr Pro
210 215 220
Gln Leu Thr Asp Ser Ile Glu Ile Pro Glu Ser Val Glu Val Leu Gly
225 230 235 240
Gln Lys Ile Asp Leu Asn Pro Ile Lys Gly Leu Leu Thr Ser Val Gln
245 250 255
Asp Thr Ala Ser Ser Val Ala Arg Thr Ile Ser Asn Gln Pro Pro Leu
260 265 270
Lys Phe Ser Leu Pro Ser Asp Asn Thr Gln Ser Trp Leu Leu Thr Thr
275 280 285
Tyr Leu Asp Lys Asp Leu Arg Ile Ser Arg Gly Asp Gly Gly Ser Val
290 295 300
Tyr Val Leu Ile Lys Glu Gly Ser Ser Leu Leu Asn Pro
305 310 315
(2) INFORMATION FOR SEQ ID NO:215:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 655 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..655
(D) OTHER INFORMATION: / Ceres Seq. ID 1566214

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:215:
aatggttact ttacttctct ctctctctct tcttgttcca tctttcatgt gaaagagaga 60
gttgaatttt gcagatgagt atgagaagaa gcaaaagcgga agggaaagag agcttacagag 120
aactgagtga ggaagagaaa gaagaagaag aaactgaaga tgaagatact tttagaagaa 180
aagaggcttt ggagaagaag cagaaaagga aagctacaag tagtagtgga gtttgcagg 240
tcgagagttg taccgcggat ataagcaaaag ccaaacagta ccacaaacga cacaaagtct 300
gcagatttca tgccaaagct cctcatgttc ggatctcttg tcttcaccaa cgtttctgcc 360
aacaatgcag caggttttcac gcgctcagtg agtttgatga agccaagcgg agttgcagga 420
gacgcttagc tggacacaac gagagaaggg ggaagagcac aactgactaa agacgggtgaa 480
acgtgtgaga tccCggtttg aaggttaatg aaacaggGct ttgGcttact ctcttctgtc 540
agtctctttt agctccttgt aatcctctgt gtctctgtct gtccccata ttacctgtaa 600
tcaaagctat ctgctaaacc tacgacatgg ttaataaat gcattgagac ttagc

(2) INFORMATION FOR SEQ ID NO:216:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 131 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..131

(D) OTHER INFORMATION: / Ceres Seq. ID 1566215

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:216:

Met	Ser	Met	Arg	Arg	Ser	Lys	Ala	Glu	Gly	Lys	Arg	Ser	Leu	Arg	Glu
1			5					10					15		
Leu	Ser	Glu	Glu	Glu	Glu	Glu	Glu	Glu	Thr	Glu	Asp	Glu	Asp	Thr	
			20					25				30			
Phe	Glu	Glu	Glu	Glu	Ala	Leu	Glu	Lys	Lys	Gln	Lys	Gly	Lys	Ala	Thr
			35				40				45				
Ser	Ser	Ser	Gly	Val	Cys	Gln	Val	Glu	Ser	Cys	Thr	Ala	Asp	Ile	Ser
			50				55				60				
Lys	Ala	Lys	Gln	Tyr	His	Lys	Arg	His	Lys	Val	Cys	Gln	Phe	His	Ala
65				70					75					80	
Lys	Ala	Pro	His	Val	Arg	Ile	Ser	Gly	Leu	His	Gln	Arg	Phe	Cys	Gln
			85					90					95		
Gln	Cys	Ser	Arg	Phe	His	Ala	Leu	Ser	Glu	Phe	Asp	Glu	Ala	Lys	Arg
			100					105					110		
Ser	Cys	Arg	Arg	Arg	Leu	Ala	Gly	His	Asn	Glu	Arg	Arg	Arg	Lys	Ser
			115				120						125		
Thr	Thr	Asp													
			130												

(2) INFORMATION FOR SEQ ID NO:217:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..129

(D) OTHER INFORMATION: / Ceres Seq. ID 1566216

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:217:

Met	Arg	Arg	Ser	Lys	Ala	Glu	Gly	Lys	Arg	Ser	Leu	Arg	Glu	Leu	Ser
1				5					10				15		
Glu	Glu	Glu	Glu	Glu	Glu	Glu	Glu	Thr	Glu	Asp	Glu	Asp	Thr	Phe	Glu
				20				25					30		
Glu	Glu	Glu	Ala	Leu	Glu	Lys	Lys	Gln	Lys	Gly	Lys	Ala	Thr	Ser	Ser
			35				40					45			
Ser	Gly	Val	Cys	Gln	Val	Glu	Ser	Cys	Thr	Ala	Asp	Ile	Ser	Lys	Ala

50	55	60
Lys Gln Tyr His Lys Arg His Lys Val Cys Gln Phe His Ala Lys Ala		
65	70	75
Pro His Val Arg Ile Ser Gly Leu His Gln Arg Phe Cys Gln Gln Cys		80
	85	90
Ser Arg Phe His Ala Leu Ser Glu Phe Asp Glu Ala Lys Arg Ser Cys		95
	100	105
Arg Arg Arg Leu Ala Gly His Asn Glu Arg Arg Arg Lys Ser Thr Thr		110
	115	120
		125

Asp

(2) INFORMATION FOR SEQ ID NO:218:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 631 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..631
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566220

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:218:

atatttatat	tttccaataa	tctcaaaaaa	aaActctctg	attcgaaaaa	tgaatttga	60
ttttgacaaa	aaaaaaatga	gctacgacag	agtcccaccg	gaatcgatc	ctcctccagg	120
ataccaatct	cactatccac	ctccggggtta	tccatcagca	ccgccaccgc	cgggatatcc	180
ttctctctcg	tcgcatcacg	aaggatatcc	tccacctcac	ccttacggag	gatatccacc	240
acgcctctca	cgtccttacg	aaggcgggtta	tcaagggtac	tgcgcggag	gagggttatcc	300
tcatcagcat	caaggaccac	cacctctctc	tccgccgcaa	aattacgacc	actgccatca	360
tgatcatcac	cattaccaag	attctgactc	tggttgcttc	tctttcatcc	gtggctgtct	420
tgctgctctt	tgctgttgct	gtttgttgga	ggaatgctgc	ttctgagaat	gcgcgcagtc	480
tctgtggtac	tcgtgtgtta	ctgtcagcat	tatgtgtcta	atcgaagaca	tatgccataa	540
cactctatgt	cttatatgta	tccatcaaaa	taaacattgg	tgagtttcta	atgcagttcc	600
ttcagaaatg	tgtggaataa	tgtttcacaa	t			

(2) INFORMATION FOR SEQ ID NO:219:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 154 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..154
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566221

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:219:

Tyr	Leu	Tyr	Phe	Pro	Ile	Ile	Ser	Lys	Lys	Asn	Ser	Leu	Ile	Arg	Lys
1		5						10				15			
Val	Lys	Phe	Asp	Phe	Asp	Lys	Lys	Lys	Met	Ser	Tyr	Asp	Arg	Val	Pro
			20					25				30			
Pro	Glu	Ser	Tyr	Pro	Pro	Pro	Gly	Tyr	Gln	Ser	His	Tyr	Pro	Pro	Pro
			35				40					45			
Gly	Tyr	Pro	Ser	Ala	Pro	Pro	Pro	Pro	Gly	Tyr	Pro	Ser	Pro	Pro	Ser
			50				55					60			
His	His	Glu	Gly	Tyr	Pro	Pro	Pro	Gln	Pro	Tyr	Gly	Gly	Tyr	Pro	Pro
			65				70			75				80	
Pro	Ser	Ser	Arg	Pro	Tyr	Glu	Gly	Gly	Tyr	Gln	Gly	Tyr	Phe	Ala	Gly
			85				90					95			
Gly	Gly	Tyr	Pro	His	Gln	His	His	Gly	Pro	Pro	Pro	Pro	Pro	Pro	Pro
			100				105					110			
Gln	Asn	Tyr	Asp	His	Cys	His	His	Asp	His	His	His	Tyr	Gln	Asp	Ser

115 120 125
Asp Ser Gly Cys Phe Ser Phe Ile Arg Gly Cys Leu Ala Ala Leu Cys
130 135 140
Cys Cys Cys Leu Leu Glu Glu Cys Cys Phe
145 150

(2) INFORMATION FOR SEQ ID NO:220:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..129
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566222

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:220:

Met	Ser	Tyr	Asp	Arg	Val	Pro	Pro	Glu	Ser	Tyr	Pro	Pro	Pro	Gly	Tyr
1			5					10						15	
Gln	Ser	His	Tyr	Pro	Pro	Pro	Gly	Tyr	Pro	Ser	Ala	Pro	Pro	Pro	Pro
			20					25						30	
Gly	Tyr	Pro	Ser	Pro	Pro	Ser	His	His	Glu	Gly	Tyr	Pro	Pro	Pro	Gln
			35				40							45	
Pro	Tyr	Gly	Gly	Tyr	Pro	Pro	Pro	Ser	Ser	Arg	Pro	Tyr	Glu	Gly	Gly
			50				55							60	
Tyr	Gln	Gly	Tyr	Phe	Ala	Gly	Gly	Gly	Tyr	Pro	His	Gln	His	His	Gly
							70							80	
Pro	Pro	Pro	Pro	Pro	Pro	Pro	Gln	Asn	Tyr	Asp	His	Cys	His	His	Asp
							85							95	
His	His	His	Tyr	Gln	Asp	Ser	Asp	Ser	Gly	Cys	Phe	Ser	Phe	Ile	Arg
														110	
Gly	Cys	Leu	Ala	Ala	Leu	Cys	Cys	Cys	Cys	Leu	Leu	Glu	Gly	Cys	Cys
														125	
Phe															

(2) INFORMATION FOR SEQ ID NO:221:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 771 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..771
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566223

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:221:

aaaaaattag	tctgtcgaag	catcgtgaaa	atgatcgtac	ttctctgttg	ttccgctttct	60
tcatactcga	tctgtcgtcgt	cttttcctgc	gcgctttctc	tgtttctact	ctctgaaact	120
tctctaggag	ctccttctgc	catcaatggc	ttgccaatcg	tgaggaatat	tagtgacctt	180
cctcaggata	actatggaag	accaggtctt	tccacatgta	ctgttgctgg	ctccgtattg	240
catggaatga	aagagggttg	aatatggctt	cagacatttg	ctccagggtc	agagacacca	300
attcacaggc	actcctgtga	agagggtttt	gttctcctaa	agggcagtg	tactctgtat	360
ctcgtcgaaa	cacatggaaa	tttccctggg	aaaccaatcg	aatttccaat	ctttgccaac	420
agtacaattc	atatcccgat	caatgatgct	catcagggtc	aaaacaccgg	tcattgaggac	480
ctgcaggtgt	tgggttatcat	atctcggcgc	ccattataaaa	tcttcatcta	cgaagactgg	540
tttatgccac	acaactgctgc	aaggctgaag	ttCccttact	attgggatga	gcaatgcatt	600
caagaatcac	aaaaagacga	gctttaaagc	aaagtccgag	gctaaaagca	agcacacctt	660
ttagatagta	aaatcatatg	tgagggtttt	tgacActacg	tagatactgg	taaatgtggca	720
aggattttac	atgaatgttg	ttgttaccag	aaagtaataa	aatgttcaag	c	

(2) INFORMATION FOR SEQ ID NO:222:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 208 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..208
(D) OTHER INFORMATION: / Ceres Seq. ID 1566224
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:222:

Lys	Lys	Leu	Val	Arg	Arg	Ser	Ile	Val	Lys	Met	Ile	Val	Leu	Ser	Val
1				5				10					15		
Gly	Ser	Ala	Ser	Ser	Ser	Pro	Ile	Val	Val	Val	Phe	Ser	Val	Ala	Leu
				20				25					30		
Leu	Leu	Phe	Tyr	Phe	Ser	Glu	Thr	Ser	Leu	Gly	Ala	Pro	Cys	Pro	Ile
				35				40					45		
Asn	Gly	Leu	Pro	Ile	Val	Arg	Asn	Ile	Ser	Asp	Leu	Pro	Gln	Asp	Asn
				50				55					60		
Tyr	Gly	Arg	Pro	Gly	Leu	Ser	His	Met	Thr	Val	Ala	Gly	Ser	Val	Leu
65					70				75					80	
His	Gly	Met	Lys	Glu	Val	Glu	Ile	Trp	Leu	Gln	Thr	Phe	Ala	Pro	Gly
				85					90					95	
Ser	Glu	Thr	Pro	Ile	His	Arg	His	Ser	Cys	Glu	Glu	Val	Phe	Val	Leu
				100				105					110		
Leu	Lys	Gly	Ser	Gly	Thr	Leu	Tyr	Leu	Ala	Glu	Thr	His	Gly	Asn	Phe
				115				120					125		
Pro	Gly	Lys	Pro	Ile	Glu	Phe	Pro	Ile	Phe	Ala	Asn	Ser	Thr	Ile	His
				130				135					140		
Ile	Pro	Ile	Asn	Asp	Ala	His	Gln	Val	Lys	Asn	Thr	Gly	His	Glu	Asp
145					150				155					160	
Leu	Gln	Val	Leu	Val	Ile	Ile	Ser	Arg	Pro	Pro	Ile	Lys	Ile	Phe	Ile
				165					170					175	
Tyr	Glu	Asp	Trp	Phe	Met	Pro	His	Thr	Ala	Ala	Arg	Leu	Lys	Phe	Pro
				180				185					190		
Tyr	Tyr	Trp	Asp	Glu	Gln	Cys	Ile	Gln	Glu	Ser	Gln	Lys	Asp	Glu	Leu
				195				200					205		

- (2) INFORMATION FOR SEQ ID NO:223:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 198 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..198
(D) OTHER INFORMATION: / Ceres Seq. ID 1566225
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:223:

Met	Ile	Val	Leu	Ser	Val	Gly	Ser	Ala	Ser	Ser	Ser	Pro	Ile	Val	Val
1				5				10					15		
Val	Phe	Ser	Val	Ala	Leu	Leu	Leu	Phe	Tyr	Phe	Ser	Glu	Thr	Ser	Leu
				20				25					30		
Gly	Ala	Pro	Cys	Pro	Ile	Asn	Gly	Leu	Pro	Ile	Val	Arg	Asn	Ile	Ser
				35				40					45		
Asp	Leu	Pro	Gln	Asp	Asn	Tyr	Gly	Arg	Pro	Gly	Leu	Ser	His	Met	Thr
				50				55					60		
Val	Ala	Gly	Ser	Val	Leu	His	Gly	Met	Lys	Glu	Val	Glu	Ile	Trp	Leu
65					70				75					80	

```

Gln Thr Phe Ala Pro Gly Ser Glu Thr Pro Ile His Arg His Ser Cys
      85                      90                      95
Glu Glu Val Phe Val Leu Leu Lys Gly Ser Gly Thr Leu Tyr Leu Ala
      100                      105                      110
Glu Thr His Gly Asn Phe Pro Gly Lys Pro Ile Glu Phe Pro Ile Phe
      115                      120                      125
Ala Asn Ser Thr Ile His Ile Pro Ile Asn Asp Ala His Gln Val Lys
      130                      135                      140
Asn Thr Gly His Glu Asp Leu Gln Val Leu Val Ile Ile Ser Arg Pro
      145                      150                      155                      160
Pro Ile Lys Ile Phe Ile Tyr Glu Asp Trp Phe Met Pro His Thr Ala
      165                      170                      175
Ala Arg Leu Lys Phe Pro Tyr Tyr Trp Asp Glu Gln Cys Ile Gln Glu
      180                      185                      190
Ser Gln Lys Asp Glu Leu
      195

```

(2) INFORMATION FOR SEQ ID NO:224:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 136 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..136
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566226

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:224:

```

Met Thr Val Ala Gly Ser Val Leu His Gly Met Lys Glu Val Glu Ile
1      5      10      15
Trp Leu Gln Thr Phe Ala Pro Gly Ser Glu Thr Pro Ile His Arg His
      20      25      30
Ser Cys Glu Glu Val Phe Val Leu Lys Gly Ser Gly Thr Leu Tyr
      35      40      45
Leu Ala Glu Thr His Gly Asn Phe Pro Gly Lys Pro Ile Glu Phe Pro
      50      55      60
Ile Phe Ala Asn Ser Thr Ile His Ile Pro Ile Asn Asp Ala His Gln
      65      70      75      80
Val Lys Asn Thr Gly His Glu Asp Leu Gln Val Leu Val Ile Ile Ser
      85      90      95
Arg Pro Pro Ile Lys Ile Phe Ile Tyr Glu Asp Trp Phe Met Pro His
      100      105      110
Thr Ala Ala Arg Leu Lys Phe Pro Tyr Tyr Trp Asp Glu Gln Cys Ile
      115      120      125
Gln Glu Ser Gln Lys Asp Glu Leu
      130      135

```

(2) INFORMATION FOR SEQ ID NO:225:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1256 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1256
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566234

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:225:

```

aaacaaaaca caggtttggt cggagaaggc ttatattaac cacttgtcct cctctcagac      60
tctacaaagt caaagtgtgt cactttacct ataaaaacgc ttctctttca atggctctct      120
ctcttgtgtt ccttgctctg attctctctt cttctctctac taaccttcgt tcaaatcacc      180

```

```

atctccccc tttcttcccc aagaatcatc tcatttgctc tcattccact tctctctgct 240
tcgaatcgct ctggttttca tgcgtcgcaa ctggatctac caagaaatca tccgatactc 300
ggagaaagggt aaagagcatg gctacgacaa atataggaaa gaggaggag aaagagctcg 360
agatttatga tctcgaagAg aatttagcga ttgatttgcc taaattcaca gcagatctct 420
ccgataagtt ttgtaaagag agaggcgctt tcaccgtcgt tgtctccggt ggctctctca 480
tcaaatcact ccgaaaatta gtagaatctc cttacgttga tctctatagat tgggcaagggt 540
ggcatttttt ctgggttgac gagagagttg ttcccaagaa tcacgatgat agcaactata 600
aactcgttta tgatagtttt ctatcccaag taccaattcc gcttggaagt gtatatgcga 660
tcaacgaagc cctctccgct gaggtcgtag cggatgatta cgagacctcg ctcaaacatt 720
tggtcaacac caacattctc cgtgtatctg aatcaactgg ctttcccaaa ttgtatctca 780
tgctctaggt tatgggacct gatggtcatc tggcatcatt attccctggg catggtctct 840
gcaacgagag caagaaatgg gtagtttcaa tctctgactc tccaaaacca ccgtctgaga 900
gaatcacctt cactgtcccc gtcatacaat catctgcaca tgtagctcta gttgtttcgg 960
gttctgggaa agctgaagct gtggaggcag ctttaagaaa gactgggaat gtaccacctg 1020
ctggttctgt ttctgctgaa gacgagttgg tttggttctt ggacaaaacca gcatcttcca 1080
agctctaaaa acaggtggta tgcttcccat tccagtgaa ttaccaatgt gactagctcg 1140
gtttagtttt tggattttga ctcttttggt ctctccattt atgttgtggg aagagaactg 1200
tgtgataaaa gcgtgtactt tacatggaaa taatgaacta atcaatggtt tctctg

```

(2) INFORMATION FOR SEQ ID NO:226:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 325 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..325

(D) OTHER INFORMATION: / Ceres Seq. ID 1566235

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:226:

```

Met Ala Ser Ser Ser Cys Phe Leu Arg Ser Ile Leu Phe Ser Ser Pro
1      5      10      15
Thr Asn Leu Arg Ser Asn His His Leu Pro Thr Phe Phe Pro Lys Asn
20     25
His Leu Ile Cys Ser His Ser Thr Ser Ser Arg Phe Glu Ser Leu Ser
35     40     45
Val Ser Ser Ile Gly Thr Gly Ser Thr Lys Lys Ser Ser Asp Thr Arg
50     55     60
Arg Lys Val Lys Ser Met Ala Thr Thr Asn Ile Gly Lys Glu Glu Lys
65     70     75     80
Lys Arg Val Glu Ile Tyr Asp Leu Glu Glu Asn Leu Ala Ile Asp Leu
85     90     95
Ala Lys Phe Thr Ala Asp Leu Ser Asp Lys Phe Cys Lys Glu Arg Gly
100    105    110
Ala Phe Thr Val Val Val Ser Gly Gly Ser Leu Ile Lys Ser Leu Arg
115    120    125
Lys Leu Val Glu Ser Pro Tyr Val Asp Ser Ile Asp Trp Ala Arg Trp
130    135    140
His Phe Phe Trp Val Asp Glu Arg Val Val Pro Lys Asn His Asp Asp
145    150    155    160
Ser Asn Tyr Lys Leu Ala Tyr Asp Ser Phe Leu Ser Lys Val Pro Ile
165    170    175
Pro Pro Gly Asn Val Tyr Ala Ile Asn Glu Ala Leu Ser Ala Glu Ala
180    185    190
Ala Ala Asp Asp Tyr Glu Thr Cys Leu Lys His Leu Val Asn Thr Asn
195    200    205
Ile Leu Arg Val Ser Glu Ser Thr Gly Phe Pro Lys Phe Asp Leu Met
210    215    220
Leu Leu Gly Met Gly Pro Asp Gly His Val Ala Ser Leu Phe Pro Gly
225    230    235    240
His Gly Leu Cys Asn Glu Ser Lys Lys Trp Val Ser Ile Ser Asp

```

245 250 255
Ser Pro Lys Pro Pro Ser Glu Arg Ile Thr Phe Thr Phe Pro Val Ile
260 265 270
Asn Ser Ser Ala His Val Ala Leu Val Val Cys Gly Ser Gly Lys Ala
275 280 285
Glu Ala Val Glu Ala Ala Leu Lys Lys Thr Gly Asn Val Pro Pro Ala
290 295 300
Gly Ser Val Ser Ala Glu Asp Glu Leu Val Trp Phe Leu Asp Lys Pro
305 310 315 320
Ala Ser Ser Lys Leu
325

(2) INFORMATION FOR SEQ ID NO:227:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 256 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..256

(D) OTHER INFORMATION: / Ceres Seq. ID 1566236

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:227:

Met Ala Thr Thr Asn Ile Gly Lys Glu Glu Lys Lys Arg Val Glu Ile
1 5 10 15
Tyr Asp Leu Glu Glu Asn Leu Ala Ile Asp Leu Ala Lys Phe Thr Ala
20 25 30
Asp Leu Ser Asp Lys Phe Cys Lys Glu Arg Gly Ala Phe Thr Val Val
35 40 45
Val Ser Gly Gly Ser Leu Ile Lys Ser Leu Arg Lys Leu Val Glu Ser
50 55 60
Pro Tyr Val Asp Ser Ile Asp Trp Ala Arg Trp His Phe Phe Trp Val
65 70 75 80
Asp Glu Arg Val Val Pro Lys Asn His Asp Asp Ser Asn Tyr Lys Leu
85 90 95
Ala Tyr Asp Ser Phe Leu Ser Lys Val Pro Ile Pro Pro Gly Asn Val
100 105 110
Tyr Ala Ile Asn Glu Ala Leu Ser Ala Glu Ala Ala Asp Asp Tyr
115 120 125
Glu Thr Cys Leu Lys His Leu Val Asn Thr Asn Ile Leu Arg Val Ser
130 135 140
Glu Ser Thr Gly Phe Pro Lys Phe Asp Leu Met Leu Leu Gly Met Gly
145 150 155 160
Pro Asp Gly His Val Ala Ser Leu Phe Pro Gly His Gly Leu Cys Asn
165 170 175
Glu Ser Lys Lys Trp Val Val Ser Ile Ser Asp Ser Pro Lys Pro Pro
180 185 190
Ser Glu Arg Ile Thr Phe Thr Phe Pro Val Ile Asn Ser Ser Ala His
195 200 205
Val Ala Leu Val Val Cys Gly Ser Gly Lys Ala Glu Ala Val Glu Ala
210 215 220
Ala Leu Lys Lys Thr Gly Asn Val Pro Pro Ala Gly Ser Val Ser Ala
225 230 235 240
Glu Asp Glu Leu Val Trp Phe Leu Asp Lys Pro Ala Ser Ser Lys Leu
245 250 255

(2) INFORMATION FOR SEQ ID NO:228:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 640 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
 (A) NAME/KEY: -
 (B) LOCATION: 1..640
 (D) OTHER INFORMATION: / Ceres Seq. ID 1566237
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:228:
aactaccacc aattcaatcc attgctcaaa ctctcttctc atctctcaaca caccaccctt 60
acctaccctc atctctctct ctgcaacaga gcacaaaaat ggattctgca tcgtccaaca 120
ccaaagctat agaccctcca ctccacatgt tgggtttcga gttcgatgaa ttatctccga 180
cacgtatcac aggtgcgctt cctgtttctc cctgtctgtg ccagcctttc aaggtgttac 240
acggtgggtg atctgtcttg atagccgagt ctttagcaag tatgggagct cacatggcct 300
ctgggtttcaa aagggtgcgt ggaattcaac tctcaatcaa ccatttgaag agtgcgtgat 360
ttggagacct tgtcttcgcc gaagcaactc ctgtaagcac aggggaagact attcaggttt 420
gggaagtcac gttatggaaa acaacacaga aagataaagc taacaaaatc Tttaatatct 480
tcctctagag ttacacttat ctgtaattcta cctatccctg ataacgccaa agatgcagca 540
aacatgctca aaatggctgc aaagtgttag atttcttcag gcttttttgt ttactctgta 600
ttgtatgtaa tgaccatct tctcgaattt gataataagc
(2) INFORMATION FOR SEQ ID NO:229:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 161 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..161
 (D) OTHER INFORMATION: / Ceres Seq. ID 1566238
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:229:
Leu Pro Pro Ile Gln Ser Ile Ala Gln Thr Leu Leu Ser Ser Leu Thr
1 5 10 15
His Pro Pro Tyr Leu Pro Pro Ser Leu Gln Gln Ser Thr Lys
20 25 30
Met Asp Ser Ala Ser Ser Asn Thr Lys Ala Ile Asp Pro Pro Leu His
35 40 45
Met Leu Gly Phe Glu Phe Asp Glu Leu Ser Pro Thr Arg Ile Thr Gly
50 55 60
Arg Leu Pro Val Ser Pro Val Cys Cys Gln Pro Phe Lys Val Leu His
65 70 75 80
Gly Gly Val Ser Ala Leu Ile Ala Glu Ser Leu Ala Ser Met Gly Ala
85 90 95
His Met Ala Ser Gly Phe Lys Arg Val Ala Gly Ile Gln Leu Ser Ile
100 105 110
Asn His Leu Lys Ser Ala Asp Leu Gly Asp Leu Val Phe Ala Glu Ala
115 120 125
Thr Pro Val Ser Thr Gly Lys Thr Ile Gln Val Trp Glu Val Lys Leu
130 135 140
Trp Lys Thr Thr Gln Lys Asp Lys Ala Asn Lys Ile Phe Asn Ile Phe
145 150 155 160
Leu

(2) INFORMATION FOR SEQ ID NO:230:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 129 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1..129
(D) OTHER INFORMATION: / Ceres Seq. ID 1566239

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:230:

```
Met Asp Ser Ala Ser Ser Asn Thr Lys Ala Ile Asp Pro Pro Leu His
1          5          10          15
Met Leu Gly Phe Glu Phe Asp Glu Leu Ser Pro Thr Arg Ile Thr Gly
20          25          30
Arg Leu Pro Val Ser Pro Val Cys Cys Gln Pro Phe Lys Val Leu His
35          40          45
Gly Gly Val Ser Ala Leu Ile Ala Glu Ser Leu Ala Ser Met Gly Ala
50          55          60
His Met Ala Ser Gly Phe Lys Arg Val Ala Gly Ile Gln Leu Ser Ile
65          70          75
Asn His Leu Lys Ser Ala Asp Leu Gly Asp Leu Val Phe Ala Glu Ala
85          90          95
Thr Pro Val Ser Thr Gly Lys Thr Ile Gln Val Trp Glu Val Lys Leu
100         105         110
Trp Lys Thr Thr Gln Lys Asp Lys Ala Asn Lys Ile Phe Asn Ile Phe
115         120         125
Leu
```

(2) INFORMATION FOR SEQ ID NO:231:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 113 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1..113
(D) OTHER INFORMATION: / Ceres Seq. ID 1566240

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:231:

```
Met Leu Gly Phe Glu Phe Asp Glu Leu Ser Pro Thr Arg Ile Thr Gly
1          5          10          15
Arg Leu Pro Val Ser Pro Val Cys Cys Gln Pro Phe Lys Val Leu His
20          25          30
Gly Gly Val Ser Ala Leu Ile Ala Glu Ser Leu Ala Ser Met Gly Ala
35          40          45
His Met Ala Ser Gly Phe Lys Arg Val Ala Gly Ile Gln Leu Ser Ile
50          55          60
Asn His Leu Lys Ser Ala Asp Leu Gly Asp Leu Val Phe Ala Glu Ala
65          70          75
Thr Pro Val Ser Thr Gly Lys Thr Ile Gln Val Trp Glu Val Lys Leu
85          90          95
Trp Lys Thr Thr Gln Lys Asp Lys Ala Asn Lys Ile Phe Asn Ile Phe
100         105         110
Leu
```

(2) INFORMATION FOR SEQ ID NO:232:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1090 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -
(B) LOCATION: 1..1090
(D) OTHER INFORMATION: / Ceres Seq. ID 1566241

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:232:

actcttttctt	cttctctctcg	tgtctgtttg	tcacttttaga	gtactcttctt	cttcttctctt	60
gttaagcggtt	ctctctcgac	ttgatacttt	tctccagtaa	gggtttgcaa	agatgaagct	120
tgatactagt	gggttcgaga	cttccatgcc	tatgatitgga	tttggtctga	gcagtgatat	180
gcttgatgag	cttctctctg	tacctctgtt	tgatctaccc	cgtactaaag	agtttgatgg	240
atttcagaaa	aaagctaaaag	acatgttgaa	gcatgcacaa	ggaaacacaa	ctctcgcttt	300
tatcttcaaa	gggtgtgtta	tggtcgctgc	tgattctcgg	gctagcatgg	gaggtatatat	360
ctcttcacaa	tctgtgaaga	agattattga	aatcaatcct	tatatgctcg	gtacaatggc	420
tgaggagcgt	gctgattgcc	aattctggca	cagaaatctt	ggaatataag	gcgcctacaa	480
tgagctggca	aacaagagga	gaatctctgt	tccggagcgt	tcgaaacttc	ttgcacacat	540
gctctattca	taccgtggaa	tgggacttct	tggtgtgtaca	atgattgctg	gatggagcga	600
aactggtccc	ggactatact	atgtcgacaa	cgaaggagga	cgctcaagg	gagacaggtt	660
ttcagtcggt	tctggttcac	catatgccta	cggtgtgctg	gacagcgggt	acaaatatga	720
tatgtcagtt	gaagaagcct	ccgagttaga	ggagatcaat	ctaccatcgc	acattccgtg	780
atggagccag	tggtggagtt	gctagcgtgt	accacgttgg	tcccgaagga	tggaagaaac	840
tatcaggaga	tgatgttggg	gagctacact	accattacta	ccccgtggca	ccagctaccg	900
cagaacaagt	catggaggaa	gcaacagccg	aataaaaaatc	ctgttttagtt	ttctaactgt	960
tcactccctt	tcttgttgtt	gcatttttgt	gtagtatata	ctgagttgtc	tctagctgaa	1020
gcttgggtat	tctattttat	tgatctgaaa	tggtgctcgc	ggattattct	ctataagatt	1080
ctcttttctt						

(2) INFORMATION FOR SEQ ID NO:233:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 222 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..222

(D) OTHER INFORMATION: / Ceres Seq. ID 1566242

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:233:

Met	Lys	Leu	Asp	Thr	Ser	Gly	Phe	Glu	Thr	Ser	Met	Pro	Met	Ile	Gly
1			5					10						15	
Phe	Gly	Ser	Ser	Ser	Asp	Met	Leu	Asp	Glu	Leu	Ser	Ser	Val	Pro	Ser
			20					25					30		
Phe	Asp	Leu	Pro	Arg	Thr	Lys	Glu	Phe	Asp	Gly	Phe	Gln	Lys	Lys	Ala
			35				40					45			
Lys	Asp	Met	Leu	Lys	His	Ala	Lys	Gly	Thr	Thr	Thr	Leu	Ala	Phe	Ile
			50			55					60				
Phe	Lys	Gly	Gly	Val	Met	Val	Ala	Ala	Asp	Ser	Arg	Ala	Ser	Met	Gly
65				70					75					80	
Gly	Tyr	Ile	Ser	Ser	Gln	Ser	Val	Lys	Lys	Ile	Ile	Glu	Ile	Asn	Pro
			85						90					95	
Tyr	Met	Leu	Gly	Thr	Met	Ala	Gly	Gly	Ala	Ala	Asp	Cys	Gln	Phe	Trp
			100					105					110		
His	Arg	Asn	Leu	Gly	Ile	Lys	Cys	Arg	Leu	His	Glu	Leu	Ala	Asn	Lys
		115				120					125				
Arg	Arg	Ile	Ser	Val	Ser	Gly	Ala	Ser	Lys	Leu	Leu	Ala	Asn	Met	Leu
		130				135					140				
Tyr	Ser	Tyr	Arg	Gly	Met	Gly	Leu	Ser	Val	Gly	Thr	Met	Ile	Ala	Gly
145				150						155					160
Trp	Asp	Glu	Thr	Gly	Pro	Gly	Leu	Tyr	Tyr	Val	Asp	Asn	Glu	Gly	Gly
			165						170				175		
Arg	Leu	Lys	Gly	Asp	Arg	Phe	Ser	Val	Gly	Ser	Gly	Ser	Pro	Tyr	Ala
			180					185					190		
Tyr	Gly	Val	Leu	Asp	Ser	Gly	Tyr	Lys	Tyr	Asp	Met	Ser	Val	Glu	Glu
			195				200				205				
Ala	Ser	Glu	Leu	Glu	Glu	Ile	Asn	Leu	Pro	Cys	Asp	Ile	Pro		
		210				215					220				

(2) INFORMATION FOR SEQ ID NO:234:

[illegible]

```
(ii) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 209 amino acids
      (B) TYPE: amino acid
      (C) STRANDEDNESS:
      (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
      (A) NAME/KEY: peptide
      (B) LOCATION: 1..209
      (D) OTHER INFORMATION: / Ceres Seq. ID 1566244
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:235:
```

Met	Ile	Gly	Phe	Gly	Ser	Ser	Ser	Asp	Met	Leu	Asp	Glu	Leu	Ser	Ser
1				5					10					15	
Val	Pro	Ser	Phe	Asp	Leu	Pro	Arg	Thr	Lys	Glu	Phe	Asp	Gly	Phe	Gln
			20					25					30		
Lys	Lys	Ala	Lys	Asp	Met	Leu	Lys	His	Ala	Lys	Gly	Thr	Thr	Thr	Leu
		35					40					45			
Ala	Phe	Ile	Phe	Lys	Gly	Gly	Val	Met	Val	Ala	Ala	Asp	Ser	Arg	Ala
	50					55				60					
Ser	Met	Gly	Gly	Tyr	Ile	Ser	Ser	Gln	Ser	Val	Lys	Lys	Ile	Ile	Glu
65				70						75				80	

Ile	Asn	Pro	Tyr	Met	Leu	Gly	Thr	Met	Ala	Gly	Gly	Ala	Ala	Asp	Cys	
				85						90				95		
Gln	Phe	Trp	His	Arg	Asn	Leu	Gly	Ile	Lys	Cys	Arg	Leu	His	Glu	Leu	
			100					105					110			
Ala	Asn	Lys	Arg	Arg	Ile	Ser	Val	Ser	Gly	Ala	Ser	Lys	Leu	Leu	Ala	
		115					120					125				
Asn	Met	Leu	Tyr	Ser	Tyr	Arg	Gly	Met	Gly	Leu	Ser	Val	Gly	Thr	Met	
	130					135						140				
Ile	Ala	Gly	Trp	Asp	Glu	Thr	Gly	Pro	Gly	Leu	Tyr	Tyr	Val	Asp	Asn	
	145				150					155				160		
Glu	Gly	Gly	Arg	Leu	Lys	Gly	Asp	Arg	Phe	Ser	Val	Gly	Ser	Gly	Ser	
			165						170					175		
Pro	Tyr	Ala	Tyr	Gly	Val	Leu	Asp	Ser	Gly	Tyr	Lys	Tyr	Asp	Met	Ser	
			180					185					190			
Val	Glu	Glu	Ala	Ser	Glu	Leu	Glu	Glu	Ile	Asn	Leu	Pro	Cys	Asp	Ile	
			195				200						205			

(2) INFORMATION FOR SEQ ID NO:236:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1498 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1498

(D) OTHER INFORMATION: / Ceres Seq. ID 1566253

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:236:

aggaagaaga	gaacacctgat	tctattcttg	aggaacctga	agattctaac	atcaaagctg	60
ttactttctg	tgaacacacca	tatacatcag	caagtagatt	tgaagacttg	aactgtgtcac	120
ctgaattgat	gaaggcttg	tacgttgaga	tgaattctga	aaagcctagc	aagatccaaag	180
ctattagttt	gactatgata	atgacgcgcg	cacacaagca	tctgattgcc	caggctcata	240
acggatctgg	aaagacgact	tgtttcgttc	tgtgaattgt	gagtcgtgtt	gatccacat	300
tgagagagcc	tcaagctctc	tgtatttgtc	ccactagaga	attagctaat	cagaatatgg	360
aagtctctca	gaagatgggg	aagtttactg	ggatcactgc	tgagttggct	gtgCctgact	420
caacgagagg	tgacccggcg	gcaacaagag	gagctcctgt	tctgtgctat	gttgtgattg	480
gcaccctctg	aagccttaag	aaatggatgg	catttaagag	actaggtcta	aatcattttga	540
agattctggg	ttttgatgag	gctgcaccata	tgcttgctac	ggatgggttt	agggatgatt	600
ctttgaagat	aatgaagagc	attggggag	ttaatcccaa	tttccaggtt	ctctttttct	660
cggaacattt	taacgaaact	gtcaaaagatt	ttgttgcgcg	gacagtcaaa	gatccccacc	720
aattgtttgt	caaaagagag	gatctggcct	togactcggt	gaagcagtat	aaagtgtgtt	780
gcccgaaagg	gcacaaacaga	atcgaaagta	tcaaggatca	gattatggag	cttggggata	840
ttgggcaaac	cattatcttt	gtgaaaaaca	aagcgtttct	ctcaaaaagt	gcacaaagcc	900
ttgcgggaaa	tgggatatga	cgttaccagt	gtccatggta	atctgactga	atcggaacag	960
gataagatag	ttaaaagatg	taaagaatgc	cttactcaag	tgctcatatg	taccgatgtc	1020
attgcaagag	gtttttgacca	acagcgggtg	aatttgggtg	tcaattataa	tcttccactt	1080
aaatatgaaa	ctggagagcc	agattatgag	gtgtaccttc	acaggggttg	gagagctggc	1140
cggtttctgc	gcacaaagagc	ggttttcaac	tgtctgcttg	atgatggctg	ggataaagag	1200
gtgattggaga	agatcgagaa	gtattttgaa	gcacaaatga	aggagatcaa	gtcgtggaa	1260
tcagaggaag	agataaagag	tgcattaaag	gaagctggct	tgtctgacga	gtgaggaaga	1320
gagacagcat	gtgttcaaac	catcttaaaa	gaactatgct	tctgtttttc	tgagattgtt	1380
ttaagaaaaga	aacttgtata	cctctttgag	gttttctgt	aattctttgt	tctgattgtt	1440
gagattttca	gacttttgat	attttttgtt	aagggaaaag	gaaaacattt	tttatgtc	

(2) INFORMATION FOR SEQ ID NO:237:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 305 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ix) FEATURE:

(B) LOCATION: 1..305

SEQUENCE DESCRIPTION: SEQ ID NO:237:

Glu Glu Lys Pro Asp Ser Ile Leu Glu Glu P

Ile
305

(2) INFORMATION FOR SEO ID NO:238:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 263 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..263

(D) OTHER INFORMATION: / Ceres Seq. ID 1566255

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:238:

Met Lys Gly Leu Tyr Val Glu Met Lys Phe Glu Lys Pro Ser Lys Ile
1 5 10 15
Gln Ala Ile Ser Leu Pro Met Ile Met Thr Pro Pro His Lys His Leu

Met	Lys	Phe	Glu	Lys	Pro	Ser	Lys	Ile	Gln	Ala	Ile	Ser	Leu	Pro	Met
1				5				10					15		
Ile	Met	Thr	Pro	Pro	His	Lys	His	Leu	Ile	Ala	Gln	Ala	His	Asn	Gly
			20					25					30		
Ser	Gly	Lys	Thr	Thr	Cys	Phe	Val	Leu	Gly	Met	Leu	Ser	Arg	Val	Asp
		35					40					45			
Pro	Thr	Leu	Arg	Glu	Pro	Gln	Ala	Leu	Cys	Ile	Cys	Pro	Thr	Arg	Glu
		50				55					60				
Leu	Ala	Asn	Gln	Asn	Met	Glu	Val	Leu	Gln	Lys	Met	Gly	Lys	Phe	Thr
65				70						75				80	
Gly	Ile	Thr	Ala	Glu	Leu	Ala	Val	Pro	Asp	Ser	Thr	Arg	Gly	Ala	Pro
			85						90					95	
Ala	Ala	Thr	Arg	Gly	Ala	Pro	Val	Ser	Ala	His	Val	Val	Ile	Gly	Thr
			100					105					110		
Pro	Gly	Thr	Leu	Lys	Lys	Trp	Met	Ala	Phe	Lys	Arg	Leu	Gly	Leu	Asn
		115					120					125			
His	Leu	Lys	Ile	Leu	Val	Phe	Asp	Glu	Ala	Asp	His	Met	Leu	Ala	Thr
130						135					140				

Asp Gly Phe Arg Asp Asp Ser Leu Lys Ile Met Lys Asp Ile Gly Arg	
145 150 155 160	
Val Asn Pro Asn Phe Gln Val Leu Leu Phe Ser Ala Thr Phe Asn Glu	
165 170 175	
Thr Val Lys Asp Phe Val Ala Arg Thr Val Lys Asp Pro Asn Gln Leu	
180 185 190	
Phe Val Lys Arg Glu Asp Leu Ala Phe Asp Ser Val Lys Gln Tyr Lys	
195 200 205	
Val Val Cys Pro Lys Glu Gln Asn Lys Ile Glu Val Ile Lys Asp Gln	
210 215 220	
Ile Met Glu Leu Gly Asp Ile Gly Gln Thr Ile Ile Phe Val Lys Thr	
225 230 235 240	
Lys Ala Phe Cys Ser Lys Gly Ala Gln Ser Pro Cys Gly Asn Gly Ile	
245 250 255	

(2) INFORMATION FOR SEQ ID NO:240:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 637 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..637
(D) OTHER INFORMATION: / Ceres Seq. ID 1566257

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:240:

acgatacc	caaa	ctcttctt	cttccctt	cttctctt	ctcttctt	60
cacgtttac	cgatataca	ctctataca	tacattaat	ttgatcttc	tttatcttt	120
tgcttccaa	aaactccaa	gaacagctc	ttcttttt	cattcttct	atcatcata	180
atggagag	aagacttga	cgctgtct	gattgaaca	acgaatgt	acaaggaga	240
ctcagact	tttacaaga	ccttgtct	aaatggcat	cagatcggt	tcttgaaga	300
atagagaaa	atgaagctaa	gatgaaatt	cagtccttc	aacgagcct	ttctgtttt	360
tcggattcc	acaagaggct	tttgtatga	gtcgggtgt	atgatagt	tgacagcaa	420
actggaat	gtgatttcat	aaatgagat	gtgacgcta	tggtccaaa	tcaatctac	480
ggggacgaa	atttagagga	atttgaaga	ttatttcaa	aattgttga	ggatgatgt	540
aatcaatt	caaatcgctc	atcttctgc	ttcatgttc	caatttagt	gcacgtcgc	600
tttgcctat	tgcatgatt	tatcaaatc	aaatgat			

(2) INFORMATION FOR SEQ ID NO:241:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 135 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..135
(D) OTHER INFORMATION: / Ceres Seq. ID 1566258

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:241:

Met Glu Arg Glu Asp Leu Tyr Ala Val Leu Asp Leu Asn Asn Glu Cys	
1 5 10 15	
Thr Gln Gly Asp Leu Arg Leu Ser Tyr Lys Asn Leu Val Leu Lys Trp	
20 25 30	
His Pro Asp Arg Phe Leu Glu Glu Ile Glu Lys Asp Glu Ala Lys Met	
35 40 45	
Lys Phe Gln Ser Ile Gln Arg Ala Tyr Ser Val Leu Ser Asp Ser Asn	
50 55 60	
Lys Arg Leu Leu Tyr Asp Val Gly Ala Tyr Asp Ser Asp Asp Asp Glu	
65 70 75 80	

Thr Gly Met Ala Asp Phe Ile Asn Glu Met Val Thr Leu Met Ala Gln
85 90 95
Thr Gln Ser Thr Gly Asp Glu Asn Leu Glu Glu Phe Glu Glu Leu Phe
100 105 110
Gln Glu Leu Leu Lys Asp Asp Val Asn Gln Phe Lys Thr Arg Ser Ser
115 120 125
Phe Val Phe Met Phe Ala Ile
130 135

(2) INFORMATION FOR SEQ ID NO:242:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 88 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..88

(D) OTHER INFORMATION: / Ceres Seq. ID 1566259

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:242:

Met Lys Phe Gln Ser Ile Gln Arg Ala Tyr Ser Val Leu Ser Asp Ser
1 5 10 15
Asn Lys Arg Leu Leu Tyr Asp Val Gly Ala Tyr Asp Ser Asp Asp
20 25 30
Glu Thr Gly Met Ala Asp Phe Ile Asn Glu Met Val Thr Leu Met Ala
35 40 45
Gln Thr Gln Ser Thr Gly Asp Glu Asn Leu Glu Glu Phe Glu Glu Leu
50 55 60
Phe Gln Glu Leu Leu Lys Asp Asp Val Asn Gln Phe Lys Thr Arg Ser
65 70 75 80
Ser Phe Val Phe Met Phe Ala Ile
85

(2) INFORMATION FOR SEQ ID NO:243:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 477 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..477

(D) OTHER INFORMATION: / Ceres Seq. ID 1566268

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:243:

cgggttgccg caccctgcttc gcttctcttc tctcgtcttc tactcaggac tcgtttactc 60
tttcaaaagt aagcttttcaa gatgcaaaac gaagagggtc aagtcactga gctttacatt 120
cctaggaaat gttctgctac taaccgggtg atcacatcca aggatcatgc ctctgttcag 180
ctcaacattg gtcattttaga tgctaattgac ttgtacacgc gacagttcac aacctttgtc 240
ctctgcggtt ttgtccgtgc tcaggggagac gctgacagtg gtgtcgacag gttgtggcag 300
aagaagaagg ttgaagccaa acaaaactaa gagcttaatc tgtcttggtt ttgtcgaat 360
ctgttttttt tttttccgaa agatttgctc atactgaagt aatgattttg gotttgggtc 420
gtggaaacta acttaataac ttttgtgcac catgtcttct aatttttcac cagttcg

(2) INFORMATION FOR SEQ ID NO:244:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 82 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..82

(D) OTHER INFORMATION: / Ceres Seq. ID 1566269

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:244:

Met	Gln	Asn	Glu	Glu	Gly	Gln	Val	Thr	Glu	Leu	Tyr	Ile	Pro	Arg	Lys	
1			5						10						15	
Cys	Ser	Ala	Thr	Asn	Arg	Leu	Ile	Thr	Ser	Lys	Asp	His	Ala	Ser	Val	
			20						25					30		
Gln	Leu	Asn	Ile	Gly	His	Leu	Asp	Ala	Asn	Gly	Leu	Tyr	Thr	Gly	Gln	
			35						40					45		
Phe	Thr	Thr	Phe	Ala	Leu	Cys	Gly	Phe	Val	Arg	Ala	Gln	Gly	Asp	Ala	
			50				55					60				
Asp	Ser	Gly	Val	Asp	Arg	Leu	Trp	Gln	Lys	Lys	Val	Glu	Ala	Lys		
						70				75				80		
65																
Gln	Asn															

(2) INFORMATION FOR SEQ ID NO:245:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 65 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..65

(D) OTHER INFORMATION: / Ceres Seq. ID 1566270

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:245:

Met	Leu	Met	Ala	Cys	Thr	Pro	Asp	Ser	Ser	Gln	Pro	Leu	Leu	Ser	Ala	
1				5						10					15	
Val	Leu	Ser	Val	Leu	Arg	Glu	Thr	Leu	Thr	Val	Val	Ser	Thr	Gly	Cys	
				20					25					30		
Gly	Arg	Arg	Arg	Arg	Leu	Lys	Pro	Asn	Lys	Thr	Lys	Ser	Leu	Ile	Cys	
				35					40					45		
Leu	Val	Phe	Cys	Arg	Ile	Leu	Phe	Phe	Phe	Phe	Arg	Lys	Ile	Ala	Ser	
						55						60				
50																
Tyr																
65																

(2) INFORMATION FOR SEQ ID NO:246:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 63 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..63

(D) OTHER INFORMATION: / Ceres Seq. ID 1566271

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:246:

Met	Ala	Cys	Thr	Pro	Asp	Ser	Ser	Gln	Pro	Leu	Leu	Ser	Ala	Val	Leu	
1				5						10					15	
Ser	Val	Leu	Arg	Glu	Thr	Leu	Thr	Val	Val	Ser	Thr	Gly	Cys	Gly	Arg	
				20					25					30		
Arg	Arg	Arg	Leu	Lys	Pro	Asn	Lys	Thr	Lys	Ser	Leu	Ile	Cys	Leu	Val	
				35					40					45		
Phe	Cys	Arg	Ile	Leu	Phe	Phe	Phe	Phe	Arg	Lys	Ile	Ala	Ser	Tyr		
				50			55					60				

(2) INFORMATION FOR SEQ ID NO:247:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 988 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
 (A) NAME/KEY: -
 (B) LOCATION: 1..988
 (D) OTHER INFORMATION: / Ceres Seq. ID 1566276
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:247:

aaaagaagac	ttttgtaag	aaataaacac	acaactaaag	agatgtcgtc	aaccttggagc	60
aacgaagagt	caggactcgg	tgattcaaat	cgttcgacgg	aagtagatag	cgcgacgga	120
ggaaacttca	cggcttacga	gtctcgattc	cagtcgcagc	ggtttgactc	ttccttctct	180
aattttgact	cccaaccgga	gaaagagtca	gacttaccag	gcggcgattc	atctccttca	240
cccgaacctc	aatctccgcc	gtcgtataat	agtttcgatg	atacaaacgg	ttcgatcttg	300
ccgccaccat	cggccatgga	gaaagaggaa	ggtttcgctc	ttagagagtg	gcgaaggcta	360
aatgctctga	gatctggaag	gaaagaaaag	gaagagaaa	aaatggttca	acaaattcta	420
gaagcagcag	agcaatataa	ggctgagttc	tatagcaagc	gtaacgttac	tattgaaaaa	480
aacaagaaac	taaaaccgga	gaaagagaag	ttttttttgg	agaatcaaga	aaagtttttac	540
gctgaagctg	acaaaaacaa	ttggaaggcg	attgcagaac	tcattcctcg	tgaagtgccca	600
gtttatagaga	atagagggaa	caagaagaaa	acagcaacca	taactgtaac	ccaggggacca	660
aagccaggga	agcccatcta	tctgtGctcg	tatgcgtcaa	gtgctcacga	aactcaagca	720
caatccgcca	actcatatga	agccaaaact	gccctcacca	tctggagctg	accggaatgt	780
gagtgctgagt	gaacagggtca	cagttacaga	gaagtgttag	ttgtgtatgt	gacaaagttaa	840
cttctctttg	attgatgtta	aacgcgtctt	actttgttag	cttcctcatc	gttcagcttc	900
gactattggt	tgttttgatt	tcgtcttttg	tcttaccatt	gttggtttcc	cacacagttt	960
ttactcttga	tgtatatata	atatattc				

(2) INFORMATION FOR SEQ ID NO:248:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 242 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..242
 (D) OTHER INFORMATION: / Ceres Seq. ID 1566277
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:248:

Met	Ser	Ser	Thr	Leu	Ser	Asn	Glu	Glu	Ser	Gly	Leu	Gly	Asp	Ser	Asn	
1			5					10					15			
Arg	Ser	Thr	Glu	Val	Asp	Ser	Gly	Asp	Gly	Gly	Asn	Phe	Thr	Ala	Tyr	
			20					25				30				
Glu	Ser	Arg	Phe	Gln	Ser	Gln	Arg	Phe	Asp	Ser	Ser	Phe	Ser	Asn	Phe	
			35					40				45				
Asp	Ser	Gln	Pro	Glu	Lys	Glu	Ser	Asp	Leu	Pro	Gly	Gly	Asp	Ser	Ser	
			50					55				60				
Pro	Arg	Pro	Glu	Thr	Gln	Ser	Pro	Pro	Ser	Ile	Asn	Ser	Phe	Asp	Asp	
			65					70				75			80	
Thr	Asn	Gly	Ser	Ile	Leu	Pro	Pro	Pro	Ser	Ala	Met	Glu	Lys	Glu	Glu	
			85					90				95				
Gly	Phe	Ala	Leu	Arg	Glu	Trp	Arg	Arg	Leu	Asn	Ala	Leu	Arg	Leu	Glu	
			100					105				110				
Glu	Lys	Glu	Lys	Glu	Glu	Lys	Glu	Met	Val	Gln	Gln	Ile	Leu	Glu	Ala	
			115					120				125				
Ala	Glu	Gln	Tyr	Lys	Ala	Glu	Phe	Tyr	Ser	Lys	Arg	Asn	Val	Thr	Ile	
			130					135				140				
Glu	Asn	Asn	Lys	Lys	Leu	Asn	Arg	Glu	Lys	Glu	Lys	Phe	Phe	Leu	Glu	
			145					150				155			160	
Asn	Gln	Glu	Lys	Phe	Tyr	Ala	Glu	Ala	Asp	Lys	Asn	Asn	Trp	Lys	Ala	
			165					170				175				
Ile	Ala	Glu	Leu	Ile	Pro	Arg	Glu	Val	Pro	Val	Ile	Glu	Asn	Arg	Gly	
			180					185				190				

Asn Lys Lys Lys Thr Ala Thr Ile Thr Val Ile Gln Gly Pro Lys Pro
195 200 205
Gly Lys Pro Thr Asp Leu Cys Ser Tyr Ala Ser Ser Ala His Glu Thr
210 215 220
Gln Ala Gln Ser Ala Asn Ser Tyr Glu Ala Lys Thr Ala Leu Thr Ile
225 230 235 240
Trp Ser

(2) INFORMATION FOR SEQ ID NO:249:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 151 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..151

(D) OTHER INFORMATION: / Ceres Seq. ID 1566278

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:249:

Met Glu Lys Glu Glu Phe Ala Leu Arg Glu Trp Arg Arg Leu Asn
1 5 10 15
Ala Leu Arg Leu Glu Glu Lys Glu Lys Glu Lys Glu Met Val Gln
20 25 30
Gln Ile Leu Glu Ala Ala Glu Gln Tyr Lys Ala Glu Phe Tyr Ser Lys
35 40 45
Arg Asn Val Thr Ile Glu Asn Asn Lys Lys Leu Asn Arg Glu Lys Glu
50 55 60
Lys Phe Phe Leu Glu Asn Gln Glu Lys Phe Tyr Ala Glu Ala Asp Lys
65 70 75 80
Asn Asn Trp Lys Ala Ile Ala Glu Leu Ile Pro Arg Glu Val Pro Val
85 90 95
Ile Glu Asn Arg Gly Asn Lys Lys Lys Thr Ala Thr Ile Thr Val Ile
100 105 110
Gln Gly Pro Lys Pro Gly Lys Pro Thr Asp Leu Cys Ser Tyr Ala Ser
115 120 125
Ser Ala His Glu Thr Gln Ala Gln Ser Ala Asn Ser Tyr Glu Ala Lys
130 135 140
Thr Ala Leu Thr Ile Trp Ser
145 150

(2) INFORMATION FOR SEQ ID NO:250:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 122 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..122

(D) OTHER INFORMATION: / Ceres Seq. ID 1566279

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:250:

Met Val Gln Gln Ile Leu Glu Ala Ala Glu Gln Tyr Lys Ala Glu Phe
1 5 10 15
Tyr Ser Lys Arg Asn Val Thr Ile Glu Asn Asn Lys Lys Leu Asn Arg
20 25 30
Glu Lys Glu Lys Phe Phe Leu Glu Asn Gln Glu Lys Phe Tyr Ala Glu
35 40 45
Ala Asp Lys Asn Asn Trp Lys Ala Ile Ala Glu Leu Ile Pro Arg Glu
50 55 60
Val Pro Val Ile Glu Asn Arg Gly Asn Lys Lys Lys Thr Ala Thr Ile

65	70	75	80
Thr Val Ile Gln Gly	Pro Lys Pro Gly	Lys Pro Thr Asp Leu Cys Ser	
	85	90	95
Tyr Ala Ser Ser Ala His Glu Thr Gln Ala Gln Ser Ala Asn Ser Tyr			
	100	105	110
Glu Ala Lys Thr Ala Leu Thr Ile Trp Ser			
	115	120	

(2) INFORMATION FOR SEQ ID NO:251:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1643 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1643
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566290

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:251:

aaagaaaaga	ccttattcac	acagggtcgt	tttgcgaagC	tcactcgtca	cgatgaccat	60
gatggatata	gcgaagggga	agacagtgat	gtgtctgtta	acagaccag	aaggaactca	120
tttaggttct	gccatgtata	ttctcctaaa	ggctgtgtct	ttgcaactta	ctcagctcgt	180
caatagggtc	ctcgacaacg	aggagatggt	accttacagt	ttctatgtat	cgacgcaaga	240
gcttcttgta	cagatgtgga	cgactctgga	gaaaaacaaa	gtgtctgtgg	agaagggttt	300
gacgattggt	tatcaacaac	aagctgtttt	tcgaattcgt	cctgttaacc	gttgctcaca	360
gacaattgct	ggctacggcg	aagctgttct	ttgtgtttcg	tttagtcctg	atggaaagca	420
attagctagt	gggtcagggt	atactactgt	caggcttttg	gatctctaca	ctgaaactcc	480
attgtttact	tgcaaaaggcc	acaagaattg	ggttctcaca	gtgcgtggt	ctcgtgatgg	540
taagcatctt	gtgagtggta	gtaaatccgg	tgaaatctgt	tgttggaatc	caaagaaagg	600
agaaattgaa	ggcagccocac	ttacgggtca	caagaatagg	attactggta	tctcgtggga	660
accagtcacac	cttagttctc	catgccgtcg	atttgtgact	tctagttaag	atggggatgc	720
aaggatttgg	gatattacac	tgaaaaaatc	tattatttgt	ctcagtgggc	acacacttgc	780
tgtgacttgt	gtcaaatggg	gcggagatgg	aattatttat	acaggttcgc	aagattgtac	840
gattaagatg	tgggagacta	ctcaggggaa	gcttattcgt	gaattgaagg	ggcatgggca	900
ttggattaac	tcctctgcgt	tgagcacaga	atatgttctt	cgaaacaggag	cttttgacca	960
cactggaaga	caatatccct	caaatgaaga	aaagcaaaag	gcgctcgaaa	gatacaacaa	1020
aacaaaaggg	gattccctgt	aaagattagt	ctcaggttct	gatgatttca	ctatgttctt	1080
ttgggaacca	tcgtgttaga	aacaacctaa	aaagcgctta	accggtcctc	aacagcttgt	1140
aaatcatatc	tattttccac	ctgatgggaa	atggatttga	atgtgcctgt	tcgataaaat	1200
agttaggtta	tggaaatgga	tcacaggaca	atttgttaca	gttttccggg	gccatgtttg	1260
acctgtttat	caggtcagtt	gttccgcaga	cagtagattg	cttttgagtg	cgagtaaaaga	1320
ctctactctc	aaagatttgg	aaattaggac	gaaaaagtta	aaacaagatc	tttctgtgtca	1380
tgtcgtgagc	gtttttcggg	tgagattggg	tccagatgga	gagaaagtgc	tttctgtgtg	1440
taaagataga	gtgttgaagc	tatggaaggg	ttaaaatgga	agaccatttt	ggagtttttg	1500
tttactcaac	caacacttat	tttacacata	tttatctatt	tcgccttggt	tggtttctac	1560
acataaatgc	ttctctatgg	gtctcttttt	gatcttatgc	ttagtaaaac	aactcttttt	1620
tcttacctca	agttgttact	gtc				

(2) INFORMATION FOR SEQ ID NO:252:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 490 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..490
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566291

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:252:

Lys Lys Arg Pro Tyr Ser His Arg Ser Ser Leu Arg Ser Ser Ser Ser			
1	5	10	15

Thr Met Thr Met Met Asp Thr Asp Glu Gly Lys Thr Val Met Cys Leu
20 25 30
Leu Thr Asp Pro Glu Gly Thr His Leu Gly Ser Ala Met Tyr Ile Pro
35 40 45
Gln Lys Ala Gly Pro Leu Gln Leu Thr Gln Leu Val Asn Arg Phe Leu
50 55 60
Asp Asn Glu Glu Met Leu Pro Tyr Ser Phe Tyr Val Ser Asp Glu Glu
65 70 75 80
Leu Leu Val Pro Val Gly Thr Tyr Leu Glu Lys Asn Lys Val Ser Val
85 90 95
Glu Lys Val Leu Thr Ile Val Tyr Gln Gln Ala Val Phe Arg Ile
100 105 110
Arg Pro Val Asn Arg Cys Ser Gln Thr Ile Ala Gly His Ala Glu Ala
115 120 125
Val Leu Cys Val Ser Phe Ser Pro Asp Gly Lys Gln Leu Ala Ser Gly
130 135 140
Ser Gly Asp Thr Thr Val Arg Leu Trp Asp Leu Tyr Thr Glu Thr Pro
145 150 155 160
Leu Phe Thr Cys Lys Gly His Lys Asn Trp Val Leu Thr Val Ala Trp
165 170 175
Ser Pro Asp Gly Lys His Leu Val Ser Gly Ser Lys Ser Gly Glu Ile
180 185 190
Cys Cys Trp Asn Pro Lys Lys Gly Glu Leu Glu Gly Ser Pro Leu Thr
195 200 205
Gly His Lys Lys Trp Ile Thr Gly Ile Ser Trp Glu Pro Val His Leu
210 215 220
Ser Ser Pro Cys Arg Arg Phe Val Thr Ser Ser Lys Asp Gly Asp Ala
225 230 235 240
Arg Ile Trp Asp Ile Thr Leu Lys Lys Ser Ile Ile Cys Leu Ser Gly
245 250 255
His Thr Leu Ala Val Thr Cys Val Lys Trp Gly Gly Asp Gly Ile Ile
260 265 270
Tyr Thr Gly Ser Gln Asp Cys Thr Ile Lys Met Trp Glu Thr Thr Gln
275 280 285
Gly Lys Leu Ile Arg Glu Leu Lys Gly His Gly His Trp Ile Asn Ser
290 295 300
Leu Ala Leu Ser Thr Glu Tyr Val Leu Arg Thr Gly Ala Phe Asp His
305 310 315 320
Thr Gly Arg Gln Tyr Pro Pro Asn Glu Glu Lys Gln Lys Ala Leu Glu
325 330 335
Arg Tyr Asn Lys Thr Lys Gly Asp Ser Pro Glu Arg Leu Val Ser Gly
340 345 350
Ser Asp Asp Phe Thr Met Phe Leu Trp Glu Pro Ser Val Ser Lys Gln
355 360 365
Pro Lys Lys Arg Leu Thr Gly His Gln Gln Leu Val Asn His Val Tyr
370 375 380
Phe Ser Pro Asp Gly Lys Trp Ile Ala Ser Ala Ser Phe Asp Lys Ser
385 390 395 400
Val Arg Leu Trp Asn Gly Ile Thr Gly Gln Phe Val Thr Val Phe Arg
405 410 415
Gly His Val Gly Pro Val Tyr Gln Val Ser Trp Ser Ala Asp Ser Arg
420 425 430
Leu Leu Leu Ser Gly Ser Lys Asp Ser Thr Leu Lys Ile Trp Glu Ile
435 440 445
Arg Thr Lys Lys Leu Lys Gln Asp Leu Pro Gly His Ala Asp Glu Val
450 455 460
Phe Ala Val Asp Trp Ser Pro Asp Gly Glu Lys Val Val Ser Gly Gly
465 470 475 480
Lys Asp Arg Val Leu Lys Leu Trp Lys Gly
485 490

(2) INFORMATION FOR SEQ ID NO:253:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 473 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..473
 (D) OTHER INFORMATION: / Ceres Seq. ID 1566292
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:253:

Met	Thr	Met	Met	Asp	Thr	Asp	Glu	Gly	Lys	Thr	Val	Met	Cys	Leu	Leu
1			5						10				15		
Thr	Asp	Pro	Glu	Gly	Thr	His	Leu	Gly	Ser	Ala	Met	Tyr	Ile	Pro	Gln
			20				25						30		
Lys	Ala	Gly	Pro	Leu	Gln	Leu	Thr	Gln	Leu	Val	Asn	Arg	Phe	Leu	Asp
			35				40					45			
Asn	Glu	Glu	Met	Leu	Pro	Tyr	Ser	Phe	Tyr	Val	Ser	Asp	Glu	Glu	Leu
			50			55					60				
Leu	Val	Pro	Val	Gly	Thr	Tyr	Leu	Glu	Lys	Asn	Lys	Val	Ser	Val	Glu
65					70				75						80
Lys	Val	Leu	Thr	Ile	Val	Tyr	Gln	Gln	Gln	Ala	Val	Phe	Arg	Ile	Arg
				85					90					95	
Pro	Val	Asn	Arg	Cys	Ser	Gln	Thr	Ile	Ala	Gly	His	Ala	Glu	Ala	Val
			100				105						110		
Leu	Cys	Val	Ser	Phe	Ser	Pro	Asp	Gly	Lys	Gln	Leu	Ala	Ser	Gly	Ser
			115				120					125			
Gly	Asp	Thr	Thr	Val	Arg	Leu	Trp	Asp	Leu	Tyr	Thr	Glu	Thr	Pro	Leu
			130			135					140				
Phe	Thr	Cys	Lys	Gly	His	Lys	Asn	Trp	Val	Leu	Thr	Val	Ala	Trp	Ser
145				150					155					160	
Pro	Asp	Gly	Lys	His	Leu	Val	Ser	Gly	Ser	Lys	Ser	Gly	Glu	Ile	Cys
			165						170					175	
Cys	Trp	Asn	Pro	Lys	Lys	Gly	Glu	Leu	Glu	Gly	Ser	Pro	Leu	Thr	Gly
			180				185						190		
His	Lys	Lys	Trp	Ile	Thr	Gly	Ile	Ser	Trp	Glu	Pro	Val	His	Leu	Ser
			195				200					205			
Ser	Pro	Cys	Arg	Arg	Phe	Val	Thr	Ser	Ser	Lys	Asp	Gly	Asp	Ala	Arg
			210			215					220				
Ile	Trp	Asp	Ile	Thr	Leu	Lys	Lys	Ser	Ile	Ile	Cys	Leu	Ser	Gly	His
225				230					235					240	
Thr	Leu	Ala	Val	Thr	Cys	Val	Lys	Trp	Gly	Gly	Asp	Gly	Ile	Ile	Tyr
				245					250					255	
Thr	Gly	Ser	Gln	Asp	Cys	Thr	Ile	Lys	Met	Trp	Glu	Thr	Thr	Gln	Gly
			260					265					270		
Lys	Leu	Ile	Arg	Glu	Leu	Lys	Gly	His	Gly	His	Trp	Ile	Asn	Ser	Leu
			275				280					285			
Ala	Leu	Ser	Thr	Glu	Tyr	Val	Leu	Arg	Thr	Gly	Ala	Phe	Asp	His	Thr
			290			295					300				
Gly	Arg	Gln	Tyr	Pro	Pro	Asn	Glu	Glu	Lys	Gln	Lys	Ala	Leu	Glu	Arg
305				310					315					320	
Tyr	Asn	Lys	Thr	Lys	Gly	Asp	Ser	Pro	Glu	Arg	Leu	Val	Ser	Gly	Ser
			325					330					335		
Asp	Asp	Phe	Thr	Met	Phe	Leu	Trp	Glu	Pro	Ser	Val	Ser	Lys	Gln	Pro
			340				345						350		
Lys	Lys	Arg	Leu	Thr	Gly	His	Gln	Gln	Leu	Val	Asn	His	Val	Tyr	Phe
			355				360				365				
Ser	Pro	Asp	Gly	Lys	Trp	Ile	Ala	Ser	Ala	Ser	Phe	Asp	Lys	Ser	Val
			370			375					380				
Arg	Leu	Trp	Asn	Gly	Ile	Thr	Gly	Gln	Phe	Val	Thr	Val	Phe	Arg	Gly
385				390					395						400

His Val Gly Pro Val Tyr Gln Val Ser Trp Ser Ala Asp Ser Arg Leu
405 410 415
Leu Leu Ser Gly Ser Lys Asp Ser Thr Leu Lys Ile Trp Glu Ile Arg
420 425 430
Thr Lys Lys Leu Lys Gln Asp Leu Pro Gly His Ala Asp Glu Val Phe
435 440 445
Ala Val Asp Trp Ser Pro Asp Gly Glu Lys Val Val Ser Gly Gly Lys
450 455 460

Asp Arg Val Leu Lys Leu Trp Lys Gly
465 470

(2) INFORMATION FOR SEQ ID NO:254:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 471 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..471

(D) OTHER INFORMATION: / Ceres Seq. ID 1566293

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:254:

Met Met Asp Thr Asp Glu Gly Lys Thr Val Met Cys Leu Leu Thr Asp
1 5 10 15
Pro Glu Gly Thr His Leu Gly Ser Ala Met Tyr Ile Pro Gln Lys Ala
20 25 30
Gly Pro Leu Gln Leu Thr Gln Leu Val Asn Arg Phe Leu Asp Asn Glu
35 40 45
Glu Met Leu Pro Tyr Ser Phe Tyr Val Ser Asp Glu Glu Leu Leu Val
50 55 60
Pro Val Gly Thr Tyr Leu Glu Lys Asn Lys Val Ser Val Glu Lys Val
65 70 75 80
Leu Thr Ile Val Tyr Gln Gln Gln Ala Val Phe Arg Ile Arg Pro Val
85 90 95
Asn Arg Cys Ser Gln Thr Ile Ala Gly His Ala Glu Ala Val Leu Cys
100 105 110
Val Ser Phe Ser Pro Asp Gly Lys Gln Leu Ala Ser Gly Ser Gly Asp
115 120 125
Thr Thr Val Arg Leu Trp Asp Leu Tyr Thr Glu Thr Pro Leu Phe Thr
130 135 140
Cys Lys Gly His Lys Asn Trp Val Leu Thr Val Ala Trp Ser Pro Asp
145 150 155 160
Gly Lys His Leu Val Ser Gly Ser Lys Ser Gly Glu Ile Cys Cys Trp
165 170 175
Asn Pro Lys Lys Gly Glu Leu Glu Gly Ser Pro Leu Thr Gly His Lys
180 185 190
Lys Trp Ile Thr Gly Ile Ser Trp Glu Pro Val His Leu Ser Ser Pro
195 200 205
Cys Arg Arg Phe Val Thr Ser Ser Lys Asp Gly Asp Ala Arg Ile Trp
210 215 220
Asp Ile Thr Leu Lys Lys Ser Ile Ile Cys Leu Ser Gly His Thr Leu
225 230 235 240
Ala Val Thr Cys Val Lys Trp Gly Gly Asp Gly Ile Ile Tyr Thr Gly
245 250 255
Ser Gln Asp Cys Thr Ile Lys Met Trp Glu Thr Thr Gln Gly Lys Leu
260 265 270
Ile Arg Glu Leu Lys Gly His Gly His Trp Ile Asn Ser Leu Ala Leu
275 280 285
Ser Thr Glu Tyr Val Leu Arg Thr Gly Ala Phe Asp His Thr Gly Arg
290 295 300
Gln Tyr Pro Pro Asn Glu Lys Lys Ala Leu Glu Arg Tyr Asn

305 310 315 320
Lys Thr Lys Gly Asp Ser Pro Glu Arg Leu Val Ser Gly Ser Asp Asp
325 330 335
Phe Thr Met Phe Leu Trp Glu Pro Ser Val Ser Lys Gln Pro Lys Lys
340 345 350
Arg Leu Thr Gly His Gln Gln Leu Val Asn His Val Tyr Phe Ser Pro
355 360 365
Asp Gly Lys Trp Ile Ala Ser Ala Ser Phe Asp Lys Ser Val Arg Leu
370 375 380
Trp Asn Gly Ile Thr Gly Gln Phe Val Thr Val Phe Arg Gly His Val
385 390 395 400
Gly Pro Val Tyr Gln Val Ser Trp Ser Ala Asp Ser Arg Leu Leu Leu
405 410 415
Ser Gly Ser Lys Asp Ser Thr Leu Lys Ile Trp Glu Ile Arg Thr Lys
420 425 430
Lys Leu Lys Gln Asp Leu Pro Gly His Ala Asp Glu Val Phe Ala Val
435 440 445
Asp Trp Ser Pro Asp Gly Glu Lys Val Val Ser Gly Gly Lys Asp Arg
450 455 460
Val Leu Lys Leu Trp Lys Gly
465 470

(2) INFORMATION FOR SEQ ID NO:255:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 944 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..944

(D) OTHER INFORMATION: / Ceres Seq. ID 1566297

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:255:

```
attttttttc ataattgtat caaattgtga gaggaaaaaa agaagttcaa gaaatggaga      60
aggaaggact cgggcttgag ataacggagc tgagattggg gcttcggggg agagatgtgg      120
cagagaagat gatgaagaag agagcttttca cggagatgaa tatgacgtcg tcgggtagta      180
atagtgatca atgtgaaagc ggcgtcggtt catctgggtg tgacgctgag aaggttaatg      240
attcgcgggc ggcGaaaagc caggtgggtg ggtggccacc ggtttgtctt taccggaaga      300
aaaacagctg taaggaaagc tcgaccacga aagtgggStt agggatgtg aaagtgaagca      360
tgagatgggt gccattattg aggaagatgg atcttggttc gagccaaggc tatgatgatc      420
tagcttttct tcttgataag ctcttcggtt tccgtggcat cggtgtggcc ttgaaagatg      480
gtgacaaact cgaatacgtt accatatacg aagacaaaga tggagactgg atgctcgcgg      540
gtgatghacc ttgggggatg tGttctagag tcatgcaaga ggttgagaat aatgaaaaa      600
tcggatgccta ccgggtttgg gctgcagcct agaggagtag acgagtgatg atgacttgaa      660
caagaagcaa ggagctgggt cattaattta atcttaaat tgatcatcaa gatcctttag      720
aacatttttc ctattcatgt tatataaata tatatgttat agtatattat ttgcaacaaa      780
atttcaagtt atggtttgca taattatctt cagaaagaca gcattatata tatcacacta      840
ttgtttcttg agtgttgagt taaaaacatta atctgtttca aaattatttg ttatttcgga      900
cttatatatg tgtgtagaaa catatgtaat aagtatccat tatt
```

(2) INFORMATION FOR SEQ ID NO:256:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 192 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..192

(D) OTHER INFORMATION: / Ceres Seq. ID 1566298

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:256:

Met Glu Lys Glu Gly Leu Gly Leu Glu Ile Thr Glu Leu Arg Leu Gly
1 5 10 15
Leu Pro Gly Arg Asp Val Ala Glu Lys Met Met Lys Lys Arg Ala Phe
20 25 30
Thr Glu Met Asn Met Thr Ser Ser Gly Ser Asn Ser Asp Gln Cys Glu
35 40 45
Ser Gly Val Val Ser Ser Gly Gly Asp Ala Glu Lys Val Asn Asp Ser
50 55 60
Pro Ala Ala Lys Ser Gln Val Val Gly Trp Pro Val Cys Ser Tyr
65 70 75 80
Arg Lys Lys Asn Ser Cys Lys Glu Ala Ser Thr Thr Lys Val Xaa Leu
85 90 95
Gly Tyr Val Lys Val Ser Met Asp Gly Val Pro Tyr Leu Arg Lys Met
100 105 110
Asp Leu Gly Ser Ser Gln Gly Tyr Asp Asp Leu Ala Phe Ser Leu Asp
115 120 125
Lys Leu Phe Gly Phe Arg Gly Ile Gly Val Ala Leu Lys Asp Gly Asp
130 135 140
Asn Cys Glu Tyr Val Thr Ile Tyr Glu Asp Lys Asp Gly Asp Trp Met
145 150 155 160
Leu Ala Gly Asp Xaa Pro Trp Gly Met Cys Ser Arg Val Met Gln Glu
165 170 175
Val Glu Asn Asn Glu Lys Ile Gly Cys Tyr Arg Val Trp Ala Ala Ala
180 185 190

(2) INFORMATION FOR SEQ ID NO:257:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 167 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..167

(D) OTHER INFORMATION: / Ceres Seq. ID 1566299

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:257:

Met Met Lys Lys Arg Ala Phe Thr Glu Met Asn Met Thr Ser Ser Gly
1 5 10 15
Ser Asn Ser Asp Gln Cys Glu Ser Gly Val Val Ser Ser Gly Gly Asp
20 25 30
Ala Glu Lys Val Asn Asp Ser Pro Ala Ala Lys Ser Gln Val Val Gly
35 40 45
Trp Pro Pro Val Cys Ser Tyr Arg Lys Lys Asn Ser Cys Lys Glu Ala
50 55 60
Ser Thr Thr Lys Val Xaa Leu Gly Tyr Val Lys Val Ser Met Asp Gly
65 70 75 80
Val Pro Tyr Leu Arg Lys Met Asp Leu Gly Ser Ser Gln Gly Tyr Asp
85 90 95
Asp Leu Ala Phe Ser Leu Asp Lys Leu Phe Gly Phe Arg Gly Ile Gly
100 105 110
Val Ala Leu Lys Asp Gly Asp Asn Cys Glu Tyr Val Thr Ile Tyr Glu
115 120 125
Asp Lys Asp Gly Asp Trp Met Leu Ala Gly Asp Xaa Pro Trp Gly Met
130 135 140
Cys Ser Arg Val Met Gln Glu Val Glu Asn Asn Glu Lys Ile Gly Cys
145 150 155 160
Tyr Arg Val Trp Ala Ala Ala
165

(2) INFORMATION FOR SEQ ID NO:258:

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(2) INFORMATION FOR SEQ ID NO:259:
  (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 2363 base pairs
      (B) TYPE: nucleic acid
      (C) STRANDEDNESS: single
      (D) TOPOLOGY: linear
  (ii) MOLECULE TYPE: DNA (genomic)
  (ix) FEATURE:
      (A) NAME/KEY: -
      (B) LOCATION: 1..2363
      (D) OTHER INFORMATION: / Ceres Seq. ID 1566353
  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:259:

actcaaacccg  tgcattctcat  gcagaaacccg  actacccttc  ctttaaaagt  gtcaaaaattg  60
ttgtcccgca  aatttcttgt  gaacacagaat  gtctcagaag  atttccagaat  ctttaattggt  120
ctcaacagct  aagaactaca  acagctacagg  aggatcaatt  gccgggtgtg  tctaatgatgt  180
ataaagcagg  ccgtggcttc  gagttattga  cccataacgt  ggacaacccg  ggaaaaaacc  240
aagcacttca  acaagatgtt  caaagtttcg  taagattaag  tgatcaacct  tttttgtcaa  300
actcggcac  agatccagaa  gctcacaact  tgatcacgga  tgaggaatgt  tgtagggttc  360
tttttcgaca  taacatgaaa  gatcagagta  catcttctgg  tgagcaaggt  cggaaattgg  420
ttgaccctca  aaacggcaaa  ggatcttttt  gtcttcaggc  tgcagaaacc  catgctcatg  480
aaactggaaa  agttccagct  ttaccgtggc  atccttcaag  ttctgagggc  ctggccgggtc  540
ataatttgtt  cccttttgtt  gatcagaact  tgaaggactc  acctttacc  cgtaatgatt  600
ccaacgctc  tatacaagg  ttgcgctctt  ttgagctac  cgaattagaa  ttgaagactg  660
atacaaatga  cggtttcac  gatacttaag  gacatgtaac  ttccatggc  aatgatgata  720
atggttggtt  ccagcaaaaa  tgcggcgctg  catatattcc  caaggattct  ttgaagctga  780
tacctttgaa  tctgttttct  tcctcttctt  gagtgaacaa  gatttatatt  cctatgtacg  840
acagacccgc  ttgaaaagac  aaagagctct  ttgttatga  accctcaagt  tttccaagt  900
cataatcttc  ttcttcaag  taagtacttg  taccatcaa  tagtgactta  cggcaagatg  960

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acagtcacct	tggtatccgt	cagttgatga	ttcttccaat	gaattgtaca	actccggttaa	1020
ggttatggga	ttcacccgtg	caacgatagga	gcctctgatgt	catgctttaat	gatactgcga	1080
aaagttttta	tggtgcacga	tccatcttaa	agaagcggca	tcgagacttg	ctttcacctg	1140
tgcttgatag	aaagaaagac	aaaaagccta	aaagggtctg	gacttctccc	ttggcctaag	1200
atttttcg	cttagatgta	atgcttgatg	aaggagatga	ttgcattgacc	ttcgtccgtg	1260
cagagttctc	tgaagataaa	aatatatgtg	cctccccttc	catagccaga	gataacagaa	1320
atttgcgcat	attctcggtta	tatcaagaaa	tgattccgat	agatgaggaa	ccaaagggaaa	1380
ccctagaatc	agggtggagt	acttctatgc	aaaaagaaa	tgatgtaat	gacggtgggtg	1440
cttcacgtaa	aaatgaccaa	gaaacttctg	gaagtttttt	tgagttacga	ctgtgtctct	1500
ctggtagtag	tcgagctaga	ccagataaca	aagttaatgc	aagtgcgaaa	gatctatcaa	1560
accagacaaa	aatatcattc	gggtgatttc	caacagaaga	aatgtcatca	gaacctctat	1620
gcacagtga	ctctattcct	ttatctgcga	tcgataaaac	taaacactga	gagaccagct	1680
ttgatattga	aaacttcaac	atatttgatg	gaactccgtt	cagaaaaactc	cttgataccc	1740
catcaccttg	gaaatctcct	ttactctttg	gttcttctct	gcaaaagtcca	aagttgcttc	1800
cagaaatcac	atttggagat	attgggtgtt	ttatgagtc	cggcgagaga	agtttatgat	1860
ccataggact	gatgaagcat	ttgagtgaac	actcagctac	ggcatatgca	gatgccttgc	1920
aagttctggg	taatgacaca	cctgaatcga	tactcaagaa	gagacagctg	aacaagtcca	1980
ttcaaggaaa	agaaaatcag	caccagcttc	atgatcagct	tgggaaccga	tcccacgtgg	2040
agtgctcgcc	cttagacttc	agcgattgtg	ggacaccagg	gaaagctaa	gtacCttcgg	2100
cttctccggg	aggctactca	agccatcatc	cttacctttt	gaagagtgtc	agatagagaa	2160
gggtgggttt	gttcatagag	ttctgaagg	agtcctgcct	tcaatttttt	gatcccatct	2220
gtgtatgtct	tttttatctc	ctcctgtctc	aattttcttg	tttctaattt	ttttaaatgt	2280
tgagatctct	caactctgga	catcatacca	ttgattaaat	agcgaaaaag	taacttgttc	2340
tcaagtaatt	aacttgtaac	tcc				

(2) INFORMATION FOR SEQ ID NO:260:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 717 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..717
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1566354

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:260:

Ser	Asn	Ala	Ala	Ser	His	Ala	Glu	Pro	Tyr	Tyr	Pro	Ser	Phe	Lys	Asp
1			5						10					15	
Val	Lys	Ile	Val	Val	Pro	Glu	Ile	Ser	Cys	Glu	Thr	Glu	Cys	Ser	Lys
			20					25					30		
Lys	Phe	Gln	Asn	Leu	Asn	Cys	Ser	His	Glu	Leu	Arg	Thr	Thr	Thr	Ala
			35				40					45			
Thr	Glu	Asp	Gln	Leu	Pro	Gly	Val	Ser	Asn	Asp	Ala	Lys	Gln	Asp	Arg
			50				55				60				
Gly	Leu	Glu	Leu	Leu	Thr	His	Asn	Met	Asp	Asn	Gly	Gly	Lys	Asn	Gln
			65			70			75					80	
Ala	Leu	Gln	Gln	Asp	Phe	Gln	Ser	Ser	Val	Arg	Leu	Ser	Asp	Gln	Pro
			85					90					95		
Phe	Leu	Ser	Asn	Ser	Asp	Thr	Asp	Pro	Glu	Ala	Gln	Thr	Leu	Ile	Thr
			100				105					110			
Asp	Glu	Glu	Cys	Cys	Arg	Val	Leu	Phe	Pro	Asp	Asn	Met	Lys	Asp	Ser
			115				120					125			
Ser	Thr	Ser	Ser	Gly	Glu	Gln	Gly	Arg	Asn	Met	Val	Asp	Pro	Gln	Asn
			130				135				140				
Gly	Lys	Gly	Ser	Leu	Cys	Ser	Gln	Ala	Ala	Glu	Thr	His	Ala	His	Glu
			145			150				155				160	
Thr	Gly	Lys	Val	Pro	Ala	Leu	Pro	Trp	His	Pro	Ser	Ser	Ser	Glu	Gly
			165				170						175		
Leu	Ala	Gly	His	Asn	Cys	Val	Pro	Leu	Leu	Asp	Ser	Asp	Leu	Lys	Asp
			180				185					190			
Ser	Leu	Leu	Pro	Arg	Asn	Asp	Ser	Asn	Ala	Pro	Ile	Gln	Gly	Cys	Arg

195	200	205
Leu Phe Gly Ala Thr Glu	Leu Glu Cys Lys Thr Asp	Thr Asn Asp Gly
210	215	220
Phe Ile Asp Thr Tyr Glu	His Val Thr Ser His	Gly Asn Asp Asp Asn
225	230	235
Gly Gly Phe Pro Glu Gln Gln Gly	Leu Ser Tyr Ile Pro	Lys Asp Ser
245	250	255
Leu Lys Leu Val Pro Leu Asn Ser	Phe Ser Pro Ser Arg	Val Asn
260	265	270
Lys Ile Tyr Phe Pro Ile Asp	Asp Lys Pro Ala Glu	Lys Asp Lys Gly
275	280	285
Ala Leu Cys Tyr Glu Pro Pro Arg	Phe Pro Ser Ala Asp	Ile Pro Phe
290	295	300
Phe Ser Cys Asp Leu Val Pro Ser	Asn Ser Asp Leu Arg	Gln Glu Tyr
305	310	315
Ser Pro Phe Gly Ile Arg Gln	Leu Met Ile Ser Ser Met	Asn Cys Thr
325	330	335
Thr Pro Leu Arg Leu Trp Asp	Ser Pro Cys His Asp	Arg Ser Pro Asp
340	345	350
Val Met Leu Asn Asp Thr Ala Lys	Ser Phe Ser Gly Ala Pro	Ser Ile
355	360	365
Leu Lys Lys Arg His Arg Asp	Leu Leu Ser Pro Val	Leu Asp Arg Arg
370	375	380
Lys Asp Lys Lys Leu Lys Arg	Ala Ala Thr Ser Ser	Leu Ala Asn Asp
385	390	395
Phe Ser Arg Leu Asp Val Met	Leu Asp Glu Gly Asp	Asp Cys Met Thr
405	410	415
Ser Arg Pro Ser Glu Ser Pro Glu	Asp Lys Asn Ile Cys	Ala Ser Pro
420	425	430
Ser Ile Ala Arg Asp Asn Arg	Asn Cys Ala Ser Ser	Arg Leu Tyr Gln
435	440	445
Glu Met Ile Pro Ile Asp Glu	Glu Pro Lys Glu Thr	Leu Glu Ser Gly
450	455	460
Gly Val Thr Ser Met Gln Asn	Glu Asn Gly Cys Asn	Asp Gly Gly Ala
465	470	475
Ser Ala Lys Asn Asp Gln Glu	Thr Ser Gly Ser Phe	Phe Glu Leu Arg
485	490	495
Leu Cys Ser Pro Gly Met Thr	Arg Ala Arg Pro Asp	Asn Lys Val Asn
500	505	510
Ala Ser Ala Lys Asp Leu Ser	Asn Gln His Lys Ile	Ser Leu Gly Asp
515	520	525
Phe Pro Thr Glu Glu Met Ser	Ser Glu Pro Leu Cys	Thr Val Asp Ser
530	535	540
Ile Pro Leu Ser Ala Ile Asp	Lys Thr Asn Thr Ala	Glu Thr Ser Phe
545	550	555
Asp Ile Glu Asn Phe Asn Ile	Phe Asp Gly Thr Pro	Phe Arg Lys Leu
565	570	575
Leu Asp Thr Pro Ser Pro Trp	Lys Ser Pro Leu Leu	Phe Gly Ser Phe
580	585	590
Leu Gln Ser Pro Lys Leu Pro	Pro Glu Ile Thr Phe	Glu Asp Ile Gly
595	600	605
Cys Phe Met Ser Pro Gly Glu	Arg Ser Tyr Asp Ala	Ile Gly Leu Met
610	615	620
Lys His Leu Ser Glu His Ser	Ala Thr Ala Tyr Ala	Asp Ala Leu Glu
625	630	635
Val Leu Gly Asn Asp Thr Pro	Glu Ser Ile Leu Lys	Lys Arg Glu Leu
645	650	655
Asn Lys Ser Ile Gln Gly Lys	Glu Asn Gln His Gln	Pro His Asp Gln
660	665	670
Leu Gly Asn Arg Ser His Val	Glu Cys Arg Ala Leu	Asp Phe Ser Asp
675	680	685

Cys Gly Thr Pro Gly Lys Ala Lys Val Pro Ser Ala Ser Pro Gly Gly
690 695 700
Tyr Ser Ser Pro Ser Ser Tyr Leu Leu Lys Ser Cys Arg
705 710 715

(2) INFORMATION FOR SEQ ID NO:261:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 645 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..645

(D) OTHER INFORMATION: / Ceres Seq. ID 1566355

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:261:

Met Asp Asn Gly Gly Lys Asn Gln Ala Leu Gln Gln Asp Phe Gln Ser
1 5 10 15
Ser Val Arg Leu Ser Asp Gln Pro Phe Leu Ser Asn Ser Asp Thr Asp
20 25 30
Pro Glu Ala Gln Thr Leu Ile Thr Asp Glu Glu Cys Cys Arg Val Leu
35 40 45
Phe Pro Asp Asn Met Lys Asp Ser Ser Thr Ser Ser Gly Glu Gln Gly
50 55 60
Arg Asn Met Val Asp Pro Gln Asn Gly Lys Gly Ser Leu Cys Ser Gln
65 70 75 80
Ala Ala Glu Thr His Ala His Glu Thr Gly Lys Val Pro Ala Leu Pro
85 90 95
Trp His Pro Ser Ser Ser Glu Gly Leu Ala Gly His Asn Cys Val Pro
100 105 110
Leu Leu Asp Ser Asp Leu Lys Asp Ser Leu Leu Pro Arg Asn Asp Ser
115 120 125
Asn Ala Pro Ile Gln Gly Cys Arg Leu Phe Gly Ala Thr Glu Leu Glu
130 135 140
Cys Lys Thr Asp Thr Asn Asp Gly Phe Ile Asp Thr Tyr Gly His Val
145 150 155 160
Thr Ser His Gly Asn Asp Asp Asn Gly Gly Phe Pro Glu Gln Gln Gly
165 170 175
Leu Ser Tyr Ile Pro Lys Asp Ser Leu Lys Leu Val Pro Leu Asn Ser
180 185 190
Phe Ser Ser Pro Ser Arg Val Asn Lys Ile Tyr Phe Pro Ile Asp Asp
195 200 205
Lys Pro Ala Glu Lys Asp Lys Gly Ala Leu Cys Tyr Glu Pro Pro Arg
210 215 220
Phe Pro Ser Ala Asp Ile Pro Phe Phe Ser Cys Asp Leu Val Pro Ser
225 230 235 240
Asn Ser Asp Leu Arg Gln Glu Tyr Ser Pro Phe Gly Ile Arg Gln Leu
245 250 255
Met Ile Ser Ser Met Asn Cys Thr Thr Pro Leu Arg Leu Trp Asp Ser
260 265 270
Pro Cys His Asp Arg Ser Pro Asp Val Met Leu Asn Asp Thr Ala Lys
275 280 285
Ser Phe Ser Gly Ala Pro Ser Ile Leu Lys Lys Arg His Arg Asp Leu
290 295 300
Leu Ser Pro Val Leu Asp Arg Arg Lys Asp Lys Lys Leu Lys Arg Ala
305 310 315 320
Ala Thr Ser Ser Leu Ala Asn Asp Phe Ser Arg Leu Asp Val Met Leu
325 330 335
Asp Glu Gly Asp Asp Cys Met Thr Ser Arg Pro Ser Glu Ser Pro Glu
340 345 350
Asp Lys Asn Ile Cys Ala Ser Pro Ser Ile Ala Arg Asp Asn Arg Asn

355 360 365
Cys Ala Ser Ser Arg Leu Tyr Gln Glu Met Ile Pro Ile Asp Glu Glu
370 375 380
Pro Lys Glu Thr Leu Glu Ser Gly Gly Val Thr Ser Met Gln Asn Glu
385 390 395 400
Asn Gly Cys Asn Asp Gly Gly Ala Ser Ala Lys Asn Asp Gln Glu Thr
405 410 415
Ser Gly Ser Phe Phe Glu Leu Arg Leu Cys Ser Pro Gly Met Thr Arg
420 425 430
Ala Arg Pro Asp Asn Lys Val Asn Ala Ser Ala Lys Asp Leu Ser Asn
435 440 445
Gln His Lys Ile Ser Leu Gly Asp Phe Pro Thr Glu Glu Met Ser Ser
450 455 460
Glu Pro Leu Cys Thr Val Asp Ser Ile Pro Leu Ser Ala Ile Asp Lys
465 470 475 480
Thr Asn Thr Ala Glu Thr Ser Phe Asp Ile Glu Asn Phe Asn Ile Phe
485 490 495
Asp Gly Thr Pro Phe Arg Lys Leu Leu Asp Thr Pro Ser Pro Trp Lys
500 505 510
Ser Pro Leu Leu Phe Gly Ser Phe Leu Gln Ser Pro Lys Leu Pro Pro
515 520 525
Glu Ile Thr Phe Glu Asp Ile Gly Cys Phe Met Ser Pro Gly Glu Arg
530 535 540
Ser Tyr Asp Ala Ile Gly Leu Met Lys His Leu Ser Glu His Ser Ala
545 550 555 560
Thr Ala Tyr Ala Asp Ala Leu Glu Val Leu Gly Asn Asp Thr Pro Glu
565 570 575
Ser Ile Leu Lys Lys Arg Gln Leu Asn Lys Ser Ile Gln Gly Lys Glu
580 585 590
Asn Gln His Gln Pro His Asp Gln Leu Gly Asn Arg Ser His Val Glu
595 600 605
Cys Arg Ala Leu Asp Phe Ser Asp Cys Gly Thr Pro Gly Lys Ala Lys
610 615 620
Val Pro Ser Ala Ser Pro Gly Gly Tyr Ser Ser Pro Ser Ser Tyr Leu
625 630 635 640
Leu Lys Ser Cys Arg
645

(2) INFORMATION FOR SEQ ID NO:262:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 593 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..593

(D) OTHER INFORMATION: / Ceres Seq. ID 1566356

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:262:

Met Lys Asp Ser Ser Thr Ser Ser Gly Glu Gln Gly Arg Asn Met Val
1 5 10 15
Asp Pro Gln Asn Gly Lys Gly Ser Leu Cys Ser Gln Ala Ala Glu Thr
20 25 30
His Ala His Glu Thr Gly Lys Val Pro Ala Leu Pro Trp His Pro Ser
35 40 45
Ser Ser Glu Gly Leu Ala Gly His Asn Cys Val Pro Leu Leu Asp Ser
50 55 60
Asp Leu Lys Asp Ser Leu Leu Pro Arg Asn Asp Ser Asn Ala Pro Ile
65 70 75 80
Gln Gly Cys Arg Leu Phe Gly Ala Thr Glu Leu Glu Cys Lys Thr Asp
85 90 95

Thr	Asn	Asp	Gly	Phe	Ile	Asp	Thr	Tyr	Gly	His	Val	Thr	Ser	His	Gly	
			100					105					110			
Asn	Asp	Asp	Asn	Gly	Gly	Phe	Pro	Glu	Gln	Gln	Gly	Leu	Ser	Tyr	Ile	
	115						120					125				
Pro	Lys	Asp	Ser	Leu	Lys	Leu	Val	Pro	Leu	Asn	Ser	Phe	Ser	Ser	Pro	
	130					135					140					
Ser	Arg	Val	Asn	Lys	Ile	Tyr	Phe	Pro	Ile	Asp	Asp	Lys	Pro	Ala	Glu	
	145			150					155				160			
Lys	Asp	Lys	Gly	Ala	Leu	Cys	Tyr	Glu	Pro	Pro	Arg	Phe	Pro	Ser	Ala	
			165					170					175			
Asp	Ile	Pro	Phe	Phe	Ser	Cys	Asp	Leu	Val	Pro	Ser	Asn	Ser	Asp	Leu	
			180					185					190			
Arg	Gln	Glu	Tyr	Ser	Pro	Phe	Gly	Ile	Arg	Gln	Leu	Met	Ile	Ser	Ser	
	195						200					205				
Met	Asn	Cys	Thr	Thr	Pro	Leu	Arg	Leu	Trp	Asp	Ser	Pro	Cys	His	Asp	
	210				215						220					
Arg	Ser	Pro	Asp	Val	Met	Leu	Asn	Asp	Thr	Ala	Lys	Ser	Phe	Ser	Gly	
	225			230					235						240	
Ala	Pro	Ser	Ile	Leu	Lys	Lys	Arg	His	Arg	Asp	Leu	Leu	Ser	Pro	Val	
			245					250					255			
Leu	Asp	Arg	Arg	Lys	Asp	Lys	Lys	Leu	Lys	Arg	Ala	Ala	Thr	Ser	Ser	
	260					265							270			
Leu	Ala	Asn	Asp	Phe	Ser	Arg	Leu	Asp	Val	Met	Leu	Asp	Glu	Gly	Asp	
	275					280					285					
Asp	Cys	Met	Thr	Ser	Arg	Pro	Ser	Glu	Ser	Pro	Glu	Asp	Lys	Asn	Ile	
	290				295						300					
Cys	Ala	Ser	Pro	Ser	Ile	Ala	Arg	Asp	Asn	Arg	Asn	Cys	Ala	Ser	Ser	
	305			310					315						320	
Arg	Leu	Tyr	Gln	Glu	Met	Ile	Pro	Ile	Asp	Glu	Glu	Pro	Lys	Glu	Thr	
			325					330					335			
Leu	Glu	Ser	Gly	Gly	Val	Thr	Ser	Met	Gln	Asn	Glu	Asn	Gly	Cys	Asn	
			340					345					350			
Asp	Gly	Gly	Ala	Ser	Ala	Lys	Asn	Asp	Gln	Glu	Thr	Ser	Gly	Ser	Phe	
	355					360						365				
Phe	Glu	Leu	Arg	Leu	Cys	Ser	Pro	Gly	Met	Thr	Arg	Ala	Arg	Pro	Asp	
	370				375						380					
Asn	Lys	Val	Asn	Ala	Ser	Ala	Lys	Asp	Leu	Ser	Asn	Gln	His	Lys	Ile	
	385			390					395						400	
Ser	Leu	Gly	Asp	Phe	Pro	Thr	Glu	Glu	Met	Ser	Ser	Glu	Pro	Leu	Cys	
			405					410					415			
Thr	Val	Asp	Ser	Ile	Pro	Leu	Ser	Ala	Ile	Asp	Lys	Thr	Asn	Thr	Ala	
			420					425					430			
Glu	Thr	Ser	Phe	Asp	Ile	Glu	Asn	Phe	Asn	Ile	Phe	Asp	Gly	Thr	Pro	
	435					440						445				
Phe	Arg	Lys	Leu	Leu	Asp	Thr	Pro	Ser	Pro	Trp	Lys	Ser	Pro	Leu	Leu	
	450				455						460					
Phe	Gly	Ser	Phe	Leu	Gln	Ser	Pro	Lys	Leu	Pro	Pro	Glu	Ile	Thr	Phe	
	465			470					475						480	
Glu	Asp	Ile	Gly	Cys	Phe	Met	Ser	Pro	Gly	Glu	Arg	Ser	Tyr	Asp	Ala	
			485					490					495			
Ile	Gly	Leu	Met	Lys	His	Leu	Ser	Glu	His	Ser	Ala	Thr	Ala	Tyr	Ala	
			500					505					510			
Asp	Ala	Leu	Glu	Val	Leu	Gly	Asn	Asp	Thr	Pro	Glu	Ser	Ile	Leu	Lys	
	515						520					525				
Lys	Arg	Gln	Leu	Asn	Lys	Ser	Ile	Gln	Gly	Lys	Glu	Asn	Gln	His	Gln	
	530				535						540					
Pro	His	Asp	Gln	Leu	Gly	Asn	Arg	Ser	His	Val	Glu	Cys	Arg	Ala	Leu	
	545			550					555						560	
Asp	Phe	Ser	Asp	Cys	Gly	Thr	Pro	Gly	Lys	Ala	Lys	Val	Pro	Ser	Ala	
			565					570					575			
Ser	Pro	Gly	Gly	Tyr	Ser	Ser	Pro	Ser	Ser	Tyr	Leu	Leu	Lys	Ser	Cys	

Arg 580 585 590

(2) INFORMATION FOR SEQ ID NO:263:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 574 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..574

(D) OTHER INFORMATION: / Ceres Seq. ID 1566364

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:263:

actagaaatt	ttgtctctct	cgccgccttg	cgaaaaagcat	tttcgatctt	actcttagga	60
taaaaaaatg	tcgacagtgt	gagagcttgc	tntGCagcta	cgctgttatg	atcctcgagg	120
acgagggtat	cgctatcacg	gctgacaaaa	tcgcgacctt	ggtgaaagct	gctggtgtta	180
gtattgagtc	atactggcca	atgctatttc	ccaagatggc	tgagaaaagt	aacgtgactg	240
atctcatcat	gaacgttggt	gctggtggtg	gaggtggtgc	tccggttgca	gctgctgctc	300
caagctgctgg	cggtggtgcg	gcaGctgctc	ctgctgctga	ggagaagaag	aaggatgagc	360
cagcagaaga	gagtgacgga	gatttggggt	tcggtttgtt	tgactaaacg	caGtcaactg	420
tctttctctc	ttgtagtgtg	atattggaga	ctatattttg	tcgtatgagt	tattattact	480
tgtttgatct	ggctaaagga	ctattagtgt	gtttatgatg	cgtatgtgtg	ataactcaag	540
ttctctagca	aaccaatcgg	ctcgggcttt	tggt			

(2) INFORMATION FOR SEQ ID NO:264:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 99 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..99

(D) OTHER INFORMATION: / Ceres Seq. ID 1566365

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:264:

Met	Ile	Leu	Glu	Asp	Glu	Gly	Ile	Ala	Ile	Thr	Ala	Asp	Lys	Ile	Ala
1			5						10					15	
Thr	Leu	Val	Lys	Ala	Ala	Gly	Val	Ser	Ile	Glu	Ser	Tyr	Trp	Pro	Met
			20					25					30		
Leu	Phe	Ala	Lys	Met	Ala	Glu	Lys	Arg	Asn	Val	Thr	Asp	Leu	Ile	Met
			35				40					45			
Asn	Val	Gly	Ala	Gly	Gly	Gly	Gly	Ala	Pro	Val	Ala	Ala	Ala	Ala	Ala
			50				55				60				
Pro	Ala	Ala	Gly	Gly	Gly	Ala	Ala	Ala	Ala	Pro	Ala	Ala	Glu	Glu	Lys
			65				70			75			80		
Lys	Lys	Asp	Glu	Pro	Ala	Glu	Glu	Ser	Asp	Gly	Asp	Leu	Gly	Phe	Gly
			85					90					95		
Leu	Phe	Asp													

(2) INFORMATION FOR SEQ ID NO:265:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 68 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..68

(D) OTHER INFORMATION: / Ceres Seq. ID 1566366
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:265:
Met Leu Phe Ala Lys Met Ala Glu Lys Arg Asn Val Thr Asp Leu Ile
1 5 10 15
Met Asn Val Gly Ala Gly Gly Gly Gly Ala Pro Val Ala Ala Ala
20 25 30
Ala Pro Ala Ala Gly Gly Gly Ala Ala Ala Pro Ala Ala Glu Glu
35 40 45
Lys Lys Lys Asp Glu Pro Ala Glu Glu Ser Asp Gly Asp Leu Gly Phe
50 55 60
Gly Leu Phe Asp
65

(2) INFORMATION FOR SEQ ID NO:266:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 63 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..63

(D) OTHER INFORMATION: / Ceres Seq. ID 1566367

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:266:

Met Ala Glu Lys Arg Asn Val Thr Asp Leu Ile Met Asn Val Gly Ala
1 5 10 15
Gly Gly Gly Gly Gly Ala Pro Val Ala Ala Ala Pro Ala Ala Gly
20 25 30
Gly Gly Ala Ala Ala Ala Pro Ala Ala Glu Glu Lys Lys Lys Asp Glu
35 40 45
Pro Ala Glu Glu Ser Asp Gly Asp Leu Gly Phe Gly Leu Phe Asp
50 55 60

(2) INFORMATION FOR SEQ ID NO:267:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1582 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..1582

(D) OTHER INFORMATION: / Ceres Seq. ID 1566379

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:267:

tgagaaaaatg	octgagagaa	atgcagtgct	atgatcactg	ggctttgtca	60	
gaacgggtgaa	gtggatcgcg	cggttggtgt	gtttcggaaa	atgcctgtga	aggattcgctc	120
tcctctatgt	gcactgttgg	ctggtcttat	taaaaacgag	agactttcac	aagctgcggtg	180
ggttttgggt	cagtatggga	gtttagtttc	aggaagggaa	gatttggtgt	atgcttataa	240
caacttgatt	gttgatattg	gacagcgagg	acaagtagaa	gcagctcgat	gtctgtttga	300
tcagattcct	gatctctgtg	gtgatgatca	tggtggagag	tttagagaga	ggttctgtaa	360
aaatgttggt	tcatggaaat	ctatgatcaa	agcttacttg	aaagtgggtg	atgtgggtctc	420
tgctagggtg	ctattttgatc	agatgaaaga	ccgcgataca	atttcttgga	acacaatgat	480
tgatggatgc	gtacatgttt	ccaggatgga	agatgctttt	gctctgtttt	cggaaatgcc	540
gaaccgtgat	gcacattcgt	ggaacatgat	ggtctcgggt	tatgctagtgt	ttggcgaagt	600
agagcttgct	cgccactact	ttgaaaaaac	acctgagaaa	catacagttc	cgtggaactc	660
gataatatga	gcttatgaga	aaaacaagga	ctacaagaaa	gctgttgatt	tgtttatccg	720
gatgaacatt	gaaggagaga	agcctgaccc	acatacttta	acctctcttc	tcagtgcaatc	780
taccgggctt	gtaaatctgc	gttttagaat	gcagatgcac	caaactggtt	tcaagactgt	840
gatcccgat	gttccagctc	acaatgcocct	tatcaactatg	tattcaagat	cggggtgaaat	900
aatggagtcg	aggagaaatc	tcgatgaaat	gaaactcaaa	agagaagtaa	tcacatggaa	960
tgcaatgata	ggaggatatg	catttcgatg	taatgcctca	gaggcccttga	atctgttcgg	1020

gtcgatgaaa	agcaacggga	tatatccttc	tcacataaca	ttcgtctcag	ttctgaacgc	1080
ttgtgCtca	gogggacttg	ttgatgaggc	taaagcacag	ttgtgtccca	tgatgagtgt	1140
gtacaagatc	gagccgatga	tggaaacatta	ttcttccctg	gtcaacgtta	ccagtggaca	1200
agggcagttt	gaagaggcca	tgtatatcat	aaagagtatg	ccttttgagc	cagacaaaac	1260
ggatgggggt	gcattattgg	atgctttgtg	gatataacaa	tgtaggggctt	gcacatgttg	1320
cagctgaagc	aatgtcgaga	ctcgaaccag	agagctcaac	accttatgta	ctgttataca	1380
acatgtacgc	ggatatggga	ctatggggagc	aagcttctca	agtgagaatg	aaatgggaga	1440
gtaaaagaat	caagaaggaa	agaggatcca	gttgggttga	ctctctcaacg	taaaaagcag	1500
cttttattta	tgtttactta	aacataaaaa	ttgatttggg	atcagaattg	agatagaaat	1560
tgataaggta	ctcttgaag	tt				

(2) INFORMATION FOR SEQ ID NO:268:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 431 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..431

(D) OTHER INFORMATION: / Ceres Seq. ID 1566380

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:268:

Glu	Lys	Met	Pro	Glu	Arg	Asn	Ala	Val	Ser	Trp	Ser	Ala	Met	Ile	Thr
1			5						10					15	
Gly	Leu	Cys	Gln	Asn	Gly	Glu	Val	Asp	Arg	Ala	Val	Val	Leu	Phe	Arg
			20					25					30		
Lys	Met	Pro	Val	Lys	Asp	Ser	Ser	Pro	Leu	Cys	Ala	Leu	Val	Ala	Gly
			35				40					45			
Leu	Ile	Lys	Asn	Glu	Arg	Leu	Ser	Glu	Ala	Ala	Trp	Val	Leu	Gly	Gln
			50				55				60				
Tyr	Gly	Ser	Leu	Val	Ser	Gly	Arg	Glu	Asp	Leu	Val	Tyr	Ala	Tyr	Asn
			65			70			75					80	
Thr	Leu	Ile	Val	Gly	Tyr	Gly	Gln	Arg	Gly	Gln	Val	Glu	Ala	Ala	Arg
			85						90					95	
Cys	Leu	Phe	Asp	Gln	Ile	Pro	Asp	Leu	Cys	Gly	Asp	Asp	His	Gly	Gly
			100				105						110		
Glu	Phe	Arg	Gly	Arg	Phe	Cys	Lys	Asn	Val	Val	Ser	Trp	Asn	Ser	Met
			115				120					125			
Ile	Lys	Ala	Tyr	Leu	Lys	Val	Gly	Asp	Val	Val	Ser	Ala	Arg	Leu	Leu
			130				135				140				
Phe	Asp	Gln	Met	Lys	Asp	Arg	Asp	Thr	Ile	Ser	Trp	Asn	Thr	Met	Ile
			145			150			155					160	
Asp	Gly	Tyr	Val	His	Val	Ser	Arg	Met	Glu	Asp	Ala	Phe	Ala	Leu	Phe
			165						170					175	
Ser	Glu	Met	Pro	Asn	Arg	Asp	Ala	His	Ser	Trp	Asn	Met	Met	Val	Ser
			180				185							190	
Gly	Tyr	Ala	Ser	Val	Gly	Asn	Val	Glu	Leu	Ala	Arg	His	Tyr	Phe	Glu
			195				200					205			
Lys	Thr	Pro	Glu	Lys	His	Thr	Val	Ser	Trp	Asn	Ser	Ile	Ile	Ala	Ala
			210				215				220				
Tyr	Glu	Lys	Asn	Lys	Asp	Tyr	Lys	Glu	Ala	Val	Asp	Leu	Phe	Ile	Arg
			225			230			235					240	
Met	Asn	Ile	Glu	Gly	Glu	Lys	Pro	Asp	Pro	His	Thr	Leu	Thr	Ser	Leu
			245						250					255	
Leu	Ser	Ala	Ser	Thr	Gly	Leu	Val	Asn	Leu	Arg	Leu	Gly	Met	Gln	Met
			260					265						270	
His	Gln	Ile	Val	Val	Lys	Thr	Val	Ile	Pro	Asp	Val	Pro	Val	His	Asn
			275				280					285			
Ala	Leu	Ile	Thr	Met	Tyr	Ser	Arg	Cys	Gly	Glu	Ile	Met	Glu	Ser	Arg
			290			295					300				
Arg	Ile	Phe	Asp	Glu	Met	Lys	Leu	Lys	Arg	Glu	Val	Ile	Thr	Trp	Asn

305	310	315	320
Ala Met Ile Gly	Gly Tyr Ala Phe His	Gly Asn Ala Ser	Glu Ala Leu
	325	330	335
Asn Leu Phe Gly	Ser Met Lys Ser Asn Gly	Ile Tyr Pro Ser	His Ile
	340	345	350
Thr Phe Val Ser	Val Leu Asn Ala Cys Ala His	Ala Gly Leu Val	Asp
	355	360	365
Glu Ala Lys Ala	Gln Phe Val Ser Met Met Ser	Val Tyr Lys Ile	Glu
	370	375	380
Pro Met Met Glu	His Tyr Ser Ser Leu Val Asn Val	Thr Ser Gly Gln	
	385	390	395
Gly Gln Phe Glu	Glu Ala Met Tyr Ile Ile Lys	Ser Met Pro Phe	Glu
	405	410	415
Pro Asp Lys Thr	Val Trp Gly Ala Leu Leu Asp	Ala Cys Arg Ile	
	420	425	430

(2) INFORMATION FOR SEQ ID NO:269:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 429 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..429

(D) OTHER INFORMATION: / Ceres Seq. ID 1566381

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:269:

Met Pro Glu Arg	Asn Ala Val Ser Trp Ser	Ala Met Ile Thr Gly Leu
1	5	10
Cys Gln Asn Gly	Glu Val Asp Arg Ala Val	Val Leu Phe Arg Lys Met
	20	25
Pro Val Lys Asp	Ser Ser Pro Leu Cys Ala Leu	Val Ala Gly Leu Ile
	35	40
Lys Asn Glu Arg	Leu Ser Glu Ala Ala Trp Val	Leu Gly Gln Tyr Gly
	50	55
Ser Leu Val Ser	Gly Arg Glu Asp Leu Val Tyr	Ala Tyr Asn Thr Leu
	65	70
Ile Val Gly Tyr	Gln Arg Gly Gln Val Glu Ala	Ala Arg Cys Leu
	85	90
Phe Asp Gln Ile	Pro Asp Leu Cys Gly Asp Asp	His Gly Gly Glu Phe
	100	105
Arg Glu Arg Phe	Cys Lys Asn Val Val Ser Trp Asn	Ser Met Ile Lys
	115	120
Ala Tyr Leu Lys	Val Gly Asp Val Val Ser Ala Arg	Leu Leu Phe Asp
	130	135
Gln Met Lys Asp	Arg Asp Thr Ile Ser Trp Asn Thr	Met Ile Asp Gly
	145	150
Tyr Val His Val	Ser Arg Met Glu Asp Ala Phe	Ala Leu Phe Ser Gly
	165	170
Met Pro Asn Arg	Asp Ala His Ser Trp Asn Met Met	Val Ser Gly Tyr
	180	185
Ala Ser Val Gly	Asn Val Glu Leu Ala Arg His Tyr	Phe Glu Lys Thr
	195	200
Pro Glu Lys His	Thr Val Ser Trp Asn Ser Ile Ile	Ala Ala Tyr Glu
	210	215
Lys Asn Lys Asp	Tyr Lys Glu Ala Val Asp Leu Phe	Ile Arg Met Asn
	225	230
Ile Glu Gly Glu	Lys Pro Asp Pro His Thr Leu Thr	Ser Leu Leu Ser
	245	250
Ala Ser Thr Gly	Leu Val Asn Leu Arg Leu Gly	Met Gln Met His Gln
	260	265
		270

Ile	Val	Val	Lys	Thr	Val	Ile	Pro	Asp	Val	Pro	Val	His	Asn	Ala	Leu
	275						280					285			
Ile	Thr	Met	Tyr	Ser	Arg	Cys	Gly	Glu	Ile	Met	Glu	Ser	Arg	Arg	Ile
	290						295				300				
Phe	Asp	Glu	Met	Lys	Leu	Lys	Arg	Glu	Val	Ile	Thr	Trp	Asn	Ala	Met
	305				310					315				320	
Ile	Gly	Gly	Tyr	Ala	Phe	His	Gly	Asn	Ala	Ser	Glu	Ala	Leu	Asn	Leu
				325					330					335	
Phe	Gly	Ser	Met	Lys	Ser	Asn	Gly	Ile	Tyr	Pro	Ser	His	Ile	Thr	Phe
			340					345					350		
Val	Ser	Val	Leu	Asn	Ala	Cys	Ala	His	Ala	Gly	Leu	Val	Asp	Glu	Ala
			355				360					365			
Lys	Ala	Gln	Phe	Val	Ser	Met	Met	Ser	Val	Tyr	Lys	Ile	Glu	Pro	Met
	370					375					380				
Met	Glu	His	Tyr	Ser	Ser	Leu	Val	Asn	Val	Thr	Ser	Gly	Gln	Gly	Gln
	385					390				395				400	
Phe	Glu	Glu	Ala	Met	Tyr	Ile	Ile	Lys	Ser	Met	Pro	Phe	Glu	Pro	Asp
				405					410					415	
Lys	Thr	Val	Trp	Gly	Ala	Leu	Leu	Asp	Ala	Cys	Arg	Ile			
			420					425							

- (2) INFORMATION FOR SEQ ID NO:270:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 418 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..418
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1566382

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:270:

Met	Ile	Thr	Gly	Leu	Cys	Gln	Asn	Gly	Glu	Val	Asp	Arg	Ala	Val	Val
1				5					10					15	
Leu	Phe	Arg	Lys	Met	Pro	Val	Lys	Asp	Ser	Ser	Pro	Leu	Cys	Ala	Leu
			20					25					30		
Val	Ala	Gly	Leu	Ile	Lys	Asn	Glu	Arg	Leu	Ser	Glu	Ala	Ala	Trp	Val
		35				40					45				
Leu	Gly	Gln	Tyr	Gly	Ser	Leu	Val	Ser	Gly	Arg	Glu	Asp	Leu	Val	Tyr
	50				55						60				
Ala	Tyr	Asn	Thr	Leu	Ile	Val	Gly	Tyr	Gly	Gln	Arg	Gly	Gln	Val	Glu
	65				70				75					80	
Ala	Ala	Arg	Cys	Leu	Phe	Asp	Gln	Ile	Pro	Asp	Leu	Cys	Gly	Asp	Asp
			85						90					95	
His	Gly	Gly	Glu	Phe	Arg	Glu	Arg	Phe	Cys	Lys	Asn	Val	Val	Ser	Trp
			100				105						110		
Asn	Ser	Met	Ile	Lys	Ala	Tyr	Leu	Lys	Val	Gly	Asp	Val	Val	Ser	Ala
		115					120						125		
Arg	Leu	Leu	Phe	Asp	Gln	Met	Lys	Asp	Arg	Asp	Thr	Ile	Ser	Trp	Asn
	130					135					140				
Thr	Met	Ile	Asp	Gly	Tyr	Val	His	Val	Ser	Arg	Met	Glu	Asp	Ala	Phe
	145				150					155				160	
Ala	Leu	Phe	Ser	Glu	Met	Pro	Asn	Arg	Asp	Ala	His	Ser	Trp	Asn	Met
				165					170					175	
Met	Val	Ser	Gly	Tyr	Ala	Ser	Val	Gly	Asn	Val	Glu	Leu	Ala	Arg	His
			180					185						190	
Tyr	Phe	Glu	Lys	Thr	Pro	Glu	Lys	His	Thr	Val	Ser	Trp	Asn	Ser	Ile
			195				200					205			
Ile	Ala	Ala	Tyr	Glu	Lys	Asn	Lys	Asp	Tyr	Lys	Glu	Ala	Val	Asp	Leu
	210					215					220				
Phe	Ile	Arg	Met	Asn	Ile	Glu	Gly	Glu	Lys	Pro	Asp	Pro	His	Thr	Leu

225				230				235				240
Thr	Ser	Leu	Leu	Ser	Ala	Ser	Thr	Gly	Leu	Val	Asn	Leu
				245				250				255
Met	Gln	Met	His	Gln	Ile	Val	Val	Lys	Thr	Val	Ile	Pro
			260					265			270	275
Val	His	Asn	Ala	Leu	Ile	Thr	Met	Tyr	Ser	Arg	Cys	Gly
			275				280				285	290
Glu	Ser	Arg	Arg	Ile	Phe	Asp	Glu	Met	Lys	Leu	Lys	Arg
						295					300	305
Thr	Trp	Asn	Ala	Met	Ile	Gly	Gly	Tyr	Ala	Phe	His	Gly
						310			315			320
Glu	Ala	Leu	Asn	Leu	Phe	Gly	Ser	Met	Lys	Ser	Asn	Gly
						325			330			335
Ser	His	Ile	Thr	Phe	Val	Ser	Val	Leu	Asn	Ala	Cys	Ala
			340					345				350
Leu	Val	Asp	Glu	Ala	Lys	Ala	Gln	Phe	Val	Ser	Met	Ser
			355				360				365	370
Lys	Ile	Glu	Pro	Met	Met	Glu	His	Tyr	Ser	Ser	Leu	Val
						375					380	385
Ser	Gly	Gln	Gly	Gln	Phe	Glu	Glu	Ala	Met	Tyr	Ile	Ile
						390			395			400
Pro	Phe	Glu	Pro	Asp	Lys	Thr	Val	Trp	Gly	Ala	Leu	Leu
				405					410			415
Arg	Ile											

(2) INFORMATION FOR SEQ ID NO:271:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 974 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..974

(D) OTHER INFORMATION: / Ceres Seq. ID 1566387

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:271:

aaMcaacgaa	cgccgagagc	tctcacttca	cactttatcc	acttggagct	tcgacaaatgg	60
cgtctccttc	gcttctcgag	tcttcgcgtt	cttcggtttc	cggacgtttc	tcacattag	120
cggtctccatc	ctccgcacga	atgctctctc	cgccgcctcag	aaacgttggtg	aaagtctcgg	180
cgtctggaaac	tgtaactggc	gagaaatctg	aagccgagaa	aactcaacgc	ctcaaaacgg	240
cttacctcga	gaggattatc	cctgcgcctc	aagaagagtt	caagtacgtt	aatattcacc	300
aggttccaaa	ggtacagaag	attgtagtga	attgtggtat	tggagatgcg	gcgcagaaag	360
acaagggttt	ggaggctgcg	atgaaggata	tcgcgcctat	cacaggggcag	aaacctatta	420
agacacgagc	tagagcttcc	attgctactt	tcaagatcag	ggaagatcaa	cctctggga	480
ttgctgtcac	tctcagagga	gatgtaattg	actcctctct	ggatcgctct	atcaacttag	540
cccttcgcag	aactcgagat	ttccaagggt	tgagtcgccg	tatctttgat	gggaacggaa	600
actactcgat	tgggtgtgaa	gaccaagggt	tattccctga	aatcaggttt	gatgcctgtg	660
gaaaaacgag	aggaatggat	gtatgcatca	gcacaacggc	taaaagcgat	caagaaggac	720
agaaactatt	ggctctaatg	ggaatgcctt	tcagggaagg	aggtgtgtggc	agccaggcgc	780
cgatagtgcg	gaagaagaaa	ctaaagtctc	atcaactttg	tgctaaagga	aaaggaaaaga	840
gatgatgaac	atagctgcct	attgtatgta	tcgtctctcg	taaccaacca	tttcagtgtt	900
cagaaaaacc	atctcctctt	gtaatgcttt	atgagtcagt	ttgaaaataa	tatcaggagat	960
cttgtgttta	tggt					

(2) INFORMATION FOR SEQ ID NO:272:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 280 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..280

(D) OTHER INFORMATION: / Ceres Seq. ID 1566388

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:272:

Xaa Thr Asn Ala Glu Ser Ser His Phe Thr Leu Tyr Pro Leu Gly Ala
1 5 10 15
Ser Thr Met Ala Ser Pro Ser Leu Leu Gln Ser Ser Ala Ser Ser Phe
20 25 30
His Gly Arg Phe Ser Pro Leu Ala Ala Pro Ser Ser Ala Arg Met Leu
35 40 45
Ser Pro Pro Leu Arg Asn Val Val Lys Val Ser Ala Ser Gly Thr Val
50 55 60
Leu Val Glu Lys Ser Glu Ala Glu Lys Thr Gln Arg Leu Lys Thr Ala
65 70 75 80
Tyr Leu Glu Arg Ile Ile Pro Ala Leu Lys Glu Glu Phe Lys Tyr Val
85 90 95
Asn Ile His Gln Val Pro Lys Val Gln Lys Ile Val Val Asn Cys Gly
100 105 110
Ile Gly Asp Ala Ala Gln Asn Asp Lys Gly Leu Glu Ala Ala Met Lys
115 120 125
Asp Ile Ala Leu Ile Thr Gly Gln Lys Pro Ile Lys Thr Arg Ala Arg
130 135 140
Ala Ser Ile Ala Thr Phe Lys Ile Arg Glu Asp Gln Pro Leu Gly Ile
145 150 155 160
Ala Val Thr Leu Arg Gly Asp Val Met Tyr Ser Phe Leu Asp Arg Leu
165 170 175
Ile Asn Leu Ala Leu Pro Arg Thr Arg Asp Phe Gln Gly Val Ser Pro
180 185 190
Ser Ser Phe Asp Gly Asn Gly Asn Tyr Ser Ile Gly Val Lys Asp Gln
195 200 205
Gly Val Phe Pro Glu Ile Arg Phe Asp Ala Val Gly Lys Thr Arg Gly
210 215 220
Met Asp Val Cys Ile Ser Thr Thr Ala Lys Ser Asp Gln Glu Gly Gln
225 230 235 240
Lys Leu Leu Ala Leu Met Gly Met Pro Phe Arg Glu Gly Gly Gly Gly
245 250 255
Ser Thr Gly Ala Ile Val Arg Lys Lys Lys Leu Lys Ser His His Phe
260 265 270
Asp Ala Lys Gly Lys Gly Lys Arg
275 280

(2) INFORMATION FOR SEQ ID NO:273:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 262 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..262

(D) OTHER INFORMATION: / Ceres Seq. ID 1566389

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:273:

Met Ala Ser Pro Ser Leu Leu Gln Ser Ser Ala Ser Ser Phe His Gly
1 5 10 15
Arg Phe Ser Pro Leu Ala Ala Pro Ser Ser Ala Arg Met Leu Ser Pro
20 25 30
Pro Leu Arg Asn Val Val Lys Val Ser Ala Ser Gly Thr Val Leu Val
35 40 45
Glu Lys Ser Glu Ala Glu Lys Thr Gln Arg Leu Lys Thr Ala Tyr Leu
50 55 60

Glu Arg Ile Ile Pro Ala Leu Lys Glu Glu Phe Lys Tyr Val Asn Ile
65 70 75 80
His Gln Val Pro Lys Val Gln Lys Ile Val Val Asn Cys Gly Ile Gly
85 90 95
Asp Ala Ala Gln Asn Asp Lys Gly Leu Glu Ala Ala Met Lys Asp Ile
100 105 110
Ala Leu Ile Thr Gly Gln Lys Pro Ile Lys Thr Arg Ala Arg Ala Ser
115 120 125
Ile Ala Thr Phe Lys Ile Arg Glu Asp Gln Pro Leu Gly Ile Ala Val
130 135 140
Thr Leu Arg Gly Asp Val Met Tyr Ser Phe Leu Asp Arg Leu Ile Asn
145 150 155 160
Leu Ala Leu Pro Arg Thr Arg Asp Phe Gln Gly Val Ser Pro Ser Ser
165 170 175
Phe Asp Gly Asn Gly Asn Tyr Ser Ile Gly Val Lys Asp Gln Gly Val
180 185 190
Phe Pro Glu Ile Arg Phe Asp Ala Val Gly Lys Thr Arg Gly Met Asp
195 200 205
Val Cys Ile Ser Thr Thr Ala Lys Ser Asp Gln Glu Gly Gln Lys Leu
210 215 220
Leu Ala Leu Met Gly Met Pro Phe Arg Glu Gly Gly Gly Ser Thr
225 230 235 240
Gly Ala Ile Val Arg Lys Lys Leu Lys Ser His His Phe Asp Ala
245 250 255
Lys Gly Lys Gly Lys Arg
260

(2) INFORMATION FOR SEQ ID NO:274:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 234 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..234

(D) OTHER INFORMATION: / Ceres Seq. ID 1566390

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:274:

Met Leu Ser Pro Pro Leu Arg Asn Val Val Lys Val Ser Ala Ser Gly
1 5 10 15
Thr Val Leu Val Glu Lys Ser Glu Ala Glu Lys Thr Gln Arg Leu Lys
20 25 30
Thr Ala Tyr Leu Glu Arg Ile Ile Pro Ala Leu Lys Glu Phe Lys
35 40 45
Tyr Val Asn Ile His Gln Val Pro Lys Val Gln Lys Ile Val Val Asn
50 55 60
Cys Gly Ile Gly Asp Ala Ala Gln Asn Asp Lys Gly Leu Glu Ala Ala
65 70 75 80
Met Lys Asp Ile Ala Leu Ile Thr Gly Gln Lys Pro Ile Lys Thr Arg
85 90 95
Ala Arg Ala Ser Ile Ala Thr Phe Lys Ile Arg Glu Asp Gln Pro Leu
100 105 110
Gly Ile Ala Val Thr Leu Arg Gly Asp Val Met Tyr Ser Phe Leu Asp
115 120 125
Arg Leu Ile Asn Leu Ala Leu Pro Arg Thr Arg Asp Phe Gln Gly Val
130 135 140
Ser Pro Ser Ser Phe Asp Gly Asn Gly Asn Tyr Ser Ile Gly Val Lys
145 150 155 160
Asp Gln Gly Val Phe Pro Glu Ile Arg Phe Asp Ala Val Gly Lys Thr
165 170 175
Arg Gly Met Asp Val Cys Ile Ser Thr Thr Ala Lys Ser Asp Gln Glu

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 103 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..103
(D) OTHER INFORMATION: / Ceres Seq. ID 1566397
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:277:
Met Ala Gln Lys Val Val Leu Lys Val Leu Thr Met Thr Asp Asp Lys
1 5 10 15
Thr Lys Gln Lys Ala Ile Glu Ala Ala Asp Ile Phe Gly Val Asp
20 25 30
Ser Ile Ala Ala Asp Met Lys Asp Gln Lys Leu Thr Val Ile Gly Leu
35 40 45
Met Asp Ala Val Ala Val Val Lys Lys Leu Lys Lys Val Gly Lys Val
50 55 60
Asp Leu Ile Ser Val Gly Pro Ala Lys Glu Glu Lys Lys Glu Glu Lys
65 70 75 80
Lys Glu Glu Lys Lys Lys Glu Lys Lys Glu Glu Lys Lys Glu Glu Lys
85 90 95
Lys Glu Glu Glu Pro Lys Lys
100

(2) INFORMATION FOR SEQ ID NO:278:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 92 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..92
(D) OTHER INFORMATION: / Ceres Seq. ID 1566398
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:278:
Met Thr Asp Asp Lys Thr Lys Gln Lys Ala Ile Glu Ala Ala Asp
1 5 10 15
Ile Phe Gly Val Asp Ser Ile Ala Ala Asp Met Lys Asp Gln Lys Leu
20 25 30
Thr Val Ile Gly Leu Met Asp Ala Val Ala Val Val Lys Lys Leu Lys
35 40 45
Lys Val Gly Lys Val Asp Leu Ile Ser Val Gly Pro Ala Lys Glu Glu
50 55 60
Lys Lys Glu Glu Lys Lys Glu Glu Lys Lys Lys Glu Lys Glu Glu
65 70 75 80
Lys Lys Glu Glu Lys Lys Glu Glu Glu Pro Lys Lys
85 90

(2) INFORMATION FOR SEQ ID NO:279:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1221 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..1221
(D) OTHER INFORMATION: / Ceres Seq. ID 1566423
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:279:
aatcaacaca cacaaacaca cacacacaca gcctttttcc tcggttgatc gattgttaag

二、三、四、五、六、七、八、九、十、十一、十二、十三、十四、十五、十六、十七、十八、十九、二十、二十一、二十二、二十三、二十四、二十五、二十六、二十七、二十八、二十九、三十、三十一、三十二、三十三、三十四、三十五、三十六、三十七、三十八、三十九、四十、四十一、四十二、四十三、四十四、四十五、四十六、四十七、四十八、四十九、五十、五十一、五十二、五十三、五十四、五十五、五十六、五十七、五十八、五十九、六十、六十一、六十二、六十三、六十四、六十五、六十六、六十七、六十八、六十九、七十、七十一、七十二、七十三、七十四、七十五、七十六、七十七、七十八、七十九、八十、八十一、八十二、八十三、八十四、八十五、八十六、八十七、八十八、八十九、九十、九十一、九十二、九十三、九十四、九十五、九十六、九十七、九十八、九十九、一百

(i) SEQUENCE CHARACTERISTICS:

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ix) FEATURE:

(B) LOCATION: 1..257

SEQUENCE DESCRIPTION: SEQ ID NO:280:

[illegible]

20 25 30

35	40	45
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50 55 60

65 70 75 80

85 90 95

100 105 110

115 120 125

[illegible]

Set	City	Inc	Mid	Inc	Mid	Val	City	Inc	Inc	City	Inc	Mid	Mid	City	City
145					150					155					160

110 var the var Ala var Tyr Sin 110 var Sin Thr Ser var var Ala
165 170 175

180 185 190

11e Gly Ala Val Leu 11e 11e Ala Gly Leu Tyr 11e Val Leu Tyr Gly
195 300 305

Lys Ser Glu Glu Arg Lys Phe Ala Ala Leu Glu Lys Ala Glu Ile Gln
210 215 220

Ser Ser Ala Glu His Gly Ile Glu Arg Ala Pro Val Ser Arg Asn Ser

225		230		235		240
Ile	Lys	Ser	Ser	Ile	Thr	Thr
				Pro	Leu	Leu
		245		250		255
				His	Gln	Ser
				Thr	Asp	Asn

Val

(2) INFORMATION FOR SEQ ID NO:281:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 234 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..234
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566425

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:281:

Met	Leu	Thr	Leu	Gln	Phe	Gly	Tyr	Ala	Gly	Phe	His	Val	Val	Ser	Arg
1			5						10					15	
Ala	Ala	Leu	Asn	Met	Gly	Ile	Ser	Lys	Leu	Val	Phe	Pro	Val	Tyr	Arg
			20					25					30		
Asn	Ile	Ile	Ala	Leu	Leu	Leu	Leu	Pro	Phe	Ala	Tyr	Phe	Leu	Glu	
		35					40					45			
Lys	Lys	Glu	Arg	Pro	Ala	Ile	Thr	Leu	Asn	Phe	Leu	Ile	Gln	Phe	Phe
	50						55				60				
Phe	Leu	Ala	Leu	Ile	Gly	Ile	Thr	Ala	Arg	Leu	Ser	Val	Thr	Ser	Tyr
	65				70				75				80		
Thr	Cys	Phe	Phe	Gly	Ile	Ile	Gln	Phe	Leu	Ile	Ile	Ala	Ala	Phe	Cys
			85					90					95		
Glu	Arg	Asp	Ser	Gln	Ala	Trp	Val	Phe	His	Ser	Gly	Trp	Glu	Leu	Phe
			100					105					110		
Thr	Ile	Leu	Tyr	Ala	Gly	Ile	Val	Ala	Ser	Gly	Ile	Ala	Phe	Ala	Val
		115					120					125			
Gln	Ile	Trp	Cys	Ile	Asp	Arg	Gly	Gly	Pro	Val	Phe	Val	Ala	Val	Tyr
	130				135					140					
Gln	Pro	Val	Gln	Thr	Leu	Val	Val	Ala	Ile	Met	Ala	Ser	Ile	Ala	Leu
	145				150					155				160	
Gly	Glu	Glu	Phe	Tyr	Leu	Gly	Gly	Ile	Ile	Gly	Ala	Val	Leu	Ile	Ile
			165						170				175		
Ala	Gly	Leu	Tyr	Phe	Val	Leu	Tyr	Gly	Lys	Ser	Glu	Glu	Arg	Lys	Phe
			180					185					190		
Ala	Ala	Leu	Glu	Lys	Ala	Glu	Ile	Gln	Ser	Ser	Ala	Glu	His	Gly	Ile
		195				200						205			
Glu	Arg	Ala	Pro	Val	Ser	Arg	Asn	Ser	Ile	Lys	Ser	Ser	Ile	Thr	Thr
	210					215					220				
Pro	Leu	Leu	His	Gln	Ser	Thr	Asp	Asn	Val						
	225				230										

(2) INFORMATION FOR SEQ ID NO:282:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 214 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..214
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566426

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:282:

Met	Gly	Ile	Ser	Lys	Leu	Val	Phe	Pro	Val	Tyr	Arg	Asn	Ile	Ile	Ala
1			5						10				15		

Leu Leu Leu Leu Leu Pro Phe Ala Tyr Phe Leu Glu Lys Lys Glu Arg
20 25 30
Pro Ala Ile Thr Leu Asn Phe Leu Ile Gln Phe Phe Phe Leu Ala Leu
35 40 45
Ile Gly Ile Thr Ala Arg Leu Ser Val Thr Ser Tyr Thr Cys Phe Phe
50 55 60
Gly Ile Ile Gln Phe Leu Ile Ile Ala Ala Phe Cys Glu Arg Asp Ser
65 70 75 80
Gln Ala Trp Val Phe His Ser Gly Trp Glu Leu Phe Thr Ile Leu Tyr
85 90 95
Ala Gly Ile Val Ala Ser Gly Ile Ala Phe Ala Val Gln Ile Trp Cys
100 105 110
Ile Asp Arg Gly Gly Pro Val Phe Val Ala Val Tyr Gln Pro Val Gln
115 120 125
Thr Leu Val Val Ala Ile Met Ala Ser Ile Ala Leu Gly Glu Glu Phe
130 135 140
Tyr Leu Gly Gly Ile Ile Gly Ala Val Leu Ile Ile Ala Gly Leu Tyr
145 150 155 160
Phe Val Leu Tyr Gly Lys Ser Glu Glu Arg Lys Phe Ala Ala Leu Glu
165 170 175
Lys Ala Glu Ile Gln Ser Ser Ala Glu His Gly Ile Glu Arg Ala Pro
180 185 190
Val Ser Arg Asn Ser Ile Lys Ser Ser Ile Thr Thr Pro Leu Leu His
195 200 205
Gln Ser Thr Asp Asn Val
210

(2) INFORMATION FOR SEQ ID NO:283:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 604 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..604
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566443

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:283:

aattcgaaga	gagttcttagc	aaaacaaaac	aaaacagagc	aaacagagta	agtgaacacgA	60
tgtctctagt	tccgagcttt	tttgaggccc	gaagaacaaa	cgtgttcgac	ccattttcac	120
tagacgtatg	ggatccgttc	gaaggattct	tgacgccccc	gttgacaaaac	gcacctgccA	180
aggacgtgtg	agcggttcaca	aacgctaagg	tggactggag	ggagacacct	gaagcgcgatg	240
tgttcaaggg	ggacgtgcct	gggcttaaga	aggaagaggt	gaaggtggag	gttgaagatg	300
gtaacataact	tcagataagc	ggtgagagga	gcagtgagaa	tgaagagaag	agtgacacat	360
ggcaccgtgt	ggagcgggtca	agtggaagat	tcatgaggag	gtttaggttg	ccagacaagt	420
caaaagtgga	ggaagtaaa	gacgatatgg	agaatgggtg	gtgtcggtt	acggtgccga	480
aagttcagga	gagtaaacgg	gaggtcaagt	ccattgatat	ctctggttaa	gaggaaactct	540
gaagttggaa	agcttaagac	agtaatatgt	gatagtgtga	aataaatggt	gcgactttcc	600
ttcc						

(2) INFORMATION FOR SEQ ID NO:284:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 175 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..175
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566444

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:284:

Phe Glu Glu Ser Ser Ser Lys Thr Lys Gln Asn Arg Ala Asn Arg Val
1 5 10 15
Ser Glu Thr Met Ser Leu Val Pro Ser Phe Phe Gly Gly Arg Arg Thr
20 25 30
Asn Val Phe Asp Pro Phe Ser Leu Asp Val Trp Asp Pro Phe Glu Gly
35 40 45
Phe Leu Thr Pro Gly Leu Thr Asn Ala Pro Ala Lys Asp Val Ala Ala
50 55 60
Phe Thr Asn Ala Lys Val Asp Trp Arg Glu Thr Pro Glu Ala His Val
65 70 75 80
Phe Lys Ala Asp Val Pro Gly Leu Lys Lys Glu Glu Val Lys Val Glu
85 90 95
Val Glu Asp Gly Asn Ile Leu Gln Ile Ser Gly Glu Arg Ser Ser Glu
100 105 110
Asn Glu Glu Lys Ser Asp Thr Trp His Arg Val Glu Arg Ser Ser Gly
115 120 125
Lys Phe Met Arg Arg Phe Arg Leu Pro Asp Asn Ala Lys Val Glu Glu
130 135 140
Val Lys Ala Ser Met Glu Asn Gly Val Leu Ser Val Thr Val Pro Lys
145 150 155 160
Val Gln Glu Ser Lys Pro Glu Val Lys Ser Ile Asp Ile Ser Gly
165 170 175

(2) INFORMATION FOR SEQ ID NO:285:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 156 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..156

(D) OTHER INFORMATION: / Ceres Seq. ID 1566445

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:285:

Met Ser Leu Val Pro Ser Phe Phe Gly Gly Arg Arg Thr Asn Val Phe
1 5 10 15
Asp Pro Phe Ser Leu Asp Val Trp Asp Pro Phe Glu Gly Phe Leu Thr
20 25 30
Pro Gly Leu Thr Asn Ala Pro Ala Lys Asp Val Ala Ala Phe Thr Asn
35 40 45
Ala Lys Val Asp Trp Arg Glu Thr Pro Glu Ala His Val Phe Lys Ala
50 55 60
Asp Val Pro Gly Leu Lys Lys Glu Glu Val Lys Val Glu Val Glu Asp
65 70 75 80
Gly Asn Ile Leu Gln Ile Ser Gly Glu Arg Ser Ser Glu Asn Glu Glu
85 90 95
Lys Ser Asp Thr Trp His Arg Val Glu Arg Ser Ser Gly Lys Phe Met
100 105 110
Arg Arg Phe Arg Leu Pro Asp Asn Ala Lys Val Glu Glu Val Lys Ala
115 120 125
Ser Met Glu Asn Gly Val Leu Ser Val Thr Val Pro Lys Val Gln Glu
130 135 140
Ser Lys Pro Glu Val Lys Ser Ile Asp Ile Ser Gly
145 150 155

(2) INFORMATION FOR SEQ ID NO:286:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1325 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1325

(D) OTHER INFORMATION: / Ceres Seq. ID 1566453

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:286:

```
aaCttctccct cggatgcact attgtccgtg agatcagaga ttccacctct ttagatatttg      60
cgcagaaaact tttgccacaca attttgtttt ctacaaatct gagctgagat ctctagagtg      120
agaaaaatgag catcactaat gaagaagcag tgaagcaatt gcgtgcttta atggaagatg      180
ttgatgattc actcagagag tcgtatcgga acattcatca agggatattccg acagagaatt      240
tgttactgctt tcttaaagcc agggatggga atgtccagaa agctcataaa attgttgctcg      300
gtgtgtttgga atggaggagt caaaacgaga ttgacaagat actaactaaa cccattgttc      360
ctgttgacct gtacagagaga atcagagaca cacaacttgt cgggtgtgct ggttactcta      420
aagaggggtct cccgtgctatt gccattggtg tggggccttag cacatatgat aaagcctccg      480
ttcactacta tgtacagtct cacattcaaa tgaatgagta ccgggatcgt gttgtattgc      540
catctgcttc aaagaaacag ggacgaccaa ttgacacttg ttggaaaatt ttggatatgt      600
ctggttttaaa gcttttcagct ttaagtcaaa ttaagttaat gactgctata acaacaatag      660
atgatttgaa ctatccagag aagacagaga catactatgt tgtcaatgtc ccgtacatat      720
tcctcgtgct ttggaaaacc ataaagcctc tgttgcaaga gagaacaaag aagaagatc      780
aagttctgaa aggttgccgg aaagatgagt tgctaaagat aatggactat gactctctcc      840
cacatttctg tagaagagaa gggctctggat ctggtaggca tatctcaaat ggaacagtag      900
acaattgttt ctctctggat cactctttcc accaagacct ttatgattat gtcaaagcagc      960
agggctctggt taaaggatca ggtgcaccga tcagacatgg ttccagtcac gttaatgttc      1020
ctgagccaag caccgaagcg aacaagatct tgcatacctt agaaaatgag ttccagaagc      1080
ttggaatatga ccagaagatc tgagtgatct acaaccctta taacacgaat tgcccataag      1140
aaaccggaaat ttgtctctgg ttgatgagca gtatttaaga taagaatcaa tcacctttac      1200
ttgtattact agtttctgct gcatacgtc gatgcaggtt ttttttaaaa agaagatgga      1260
acacaatttc ctccgaatg atcttttgat ctagtaccat tatatatata gaactcattt      1320
ctatc
```

(2) INFORMATION FOR SEQ ID NO:287:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 325 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..325

(D) OTHER INFORMATION: / Ceres Seq. ID 1566454

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:287:

```
Met Ser Ile Thr Asn Glu Glu Ala Val Lys Gln Leu Arg Ala Leu Met
1 5 10 15
Glu Asp Val Asp Ser Leu Arg Glu Ser Tyr Arg Asn Ile His Gln
20 25 30
Gly Tyr Pro Thr Glu Asn Leu Leu Arg Phe Leu Lys Ala Arg Asp Gly
35 40 45
Asn Val Gln Lys Ala His Lys Met Leu Leu Glu Cys Leu Glu Trp Arg
50 55 60
Thr Gln Asn Glu Ile Asp Lys Ile Leu Thr Lys Pro Ile Val Pro Val
65 70 75 80
Asp Leu Tyr Arg Gly Ile Arg Asp Thr Gln Leu Val Gly Val Ser Gly
85 90 95
Tyr Ser Lys Glu Gly Leu Pro Val Ile Ala Ile Gly Val Gly Leu Ser
100 105 110
Thr Tyr Asp Lys Ala Ser Val His Tyr Tyr Val Gln Ser His Ile Gln
115 120 125
Met Asn Glu Tyr Arg Asp Arg Val Val Leu Pro Ser Ala Ser Lys Lys
130 135 140
Gln Gly Arg Pro Ile Cys Thr Cys Leu Lys Ile Leu Asp Met Ser Gly
145 150 155 160
Leu Lys Leu Ser Ala Leu Ser Gln Ile Lys Leu Met Thr Ala Ile Thr
```

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(2) INFORMATION FOR SEQ ID NO:288:
  (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 310 amino acids
      (B) TYPE: amino acid
      (C) STRANDEDNESS:
      (D) TOPOLOGY: linear
  (ii) MOLECULE TYPE: peptide
  (ix) FEATURE:
      (A) NAME/KEY: peptide
      (B) LOCATION: 1..310
      (D) OTHER INFORMATION: / Ceres Seq. ID 1566455
  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:288:
Met Glu Asp Val Asp Asp Ser Leu Arg Glu Ser Tyr Arg Asn Ile His
1      5      10      15
Gln Gly Tyr Pro Thr Glu Asn Leu Leu Arg Phe Leu Cys Ala Arg Asp
      20      25
Gly Asn Val Gln Lys Ala His Lys Met Leu Leu Glu Cys Leu Glu Trp
      35      40      45
Arg Thr Gln Asn Glu Ile Asp Lys Ile Leu Thr Lys Pro Ile Val Pro
      50      55      60
Val Asp Leu Tyr Arg Gly Ile Arg Asp Thr Gln Leu Val Gly Val Ser
      65      70      75      80
Gly Tyr Ser Lys Glu Gly Leu Pro Val Ile Ala Ile Gly Val Gly Leu
      85      90      95
Ser Thr Tyr Asp Lys Ala Ser Val His Tyr Tyr Val Gln Ser His Ile
      100      105      110
Gln Met Asn Glu Tyr Arg Asp Arg Val Val Leu Pro Ser Ala Ser Lys
      115      120      125
Lys Gln Gly Arg Pro Ile Cys Thr Cys Leu Lys Ile Leu Asp Met Ser
      130      135      140
Gly Leu Lys Leu Ser Ala Leu Ser Gln Ile Lys Leu Met Thr Ala Ile
      145      150      155      160
Thr Thr Ile Asp Asp Leu Asn Tyr Pro Glu Lys Thr Glu Thr Tyr Tyr
      165      170      175
Val Val Asn Val Pro Tyr Ile Phe Ser Ala Cys Trp Lys Thr Ile Lys
      180      185      190
Pro Leu Leu Gln Glu Arg Thr Lys Lys Lys Ile Gln Val Leu Lys Gly
      195      200      205
Cys Gly Lys Asp Glu Leu Leu Lys Ile Met Asp Tyr Glu Ser Leu Pro
      210      215      220

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His Phe Cys Arg Arg Glu Gly Ser Gly Ser Gly Arg His Ile Ser Asn
225 230 235 240
Gly Thr Val Asp Asn Cys Phe Ser Leu Asp His Ser Phe His Gln Asp
245 250 255
Leu Tyr Asp Tyr Val Lys Gln Gln Ala Leu Val Lys Gly Ser Gly Ala
260 265 270
Pro Ile Arg His Gly Ser Val His Val Lys Phe Pro Glu Pro Asp Thr
275 280 285
Glu Gly Asn Lys Ile Phe Asp Thr Leu Glu Asn Glu Phe Gln Lys Leu
290 295 300
Gly Asn Asp Gln Lys Ile
305 310

(2) INFORMATION FOR SEQ ID NO:289:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 270 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..270
(D) OTHER INFORMATION: / Ceres Seq. ID 1566456

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:289:

Met Leu Leu Glu Cys Leu Glu Trp Arg Thr Gln Asn Glu Ile Asp Lys
1 5 10 15
Ile Leu Thr Lys Pro Ile Val Pro Val Asp Leu Tyr Arg Gly Ile Arg
20 25 30
Asp Thr Gln Leu Val Gly Val Ser Gly Tyr Ser Lys Glu Gly Leu Pro
35 40 45
Val Ile Ala Ile Gly Val Gly Leu Ser Thr Tyr Asp Lys Ala Ser Val
50 55 60
His Tyr Tyr Val Gln Ser His Ile Gln Met Asn Glu Tyr Arg Asp Arg
65 70 75 80
Val Val Leu Pro Ser Ala Ser Lys Lys Gln Gly Arg Pro Ile Cys Thr
85 90 95
Cys Leu Lys Ile Leu Asp Met Ser Gly Leu Lys Leu Ser Ala Leu Ser
100 105 110
Gln Ile Lys Leu Met Thr Ala Ile Thr Thr Ile Asp Asp Leu Asn Tyr
115 120 125
Pro Glu Lys Thr Glu Thr Tyr Tyr Val Val Asn Val Pro Tyr Ile Phe
130 135 140
Ser Ala Cys Trp Lys Thr Ile Lys Pro Leu Leu Gln Glu Arg Thr Lys
145 150 155 160
Lys Lys Ile Gln Val Leu Lys Gly Cys Gly Lys Asp Glu Leu Leu Lys
165 170 175
Ile Met Asp Tyr Glu Ser Leu Pro His Phe Cys Arg Arg Glu Gly Ser
180 185 190
Gly Ser Gly Arg His Ile Ser Asn Gly Thr Val Asp Asn Cys Phe Ser
195 200 205
Leu Asp His Ser Phe His Gln Asp Leu Tyr Asp Tyr Val Lys Gln Gln
210 215 220
Ala Leu Val Lys Gly Ser Gly Ala Pro Ile Arg His Gly Ser Val His
225 230 235 240
Val Lys Phe Pro Glu Pro Asp Thr Glu Gly Asn Lys Ile Phe Asp Thr
245 250 255
Leu Glu Asn Glu Phe Gln Lys Leu Gly Asn Asp Gln Lys Ile
260 265 270

(2) INFORMATION FOR SEQ ID NO:290:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1767 base pairs

- (B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..1767
(D) OTHER INFORMATION: / Ceres Seq. ID 1566468

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:290:

catcttttct	ttctccctct	gctcttgtgc	aacttgatcc	gtcgtcttct	ctcagctctc	60
cactctccgtc	ttccaaggtg	gaagaatcca	gtgcgattta	cgctcgctgc	cgaCGgNctc	120
tcggcgaggaa	caactgtgac	ggcgctgogt	tatgccacct	ctctgagatc	ttattcgacc	180
tcgtttTagg	gaggagaggg	acaccttcgg	gccgattcaa	gttctctccg	ataaattgtg	240
gggagcccg	acgcagagat	cgctgcagaa	cttcgaaatc	ggttggtgag	gcgagCGaNa	300
tgccctgaacc	aattgtccgc	gcttttggcg	tcttgaagaa	atgcgctgcg	aaggttaaca	360
tggaatccgg	tcttgatccg	acgattggga	aagcaattat	gcaagctgct	caggaagtag	420
ctgaggggaaa	gctcaatgat	catttccccc	ttgttgtctg	gcaaaactggt	agtgtgtactc	480
agagtataat	gaatgctaatt	gaggtcattg	ctaatagagc	agctgagatt	cttggctgcga	540
aacgtgtgga	gaaatgtgtg	cacccaagt	accatgtgaa	cagatcacaa	tcttctaaccg	600
acacttttcc	taccgtcatg	cacattgcag	ctgcaaccga	gattaattgc	aggctcatcc	660
ctagtttttaa	aactttgcat	agcactttgg	aatctaagtc	cttcgagttc	aaagatattg	720
tgaataattgg	aagaaactcac	actcaaatgt	ctacaccttt	gacactagga	caagaatttg	780
gtgcttatgc	tactcaagtt	aagtatggac	taaatagagt	cacctgcaact	cttcctgcgc	840
tctatcagct	tgacacaagt	ggaactgcgg	ttgggacagg	attaaacact	aagaaaaggtg	900
ttgatgtaaa	gatatgctgt	gcagtagctg	aagaaacaaa	cttgccattc	gtcactgcag	960
aaaaacaagt	tgaagctctg	gctgcacacg	atgctttgtg	tgaaaccagt	gggtcactta	1020
acacaatcgc	cacatcgctg	atgaagatcg	ccaatgatat	agcttttctt	ggaagtggcc	1080
caagatgtgg	tcttggtgaa	cttgtactac	ctgaaaatga	gccagggaagc	agtatcatgc	1140
ctgggaaggt	aaatcctaca	cagtgtagag	ccttgactat	ggtttgtgca	caggttatgg	1200
gaacacatgt	agctgtgaca	gttggtgggt	caaatgggtc	ttctgagatc	aagtattatc	1260
agccggtagt	cgcgagtgtc	ctttttacatt	cogtcaagatt	aatagcagat	gcttcagctt	1320
cgttcgagaa	aaactgtgtg	aggggcattg	agggccaacg	agaaagaaac	tcaaaagctat	1380
tgcaacgagtc	tcttatgctt	gtgacatcat	tgaatccgaa	aatcggtgat	gacaatgctg	1440
cagcagttgc	caagaaagct	cacaaagaag	gatgtacatt	gaagggaagc	gctctgaatt	1500
taggcgtgct	tactgcggaa	gagtttgata	ctctgttgtt	tcttgagaag	atgatgtgtc	1560
cttcgcgattg	atagtgtgtt	ttggagccaa	agcttcaagt	accattatcc	tcttgatgct	1620
tttatttagg	ttataataaa	aatgagcaaa	tccagaaaca	attcaaat	tcttgggagg	1680
gcaacattgt	tcttcatctt	acggctaaac	tatgatcttc	tttatgtatc	aatttttttt	1740

(2) INFORMATION FOR SEQ ID NO:291:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 522 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..522
(D) OTHER INFORMATION: / Ceres Seq. ID 1566469

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:291:

Ile	Phe	Leu	Ser	Pro	Ser	Ala	Leu	Val	Gln	Leu	Asp	Pro	Ser	Ser	Ser
1				5				10				15			
Leu	Ser	Ser	Pro	Ser	Pro	Ser	Ser	Lys	Val	Glu	Glu	Ser	Met	Ser	Ile
				20				25				30			
Tyr	Val	Ala	Ser	Arg	Arg	Xaa	Leu	Arg	Arg	Asn	Asn	Cys	Asp	Gly	Ala
				35				40				45			
Ala	Leu	Cys	His	Leu	Ser	Glu	Ile	Leu	Phe	Asp	Leu	Val	Leu	Gly	Arg
				50				55				60			
Arg	Gly	Thr	Pro	Ser	Gly	Arg	Phe	Lys	Phe	Leu	Pro	Ile	Asn	Cys	Gly
65				70				75				80			

Glu	Pro	Arg	Arg	Arg	Asp	Arg	Cys	Arg	Thr	Ser	Lys	Ser	Val	Val	Ser
				85					90					95	
Ala	Ser	Xaa	Met	Pro	Glu	Pro	Ile	Val	Arg	Ala	Phe	Gly	Val	Leu	Lys
			100					105					110		
Lys	Cys	Ala	Ala	Lys	Val	Asn	Met	Glu	Tyr	Gly	Leu	Asp	Pro	Thr	Ile
		115					120					125			
Gly	Lys	Ala	Ile	Met	Gln	Ala	Ala	Gln	Glu	Val	Ala	Glu	Gly	Lys	Leu
		130				135					140				
Asn	Asp	His	Phe	Pro	Leu	Val	Val	Trp	Gln	Thr	Gly	Ser	Gly	Thr	Gln
145				150					155					160	
Ser	Asn	Met	Asn	Ala	Asn	Glu	Val	Ile	Ala	Asn	Arg	Ala	Ala	Glu	Ile
			165						170					175	
Leu	Gly	Arg	Lys	Arg	Gly	Glu	Lys	Cys	Val	His	Pro	Asn	Asp	His	Val
			180						185					190	
Asn	Arg	Ser	Gln	Ser	Ser	Asn	Asp	Thr	Phe	Pro	Thr	Val	Met	His	Ile
			195				200					205			
Ala	Ala	Ala	Thr	Glu	Ile	Asn	Ser	Arg	Leu	Ile	Pro	Ser	Leu	Lys	Thr
			210			215					220				
Leu	His	Ser	Thr	Leu	Glu	Ser	Lys	Ser	Phe	Glu	Phe	Lys	Asp	Ile	Val
225				230					235					240	
Lys	Ile	Gly	Arg	Thr	His	Thr	Gln	Asp	Ala	Thr	Pro	Leu	Thr	Leu	Gly
			245						250					255	
Gln	Glu	Phe	Gly	Gly	Tyr	Ala	Thr	Gln	Val	Lys	Tyr	Gly	Leu	Asn	Arg
			260					265					270		
Val	Thr	Cys	Thr	Leu	Pro	Arg	Leu	Tyr	Gln	Leu	Ala	Gln	Gly	Gly	Thr
		275					280					285			
Ala	Val	Gly	Thr	Gly	Leu	Asn	Thr	Lys	Lys	Gly	Phe	Asp	Val	Lys	Ile
			290			295					300				
Ala	Ala	Ala	Val	Ala	Glu	Glu	Thr	Asn	Leu	Pro	Phe	Val	Thr	Ala	Glu
305				310					315					320	
Asn	Lys	Phe	Glu	Ala	Leu	Ala	Ala	His	Asp	Ala	Cys	Val	Glu	Thr	Ser
			325						330					335	
Gly	Ser	Leu	Asn	Thr	Ile	Ala	Thr	Ser	Leu	Met	Lys	Ile	Ala	Asn	Asp
			340					345					350		
Ile	Arg	Phe	Leu	Gly	Ser	Gly	Pro	Arg	Cys	Gly	Leu	Gly	Glu	Leu	Val
		355					360					365			
Leu	Pro	Glu	Asn	Glu	Pro	Gly	Ser	Ser	Ile	Met	Pro	Gly	Lys	Val	Asn
			370			375					380				
Pro	Thr	Gln	Cys	Glu	Ala	Leu	Thr	Met	Val	Cys	Ala	Gln	Val	Met	Gly
385				390						395				400	
Asn	His	Val	Ala	Val	Thr	Val	Gly	Gly	Ser	Asn	Gly	His	Phe	Glu	Leu
			405					410						415	
Asn	Val	Phe	Lys	Pro	Val	Ile	Ala	Ser	Ala	Leu	Leu	His	Ser	Val	Arg
			420					425				430			
Leu	Ile	Ala	Asp	Ala	Ser	Ala	Ser	Phe	Glu	Lys	Asn	Cys	Val	Arg	Gly
		435					440					445			
Ile	Glu	Ala	Asn	Arg	Glu	Arg	Ile	Ser	Lys	Leu	Leu	His	Glu	Ser	Leu
450				455							460				
Met	Leu	Val	Thr	Ser	Leu	Asn	Pro	Lys	Ile	Gly	Tyr	Asp	Asn	Ala	Ala
465				470					475					480	
Ala	Val	Ala	Lys	Lys	Ala	His	Lys	Glu	Gly	Cys	Thr	Leu	Lys	Glu	Ala
			485						490					495	
Ala	Leu	Asn	Leu	Gly	Val	Leu	Thr	Ala	Glu	Glu	Phe	Asp	Thr	Leu	Val
			500					505						510	
Val	Pro	Glu	Lys	Met	Ile	Gly	Pro	Ser	Asp						
			515				520								

(2) INFORMATION FOR SEQ ID NO:292:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 493 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:

- (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..493
 (D) OTHER INFORMATION: / Ceres Seq. ID 1566470
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:292:

Met	Ser	Ile	Tyr	Val	Ala	Ser	Arg	Arg	Xaa	Leu	Arg	Arg	Asn	Asn	Cys
1				5					10					15	
Asp	Gly	Ala	Ala	Leu	Cys	His	Leu	Ser	Glu	Ile	Leu	Phe	Asp	Leu	Val
		20						25					30		
Leu	Gly	Arg	Arg	Gly	Thr	Pro	Ser	Gly	Arg	Phe	Lys	Phe	Leu	Pro	Ile
		35					40					45			
Asn	Cys	Gly	Glu	Pro	Arg	Arg	Arg	Asp	Arg	Cys	Arg	Thr	Ser	Lys	Ser
		50				55					60				
Val	Val	Ser	Ala	Ser	Xaa	Met	Pro	Glu	Pro	Ile	Val	Arg	Ala	Phe	Gly
65					70					75					80
Val	Leu	Lys	Lys	Cys	Ala	Ala	Lys	Val	Asn	Met	Glu	Tyr	Gly	Leu	Asp
				85					90					95	
Pro	Thr	Ile	Gly	Lys	Ala	Ile	Met	Gln	Ala	Ala	Gln	Glu	Val	Ala	Glu
			100					105					110		
Gly	Lys	Leu	Asn	Asp	His	Phe	Pro	Leu	Val	Val	Trp	Gln	Thr	Gly	Ser
		115					120					125			
Gly	Thr	Gln	Ser	Asn	Met	Asn	Ala	Asn	Glu	Val	Ile	Ala	Asn	Arg	Ala
		130				135					140				
Ala	Glu	Ile	Leu	Gly	Arg	Lys	Arg	Gly	Glu	Lys	Cys	Val	His	Pro	Asn
145					150					155					160
Asp	His	Val	Asn	Arg	Ser	Gln	Ser	Ser	Asn	Asp	Thr	Phe	Pro	Thr	Val
			165						170					175	
Met	His	Ile	Ala	Ala	Ala	Thr	Glu	Ile	Asn	Ser	Arg	Leu	Ile	Pro	Ser
			180					185					190		
Leu	Lys	Thr	Leu	His	Ser	Thr	Leu	Glu	Ser	Lys	Ser	Phe	Glu	Phe	Lys
		195					200					205			
Asp	Ile	Val	Lys	Ile	Gly	Arg	Thr	His	Thr	Gln	Asp	Ala	Thr	Pro	Leu
		210				215					220				
Thr	Leu	Gly	Gln	Glu	Phe	Gly	Gly	Tyr	Ala	Thr	Gln	Val	Lys	Tyr	Gly
225					230				235					240	
Leu	Asn	Arg	Val	Thr	Cys	Thr	Leu	Pro	Arg	Leu	Tyr	Gln	Leu	Ala	Gln
			245						250					255	
Gly	Gly	Thr	Ala	Val	Gly	Thr	Gly	Leu	Asn	Thr	Lys	Lys	Gly	Phe	Asp
			260					265					270		
Val	Lys	Ile	Ala	Ala	Ala	Val	Ala	Glu	Glu	Thr	Asn	Leu	Pro	Phe	Val
		275					280					285			
Thr	Ala	Glu	Asn	Lys	Phe	Glu	Ala	Leu	Ala	Ala	His	Asp	Ala	Cys	Val
		290				295					300				
Glu	Thr	Ser	Gly	Ser	Leu	Asn	Thr	Ile	Ala	Thr	Ser	Leu	Met	Lys	Ile
305					310					315				320	
Ala	Asn	Asp	Ile	Arg	Phe	Leu	Gly	Ser	Gly	Pro	Arg	Cys	Gly	Leu	Gly
			325						330					335	
Glu	Leu	Val	Leu	Pro	Glu	Asn	Glu	Pro	Gly	Ser	Ser	Ile	Met	Pro	Gly
			340					345					350		
Lys	Val	Asn	Pro	Thr	Gln	Cys	Glu	Ala	Leu	Thr	Met	Val	Cys	Ala	Gln
			355					360					365		
Val	Met	Gly	Asn	His	Val	Ala	Val	Thr	Val	Gly	Gly	Ser	Asn	Gly	His
			370			375					380				
Phe	Glu	Leu	Asn	Val	Phe	Lys	Pro	Val	Ile	Ala	Ser	Ala	Leu	Leu	His
385					390					395				400	
Ser	Val	Arg	Leu	Ile	Ala	Asp	Ala	Ser	Ala	Ser	Phe	Glu	Lys	Asn	Cys
			405					410						415	
Val	Arg	Gly	Ile	Glu	Ala	Asn	Arg	Glu	Arg	Ile	Ser	Lys	Leu	Leu	His
			420				425						430		

Glu	Ser	Leu	Met	Leu	Val	Thr	Ser	Leu	Asn	Pro	Lys	Ile	Gly	Tyr	Asp	
	435						440					445				
Asn	Ala	Ala	Ala	Val	Ala	Lys	Lys	Ala	His	Lys	Glu	Gly	Cys	Thr	Leu	
	450					455					460					
Lys	Glu	Ala	Ala	Leu	Asn	Leu	Gly	Val	Leu	Thr	Ala	Glu	Glu	Phe	Asp	
465				470					475						480	
Thr	Leu	Val	Val	Pro	Glu	Lys	Met	Ile	Gly	Pro	Ser	Asp				
				485				490								

(2) INFORMATION FOR SEQ ID NO:293:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 423 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..423

(D) OTHER INFORMATION: / Ceres Seq. ID 1566471

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:293:

Met	Pro	Glu	Pro	Ile	Val	Arg	Ala	Phe	Gly	Val	Leu	Lys	Lys	Cys	Ala	
1			5						10					15		
Ala	Lys	Val	Asn	Met	Glu	Tyr	Gly	Leu	Asp	Pro	Thr	Ile	Gly	Lys	Ala	
		20					25						30			
Ile	Met	Gln	Ala	Ala	Gln	Glu	Val	Ala	Glu	Gly	Lys	Leu	Asn	Asp	His	
		35				40					45					
Phe	Pro	Leu	Val	Val	Trp	Gln	Thr	Gly	Ser	Gly	Thr	Gln	Ser	Asn	Met	
	50				55					60						
Asn	Ala	Asn	Glu	Val	Ile	Ala	Asn	Arg	Ala	Ala	Glu	Ile	Leu	Gly	Arg	
65				70				75						80		
Lys	Arg	Gly	Glu	Lys	Cys	Val	His	Pro	Asn	Asp	His	Val	Asn	Arg	Ser	
				85				90					95			
Gln	Ser	Ser	Asn	Asp	Thr	Phe	Pro	Thr	Val	Met	His	Ile	Ala	Ala	Ala	
			100					105				110				
Thr	Glu	Ile	Asn	Ser	Arg	Leu	Ile	Pro	Ser	Leu	Lys	Thr	Leu	His	Ser	
	115				120						125					
Thr	Leu	Glu	Ser	Lys	Ser	Phe	Glu	Phe	Lys	Asp	Ile	Val	Lys	Ile	Gly	
	130				135					140						
Arg	Thr	His	Thr	Gln	Asp	Ala	Thr	Pro	Leu	Thr	Leu	Gly	Gln	Glu	Phe	
145				150					155					160		
Gly	Gly	Tyr	Ala	Thr	Gln	Val	Lys	Tyr	Gly	Leu	Asn	Arg	Val	Thr	Cys	
			165					170					175			
Thr	Leu	Pro	Arg	Leu	Tyr	Gln	Leu	Ala	Gln	Gly	Gly	Thr	Ala	Val	Gly	
	180						185					190				
Thr	Gly	Leu	Asn	Thr	Lys	Lys	Gly	Phe	Asp	Val	Lys	Ile	Ala	Ala	Ala	
	195				200						205					
Val	Ala	Glu	Glu	Thr	Asn	Leu	Pro	Phe	Val	Thr	Ala	Glu	Asn	Lys	Phe	
	210				215					220						
Glu	Ala	Leu	Ala	Ala	His	Asp	Ala	Cys	Val	Glu	Thr	Ser	Gly	Ser	Leu	
225					230					235					240	
Asn	Thr	Ile	Ala	Thr	Ser	Leu	Met	Lys	Ile	Ala	Asn	Asp	Ile	Arg	Phe	
			245					250					255			
Leu	Gly	Ser	Gly	Pro	Arg	Cys	Gly	Leu	Gly	Glu	Leu	Val	Leu	Pro	Glu	
	260						265					270				
Asn	Glu	Pro	Gly	Ser	Ser	Ile	Met	Pro	Gly	Lys	Val	Asn	Pro	Thr	Gln	
	275					280						285				
Cys	Glu	Ala	Leu	Thr	Met	Val	Cys	Ala	Gln	Val	Met	Gly	Asn	His	Val	
290					295						300					
Ala	Val	Thr	Val	Gly	Gly	Ser	Asn	Gly	His	Phe	Glu	Leu	Asn	Val	Phe	
305					310					315						
Lys	Pro	Val	Ile	Ala	Ser	Ala	Leu	Leu	His	Ser	Val	Arg	Leu	Ile	Ala	

325 330 335
Asp Ala Ser Ala Ser Phe Glu Lys Asn Cys Val Arg Gly Ile Glu Ala
340 345 350
Asn Arg Glu Arg Ile Ser Lys Leu Leu His Glu Ser Leu Met Leu Val
355 360 365
Thr Ser Leu Asn Pro Lys Ile Gly Tyr Asp Asn Ala Ala Val Ala
370 375 380
Lys Lys Ala His Lys Glu Gly Cys Thr Leu Lys Glu Ala Ala Leu Asn
385 390 395 400
Leu Gly Val Leu Thr Ala Glu Glu Phe Asp Thr Leu Val Val Pro Glu
405 410 415
Lys Met Ile Gly Pro Ser Asp
420

(2) INFORMATION FOR SEQ ID NO:294:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1106 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1106
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566505

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:294:

aacaattcag	atttcaattt	ctcaaaatct	taaaaacttt	ctctcaattc	tctctacogt	60
gatcaagatg	cagatctttg	ttaagactct	cacccgaaag	acaatcaccc	togagggtgga	120
aagctccgac	accatcgaca	acgttaaggc	caagatccag	gataaggagg	gcattctctcc	180
ggatcgcagc	aggcttattt	tgcgcggcaa	gcagctagag	gatggccgta	cgttggctgta	240
ttacaatatc	cagaaggaat	ccaccctcca	cttggtcctc	aggctccgtg	gtgggtatgca	300
gattttcggt	aaaaccctaa	cgggaaagac	gattactctt	gaggtggaga	gttctgacac	360
catcgacaac	gtcaaaggcca	agatccaaga	caaaaggagt	attcctccgg	accagcagag	420
gctgatcttc	gccggaaagc	agttggagga	tggcagaact	cttGgctgac	tacaayatyc	480
agaaggagtc	cacmcttcA	cttgkctTG	cAgkctscgt	gwggtatgc	agatytttgt	540
kaagactctc	acyggaaaaga	ccatcacttt	ggaggtggag	agttctgaca	ccattgataa	600
cgtgaaagcc	aagatccagg	acaaagaggg	tatycctccg	taccacagca	gattgatctt	660
cgccggaaag	caacttgarg	atgghagaac	tttggcbgac	tacaacattc	agaaggagtc	720
cacmcttcac	ttggtcttgc	gtctgcgtgg	aggatgacag	attcttgtsa	agactytbac	780
cggaagagacy	atcacyytkg	argtrgarag	ctcygacacc	attgacaacg	tcaaggccaa	840
gatccaggac	aaggaaggtta	tctctccgga	ccagcagcgt	ctcatcttgg	ctggaaagca	900
gcttgaggat	ggagctactt	tggccgacta	caacatccag	aaggagctcta	ctcttcaactt	960
ggctcctgct	cttcgttggtg	gttttcaaat	ctcgtctctg	ttatgcttaa	gaagttcaat	1020
gtttcggttt	atgtaaaact	ttgggtggtt	gtgttttggg	gcctgtgata	atccctgatg	1080
aataagtggt	ctactatggt	tccggt				

(2) INFORMATION FOR SEQ ID NO:295:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 155 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..155
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566506

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:295:

Thr	Ile	Gln	Ile	Ser	Ile	Ser	Gln	Asn	Leu	Lys	Asn	Phe	Leu	Ser	Ile	
1			5					10				15				
Leu	Ser	Thr	Val	Ile	Lys	Met	Gln	Ile	Phe	Val	Lys	Thr	Leu	Thr	Gly	
			20					25				30				
Lys	Thr	Ile	Thr	Leu	Glu	Val	Glu	Ser	Ser	Asp	Thr	Ile	Asp	Asn	Val	

35 40 45
Lys Ala Lys Ile Gln Asp Lys Glu Gly Ile Pro Pro Asp Gln Gln Arg
50 55 60
Leu Ile Phe Ala Gly Lys Gln Leu Glu Asp Gly Arg Thr Leu Ala Asp
65 70 75 80
Tyr Asn Ile Gln Lys Glu Ser Thr Leu His Leu Val Leu Arg Leu Arg
85 90 95
Gly Gly Met Gln Ile Phe Val Lys Thr Leu Thr Gly Lys Thr Ile Thr
100 105 110
Leu Glu Val Glu Ser Ser Asp Thr Ile Asp Asn Val Lys Ala Lys Ile
115 120 125
Gln Asp Lys Glu Gly Ile Pro Pro Asp Gln Gln Arg Leu Ile Phe Ala
130 135 140
Gly Lys Gln Leu Glu Asp Gly Arg Thr Leu Gly
145 150 155

(2) INFORMATION FOR SEQ ID NO:296:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 133 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..133

(D) OTHER INFORMATION: / Ceres Seq. ID 1566507
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:296:

Met Gln Ile Phe Val Lys Thr Leu Thr Gly Lys Thr Ile Thr Leu Glu
1 5 10 15
Val Glu Ser Ser Asp Thr Ile Asp Asn Val Lys Ala Lys Ile Gln Asp
20 25 30
Lys Glu Gly Ile Pro Pro Asp Gln Gln Arg Leu Ile Phe Ala Gly Lys
35 40 45
Gln Leu Glu Asp Gly Arg Thr Leu Ala Asp Tyr Asn Ile Gln Lys Glu
50 55 60
Ser Thr Leu His Leu Val Leu Arg Leu Arg Gly Met Gln Ile Phe
65 70 75 80
Val Lys Thr Leu Thr Gly Lys Thr Ile Thr Leu Glu Val Glu Ser Ser
85 90 95
Asp Thr Ile Asp Asn Val Lys Ala Lys Ile Gln Asp Lys Glu Gly Ile
100 105 110
Pro Pro Asp Gln Gln Arg Leu Ile Phe Ala Gly Lys Gln Leu Glu Asp
115 120 125
Gly Arg Thr Leu Gly
130

(2) INFORMATION FOR SEQ ID NO:297:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 153 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..153

(D) OTHER INFORMATION: / Ceres Seq. ID 1566508
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:297:

Met Gln Xaa Phe Xaa Lys Thr Leu Xaa Gly Lys Thr Ile Thr Leu Glu
1 5 10 15
Val Glu Ser Ser Asp Thr Ile Asp Asn Val Lys Ala Lys Ile Gln Asp
20 25 30

```

Lys Glu Gly Xaa Pro Pro Asp Gln Gln Arg Leu Ile Phe Ala Gly Lys
      35              40              45
Gln Leu Xaa Asp Xaa Arg Thr Leu Xaa Asp Tyr Asn Ile Gln Lys Glu
      50              55              60
Ser Xaa Leu His Leu Val Leu Arg Leu Arg Gly Met Gln Ile Phe
      65              70              75              80
Xaa Lys Thr Xaa Thr Gly Lys Xaa Ile Xaa Xaa Xaa Xaa Ser Xaa
      85              90              95
Asp Thr Ile Asp Asn Val Lys Ala Lys Ile Gln Asp Lys Glu Gly Ile
      100             105             110
Pro Pro Asp Gln Gln Arg Leu Ile Phe Ala Gly Lys Gln Leu Glu Asp
      115             120             125
Gly Arg Thr Leu Ala Asp Tyr Asn Ile Gln Lys Glu Ser Thr Leu His
      130             135             140
Leu Val Leu Arg Leu Arg Gly Gly Phe
      145             150

```

(2) INFORMATION FOR SEQ ID NO:298:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1217 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1217
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566517

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:298:

```

atcttatctc aactctcaaa atcatcttct tcacccaaaa acccctaataa gcottatccc      60
ttcttctctc catgctgtct tcagctctct tctcgtctct tcttctctca accctaataac      120
tcttctctct ggcgtctcca gacctgcctc cgtttccctc ttatctcctt cctctctcctt      180
taaaactcaat tccgactccg ttctctctc catcgccgcc aatgggaact ctcccgtctc      240
tcgcttcgtc cgtaacgttg cgattacctc agagttcgag gtggaagaag atggtttcgc      300
tgacgtcgtc cgcacaaaag agcaatcttt ctctgctgac cttaaaactct tcgtttggtaa      360
ctctctcttc aacgttgaca gtgctcagct cgctcagctc ttgagagtg ccggaatagt      420
tgagatggtt gaggtaatct atgacaaaat tacaggaaga agcagaggtt ttgattcgt      480
gactatgtct tcagtttctg aagttgaggc agctgctcag cagttcaatg gctatgagtt      540
ggatggtaga cctttgagag tcaatgctgg tccccaccca ccaagagggg aagatgggtt      600
ctccagagga ctaggagca gctttggaag ctacaggttct ggataggag gaggtgggtg      660
ttctggtgct ggttcaggaa accgtgttta tgtgggtaac ctctcttggg gagttgatga      720
catggctctt gagagtttgt tctcggagca agaaaaggtt gttgaggcca gactcatcta      780
cgacagggac agtggctgat ccaaggggtt tggatttgt acatacgact ctctccaaga      840
ggtcacaaat gccatcaagt ccttggatgg tgctgatttg gacggtagac aaatagagt      900
ctcggaagct gaggctaggg ctccaaggcg ccaatatgga gcaccaatct atgacttctc      960
attctcaaaa acgcatattc tggagggcgc ttogaagtaa agagggtttg tgagatgatg      1020
gcagtttcag acggtactcaa gctcttagct tcgcctatgt ttgttcgctt ggatgcaaga      1080
aggtcgtaaa ggaatggctt tttttttttt gagaacogta taattaagat agaactgga      1140
gagaccatgt tcttgtctgt ctgaatgctg ccattgactg Cttcgttttg gttttgattc      1200
aatttttttt tctctctc

```

(2) INFORMATION FOR SEQ ID NO:299:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 312 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..312
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566518

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:299:

Ser Tyr Leu Asn Ser Gln Asn His Leu Leu His Pro Lys Thr Pro Lys
1 5 10 15
Ser Leu Ile Pro Ser Ser Ser His Gly Cys Phe Ser Ser Ser Leu Ala
20 25 30
Leu Ser Ser Phe Asn Pro Lys Ser Leu Pro Phe Gly Val Ser Arg Pro
35 40 45
Ala Ser Val Ser Leu Leu Ser Pro Ser Leu Ser Phe Lys Leu Asn Ser
50 55 60
Asp Ser Val Ser Phe Ser Ile Ala Ala Lys Trp Asn Ser Pro Ala Ser
65 70 75 80
Arg Phe Val Arg Asn Val Ala Ile Thr Ser Glu Phe Glu Val Glu Glu
85 90 95
Asp Gly Phe Ala Asp Val Ala Pro Pro Lys Glu Gln Ser Phe Ser Ala
100 105 110
Asp Leu Lys Leu Phe Val Gly Asn Leu Pro Phe Asn Val Asp Ser Ala
115 120 125
Gln Leu Ala Gln Leu Phe Glu Ser Ala Gly Asn Val Glu Met Val Glu
130 135 140
Val Ile Tyr Asp Lys Ile Thr Gly Arg Ser Arg Gly Phe Gly Phe Val
145 150 155 160
Thr Met Ser Ser Val Ser Glu Val Glu Ala Ala Gln Gln Phe Asn
165 170 175
Gly Tyr Glu Leu Asp Gly Arg Pro Leu Arg Val Asn Ala Gly Pro Pro
180 185 190
Pro Pro Lys Arg Glu Asp Gly Phe Ser Arg Gly Pro Arg Ser Ser Phe
195 200 205
Gly Ser Ser Gly Ser Gly Tyr Gly Gly Gly Gly Ser Gly Ala Gly
210 215 220
Ser Gly Asn Arg Val Tyr Val Gly Asn Leu Ser Trp Gly Val Asp Asp
225 230 235 240
Met Ala Leu Glu Ser Leu Phe Ser Glu Gln Gly Lys Val Val Glu Ala
245 250 255
Arg Val Ile Tyr Asp Arg Asp Ser Gly Arg Ser Lys Gly Phe Gly Phe
260 265 270
Val Thr Tyr Asp Ser Ser Gln Glu Val Gln Asn Ala Ile Lys Ser Leu
275 280 285
Asp Gly Ala Asp Leu Asp Gly Arg Gln Ile Arg Val Ser Glu Ala Glu
290 295 300
Ala Arg Pro Pro Arg Arg Gln Tyr
305 310

(2) INFORMATION FOR SEQ ID NO:300:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 171 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..171

(D) OTHER INFORMATION: / Ceres Seq. ID 1566519

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:300:

Met Val Glu Val Ile Tyr Asp Lys Ile Thr Gly Arg Ser Arg Gly Phe
1 5 10 15
Gly Phe Val Thr Met Ser Ser Val Ser Glu Val Glu Ala Ala Gln
20 25 30
Gln Phe Asn Gly Tyr Glu Leu Asp Gly Arg Pro Leu Arg Val Asn Ala
35 40 45
Gly Pro Pro Pro Pro Lys Arg Glu Asp Gly Phe Ser Arg Gly Pro Arg
50 55 60
Ser Ser Phe Gly Ser Ser Gly Ser Gly Tyr Gly Gly Gly Gly Ser

65		70		75		80
Gly	Ala	Gly	Ser	Gly	Asn	Arg
				85		
Val	Asp	Asp	Met	Ala	Leu	Glu
				100		
Val	Glu	Ala	Arg	Val	Ile	Tyr
				115		
Phe	Gly	Phe	Val	Thr	Tyr	Asp
				130		
Lys	Ser	Leu	Asp	Gly	Ala	Asp
				145		
Glu	Ala	Glu	Ala	Arg	Pro	Arg
				165		

(2) INFORMATION FOR SEQ ID NO:301:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1082 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1082
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566531

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:301:

atttttaagg	tttcagatat	aggcagattc	tcacatttgc	aaacatgacg	actcagatca	60
gcaagaagag	aaagtttgtg	gcggcaggtg	tggaaacatt	tgtatgttgc	aaatgttggg	120
gactcgagga	caatagtttc	taaaagctgg	aaagcgatcg	cgctatctga	tgaccataag	180
ccaaatagaa	gcgatgaag	aaagcgaaat	gaaagtgtgc	gtggtgttat	catgtgggca	240
ggaacatgga	gagtaggtgg	gggtgttgct	atgtcccggg	cctttggtaa	cagaatgctg	300
aagcaattcg	ttgtgtgtga	accgcagata	caagatctag	agatagatca	tgaggccgag	360
ttgcttggcg	ttgcaagtga	cggttttatg	gatgtggtag	caaatgagga	tgcggtatgcc	420
ctgtctcaga	gcgagggaag	gcccgaggca	gctgcccgca	agttaaactg	cactgccttc	480
agccgtggca	gtgcagacaa	catcacgtgc	attgttgtta	aattccgtca	tgataagaca	540
gaatctccta	aaatcgaaac	aaacgccatg	gctgaatcgg	aaactgaaat	gaacccccaca	600
actgaactgg	aaccggaatc	aaaccccgat	actgaaatgg	aaactgaaat	aatcccccaaa	660
gctgaaactg	aatccgaacc	tgatgtcata	cctgatccaa	aaactgaaac	cgaaccagag	720
accaagggtg	agaaagctgg	tgagtaaggt	agcagccggg	gaaagggtgc	catactgttg	780
gggacatgtg	gaaacagatg	aatataaaat	tgttagtaga	gttggtgtgg	ttgtggctac	840
ctgtaaactg	tgaggatttg	tgtttttttg	ttttgtgttg	catctcatga	catgacctatg	900
cctgccttga	ggacgacgac	gacccttttg	acatgtcccc	gatttttttg	tattcatattt	960
acctattttt	gtttttgttg	gtgtactctc	caccataaaa	agcacatttg	ttctctgttt	1020
ctctactttt	ttttctatct	ttatttaaaa	caccgtccat	tccaataaac	aatgtttttg	1080

(2) INFORMATION FOR SEQ ID NO:302:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 171 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..171
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566532

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:302:

Met	Trp	Ala	Gly	Thr	Trp	Arg	Val	Gly	Gly	Val	Leu	Ala	Met	Ser	Arg
1			5					10					15		
Ala	Phe	Gly	Asn	Arg	Met	Leu	Lys	Gln	Phe	Val	Val	Ala	Glu	Pro	Glu
								20					25		
Ile	Gln	Asp	Leu	Glu	Ile	Asp	His	Glu	Ala	Glu	Leu	Leu	Val	Leu	Ala

35 40 45
Ser Asp Gly Leu Trp Asp Val Pro Asn Glu Asp Ala Val Ala Leu
50 55 60
Ala Gln Ser Glu Glu Glu Pro Glu Ala Ala Arg Lys Leu Thr Asp
65 70 75 80
Thr Ala Phe Ser Arg Gly Ser Ala Asp Asn Ile Thr Cys Ile Val Val
85 90
Lys Phe Arg His Asp Lys Thr Glu Ser Pro Lys Ile Glu Thr Asn Ala
100 105 110
Met Ala Glu Ser Glu Pro Glu Met Asn Pro Thr Thr Glu Leu Glu Pro
115 120 125
Glu Ser Asn Pro Ser Thr Glu Met Glu Thr Glu Ser Ile Pro Lys Ala
130 135 140
Glu Leu Glu Ser Glu Pro Asp Ala Ile Pro Asp Pro Lys Pro Glu Thr
145 150 155 160
Glu Pro Glu Thr Lys Gly Glu Lys Ala Gly Glu
165 170

(2) INFORMATION FOR SEQ ID NO:303:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 158 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..158
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566533

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:303:

Met Ser Arg Ala Phe Gly Asn Arg Met Leu Lys Gln Phe Val Val Ala
1 5 10 15
Glu Pro Glu Ile Gln Asp Leu Glu Ile Asp His Glu Ala Glu Leu Leu
20 25 30
Val Leu Ala Ser Asp Gly Leu Trp Asp Val Val Pro Asn Glu Asp Ala
35 40 45
Val Ala Leu Ala Gln Ser Glu Glu Glu Pro Glu Ala Ala Arg Lys
50 55 60
Leu Thr Asp Thr Ala Phe Ser Arg Gly Ser Ala Asp Asn Ile Thr Cys
65 70 75 80
Ile Val Val Lys Phe Arg His Asp Lys Thr Glu Ser Pro Lys Ile Glu
85 90 95
Thr Asn Ala Met Ala Glu Ser Glu Pro Glu Met Asn Pro Thr Thr Glu
100 105 110
Leu Glu Pro Glu Ser Asn Pro Ser Thr Glu Met Glu Thr Glu Ser Ile
115 120 125
Pro Lys Ala Glu Leu Glu Ser Glu Pro Asp Ala Ile Pro Asp Pro Lys
130 135 140
Pro Glu Thr Glu Pro Glu Thr Lys Gly Glu Lys Ala Gly Glu
145 150 155

(2) INFORMATION FOR SEQ ID NO:304:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 150 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..150
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566534

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:304:

Met Leu Lys Gln Phe Val Val Ala Glu Pro Glu Ile Gln Asp Leu Glu
1 5 10 15
Ile Asp His Glu Ala Glu Leu Leu Val Leu Ala Ser Asp Gly Leu Trp
20 25 30
Asp Val Val Pro Asn Glu Asp Ala Val Ala Leu Ala Gln Ser Glu Glu
35 40 45
Glu Pro Glu Ala Ala Ala Arg Lys Leu Thr Asp Thr Ala Phe Ser Arg
50 55 60
Gly Ser Ala Asp Asn Ile Thr Cys Ile Val Val Lys Phe Arg His Asp
65 70 75 80
Lys Thr Glu Ser Pro Lys Ile Glu Thr Asn Ala Met Ala Glu Ser Glu
85 90 95
Pro Glu Met Asn Pro Thr Thr Glu Leu Glu Pro Glu Ser Asn Pro Ser
100 105 110
Thr Glu Met Glu Thr Glu Ser Ile Pro Lys Ala Glu Leu Glu Ser Glu
115 120 125
Pro Asp Ala Ile Pro Asp Pro Lys Pro Glu Thr Glu Pro Glu Thr Lys
130 135 140
Gly Glu Lys Ala Gly Glu
145 150

(2) INFORMATION FOR SEQ ID NO:305:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 719 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..719
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566553

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:305:

aaaaaaaaat catttcttct ctgaaacgaa aaaccaaaga aacgagaaga agaagctatg	60
goggatcagc taactgatga acagatctct gagtttaagg aagctttag cctcttcgac	120
aaagatggag atggtttgcat caccacaaag gagctgggaa cagtgtatgag gtcactaggg	180
cagaacccaa cagaagctga gctacaagac atgatcaacg aggttgacgc tgatggaaac	240
ggaaccattg acctccctga gttcttaaac ctaatggcta aaaagatgaa ggacacagac	300
tcggaggaag agctgaaaga agctttcagg gtgttcgaca aagaccagaa cggtttcata	360
tccgctcgag aGcttcgcca tgtgatgacg aatctagggt agaaactgac tgatgaagag	420
gtcgaggaga tgattctgtga agcagatgtt gatggagatg gtcagataaa ctacgaggag	480
tttgtaaga ttatgatggc taagtgatga tgataagaaa aaaatgaaga ataaaagtgg	540
tgatgtgatg accttttagc cttttactat ctacaaaaga atgattcgac ctttaattgc	600
ttgggtttga tttgagccta gtagtcttct aaggttttaa cagactgaat ttgtgactca	660
tcctttttta tttttgtgtt ttctttctcg ttggcataat ggcagtgtta gatttcggc	

(2) INFORMATION FOR SEQ ID NO:306:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 149 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..149
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566554

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:306:

Met Ala Asp Gln Leu Thr Asp Glu Gln Ile Ser Glu Phe Lys Glu Ala
1 5 10 15
Phe Ser Leu Phe Asp Lys Asp Gly Asp Gly Cys Ile Thr Thr Lys Glu
20 25 30
Leu Gly Thr Val Met Arg Ser Leu Gly Gln Asn Pro Thr Glu Ala Glu

(X1) SEQUENCE DESCRIPTION: SEQ ID: 1															
Met	Ile	Asn	Glu	Val	Asp	Ala	Asp	Gly	Asn	Gly	Thr	Ile	Asp	Phe	Pro
1				5				10						15	
Glu	Phe	Leu	Asn	Leu	Met	Ala	Lys	Lys	Met	Lys	Asp	Thr	Asp	Ser	Glu
			20					25					30		
Glu	Glu	Leu	Lys	Glu	Ala	Phe	Arg	Val	Phe	Asp	Lys	Asp	Gln	Asn	Gly
		35					40					45			

Phe Ile Ser Ala Ala Glu Leu Arg His Val Met Thr Asn Leu Gly Glu
50 55 60
Lys Leu Thr Asp Glu Glu Val Glu Glu Met Ile Arg Glu Ala Asp Val
65 70 75 80
Asp Gly Asp Gly Gln Ile Asn Tyr Glu Glu Phe Val Lys Ile Met Met
85 90 95
Ala Lys

(2) INFORMATION FOR SEQ ID NO:309:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1651 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1651

(D) OTHER INFORMATION: / Ceres Seq. ID 1566580

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:309:

aagctaaagt ctagaaacac cgcctttaac gtctcgctgc accatttttc atcggtgatc 60
agtcgtcgat cctcttgagt gatttgattt tagactttct agttatcaaa ctcgaaagat 120
ggattctgtc cttgtagtgg gcattgcato ggttattctc ggtgcgttga tcgctgta 180
cttcttcggt agctacttcc ggaagcggac atcggaggtg caatccatgg ccaaaagcga 240
gcCtcaggat ccgatccgga atccaaagtc gaatcatcct gctccgaaga agaattcatc 300
caaatctcaaa gcgtccgata agaatacaga caaacggcat catcctttag atttaaacac 360
gttgaagggc cagcgtgatg ctgttactgg actctgtttc tcgtccgatg gaaagagctt 420
ggccacagct tcgcctgatg gtttaactca ggtgttcaa gctagatgat catcaagcaa 480
aagcttcaaa tttttaagga taaatcttcc tgctggagga catccaaacc ccgtggcatt 540
tgctgacagt gcctcatcta ttgttgggc ttgtcatcat atgtctggtt catctttgta 600
catgtacggc gaagataagc aaaaggatca gcaagggaag ctctctcttc ctagtatcaa 660
atgggaccac catcatattc atgagaagag atcagtgctt accatctctg gagctaactg 720
aacttacggt actgctgatg gaagtgttgt cattgcctct tgttctgaag ggaactgatat 780
cgtcctttgg catgggaaaa cgtggaggaa tttgggacat gttgatacaa accagttgaa 840
gaaccacatg gcagctgtat caccaaatgg acgtttttt gcagctgcaag catttaactgc 900
agatgtgaaa gtgtgggaaa ttgtgtatca gaaagatggt tctgtgaaag aggtttcaag 960
agttatgcaa ctttaaaggcc acaagagtgc agtgacttgg ttatgctttt ctccaaactc 1020
agagaaaatc atcaccgctt caaagatggt ttcaataaga gctcggaaac tcaatgtccg 1080
ttatcatctt gatgaggatc caaagacttt gaagggtgtc ccgattccac ttctggactc 1140
aggaggcaat ccgbtgcact atgatcgtct cagcttatgc ccagagggaaa agatattggc 1200
agcaagcatc ggttccacat tgcagtggtt atgtgctgaa actggaatat tcttggacac 1260
agctgagaaa gccacagaga gggatatcac atgcatatct tgggcaacca aggctattac 1320
agtgtgggaa agacatgcga tggttttggg gacatcaggc tggatgacaa aagtggaagc 1380
tgtgggaagc tccaaagtcg caatctttgt aggcctctcg atacacgtag tcctcttgatg 1440
acatgaggcg tatttaaacc gtacaaacttg cgaggaaaaa aactcttaata ggttttgatt 1500
cgagtcccaa gttgggatca aatgaagggt ggtttaaagt ccttcttggt accaagtgtc 1560
ttttaacttc tgaagttttg aattttgctc ataggactag tacaacactc acagtcttct 1620
atgttttcca aattaaggaa atttaaaaag c

(2) INFORMATION FOR SEQ ID NO:310:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 261 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..261

(D) OTHER INFORMATION: / Ceres Seq. ID 1566581

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:310:

Met Ser Gly Ser Ser Leu Tyr Met Tyr Gly Glu Asp Lys Lys Asp

1	5	10	15
Gln Gln Gly Lys Leu Pro Leu Pro Ser Ile Lys Trp Asp His His His	20	25	30
Ile His Glu Lys Arg Ser Val Leu Thr Ile Ser Gly Ala Thr Ala Thr	35	40	45
Tyr Gly Thr Ala Asp Gly Ser Val Val Ile Ala Ser Cys Ser Glu Gly	50	55	60
Thr Asp Ile Val Leu Trp His Gly Lys Thr Gly Arg Asn Leu Gly His	65	70	75
Val Asp Thr Asn Gln Leu Lys Asn His Met Ala Ala Val Ser Pro Asn	80	85	90
Gly Arg Phe Leu Ala Ala Ala Phe Thr Ala Asp Val Lys Val Trp	95	100	105
Glu Ile Val Tyr Gln Lys Asp Gly Ser Val Lys Glu Val Ser Arg Val	110	115	120
Met Gln Leu Lys Gly His Lys Ser Ala Val Thr Trp Leu Cys Phe Ser	125	130	135
Pro Asn Ser Glu Lys Ile Ile Thr Ala Ser Lys Asp Gly Ser Ile Arg	140	145	150
Val Trp Asn Ile Asn Val Arg Tyr His Leu Asp Glu Asp Pro Lys Thr	155	160	165
Leu Lys Val Phe Pro Ile Pro Leu Cys Asp Ser Gly Gly Asn Pro Xaa	170	175	180
His Tyr Asp Arg Leu Ser Leu Cys Pro Glu Gly Lys Ile Leu Ala Ala	185	190	195
Ser His Gly Ser Thr Leu Gln Trp Leu Cys Ala Glu Thr Gly Asn Val	200	205	210
Leu Asp Thr Ala Glu Lys Ala His Glu Gly Asp Ile Thr Cys Ile Ser	215	220	225
Trp Ala Pro Lys Ala Ile Thr Val Gly Glu Arg His Ala Met Val Leu	230	235	240
Gly Thr Ser Gly Xaa	245	250	255
	260		

(2) INFORMATION FOR SEQ ID NO:311:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 254 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..254
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566582

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:311:

Met Tyr Gly Glu Asp Lys Gln Lys Asp Gln Gln Gly Lys Leu Pro Leu	1	5	10	15
Pro Ser Ile Lys Trp Asp His His His Ile His Glu Lys Arg Ser Val	20	25	30	35
Leu Thr Ile Ser Gly Ala Thr Ala Thr Tyr Gly Thr Ala Asp Gly Ser	40	45	50	55
Val Val Ile Ala Ser Cys Ser Glu Gly Thr Asp Ile Val Leu Trp His	60	65	70	75
Gly Lys Thr Gly Arg Asn Leu Gly His Val Asp Thr Asn Gln Leu Lys	80	85	90	95
Asn His Met Ala Ala Val Ser Pro Asn Gly Arg Phe Leu Ala Ala Ala	100	105	110	115
Ala Phe Thr Ala Asp Val Lys Val Trp Glu Ile Val Tyr Gln Lys Asp	120	125	130	135
Gly Ser Val Lys Glu Val Ser Arg Val Met Gln Leu Lys Gly His Lys	140	145	150	155

Ser Ala Val Thr Trp Leu Cys Phe Ser Pro Asn Ser Glu Lys Ile Ile
130 135 140
Thr Ala Ser Lys Asp Gly Ser Ile Arg Val Trp Asn Ile Asn Val Arg
145 150 155 160
Tyr His Leu Asp Glu Asp Pro Lys Thr Leu Lys Val Phe Pro Ile Pro
165 170 175
Leu Cys Asp Ser Ser Gly Gly Asn Pro Xaa His Tyr Asp Arg Leu Ser Leu
180 185 190
Cys Pro Glu Gly Lys Ile Leu Ala Ala Ser His Gly Ser Thr Leu Gln
195 200 205
Trp Leu Cys Ala Glu Thr Gly Asn Val Leu Asp Thr Ala Glu Lys Ala
210 215 220
His Glu Gly Asp Ile Thr Cys Ile Ser Trp Ala Pro Lys Ala Ile Thr
225 230 235 240
Val Gly Glu Arg His Ala Met Val Leu Gly Thr Ser Gly Xaa
245 250

(2) INFORMATION FOR SEQ ID NO:312:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 172 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..172
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566583

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:312:

Met Ala Ala Val Ser Pro Asn Gly Arg Phe Leu Ala Ala Ala Ala Phe
1 5 10 15
Thr Ala Asp Val Lys Val Trp Glu Ile Val Tyr Gln Lys Asp Gly Ser
20 25 30
Val Lys Glu Val Ser Arg Val Met Gln Leu Lys Gly His Lys Ser Ala
35 40 45
Val Thr Trp Leu Cys Phe Ser Pro Asn Ser Glu Lys Ile Ile Thr Ala
50 55 60
Ser Lys Asp Gly Ser Ile Arg Val Trp Asn Ile Asn Val Arg Tyr His
65 70 75 80
Leu Asp Glu Asp Pro Lys Thr Leu Lys Val Phe Pro Ile Pro Leu Cys
85 90 95
Asp Ser Gly Gly Asn Pro Xaa His Tyr Asp Arg Leu Ser Leu Cys Pro
100 105 110
Glu Gly Lys Ile Leu Ala Ala Ser His Gly Ser Thr Leu Gln Trp Leu
115 120 125
Cys Ala Glu Thr Gly Asn Val Leu Asp Thr Ala Glu Lys Ala His Glu
130 135 140
Gly Asp Ile Thr Cys Ile Ser Trp Ala Pro Lys Ala Ile Thr Val Gly
145 150 155 160
Glu Arg His Ala Met Val Leu Gly Thr Ser Gly Xaa
165 170

(2) INFORMATION FOR SEQ ID NO:313:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 781 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..781
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566588

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:313:

atagttttat	atcatatcaa	tcgacatggc	gaatgtggac	cgtgatcgcc	gtgtgcatgt	60
agaccgttact	gacaaacgtg	ttcatcagcc	aaactacgaa	gatgatgtcg	gttttgggtg	120
ctatggcggt	tatgggtcgt	gtttctgatta	taagagtcgc	ggccctccca	ctaaccaaat	180
cttggcactt	atagcaggag	ttccattgg	tggcacactg	ctaaccctag	ctggactcac	240
tctagccggt	tcggtgatcg	Cgcttgctag	tctccatacc	cctcttccct	ctcttcagtc	300
cggtgatagt	cccgccggct	ctcactattg	ggcttgctgt	gacgggaatc	ttggccttct	360
gtttgttttg	gttgacgggt	ctgagctcgg	tctcgtgggt	cctcaactac	ctccgtggga	420
cgagtgtac	agtgccagag	caattggact	acgctaaacg	gcgtatggct	gatgcggtaa	480
gctatgctgg	tatgaaggga	aaagaSATgg	gtcagtatgt	gcaagataag	gcgcagtagg	540
ctcgtgagac	tgagttcatc	actgagacc	atgagccggg	taaggccagg	agaggctcat	600
aagctaatat	aaattgcggg	agtcagttgg	aaaggcgata	aatgtagtgt	tacttttatg	660
ttccagtttc	tttctctctt	taagaatatc	tttgtctata	tgtgtacggt	cgttttgtct	720
gtcccaata	aaaatccttg	ttagtgaat	aagaaatgaa	ataaatatgt	tttctttttt	780

g

(2) INFORMATION FOR SEQ ID NO:314:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 133 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..133

(D) OTHER INFORMATION: / Ceres Seq. ID 1566589

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:314:

Met	Ala	Asn	Val	Asp	Arg	Asp	Arg	Arg	Val	His	Val	Asp	Arg	Thr	Asp
1		5						10						15	
Lys	Arg	Val	His	Gln	Pro	Asn	Tyr	Glu	Asp	Asp	Val	Gly	Phe	Gly	Gly
		20						25					30		
Tyr	Gly	Gly	Tyr	Gly	Ala	Gly	Ser	Asp	Tyr	Lys	Ser	Arg	Gly	Pro	Ser
		35						40				45			
Thr	Asn	Gln	Ile	Leu	Ala	Leu	Ile	Ala	Gly	Val	Pro	Ile	Gly	Gly	Thr
		50				55					60				
Leu	Leu	Thr	Leu	Ala	Gly	Leu	Thr	Leu	Ala	Gly	Ser	Val	Ile	Ala	Leu
		65				70				75				80	
Ala	Ser	Leu	His	Thr	Pro	Leu	Pro	Pro	Leu	Gln	Ser	Gly	Asp	Ser	Pro
			85						90				95		
Gly	Gly	Ser	His	Tyr	Trp	Ala	Cys	Cys	Asp	Gly	Asn	Leu	Gly	Phe	Trp
			100					105					110		
Phe	Val	Trp	Val	Asp	Gly	Ser	Glu	Leu	Gly	Leu	Val	Gly	Pro	Gln	Leu
		115					120					125			
Pro	Pro	Trp	Asp	Glu											
															130

(2) INFORMATION FOR SEQ ID NO:315:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 717 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..717

(D) OTHER INFORMATION: / Ceres Seq. ID 1566597

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:315:

aacacatctc	actgctcaact	actctcactg	taatccctta	gatcttcttt	tcaaatttca	60
atggcgctccg	gtgatgttga	gtatcggtgc	ttctgttggag	gtctagcatg	ggccactgat	120
gacagagctc	ttgagactgc	cttcgctcaa	tacggcgacg	ttattgattc	caagatcatt	180
aacgatcgtg	agactggaag	atcaaaggga	ttcggattcc	tcaccttcaa	ggatgagaaa	240

gccatgaagg atgcgattga gggaatgaac ggacaagatc tcgattggccg tagcatcact 300
gttaacgagg ctcaagtcacg aggaagcggt ggcggcgagg gccaccgtgg aggtggtggc 360
gggtgtggag gttactccgg tggaggtggt agctacggag gtggcgggg tasacgcgag 420
gggtggaggag gatacagcgg cgggcgcggt tactctctcaa gaggtgtgg tggcggaagc 480
tacgggtggtg gaagacgtga gggaggagga ggatacgggtg gtggtgaagg aggaggttac 540
ggaggaaagcg gtggtggtgg aggatggtaa ttcCtGthR attaggtttg ggattaccaa 600
tgaatgttct ctctctcgtc tggtatgctt ctactttggt ttgtgtgttc tctattttgt 660
tcctggtctg ctttagattt gatgtaacag ttcgtgatta ggtattttgg tatctgg

(2) INFORMATION FOR SEQ ID NO:316:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 169 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..169

(D) OTHER INFORMATION: / Ceres Seq. ID 1566598

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:316:

Met Ala Ser Gly Asp Val Glu Tyr Arg Cys Phe Val Gly Gly Leu Ala
1 5 10 15
Trp Ala Thr Asp Asp Arg Ala Leu Glu Thr Ala Phe Ala Gln Tyr Gly
20 25 30
Asp Val Ile Asp Ser Lys Ile Ile Asn Asp Arg Glu Thr Gly Arg Ser
35 40 45
Arg Gly Phe Gly Phe Val Thr Phe Lys Asp Glu Lys Ala Met Lys Asp
50 55 60
Ala Ile Glu Gly Met Asn Gly Gln Asp Leu Asp Gly Arg Ser Ile Thr
65 70 75 80
Val Asn Glu Ala Gln Ser Arg Gly Ser Gly Gly Gly Gly His Arg
85 90 95
Gly Gly Gly Gly Gly Gly Gly Tyr Ser Gly Gly Gly Gly Ser Tyr
100 105 110
Gly Gly Gly Gly Gly Xaa Arg Glu Gly Gly Gly Tyr Ser Gly Gly
115 120 125
Gly Gly Tyr Ser Ser Arg Gly Gly Gly Gly Ser Tyr Gly Gly Gly
130 135 140
Arg Arg Glu Gly Gly Gly Gly Tyr Gly Gly Gly Gly Gly Tyr
145 150 155 160
Gly Gly Ser Gly Gly Gly Gly Trp
165

(2) INFORMATION FOR SEQ ID NO:317:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 108 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..108

(D) OTHER INFORMATION: / Ceres Seq. ID 1566599

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:317:

Met Lys Asp Ala Ile Glu Gly Met Asn Gly Gln Asp Leu Asp Gly Arg
1 5 10 15
Ser Ile Thr Val Asn Glu Ala Gln Ser Arg Gly Ser Gly Gly Gly Gly
20 25 30
Gly His Arg Gly Gly Gly Gly Gly Gly Gly Tyr Ser Gly Gly Gly
35 40 45
Gly Ser Tyr Gly Gly Gly Gly Xaa Arg Glu Gly Gly Gly Tyr

50	55	60
Ser Gly Gly Gly Gly Tyr Ser Ser Arg Gly Gly Gly Gly Ser Tyr		
65	70	75
Gly Gly Gly Arg Arg Glu Gly Gly Gly Gly Tyr Gly Gly Gly Glu Gly		80
	85	90
Gly Gly Tyr Gly Gly Ser Gly Gly Gly Gly Gly Trp		95
	100	105

(2) INFORMATION FOR SEQ ID NO:318:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 130 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..130
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566600

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:318:

Met Ala Val Ala Ser Leu Leu Thr Arg Leu Ser His Glu Glu Ala Val	
1	5
Ala Ala Glu Ala Thr Val Glu Val Val Ala Val Val Glu Val Thr Pro	15
	20
Val Glu Val Val Ala Thr Glu Val Ala Ala Val Xaa Ala Arg Val Glu	25
	30
Glu Asp Thr Ala Ala Ala Ala Val Thr Pro Gln Glu Val Val Val Ala	35
	40
Glu Ala Thr Val Val Glu Asp Val Arg Glu Glu Glu Asp Thr Val Val	45
	50
65	55
Val Lys Glu Glu Val Thr Glu Glu Ala Val Val Glu Asp Gly Asn	60
	65
	70
Ser Cys Xaa Ile Arg Phe Gly Ile Thr Asn Glu Cys Ser Leu Ser Arg	75
	80
	85
Leu Leu Cys Phe Tyr Phe Val Leu Cys Val Leu Tyr Phe Val Leu Val	90
	95
	100
	105
	110
	115
	120
	125
Leu Leu	
130	

(2) INFORMATION FOR SEQ ID NO:319:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1567 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1567
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566608

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:319:

atttttgat tctatcaatt ctcttcttca tcatctttct tgtctgggcc gccttcaaac	60
gcaaaaatca tgggaaacat cgacgaatac catctctccc tggttttcca atcatcgga	120
acttacatca gctcgagaaa ttacaacatc agtctctatg gaagctctca aagaagtatg	180
gccagtgat gcttttgaa gcttgaaaag tccccacagt catactttct tcatcagaaa	240
gcacaaacaa agctctaaga gactatgacc tctattgttg tagccgtccct tccttagcag	300
gaggaagaga gctctcttca aacaatctgg atatgtcttc ctctccttat aatgaatatt	360
ggaaagaact aaggaaagctc tgacgtcaag aactctttg tgctaataaa attcaatcga	420
ttcaacctat taaggacgag gaggtaacga aagttatcga ttcaatcgcg gaatcatctt	480
ctcttaagaa tccggttaac ttgacgaaga cgtttcttgc tttaactaca agtgtagtat	540
gcaaggcagc atttggtgtg agttttgagg gaactgtgct caacagtgat agattcaata	600
agttagtccg agatactttc gagatgttgg gaagcttctc tgcctcagat ttattccgtc	660
atgtcgatg gatcatcgat aagttcaatg gtttacaagg gtggagaaga aaaagctttc	720

gagatcttga	tgcgttctat	gaacaaaattt	ttgatctgca	taaggaagag	aaggaagttag	780
gaagtgaaga	tttagtggat	gtgctcttga	ggttggagaa	agaagaaaatt	gttgttggaa	840
atggcaagct	cacaagaagt	cataatcaaa	caattttgat	gaacattctt	ttaggaggaa	900
tcgatacttc	tgcaataaca	atgacatggg	caatggcaga	acttgctaaa	aaccttagag	960
tgatgaagaa	agttcaagca	gaaatcagaa	gccaaatcaa	agaatcacgt		1020
ttgatgcac	tgataagctc	gagtacttaa	aaatggtgat	caaagaacaa	tgaggtttac	1080
atctctcaac	acctcttctc	ctcccaagag	ttgtaatcac	tgaattttgag	atcaaatggct	1140
acacgatttc	tgccaaaaaca	cgacttcaatg	tgaatttttg	ggctatttggg	cgtgatccctg	1200
atacatggaa	agatccagaa	atgtttctcc	ccgaaaggtt	taatgatagt	aacattgatg	1260
caaaaggaca	gaactttgag	ttgttgcgt	ttgggagtg	taggagaatt	tgtcctggac	1320
tgtaactggg	aacaacaatg	gtggagtttg	gcctagctaa	tatgtttgat	cattttgatt	1380
ggaagtgtacc	agaaggcatg	gtagtcagaa	gatatcgata	tggaagaagc	tcctggacctt	1440
actgtgagca	aaaaaagtga	gcttctactt	gttcacgtga	agtatttaga	ccattgattc	1500
acgtgaatta	gttcttctac	gattgtacta	tgaataagaa	cgaatgata	atgagaattt	1560
tcaatgt						

(2) INFORMATION FOR SEQ ID NO:320:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 485 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..485

(D) OTHER INFORMATION: / Ceres Seq. ID 1566609

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:320:

Ph	Trp	Ile	Leu	Ser	Leu	Leu	Phe	Phe	Ile	Phe	Leu	Leu	Leu	Ala
1			5						10				15	
Ala	Phe	Lys	Arg	Lys	Asn	His	Gly	Lys	His	Arg	Arg	Ile	Pro	Ser
			20					25				30	Ser	Pro
Pro	Gly	Phe	Pro	Ile	Ile	Gly	Asn	Leu	His	Gln	Leu	Gly	Glu	Leu
			35				40				45			Gln
His	Gln	Ser	Leu	Trp	Lys	Leu	Ser	Lys	Lys	Tyr	Gly	Pro	Val	Met
			50			55					60			Leu
Leu	Lys	Leu	Gly	Lys	Val	Pro	Thr	Val	Ile	Leu	Ser	Ser	Ser	Glu
			65		70				75					80
Ala	Lys	Gln	Ala	Leu	Arg	Asp	Tyr	Asp	Leu	Tyr	Cys	Cys	Ser	Arg
			85					90					95	Pro
Ser	Leu	Ala	Gly	Gly	Arg	Glu	Leu	Ser	Tyr	Asn	Asn	Leu	Asp	Met
			100					105					110	Ser
Ser	Ser	Pro	Tyr	Asn	Glu	Tyr	Trp	Lys	Glu	Leu	Arg	Lys	Leu	Cys
			115				120					125		Ser
Gln	Glu	Leu	Phe	Ser	Ala	Asn	Lys	Ile	Gln	Ser	Ile	Gln	Pro	Ile
			130			135					140			Lys
Asp	Glu	Glu	Val	Lys	Lys	Val	Ile	Asp	Ser	Ile	Ala	Glu	Ser	Ser
			145			150				155				Ser
Leu	Lys	Asn	Pro	Val	Asn	Leu	Ser	Lys	Thr	Phe	Leu	Ala	Leu	Thr
			165					170					175	Thr
Ser	Val	Val	Cys	Lys	Ala	Ala	Phe	Gly	Val	Ser	Phe	Glu	Gly	Thr
			180				185						190	Val
Leu	Asn	Ser	Asp	Arg	Phe	Asn	Lys	Leu	Val	Arg	Asp	Thr	Phe	Glu
			195				200				205			Met
Leu	Gly	Ser	Phe	Ser	Ala	Ser	Asp	Phe	Ile	Pro	Tyr	Val	Gly	Trp
			210			215					220			Ile
Ile	Asp	Lys	Phe	Asn	Gly	Leu	Gln	Gly	Trp	Arg	Lys	Lys	Ser	Phe
			225			230				235				Arg
Asp	Leu	Asp	Ala	Phe	Tyr	Glu	Gln	Ile	Phe	Asp	Leu	His	Lys	Glu
			245					250					255	
Lys	Glu	Val	Gly	Ser	Glu	Asp	Leu	Val	Asp	Val	Leu	Leu	Arg	Glu
			260				265						270	

Lys Glu Glu Ile Val Val Gly Asn Gly Lys Leu Thr Arg Asn His Ile
275 280 285
Lys Ala Ile Leu Met Asn Ile Leu Leu Gly Gly Ile Asp Thr Ser Ala
290 295 300
Ile Thr Met Thr Trp Ala Met Ala Glu Leu Ala Lys Asn Pro Arg Val
305 310 315 320
Met Lys Lys Val Gln Ala Glu Ile Arg Ser Gln Ile Lys Asn Lys Glu
325 330 335
Arg Ile Ser Phe Asp Asp Thr Asp Lys Leu Glu Tyr Leu Lys Met Val
340 345 350
Ile Lys Glu Thr Trp Arg Leu His Pro Pro Thr Pro Leu Leu Leu Pro
355 360 365
Arg Val Val Ile Thr Glu Phe Glu Ile Asn Gly Tyr Thr Ile Pro Ala
370 375 380
Lys Thr Arg Leu His Val Asn Val Trp Ala Ile Gly Arg Asp Pro Asp
385 390 395 400
Thr Trp Lys Asp Pro Glu Met Phe Leu Pro Glu Arg Phe Asn Asp Ser
405 410 415
Asn Ile Asp Ala Lys Gly Gln Asn Phe Glu Leu Leu Ser Phe Gly Ser
420 425 430
Gly Arg Arg Ile Cys Pro Gly Leu Tyr Met Gly Thr Thr Met Val Glu
435 440 445
Phe Gly Leu Ala Asn Met Leu Tyr His Phe Asp Trp Lys Leu Pro Glu
450 455 460
Gly Met Val Val Arg Arg Tyr Arg Tyr Gly Arg Ser Ser Trp Thr Tyr
465 470 475 480
Cys Glu Gln Lys Lys
485

(2) INFORMATION FOR SEQ ID NO:321:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 423 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..423

(D) OTHER INFORMATION: / Ceres Seq. ID 1566610

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:321:

Met Leu Leu Lys Lys Leu Gly Lys Val Pro Thr Val Ile Leu Ser Ser Ser
1 5 10 15
Glu Thr Ala Lys Gln Ala Leu Arg Asp Tyr Asp Leu Tyr Cys Cys Ser
20 25 30
Arg Pro Ser Leu Ala Gly Gly Arg Glu Leu Ser Tyr Asn Asn Leu Asp
35 40 45
Met Ser Ser Ser Pro Tyr Asn Glu Tyr Trp Lys Glu Leu Arg Lys Leu
50 55 60
Cys Ser Gln Glu Leu Phe Ser Ala Asn Lys Ile Gln Ser Ile Gln Pro
65 70 75 80
Ile Lys Asp Glu Glu Val Lys Lys Val Ile Asp Ser Ile Ala Glu Ser
85 90 95
Ser Ser Leu Lys Asn Pro Val Asn Leu Ser Lys Thr Phe Leu Ala Leu
100 105 110
Thr Thr Ser Val Val Cys Lys Ala Ala Phe Gly Val Ser Phe Glu Gly
115 120 125
Thr Val Leu Asn Ser Asp Arg Phe Asn Lys Leu Val Arg Asp Thr Phe
130 135 140
Glu Met Leu Gly Ser Phe Ser Ala Ser Asp Phe Ile Pro Tyr Val Gly
145 150 155 160
Trp Ile Ile Asp Lys Phe Asn Gly Leu Gln Gly Trp Arg Lys Lys Ser

Met	Ser	Ser	Ser	Pro	Tyr	Asn	Glu	Tyr	Trp	Lys	Glu	Leu	Arg	Lys	Leu
1				5					10					15	
Cys	Ser	Gln	Glu	Leu	Phe	Ser	Ala	Asn	Lys	Ile	Gln	Ser	Ile	Gln	Pro
			20						25				30		
Ile	Lys	Asp	Glu	Glu	Val	Lys	Lys	Val	Ile	Asp	Ser	Ile	Ala	Glu	Ser
		35					40					45			
Ser	Ser	Leu	Lys	Asn	Pro	Val	Asn	Leu	Ser	Lys	Thr	Phe	Leu	Ala	Leu
		50				55					60				
Thr	Thr	Ser	Val	Val	Cys	Lys	Ala	Ala	Phe	Gly	Val	Ser	Phe	Glu	Gly
65					70					75				80	
Thr	Val	Leu	Asn	Ser	Asp	Arg	Phe	Asn	Lys	Leu	Val	Arg	Asp	Thr	Phe
				85					90					95	
Glu	Met	Leu	Gly	Ser	Phe	Ser	Ala	Ser	Asp	Phe	Ile	Pro	Tyr	Val	Gly
			100					105					110		
Trp	Ile	Ile	Asp	Lys	Phe	Asn	Gly	Leu	Gln	Gly	Trp	Arg	Lys	Lys	Ser
		115					120					125			

Phe Arg Asp Leu Asp Ala Phe Tyr Glu Gln Ile Phe Asp Leu His Lys
130 135 140
Glu Glu Lys Glu Val Gly Ser Glu Asp Leu Val Asp Val Leu Leu Arg
145 150 155 160
Leu Glu Lys Glu Glu Ile Val Val Gly Asn Gly Lys Leu Thr Arg Asn
165 170 175
His Ile Lys Ala Ile Leu Met Asn Ile Leu Leu Gly Gly Ile Asp Thr
180 185 190
Ser Ala Ile Thr Met Thr Trp Ala Met Ala Glu Leu Ala Lys Asn Pro
195 200 205
Arg Val Met Lys Lys Val Gln Ala Glu Ile Arg Ser Gln Ile Lys Asn
210 215 220
Lys Glu Arg Ile Ser Phe Asp Asp Thr Asp Lys Leu Glu Tyr Leu Lys
225 230 235 240
Met Val Ile Lys Glu Thr Trp Arg Leu His Pro Pro Thr Pro Leu Leu
245 250 255
Leu Pro Arg Val Val Ile Thr Glu Phe Glu Ile Asn Gly Tyr Thr Ile
260 265 270
Pro Ala Lys Thr Arg Leu His Val Asn Val Trp Ala Ile Gly Arg Asp
275 280 285
Pro Asp Thr Trp Lys Asp Pro Glu Met Phe Leu Pro Glu Arg Phe Asn
290 295 300
Asp Ser Asn Ile Asp Ala Lys Gly Gln Asn Phe Glu Leu Leu Ser Phe
305 310 315 320
Gly Ser Gly Arg Arg Ile Cys Pro Gly Leu Tyr Met Gly Thr Thr Met
325 330 335
Val Glu Phe Gly Leu Ala Asn Met Leu Tyr His Phe Asp Trp Lys Leu
340 345 350
Pro Glu Gly Met Val Val Arg Arg Tyr Arg Tyr Gly Arg Ser Ser Trp
355 360 365
Thr Tyr Cys Glu Gln Lys Lys
370 375

(2) INFORMATION FOR SEQ ID NO:323:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1049 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..1049
(D) OTHER INFORMATION: / Ceres Seq. ID 1566616

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:323:

aactgccaaa	actcttcaact	taattctccg	gcgtatacaa	gtcgcggcga	aaaatgtcga	60
tgctgaaaaa	gtcccaaatg	cttcagttca	taaaactacag	gatgcgagta	acaatccaag	120
acggaagaca	gtcaatcgga	aaattcctag	cggttcgatcg	ccacatgaat	cttggtctctg	180
gcgactgcga	agagttttca	aaacttctct	cggcgaaaag	taataagaag	acgagcggaag	240
aaagagaaga	gcgtcgtaact	ctaggttttg	ttttacttag	aggagaagaa	gtgatttcga	300
tgactgtcga	aggctccaccg	ccaccgcgaag	aatctcgcgc	caaatctgga	ctgtgtaccg	360
ccgtgtcgtg	tctctggaatc	ggctgtcgtg	ctggacgcgg	agtacacct	ggctcgttag	420
ttcaagctca	gcctggttta	tctgtctctg	tctgtggaat	tggttgacct	gtcctcgtgaa	480
tgatgcagcc	tcagatctct	agaccaccac	agattattcg	tctcgcggga	caaatgccac	540
cacagcctcc	ttttgttgtt	caaggagggtc	ctcctccacc	ttatggtatg	agaccaccgt	600
atctctggtc	accacgcgct	caagtatggtg	gacagcaaa	gccaatgatg	attcctccac	660
ctggtggtat	gatgagagga	ctcctccacc	ctcatgggtat	gcaaggaccg	ctcctctctc	720
gccctggaat	acctcccccc	gggtgtgtctc	cgatgtttGc	tccgcctcat	cttggtcgtc	780
cacctgCtcc	gccaaatcac	cataatcagc	aacattgatt	aggagtcact	tcatctacaa	840
cgaagcgaac	atccacatga	ttgagttacc	ctcgggctag	tctagtcggt	ttctctccgtg	900
aagctcagag	aattgatgag	ttcatatttg	tgtattctcg	tggaaaaagc	aactgatttt	960
agaaatagtg	aactgttagg	agttacaacc	ttgctccatg	aacttgtaag	tattacttgt	1020

aaaagaggct ctcaatgggtt ttgactggc

(2) INFORMATION FOR SEQ ID NO:324:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 254 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..254

(D) OTHER INFORMATION: / Ceres Seq. ID 1566617

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:324:

Met	Ser	Met	Ser	Lys	Ser	Ser	Lys	Met	Leu	Gln	Phe	Ile	Asn	Tyr	Arg	
1				5				10						15		
Met	Arg	Val	Thr	Ile	Gln	Asp	Gly	Arg	Gln	Leu	Ile	Gly	Lys	Phe	Met	
			20					25					30			
Ala	Phe	Asp	Arg	His	Met	Asn	Leu	Val	Leu	Gly	Asp	Cys	Glu	Glu	Phe	
			35				40					45				
Arg	Lys	Leu	Pro	Pro	Ala	Lys	Gly	Asn	Lys	Lys	Thr	Ser	Glu	Glu	Arg	
			50			55					60					
Glu	Glu	Arg	Arg	Thr	Leu	Gly	Leu	Val	Leu	Leu	Arg	Gly	Glu	Glu	Val	
65					70					75					80	
Ile	Ser	Met	Thr	Val	Glu	Gly	Pro	Pro	Pro	Pro	Glu	Glu	Ser	Arg	Ala	
					85				90					95		
Lys	Ser	Gly	Ser	Val	Thr	Ala	Val	Ala	Gly	Pro	Gly	Ile	Gly	Arg	Ala	
					100			105						110		
Ala	Gly	Arg	Gly	Val	Pro	Thr	Gly	Pro	Leu	Val	Gln	Ala	Gln	Pro	Gly	
					115			120				125				
Leu	Ser	Gly	Pro	Val	Arg	Gly	Ile	Gly	Gly	Pro	Ala	Pro	Gly	Met	Met	
						135				140						
Gln	Pro	Gln	Ile	Ser	Arg	Pro	Pro	Gln	Ile	Ile	Arg	Pro	Pro	Gly	Gln	
145					150					155					160	
Met	Pro	Pro	Gln	Pro	Phe	Ala	Gly	Gln	Gly	Gly	Pro	Pro	Pro	Pro	Pro	
					165				170					175		
Tyr	Gly	Met	Arg	Pro	Pro	Tyr	Pro	Gly	Pro	Pro	Pro	Pro	Gln	Tyr	Gly	
					180			185						190		
Gly	Gln	Gln	Arg	Pro	Met	Met	Ile	Pro	Pro	Pro	Gly	Gly	Met	Met	Arg	
					195			200					205			
Gly	Pro	Pro	Pro	Pro	His	Gly	Met	Gln	Gly	Pro	Pro	Pro	Ser	Arg	Pro	
						215				220						
Gly	Ile	Pro	Pro	Pro	Gly	Gly	Ala	Pro	Met	Phe	Ala	Pro	Pro	His	Pro	
225					230					235					240	
Gly	Met	Pro	Pro	Ala	Pro	Pro	Asn	His	His	Asn	Gln	Gln	His			
					245					250						

(2) INFORMATION FOR SEQ ID NO:325:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 252 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..252

(D) OTHER INFORMATION: / Ceres Seq. ID 1566618

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:325:

Met	Ser	Lys	Ser	Ser	Lys	Met	Leu	Gln	Phe	Ile	Asn	Tyr	Arg	Met	Arg	
1					5					10				15		
Val	Thr	Ile	Gln	Asp	Gly	Arg	Gln	Leu	Ile	Gly	Lys	Phe	Met	Ala	Phe	
					20			25						30		

Asp Arg His Met Asn Leu Val Leu Gly Asp Cys Glu Glu Phe Arg Lys
35 40 45
Leu Pro Pro Ala Lys Gly Asn Lys Lys Thr Ser Glu Glu Arg Glu Glu
50 55 60
Arg Arg Thr Leu Gly Leu Val Leu Leu Arg Gly Glu Glu Val Ile Ser
65 70 75 80
Met Thr Val Glu Gly Pro Pro Pro Pro Glu Glu Ser Arg Ala Lys Ser
85 90 95
Gly Ser Val Thr Ala Val Ala Gly Pro Gly Ile Gly Arg Ala Ala Gly
100 105 110
Arg Gly Val Pro Thr Gly Pro Leu Val Gln Ala Gln Pro Gly Leu Ser
115 120 125
Gly Pro Val Arg Gly Ile Gly Gly Pro Ala Pro Gly Met Met Gln Pro
130 135 140
Gln Ile Ser Arg Pro Pro Gln Ile Ile Arg Pro Pro Gly Gln Met Pro
145 150 155 160
Pro Gln Pro Pro Phe Ala Gly Gln Gly Gly Pro Pro Pro Tyr Gly
165 170 175
Met Arg Pro Pro Tyr Pro Gly Pro Pro Pro Gln Tyr Gly Gly Gln
180 185 190
Gln Arg Pro Met Met Ile Pro Pro Pro Gly Gly Met Met Arg Gly Pro
195 200 205
Pro Pro Pro His Gly Met Gln Gly Pro Pro Pro Ser Arg Pro Gly Ile
210 215 220
Pro Pro Pro Gly Gly Ala Pro Met Phe Ala Pro His Pro Gly Met
225 230 235 240
Pro Pro Ala Pro Pro Asn His His Asn Gln His
245 250

(2) INFORMATION FOR SEQ ID NO:326:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 246 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..246

(D) OTHER INFORMATION: / Ceres Seq. ID 1566619

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:326:

Met Leu Gln Phe Ile Asn Tyr Arg Met Arg Val Thr Ile Gln Asp Gly
1 5 10 15
Arg Gln Leu Ile Gly Lys Phe Met Ala Phe Asp Arg His Met Asn Leu
20 25 30
Val Leu Gly Asp Cys Glu Glu Phe Arg Lys Leu Pro Pro Ala Lys Gly
35 40 45
Asn Lys Lys Thr Ser Glu Glu Arg Glu Glu Arg Arg Thr Leu Gly Leu
50 55 60
Val Leu Leu Arg Gly Glu Glu Val Ile Ser Met Thr Val Glu Gly Pro
65 70 75 80
Pro Pro Pro Glu Glu Ser Arg Ala Lys Ser Gly Ser Val Thr Ala Val
85 90 95
Ala Gly Pro Gly Ile Gly Arg Ala Ala Gly Arg Gly Val Pro Thr Gly
100 105 110
Pro Leu Val Gln Ala Gln Pro Gly Leu Ser Gly Pro Val Arg Gly Ile
115 120 125
Gly Gly Pro Ala Pro Gly Met Met Gln Pro Gln Ile Ser Arg Pro Pro
130 135 140
Gln Ile Ile Arg Pro Pro Gly Gln Met Pro Pro Gln Pro Pro Phe Ala
145 150 155 160
Gly Gln Gly Gly Pro Pro Pro Tyr Gly Met Arg Pro Pro Tyr Pro

(2) INFORMATION FOR SEQ ID NO:327:

(A) LENGTH: 1570 base pairs

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(C) STRANDEDNESS: single
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MOLECULE TYPE: DNA (g

(A) NAME

(B) LOCATION: 1

(D) OTHER INFORMATION

SEQUENCE DESCRIPTION: SEQ ID NO:327:

atccacccg	tctgttttt	tccgcgtgat	tcatagctg	tccgcgttcat	ctgcacacct	120
accgctctct	tctctccatt	tcagcagatt	tgttagattg	tgttagtggt	tctcaggcaaa	180
ctttattctt	aaggtccagg	ctctttgcct	gtctgaacca	accattgttat	catattatcc	240
ctctgtgagat	tgatcatgga	atggatttcat	tctctgaaga	aacattctcag	agaagtatcc	300
atagctttct	tcacaaagaa	tcogttaaaca	atcttgattt	ctccaaagt	tctggaggaa	360
gcttaccatt	gcctcttgct	cccagcttgc	gttttgcgtt	ctatcgttat	atgtcaagtg	420
cacctgggtg	tggttcagag	aagattgggt	tgattgtctga	cattgcagaa	gtcataacctg	480
actcaaacatt	gcgaagtgtg	ccagctcagg	ctgctgtctg	tgctcagtga	gttacactcg	540
cagctgtctga	ctctttcttc	ctctatcggc	cccttcagca	tgctgattgat	atggtgcata	600
catctacagg	tcttgagtgt	tggaatccca	tgtgttgtag	caacattttt	atcgcattgat	660
caacagattcc	tctcttgatc	aaacaaatga	aagacacacac	caagttatgc	ctgatgagtc	720
ccaggttgga	gtctcatcgg	gaggaatctg	aaacacacagg	aatggtctctg	gtaacgatgg	780
cagaagaatg	aaaaaagatg	aagaaattgt	ttaaagaata	tgtgtctaac	ccattcaccc	840
caatgaaagg	gatgtttatt	cagggacccg	tgttcatctg	ctttttcttc	gctattcgaa	900
atatggcgga	gaaggtacct	tcattcccca	caggagggtc	attatggttt	accgattotaa	960
caactcccgga	cagctttatc	atcttgcggg	tataaacagg	attgacattc	ttgataaacg	1020
tttgagttaa	tgcaacaagaa	ggcatctgaag	ggaactgcat	gggtggcaat	gtaaaacatg	1080
tttgcgggtg	tttgtctctc	ctccagctgc	cgatgacaat	gagttttcca	caggccattg	1140
tttgttactg	tgacacatcc	aacctgtatt	ctctcatgta	tgcacttctg	ataaaggctc	1200
ctcaagtgaa	gaagatgtta	ctactactcg	atctgcctcc	accttttcca	gtgccaacaac	1260
cttcatctga	ccgtgttttca	gctctcaaga	aaatgaaagc	gcatacacag	gaccatcac	1320
agaaccagat	aggaaccact	tcgcagcaat	accocaggct	ttctctcaac	tcgctgagtc	1380
ctgttagtaa	ggggctcaag	gctttgggaa	gccaaagtaa	gggaagggaag	agaataagca	1440
cgaaagaaag	gttgatttaa	ccaggtgcata	ctatttttgt	taaggaggcc	aaacgaaaaa	1500
aaataataaag	cttttgatgc	gaagtgatga	acagaatttt	ctcactgagt	aaactctctt	1560
gttagcttaa	aagctggagg	cagctattgt	aagtttgttt	tgaccaatta	tagaatagaa	
gattgattttt						

(2) INFORMATION FOR SEQ ID NO:328:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 429 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..429

(D) OTHER INFORMATION: / Ceres Seq. ID 1566631

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:328:

Met Ala Phe Arg Gln Thr Leu Ser Ile Arg Ser Arg Leu Phe Ala Arg
1 5 10 15
Arg Asn Gln Pro Val Tyr His Ile Ile Pro Arg Glu Ser Asp His Glu
20 25 30
Arg Asp Ser Phe Cys Gln Glu Thr Ser Gln Arg Ser Tyr His Ser Phe
35 40 45
Leu His Gln Arg Ser Val Asn Asn Ser Asp Phe Ser Lys Val Ser Gly
50 55 60
Gly Ser Leu His Leu Pro Leu Ala Pro Thr Ser Gly Phe Ala Phe Tyr
65 70 75 80
Arg Tyr Met Ser Ser Ala Pro Gly Val Gly Ser Glu Lys Ile Gly Val
85 90 95
Met Ser Asp Ile Ala Glu Val Ile Thr Asp Ser Thr Leu Gln Asp Val
100 105 110
Pro Ala Gln Ala Ala Ala Val Ser Glu Val Thr Leu Ala Ala Ala
115 120 125
Asp Ser Phe Phe Pro Ile Ala Ala Leu Gln Gln Cys Ile Asp Met Val
130 135 140
His Thr Phe Thr Gly Phe Glu Trp Trp Ala Ser Ile Val Val Ala Thr
145 150 155 160
Ile Leu Ile Arg Ser Ser Thr Val Pro Leu Leu Ile Lys Gln Met Lys
165 170 175
Asp Thr Thr Lys Leu Ala Leu Met Arg Pro Arg Leu Glu Ser Ile Arg
180 185 190
Glu Glu Met Gln Asn Lys Gly Met Asp Ser Val Thr Met Ala Glu Gly
195 200 205
Gln Lys Lys Met Lys Asn Leu Phe Lys Glu Tyr Gly Val Thr Pro Phe
210 215 220
Thr Pro Met Lys Gly Met Phe Ile Gln Gly Pro Leu Phe Ile Cys Phe
225 230 235 240
Phe Leu Ala Ile Arg Asn Met Ala Glu Lys Val Pro Ser Phe Gln Thr
245 250 255
Gly Gly Ala Leu Trp Phe Thr Asp Leu Thr Thr Pro Asp Ser Leu Tyr
260 265 270
Ile Leu Pro Val Ile Thr Gly Leu Thr Phe Leu Ile Thr Val Glu Cys
275 280 285
Asn Ala Gln Glu Gly Met Glu Gly Asn Pro Met Ala Gly Thr Val Lys
290 295 300
Thr Val Cys Arg Val Phe Ala Leu Leu Thr Val Pro Met Thr Met Ser
305 310 315 320
Phe Pro Gln Ala Ile Phe Cys Tyr Trp Ile Thr Ser Asn Leu Phe Ser
325 330 335
Leu Met Tyr Gly Leu Val Ile Lys Arg Pro Gln Val Lys Lys Met Leu
340 345 350
Arg Ile Pro Asp Leu Pro Pro Pro Pro Gly Gln Gln Pro Ser Phe
355 360 365
Asp Leu Phe Ser Ala Leu Lys Lys Met Lys Ala Met Thr Gln Asp His
370 375 380
Thr Gln Asn Gln Ile Glu Pro Pro Ser Pro Val Asn Pro Arg Leu Ser
385 390 395 400
Ser Thr Ser Leu Ser Pro Val Ser Lys Arg Leu Lys Ala Leu Glu Ser
405 410 415
Gln Val Lys Gly Arg Lys Lys Asn Ser Ser Lys Lys Lys
420 425

(2) INFORMATION FOR SEQ ID NO:329:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 347 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..347

(D) OTHER INFORMATION: / Ceres Seq. ID 1566632

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:329:

Met	Ser	Ser	Ala	Pro	Gly	Val	Gly	Ser	Glu	Lys	Ile	Gly	Val	Met	Ser
1			5					10						15	
Asp	Ile	Ala	Glu	Val	Ile	Thr	Asp	Ser	Thr	Leu	Gln	Asp	Val	Pro	Ala
			20					25					30		
Gln	Ala	Ala	Ala	Ala	Val	Ser	Glu	Val	Thr	Leu	Ala	Ala	Ala	Asp	Ser
			35					40				45			
Phe	Phe	Pro	Ile	Ala	Ala	Leu	Gln	Gln	Cys	Ile	Asp	Met	Val	His	Thr
			50					55				60			
Phe	Thr	Gly	Phe	Glu	Trp	Trp	Ala	Ser	Ile	Val	Val	Ala	Thr	Ile	Leu
			65					70				75			80
Ile	Arg	Ser	Ser	Thr	Val	Pro	Leu	Leu	Ile	Lys	Gln	Met	Lys	Asp	Thr
				85					90				95		
Thr	Lys	Leu	Ala	Leu	Met	Arg	Pro	Arg	Leu	Glu	Ser	Ile	Arg	Glu	Glu
			100					105					110		
Met	Gln	Asn	Lys	Gly	Met	Asp	Ser	Val	Thr	Met	Ala	Glu	Gly	Gln	Lys
			115					120					125		
Lys	Met	Lys	Asn	Leu	Phe	Lys	Glu	Tyr	Gly	Val	Thr	Pro	Phe	Thr	Pro
			130					135				140			
Met	Lys	Gly	Met	Phe	Ile	Gln	Gly	Pro	Leu	Phe	Ile	Cys	Phe	Phe	Leu
			145					150				155			160
Ala	Ile	Arg	Asn	Met	Ala	Glu	Lys	Val	Pro	Ser	Phe	Gln	Thr	Gly	Gly
				165					170					175	
Ala	Leu	Trp	Phe	Thr	Asp	Leu	Thr	Thr	Pro	Asp	Ser	Leu	Tyr	Ile	Leu
			180					185					190		
Pro	Val	Ile	Thr	Gly	Leu	Thr	Phe	Leu	Ile	Thr	Val	Glu	Cys	Asn	Ala
			195					200					205		
Gln	Glu	Gly	Met	Glu	Gly	Asn	Pro	Met	Ala	Gly	Thr	Val	Lys	Thr	Val
			210					215					220		
Cys	Arg	Val	Phe	Ala	Leu	Leu	Thr	Val	Pro	Met	Thr	Met	Ser	Phe	Pro
				230						235					240
Gln	Ala	Ile	Phe	Cys	Tyr	Trp	Ile	Thr	Ser	Asn	Leu	Phe	Ser	Leu	Met
				245						250				255	
Tyr	Gly	Leu	Val	Ile	Lys	Arg	Pro	Gln	Val	Lys	Lys	Met	Leu	Arg	Ile
			260					265					270		
Pro	Asp	Leu	Pro	Pro	Pro	Pro	Pro	Gly	Gln	Gln	Pro	Ser	Phe	Asp	Leu
			275					280					285		
Phe	Ser	Ala	Leu	Lys	Lys	Met	Lys	Ala	Met	Thr	Gln	Asp	His	Thr	Gln
				295								300			
Asn	Gln	Ile	Glu	Pro	Pro	Ser	Pro	Val	Asn	Pro	Arg	Leu	Ser	Ser	Thr
				310							315				320
Ser	Leu	Ser	Pro	Val	Ser	Lys	Arg	Leu	Lys	Ala	Leu	Glu	Ser	Gln	Val
				325						330				335	
Lys	Gly	Arg	Lys	Lys	Asn	Ser	Ser	Lys	Lys	Lys					
				340					345						

(2) INFORMATION FOR SEQ ID NO:330:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 333 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..333

(D) OTHER INFORMATION: / Ceres Seq. ID 1566633

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:330:

```

Met Ser Asp Ile Ala Glu Val Ile Thr Asp Ser Thr Leu Gln Asp Val
1      5      10      15
Pro Ala Gln Ala Ala Ala Val Ser Glu Val Thr Leu Ala Ala Ala
20     25
Asp Ser Phe Phe Pro Ile Ala Ala Leu Gln Gln Cys Ile Asp Met Val
35     40     45
His Thr Phe Thr Gly Phe Glu Trp Trp Ala Ser Ile Val Val Ala Thr
50     55     60
Ile Leu Ile Arg Ser Ser Thr Val Pro Leu Leu Ile Lys Gln Met Lys
65     70     75     80
Asp Thr Thr Lys Leu Ala Leu Met Arg Pro Arg Leu Glu Ser Ile Arg
85     90     95
Glu Glu Met Gln Asn Lys Gly Met Asp Ser Val Thr Met Ala Glu Gly
100    105    110
Gln Lys Lys Met Lys Asn Leu Phe Lys Glu Tyr Gly Val Thr Pro Phe
115    120    125
Thr Pro Met Lys Gly Met Phe Ile Gln Gly Pro Leu Phe Ile Cys Phe
130    135    140
Phe Leu Ala Ile Arg Asn Met Ala Glu Lys Val Pro Ser Phe Gln Thr
145    150    155    160
Gly Gly Ala Leu Trp Phe Thr Asp Leu Thr Thr Pro Asp Ser Leu Tyr
165    170    175
Ile Leu Pro Val Ile Thr Gly Leu Thr Phe Leu Ile Thr Val Glu Cys
180    185    190
Asn Ala Gln Glu Gly Met Glu Gly Asn Pro Met Ala Gly Thr Val Lys
195    200    205
Thr Val Cys Arg Val Phe Ala Leu Leu Thr Val Pro Met Thr Met Ser
210    215    220
Phe Pro Gln Ala Ile Phe Cys Tyr Trp Ile Thr Ser Asn Leu Phe Ser
225    230    235    240
Leu Met Tyr Gly Leu Val Ile Lys Arg Pro Gln Val Lys Lys Met Leu
245    250    255
Arg Ile Pro Asp Leu Pro Pro Pro Pro Gly Gln Gln Pro Ser Phe
260    265    270
Asp Leu Phe Ser Ala Leu Lys Lys Met Lys Ala Met Thr Gln Asp His
275    280    285
Thr Gln Asn Gln Ile Glu Pro Pro Ser Pro Val Asn Pro Arg Leu Ser
290    295    300
Ser Thr Ser Leu Ser Pro Val Ser Lys Arg Leu Lys Ala Leu Glu Ser
305    310    315    320
Gln Val Lys Gly Arg Lys Lys Asn Ser Ser Lys Lys Lys
325    330

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(2) INFORMATION FOR SEQ ID NO:331:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 681 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..681
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566641

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:331:

```

atcgatcact gaattcttctt ctctctcttctt ttcttcttctt ttcttcttctt ctcttcttctt
ctctcaagaa cagattttttt tttaaagcagc ttgatcaata aattctctctca agatctatggt
cggaagagcga tcgatgtcag acaccagaaaa gcaaccgtctc ctgtgtttaa acactgtggct
tctctggcag ctccgccacc atgaatctct gtctctaattg ttaacggcgat cttgtctctca
aacaacaaca acaatctctc tccatcaaat ccaccgttga atcagcaaca gagggccgaat
cgggtgcacga cgtgtaggaa acgggtcggg ttaaccggat tcaagtgcgc gtcgcgttacg
60
120
180
240
300
360

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atgtttttcgcg	gggttcacatg	gtaccgccgag	atccatggat	gcagctacga	tttcaaatcg	420
gccgcagcgtg	aagagatcgc	gaaagcSaat	ccgttggtga	aagcagcgaa	gcttcagaag	480
atatgatcag	agccggttcga	tgcggttgact	tttctctcgc	taagtcttca	tttctacgcg	540
tatgtgtgtc	ctccgcctccc	cgagaaatac	ggatggtgtc	gatttgattg	atctcagccg	600
ttggatcaaa	aatgggttat	tattgtaaaa	gattgattat	gtatttatca	aagggacacg	660
tgtaacgtgg	ttttaggatg	g				

(2) INFORMATION FOR SEQ ID NO:332:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..66
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566642

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:332:

Met	Ala	Glu	Glu	His	Arg	Cys	Gln	Thr	Pro	Glu	Ser	Asn	Arg	Leu	Cys
1				5					10					15	
Val	Asn	Asn	Cys	Gly	Phe	Leu	Gly	Ser	Ser	Ala	Thr	Met	Asn	Leu	Cys
			20					25					30		
Ser	Asn	Cys	Tyr	Gly	Asp	Leu	Cys	Leu	Lys	Gln	Gln	Gln	Gln	Ser	Ser
		35				40					45				
Ser	Ile	Lys	Ser	Thr	Val	Glu	Ser	Ala	Thr	Glu	Ala	Glu	Ser	Val	His
		50			55					60					
Asp	Val														
65															

(2) INFORMATION FOR SEQ ID NO:333:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..38
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566643

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:333:

Met	Asn	Leu	Cys	Ser	Asn	Cys	Tyr	Gly	Asp	Leu	Cys	Leu	Lys	Gln	Gln
1				5				10					15		
Gln	Gln	Ser	Ser	Ser	Ile	Lys	Ser	Thr	Val	Glu	Ser	Ala	Thr	Glu	Ala
				20				25					30		
Glu	Ser	Val	His	Asp	Val										
		35													

(2) INFORMATION FOR SEQ ID NO:334:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..41
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566644

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:334:

Met	Phe	Cys	Gly	Val	His	Arg	Tyr	Pro	Glu	Ile	His	Gly	Cys	Ser	Tyr
1				5				10				15			
Asp	Phe	Lys	Ser	Ala	Gly	Arg	Glu	Ile	Ala	Lys	Xaa	Asn	Pro	Leu	

20 25 30
Val Lys Ala Ala Lys Leu Gln Lys Ile
35 40

(2) INFORMATION FOR SEQ ID NO:335:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 556 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..556
(D) OTHER INFORMATION: / Ceres Seq. ID 1566650
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:335:
acytagaaca tcttaaatcga aaaacaaggg ttgaaaaatga agggacgtca aggagagaga 60
gttagattgt atgttcgtgg aacagtcctc ggctacaaga ggtccaagtc gaaccaatat 120
cccaacactt ctctcatcca gattgaaggt gtgaacactc aagaggagggt caattgggtac 180
aagggtgaagc gtttggctta catctacaag gcaaagacaa agaagaacgg ttctcactac 240
cgttgcattt ggggcaaaagt cactaggcct catggtaaca gcggtgttgt ccgttctaag 300
ttcacttcaa acctaccacc caagtcaatg ggagctagag tcagagtctt catgtaccct 360
agcaacatat gaggaggata gatttcaaga agtatcgtaa ggaatcgcca ttatcatttc 420
tcaggagctg tagtttatct attcactttt gttctaaact ctctgttggt ttgtatttta 480
tcttttagacg aagTwaRaac attttcttc ttgagataat attaatggaa cttcagaaaa 540
cctatgatcc cggtct

(2) INFORMATION FOR SEQ ID NO:336:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 111 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..111
(D) OTHER INFORMATION: / Ceres Seq. ID 1566651
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:336:
Met Lys Gly Arg Gln Gly Glu Arg Val Arg Leu Tyr Val Arg Gly Thr
1 5 10 15
Val Leu Gly Tyr Lys Arg Ser Lys Ser Asn Gln Tyr Pro Asn Thr Ser
20 25 30
Leu Ile Gln Ile Glu Gly Val Asn Thr Gln Glu Glu Val Asn Trp Tyr
35 40 45
Lys Gly Lys Arg Leu Ala Tyr Ile Tyr Lys Ala Lys Thr Lys Lys Asn
50 55 60
Gly Ser His Tyr Arg Cys Ile Trp Gly Lys Val Thr Arg Pro His Gly
65 70 75 80
Asn Ser Gly Val Val Arg Ser Lys Phe Thr Ser Asn Leu Pro Pro Lys
85 90 95
Ser Met Gly Ala Arg Val Arg Val Phe Met Tyr Pro Ser Asn Ile
100 105 110

(2) INFORMATION FOR SEQ ID NO:337:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 62 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..62

(D) OTHER INFORMATION: / Ceres Seq. ID 1566652

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:337:

Met	Arg	Arg	Ile	Asp	Phe	Lys	Lys	Tyr	Arg	Lys	Glu	Ser	Pro	Leu	Ser
1			5					10						15	
Phe	Leu	Arg	Ser	Cys	Ser	Leu	Ser	Ile	His	Phe	Cys	Ser	Lys	Leu	Ser
			20					25						30	
Val	Gly	Phe	Asp	Phe	Ile	Phe	Arg	Arg	Ser	Xaa	Asn	Ile	Phe	Leu	Leu
			35					40						45	
Glu	Ile	Ile	Leu	Met	Glu	Leu	Gln	Lys	Thr	Tyr	Asp	Pro	Gly		
			50					55						60	

(2) INFORMATION FOR SEQ ID NO:338:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 675 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..675

(D) OTHER INFORMATION: / Ceres Seq. ID 1566661

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:338:

atactatcaa	attgaagaag	aggaagatcc	aattggaaaag	ggttatccta	attcccagtc	60
attgatcgga	gaagatgagt	gctgttcgga	ttaaccacct	ttttggctta	ccggagacga	120
tcgagaagct	aatttcoccg	atttctcggt	ccggcgaaaag	taataacacg	agtcgtggaa	180
gaggaagtag	caataaatc	ccaatagaca	ttttggaatc	tcocaaaaaa	tacatatatt	240
atctcgatat	ccccgggaatt	tcaaaatcag	atatccaggt	tacagtggag	gaagagagga	300
ctttagtgat	aaagagtaat	gggaagagga	agagagatga	tgatgagagt	gaagaagggt	360
ctaagtatat	tagactcgag	aggagacttg	ctcagaattt	ggttaaagaag	ttccggttac	420
cagaagatgc	tgatatggct	tctgtaacgg	ctaaatatca	agaaggtatt	ttgacagttg	480
ttatcaagaa	gctaccgcga	cagcgcgcga	aacotaagac	tgttcaaatc	gctgtttctt	540
gagtagtttc	tgtgtttttg	ttttgtgtgt	gtttgttttc	tagtAttgta	attttctcgt	600
ttttggataa	aaagactctg	tttcttttat	gtgttctcta	gtcgaaattt	tgaattgaa	660
gaaataaata	ggtttt					

(2) INFORMATION FOR SEQ ID NO:339:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 155 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..155

(D) OTHER INFORMATION: / Ceres Seq. ID 1566662

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:339:

Met	Ser	Ala	Val	Ala	Ile	Asn	His	Phe	Phe	Gly	Leu	Pro	Glu	Thr	Ile
1			5					10						15	
Glu	Lys	Leu	Ile	Leu	Pro	Ile	Ser	Arg	Ser	Gly	Glu	Ser	Asn	Asn	Glu
			20					25						30	
Ser	Arg	Gly	Arg	Gly	Ser	Ser	Asn	Asn	Ile	Pro	Ile	Asp	Ile	Leu	Glu
			35					40						45	
Ser	Pro	Lys	Lys	Tyr	Ile	Phe	Tyr	Leu	Asp	Ile	Pro	Gly	Ile	Ser	Lys
			50					55						60	
Ser	Asp	Ile	Gln	Val	Thr	Val	Glu	Glu	Glu	Arg	Thr	Leu	Val	Ile	Lys
			65					70						80	
Ser	Asn	Gly	Lys	Arg	Lys	Arg	Asp	Asp	Asp	Glu	Ser	Glu	Glu	Gly	Ser
			85					90						95	
Lys	Tyr	Ile	Arg	Leu	Glu	Arg	Arg	Leu	Ala	Gln	Asn	Leu	Val	Lys	Lys
			100					105						110	
Phe	Arg	Leu	Pro	Glu	Asp	Ala	Asp	Met	Ala	Ser	Val	Thr	Ala	Lys	Tyr

115 120 125
Gln Glu Gly Ile Leu Thr Val Val Ile Lys Lys Leu Pro Pro Gln Pro
130 135 140
Pro Lys Pro Lys Thr Val Gln Ile Ala Val Ser
145 150 155

(2) INFORMATION FOR SEQ ID NO:340:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 512 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..512

(D) OTHER INFORMATION: / Ceres Seq. ID 1566663

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:340:

attttgcttt	tcactttctc	cgaacatcca	aaagcttgta	gcttgctcct	caaatcttct	60
tgaaaaatga	aggttgccgc	tgctttctct	ctcgccgttt	tgggcgga	cgtaaatcct	120
tcagccgaga	atatcaaaga	tatcatcgga	gctggttggt	ctgatgtga	tgagagagac	180
attgagcttc	tattgaaaga	agtgagtggt	aaggacattg	ctgagctgat	tgcttctggt	240
agggagaagt	tagcgctctg	gccatctggt	ggtggtgtgg	ctgtttcagc	tgctccatca	300
agcggtggtg	gtgggtgctg	tgctgtgcc	ctgcgcgaga	agaaagaagc	caagaaggaa	360
gagaaagaag	agtcctgatga	tgacatggga	ttcagctctc	tcgagtaagg	ttttgtccc	420
cacggaaagg	agtcagagatt	tgattttt	gttctcttag	tggtctggt	ttttgctcct	480
ctttgtaacc	ttggtctagt	tagcggtttt	tt			

(2) INFORMATION FOR SEQ ID NO:341:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..113

(D) OTHER INFORMATION: / Ceres Seq. ID 1566664

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:341:

Met Lys Val Ala Ala Ala Phe Leu Leu Ala Val Leu Gly Gly Asn Ala	
1 5 10 15	
Asn Pro Ser Ala Glu Asn Ile Lys Asp Ile Ile Gly Ala Val Gly Ala	
20 25 30	
Asp Val Asp Gly Glu Ser Ile Glu Leu Leu Lys Glu Val Ser Gly	
35 40 45	
Lys Asp Ile Ala Glu Leu Ile Ala Ser Gly Arg Glu Lys Leu Ala Ser	
50 55 60	
Val Pro Ser Gly Gly Gly Val Ala Val Ser Ala Ala Pro Ser Ser Gly	
65 70 75 80	
Gly Gly Gly Ala Ala Ala Ala Pro Ala Glu Lys Lys Glu Ala Lys	
85 90 95	
Lys Glu Glu Lys Glu Glu Ser Asp Asp Asp Met Gly Phe Ser Leu Phe	
100 105 110	

Glu

(2) INFORMATION FOR SEQ ID NO:342:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 822 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..822

(D) OTHER INFORMATION: / Ceres Seq. ID 1566665

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:342:

```
gtcgtctctca attaaacccct aaaaccctcc tcagaagaga ggcagagaga aaaaaaacgc      60
agTcttttcgg gaatctgtga aaggagaaaa gatgagacca ccaatgagag gcggcggggg      120
tttcctgtgga aggggaggac gagacggtgg tgggtgcggt aggttcggtg gaggagggcg      180
tagattccggt ggaggaggag gacgcttttg tgggtggaggc ggtcgtcttg gtggttttag      240
agacgaaggt cctcctagcg aagtcgtgga tgttgcaact tctgttcacg cttgcgaggg      300
agatgctgtg accaaaactct cacaggagaa gattcctcat tttaacgcct cgaatcactc      360
agagaacaaag actcagatgt ggaagtaga tgaaactcttt gcccacaatta atgaatcttt      420
gtttttctaat aaaaatgatgg aaggtattgt agccacctcg tattctccag gagataaagtt      480
tttctcagac ccttcaaacg ttttgccact cgctcgattc ctctctcagc caaagggtca      540
gtcaacgggtt ggcagctggag gtgcaggtcg tggaaagaggt gatagtagag gtcgtggaag      600
aggtggatca tttagtagag gttagaggtgc tccaagaggt ggtagatttc caccacggg      660
tggctctcgt ggaagctttg gaggccgagg aagattttag gttctctccc tgctttataa      720
gccttatcca aactgttacc cttgttttta tgaatgacta tctgttctccc gtatttctcaa      780
tttccaagac tttgttttta tctatggagt aaaaaatttt gc
```

(2) INFORMATION FOR SEQ ID NO:343:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 202 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..202

(D) OTHER INFORMATION: / Ceres Seq. ID 1566666

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:343:

```
Met Arg Pro Met Arg Gly Gly Gly Gly Phe Arg Gly Arg Gly Gly
1          5          10          15
Arg Asp Gly Gly Gly Gly Arg Phe Gly Gly Gly Gly Arg Phe
20          25          30
Gly Gly Gly Gly Gly Arg Phe Gly Gly Gly Gly Gly Arg Phe Gly Gly
35          40          45
Phe Arg Asp Glu Gly Pro Pro Ser Glu Val Val Asp Val Ala Thr Phe
50          55          60
Val His Ala Cys Glu Gly Asp Ala Val Thr Lys Leu Ser Gln Glu Lys
65          70          75
Ile Pro His Phe Asn Ala Pro Ile Tyr Leu Glu Asn Lys Thr Gln Ile
85          90          95
Gly Lys Val Asp Glu Ile Phe Gly Pro Ile Asn Glu Ser Leu Phe Ser
100         105         110
Ile Lys Met Met Glu Gly Ile Val Ala Thr Ser Tyr Ser Pro Gly Asp
115         120         125
Lys Phe Phe Ile Asp Pro Tyr Lys Leu Leu Pro Leu Ala Arg Phe Leu
130         135         140
Pro Gln Pro Lys Gly Gln Ser Thr Gly Gly Arg Gly Gly Ala Gly Arg
145         150         155
Gly Arg Gly Asp Ser Arg Gly Arg Gly Arg Gly Ser Phe Ser Arg
165         170         175
Gly Arg Gly Ala Pro Arg Gly Gly Arg Phe Pro Pro Arg Gly Gly Ser
180         185         190
Arg Gly Ser Phe Arg Gly Arg Gly Arg Phe
195         200
```

(2) INFORMATION FOR SEQ ID NO:344:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 198 amino acids

(B) TYPE: amino acid

- (C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..198
(D) OTHER INFORMATION: / Ceres Seq. ID 1566667

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:344:

Met	Arg	Gly	Gly	Gly	Gly	Phe	Arg	Gly	Arg	Gly	Gly	Arg	Asp	Gly	Gly
1			5					10					15		
Gly	Gly	Gly	Arg	Phe	Gly	Gly	Gly	Gly	Arg	Phe	Gly	Gly	Gly	Gly	Gly
			20					25					30		
Gly	Arg	Phe	Phe	Gly	Gly	Gly	Gly	Arg	Phe	Gly	Gly	Phe	Arg	Asp	Glu
			35					40				45			
Gly	Pro	Pro	Ser	Glu	Val	Val	Asp	Val	Ala	Thr	Phe	Val	His	Ala	Cys
			50					55				60			
Glu	Gly	Asp	Ala	Val	Thr	Lys	Leu	Ser	Gln	Glu	Lys	Ile	Pro	His	Phe
			65					70				75			80
Asn	Ala	Pro	Ile	Tyr	Leu	Glu	Asn	Lys	Thr	Gln	Ile	Gly	Lys	Val	Asp
			85					90				95			
Glu	Ile	Phe	Gly	Pro	Ile	Asn	Glu	Ser	Leu	Phe	Ser	Ile	Lys	Met	Met
			100					105				110			
Glu	Gly	Ile	Val	Ala	Thr	Ser	Tyr	Ser	Pro	Gly	Asp	Lys	Phe	Phe	Ile
			115					120				125			
Asp	Pro	Tyr	Lys	Leu	Leu	Pro	Leu	Ala	Arg	Phe	Leu	Pro	Gln	Pro	Lys
			130					135				140			
Gly	Gln	Ser	Thr	Gly	Gly	Arg	Gly	Gly	Ala	Gly	Arg	Gly	Arg	Gly	Asp
			145					150				155			160
Ser	Arg	Gly	Arg	Gly	Arg	Gly	Gly	Ser	Phe	Ser	Arg	Gly	Arg	Gly	Ala
			165					170				175			
Pro	Arg	Gly	Gly	Arg	Phe	Pro	Pro	Arg	Gly	Gly	Ser	Arg	Gly	Ser	Phe
			180					185				190			
Arg	Gly	Arg	Gly	Arg	Phe										
			195												

(2) INFORMATION FOR SEQ ID NO:345:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1622 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..1622
(D) OTHER INFORMATION: / Ceres Seq. ID 1566671

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:345:

ttaaaggat	aaataacgat	ggcttcgcga	tgacgagttc	gcacgccaag	ctatagctgg	60
gataaaccog	gtcaacatag	aacgagtcac	gtcttatcca	coggtcagca	atcttgaccoc	120
tgaatctctac	ggaccaggtc	ttaactccgc	tctcacggaa	gaccacatca	tcgggtcaact	180
tgatggctta	acggtacaac	aagcggtaga	gatgaaccgt	ttgtttatgg	tggactacca	240
tgacatatac	ttaccggttc	tagatagaat	caacgcgctt	gatggacgca	aggcttacgc	300
gactcgaaac	atattgtctt	tgaccogaat	cggtaacact	aagcctatcg	ccatcgagct	360
aagctccctct	tctcaatcaa	gctcaaacca	aaagtccaag	cgcgttggtca	caactccagt	420
agacgcaacc	tccaactgga	tgtggcagct	agccaaggcc	cacgtttgggt	ccaatgacgc	480
tggtgtccac	caagcttgta	atcattggtt	acgtactcat	gcgtgtttgg	aaacgcttat	540
attagctgct	catagacaaat	taagcgcaat	gcattccgata	ttcaaatatt	tagacctca	600
catgaggtac	actttggaga	tcaatgccgt	ggcacgacag	actttgatta	gtcggcagcg	660
tgtgatcgaa	tcgtgtctca	ctgctgtgtca	atacgtgtca	gagattagtt	ccgctgcgta	720
taagaacaag	tggcggtttg	atatggaag	tctccctgct	gatctcatcc	gaagggggat	780
ggctgttcca	gacccaacac	aaccacatgg	gcttaaatga	cttggtgaag	actaccatcg	840
ccaacgacgg	ttctttatta	tggtccgcga	tccaaacttg	ggtccgaacc	tacgtggaac	900

gttattacgc	aaactcgaac	ctaataccaaa	cgcatactga	gctccaagcc	tggtactctg	960
agtcacatcaa	cgtarGtcac	gctgatacacc	gcgcgcgcga	gtgggtggccg	aaagctttcca	1020
agtcggaaga	tctcgtctccc	gtcactccaaa	ccatcatctg	gctcgccctcc	gcacaaacag	1080
cgcgcactcaa	cttcgggacaa	tatccttaacg	gtggctacgt	cccgaaccga	ccaccgctaa	1140
tgctcgtggt	gattcccgac	gagtcagatc	cgcagttcac	gagttttatc	gaagatcctc	1200
aaaagttatt	tttctcgtcg	atgcccgagtt	tattgcaaac	gacgaagttt	atggcgggtg	1260
ttgatcacatt	gtcgacacat	tgcgcggatg	aggagttat	cggagagaga	caacaaccgt	1320
cgatatggac	tgagatgctc	gagatcgtag	atgcgtttta	tggaattctc	gcggaaatcg	1380
gacggataga	gaaggagatt	gacaagagga	atcgtgatcc	tagctgtagg	aatcgcgtgt	1440
gcgcgggagt	gttaccgtag	gagttgatgg	ctccgagttc	tgaaccgggt	gttacgtgta	1500
gaggagtccc	taatagtgta	tctatttaga	attattcaat	ttttcaaggt	atagagaatt	1560
ttataagtat	ataaattagat	tttgacgcag	tatggtttat	ttgcgatat	tgtaaaattc	1620

tt
(2) INFORMATION FOR SEQ ID NO:346:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 312 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..312
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566672

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:346:

Ser	Lys	Asp	Lys	Tyr	Ala	Trp	Leu	Arg	Asp	Asp	Glu	Phe	Ala	Arg	Gln
1			5					10						15	
Ala	Ile	Ala	Gly	Ile	Asn	Pro	Val	Asn	Ile	Glu	Arg	Val	Thr	Ser	Tyr
			20					25					30		
Pro	Pro	Val	Ser	Asn	Leu	Asp	Pro	Glu	Ile	Tyr	Gly	Pro	Gly	Leu	His
		35				40						45			
Ser	Ala	Leu	Thr	Glu	Asp	His	Ile	Ile	Gly	Gln	Leu	Asp	Gly	Leu	Thr
		50				55					60				
Val	Gln	Gln	Ala	Leu	Glu	Met	Asn	Arg	Leu	Phe	Met	Val	Asp	Tyr	His
65					70				75					80	
Asp	Ile	Tyr	Leu	Pro	Phe	Leu	Asp	Arg	Ile	Asn	Ala	Leu	Asp	Gly	Arg
			85						90					95	
Lys	Ala	Tyr	Ala	Thr	Arg	Thr	Ile	Leu	Phe	Leu	Thr	Arg	Leu	Gly	Thr
			100					105					110		
Leu	Lys	Pro	Ile	Ala	Ile	Glu	Leu	Ser	Leu	Pro	Ser	Gln	Ser	Ser	Ser
		115				120						125			
Asn	Gln	Lys	Ser	Lys	Arg	Val	Val	Thr	Pro	Pro	Val	Asp	Ala	Thr	Ser
		130				135						140			
Asn	Trp	Met	Trp	Gln	Leu	Ala	Lys	Ala	His	Val	Gly	Ser	Asn	Asp	Ala
145					150					155				160	
Gly	Val	His	Gln	Leu	Val	Asn	His	Trp	Leu	Arg	Thr	His	Ala	Cys	Leu
			165						170					175	
Glu	Pro	Phe	Ile	Leu	Ala	Ala	His	Arg	Gln	Leu	Ser	Ala	Met	His	Pro
			180					185						190	
Ile	Phe	Lys	Leu	Leu	Asp	Pro	His	Met	Arg	Tyr	Thr	Leu	Glu	Ile	Asn
		195				200						205			
Ala	Val	Ala	Arg	Gln	Thr	Leu	Ile	Ser	Ala	Asp	Gly	Val	Ile	Glu	Ser
		210				215						220			
Cys	Phe	Thr	Ala	Gly	Gln	Tyr	Gly	Leu	Glu	Ile	Ser	Ser	Ala	Ala	Tyr
225					230					235				240	
Lys	Asn	Lys	Trp	Arg	Phe	Asp	Met	Glu	Gly	Leu	Pro	Ala	Asp	Leu	Ile
			245					250						255	
Arg	Arg	Gly	Met	Ala	Val	Pro	Asp	Pro	Thr	Gln	Pro	His	Gly	Leu	Lys
			260					265						270	
Leu	Leu	Val	Glu	Asp	Tyr	Pro	Cys	Gln	Arg	Arg	Ser	Leu	Ile	Met	Val
		275						280						285	

Arg Asn Pro Asn Leu Gly Pro Asn Leu Arg Gly Thr Leu Leu Arg Lys
290 295 300
Leu Glu Pro Asn Pro Asn Arg Tyr
305 310

(2) INFORMATION FOR SEQ ID NO:347:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 242 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..242
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566673

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:347:

Met Asn Arg Leu Phe Met Val Asp Tyr His Asp Ile Tyr Leu Pro Phe
1 5 10 15
Leu Asp Arg Ile Asn Ala Leu Asp Gly Arg Lys Ala Tyr Ala Thr Arg
20 25 30
Thr Ile Leu Phe Leu Thr Arg Leu Gly Thr Leu Lys Pro Ile Ala Ile
35 40 45
Glu Leu Ser Leu Pro Ser Gln Ser Ser Asn Gln Lys Ser Lys Arg
50 55 60
Val Val Thr Pro Pro Val Asp Ala Thr Ser Asn Trp Met Trp Gln Leu
65 70 75 80
Ala Lys Ala His Val Gly Ser Asn Asp Ala Gly Val His Gln Leu Val
85 90 95
Asn His Trp Leu Arg Thr His Ala Cys Leu Glu Pro Phe Ile Leu Ala
100 105 110
Ala His Arg Gln Leu Ser Ala Met His Pro Ile Phe Lys Leu Leu Asp
115 120 125
Pro His Met Arg Tyr Thr Leu Glu Ile Asn Ala Val Ala Arg Gln Thr
130 135 140
Leu Ile Ser Ala Asp Gly Val Ile Glu Ser Cys Phe Thr Ala Gly Gln
145 150 155 160
Tyr Gly Leu Glu Ile Ser Ser Ala Ala Tyr Lys Asn Lys Trp Arg Phe
165 170 175
Asp Met Glu Gly Leu Pro Ala Asp Leu Ile Arg Arg Gly Met Ala Val
180 185 190
Pro Asp Pro Thr Gln Pro His Gly Leu Lys Leu Leu Val Glu Asp Tyr
195 200 205
Pro Cys Gln Arg Arg Ser Leu Ile Met Val Arg Asn Pro Asn Leu Gly
210 215 220
Pro Asn Leu Arg Gly Thr Leu Leu Arg Lys Leu Glu Pro Asn Pro Asn
225 230 235 240
Arg Tyr

(2) INFORMATION FOR SEQ ID NO:348:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 240 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..240
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566674

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:348:

Met Gly Leu Asn Tyr Leu Leu Lys Thr Thr His Ala Asn Asp Gly Leu

1	5	10	15
Leu Leu Trp Ser Ala Ile Gln Thr Trp Val Arg Thr Tyr Val Glu Arg			
	20	25	30
Tyr Tyr Ala Asn Ser Asn Leu Ile Gln Thr Asp Thr Glu Leu Gln Ala			
	35	40	45
Trp Tyr Ser Glu Ser Ile Asn Val Xaa His Ala Asp His Arg Asp Ala			
	50	55	60
Glu Trp Trp Pro Lys Leu Ser Thr Val Glu Asp Leu Val Ser Val Ile			
	65	70	75
Thr Thr Ile Ile Trp Leu Ala Ser Ala Gln His Ala Ala Leu Asn Phe			
	85	90	95
Gly Gln Tyr Pro Tyr Gly Gly Tyr Val Pro Asn Arg Pro Pro Leu Met			
	100	105	110
Arg Arg Leu Ile Pro Asp Glu Ser Asp Pro Glu Phe Thr Ser Phe Ile			
	115	120	125
Glu Asp Pro Gln Lys Tyr Phe Phe Ser Ser Met Pro Ser Leu Leu Gln			
	130	135	140
Thr Thr Lys Phe Met Ala Val Val Asp Thr Leu Ser Thr His Ser Pro			
	145	150	155
Asp Glu Glu Tyr Ile Gly Glu Arg Gln Gln Pro Ser Ile Trp Thr Gly			
	165	170	175
Asp Ala Glu Ile Val Asp Ala Phe Tyr Gly Phe Ser Ala Glu Ile Gly			
	180	185	190
Arg Ile Glu Lys Glu Ile Asp Lys Arg Asn Arg Asp Pro Ser Cys Arg			
	195	200	205
Asn Arg Cys Gly Ala Gly Val Leu Pro Tyr Glu Leu Met Ala Pro Ser			
	210	215	220
Ser Glu Pro Gly Val Thr Cys Arg Gly Val Pro Asn Ser Val Ser Ile			
	225	230	235
			240

(2) INFORMATION FOR SEQ ID NO:349:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 847 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..847
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566683

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:349:

atgactgctt	cactttctct	ttctcttttt	ttcaagtagt	ttgggagaga	gaagagaaga	60
agaagacacc	ctttaagcaa	aacagaggat	tttcattctc	tgttctggtt	gaattattac	120
taactatca	tcttgtgtgt	ctcttcgtcg	acaatgtcgg	gaaacaaga	agaagaggat	180
ctcgtatcc	atggaatcaa	aactaagatc	cgtgtcgttc	cagattttcc	caagaaagga	240
ataatgtttc	aagacataac	aacagtgttg	ttggatccga	aagccctcaa	agacacaatt	300
gatctgtttg	tggagaggtta	cagagacaag	aacatctcag	tggttcgagg	aatagaggct	360
cgtgtgtttc	tattcgttcc	accgatcgcg	ctaGccattg	gagcaaaaatt	tgttcctctg	420
cgcaaaccca	agaaactacc	tggtgaaaca	atatttgagg	aatacagagt	ggaatatgga	480
aatgacgcgc	tagagatgca	cataggagcc	gtcgaggctg	gcgatcgatc	tttgttgttt	540
gatgatctta	tcgcgactgg	tggtactctc	tcgcgctgcc	ttaaacttgt	cgagagggtt	600
ggagcagaag	ttgtggaaatg	tgcatgtgtg	atcgagttac	ccgaattaaa	gggaaggcag	660
agacttaagg	ggaagccact	atgtatgctt	gtggagtacc	gatgatgatt	ttagctttac	720
ttatttggat	aaaattattc	gggttaattaa	tttatgctcc	gaaaattcgg	attatgcaga	780
ctcttattta	tgggattcta	caatattttg	atttaaattc	tagcggatta	gctggaagaa	840
ataatcc						

(2) INFORMATION FOR SEQ ID NO:350:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 183 amino acids

- (B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..183
(D) OTHER INFORMATION: / Ceres Seq. ID 1566684
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:350:

Met	Ser	Gly	Asn	Lys	Glu	Glu	Glu	Asp	Pro	Arg	Ile	His	Gly	Ile	Lys
1			5					10					15		
Thr	Lys	Ile	Arg	Val	Val	Pro	Asp	Phe	Pro	Lys	Lys	Gly	Ile	Met	Phe
		20					25					30			
Gln	Asp	Ile	Thr	Thr	Val	Leu	Leu	Asp	Pro	Lys	Ala	Phe	Lys	Asp	Thr
	35					40					45				
Ile	Asp	Leu	Phe	Val	Glu	Arg	Tyr	Arg	Asp	Lys	Asn	Ile	Ser	Val	Val
	50				55					60					
Ala	Gly	Ile	Glu	Ala	Arg	Gly	Phe	Leu	Phe	Gly	Pro	Pro	Ile	Ala	Leu
65			70				75							80	
Ala	Ile	Gly	Ala	Lys	Phe	Val	Pro	Leu	Arg	Lys	Pro	Lys	Lys	Leu	Pro
			85				90						95		
Gly	Glu	Thr	Ile	Phe	Glu	Glu	Tyr	Glu	Leu	Glu	Tyr	Gly	Asn	Asp	Arg
	100						105					110			
Leu	Glu	Met	His	Ile	Gly	Ala	Val	Glu	Ala	Gly	Asp	Arg	Ser	Leu	Val
	115					120					125				
Val	Asp	Asp	Leu	Ile	Ala	Thr	Gly	Thr	Leu	Cys	Ala	Ala	Ile	Asn	
	130				135				140						
Leu	Leu	Glu	Arg	Val	Gly	Ala	Glu	Val	Val	Glu	Cys	Ala	Cys	Val	Ile
145			150				155							160	
Glu	Leu	Pro	Glu	Leu	Lys	Gly	Arg	Gln	Arg	Leu	Lys	Gly	Lys	Pro	Leu
			165				170						175		
Cys	Met	Leu	Val	Glu	Tyr	Arg									
			180												

(2) INFORMATION FOR SEQ ID NO:351:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 153 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..153
(D) OTHER INFORMATION: / Ceres Seq. ID 1566685
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:351:

Met	Phe	Gln	Asp	Ile	Thr	Thr	Val	Leu	Leu	Asp	Pro	Lys	Ala	Phe	Lys
1			5					10					15		
Asp	Thr	Ile	Asp	Leu	Phe	Val	Glu	Arg	Tyr	Arg	Asp	Lys	Asn	Ile	Ser
		20					25					30			
Val	Val	Ala	Gly	Ile	Glu	Ala	Arg	Gly	Phe	Leu	Phe	Gly	Pro	Pro	Ile
	35				40					45					
Ala	Leu	Ala	Ile	Gly	Ala	Lys	Phe	Val	Pro	Leu	Arg	Lys	Pro	Lys	Lys
	50				55					60					
Leu	Pro	Gly	Glu	Thr	Ile	Phe	Glu	Glu	Tyr	Glu	Leu	Glu	Tyr	Gly	Asn
65			70				75							80	
Asp	Arg	Leu	Glu	Met	His	Ile	Gly	Ala	Val	Glu	Ala	Gly	Asp	Arg	Ser
		85					90					95			
Leu	Val	Val	Asp	Asp	Leu	Ile	Ala	Thr	Gly	Gly	Thr	Leu	Cys	Ala	Ala
	100					105						110			
Ile	Asn	Leu	Leu	Glu	Arg	Val	Gly	Ala	Glu	Val	Val	Glu	Cys	Ala	Cys
	115					120						125			

Val Ile Glu Leu Pro Glu Leu Lys Gly Arg Gln Arg Leu Lys Gly Lys
130 135 140
Pro Leu Cys Met Leu Val Glu Tyr Arg
145 150

(2) INFORMATION FOR SEQ ID NO:352:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 604 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..604
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566691

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:352:

gcgactctcc	tctctgtttc	gttttttttt	cccttcattc	ttcttatctc	ctcactactt	60
tcgaacaagg	aggaacccta	atctcaagat	gaatagggaa	aagttgatga	agatggctaa	120
caccgtccgc	actggcgga	aggggtacagt	cagaagaaag	aagaaggctg	tgcaacaagac	180
caatacaact	gatgacaaga	ggctccagag	cacacttaag	agaattggag	ttaactccat	240
tcccgtattt	gaagaagtta	acatctttta	ggatgatgtt	gttattcagt	tcatacaacc	300
taaggttcaa	gcttcaattg	ctgcaaacac	atgggttggt	agcgggttct	ctcagaccaa	360
aaaattgcaa	gatatccctc	ctcagatcat	cagccaaact	ggaccagaca	acatggacaa	420
cctgaagaag	ctagcagagc	agttccagaa	acaggtctct	ggtgaaggta	atgccgcctc	480
agcaaccatt	caagaagagg	atgatgacga	tgtccCagag	cttgttggag	agacattcga	540
aactgctgct	gaagagaaag	caccagctgc	tgctgcttct	tcttagagag	aaaagagcga	600

gacc

(2) INFORMATION FOR SEQ ID NO:353:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 194 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..194
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566692

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:353:

Arg	Leu	Ser	Ser	Leu	Phe	Arg	Phe	Phe	Phe	Leu	Ser	Phe	Phe	Leu	Ser
1			5					10					15		
Pro	His	Thr	Leu	Arg	Thr	Arg	Arg	Asn	Pro	Asn	Leu	Lys	Met	Asn	Arg
			20					25					30		
Glu	Lys	Leu	Met	Lys	Met	Ala	Asn	Thr	Val	Arg	Thr	Gly	Gly	Lys	Gly
			35				40					45			
Thr	Val	Arg	Arg	Lys	Lys	Lys	Ala	Val	His	Lys	Thr	Asn	Thr	Thr	Asp
			50			55					60				
Asp	Lys	Arg	Leu	Gln	Ser	Thr	Leu	Lys	Arg	Ile	Gly	Val	Asn	Ser	Ile
			65			70				75				80	
Pro	Ala	Ile	Glu	Glu	Val	Asn	Ile	Phe	Lys	Asp	Asp	Val	Val	Ile	Gln
			85					90					95		
Phe	Ile	Asn	Pro	Lys	Val	Gln	Ala	Ser	Ile	Ala	Ala	Asn	Thr	Trp	Val
			100				105						110		
Val	Ser	Gly	Ser	Pro	Gln	Thr	Lys	Lys	Leu	Gln	Asp	Ile	Leu	Pro	Gln
			115				120					125			
Ile	Ile	Ser	Gln	Leu	Gly	Pro	Asp	Asn	Met	Asp	Asn	Leu	Lys	Lys	Leu
			130			135					140				
Ala	Glu	Gln	Phe	Gln	Lys	Gln	Ala	Ser	Gly	Glu	Gly	Asn	Ala	Ala	Ser
			145			150				155				160	
Ala	Thr	Ile	Gln	Glu	Glu	Asp	Asp	Asp	Asp	Val	Pro	Glu	Leu	Val	Gly
			165					170						175	

Glu Thr Phe Glu Thr Ala Ala Glu Glu Lys Ala Pro Ala Ala Ala Ala
180 185 190
Ser Ser

(2) INFORMATION FOR SEQ ID NO:354:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 165 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..165
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566693

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:354:

Met Asn Arg Glu Lys Leu Met Lys Met Ala Asn Thr Val Arg Thr Gly
1 5 10 15
Gly Lys Gly Thr Val Arg Arg Lys Lys Lys Ala Val His Lys Thr Asn
20 25 30
Thr Thr Asp Asp Lys Arg Leu Gln Ser Thr Leu Lys Arg Ile Gly Val
35 40 45
Asn Ser Ile Pro Ala Ile Glu Glu Val Asn Ile Phe Lys Asp Asp Val
50 55 60
Val Ile Gln Phe Ile Asn Pro Lys Val Gln Ala Ser Ile Ala Ala Asn
65 70 75 80
Thr Trp Val Val Ser Gly Ser Pro Gln Thr Lys Lys Leu Gln Asp Ile
85 90 95
Leu Pro Gln Ile Ile Ser Gln Leu Gly Pro Asp Asn Met Asp Asn Leu
100 105 110
Lys Lys Leu Ala Glu Gln Phe Gln Lys Gln Ala Ser Gly Glu Gly Asn
115 120 125
Ala Ala Ser Ala Thr Ile Gln Glu Glu Asp Asp Asp Val Pro Glu
130 135 140
Leu Val Gly Glu Thr Phe Glu Thr Ala Ala Glu Glu Lys Ala Pro Ala
145 150 155 160
Ala Ala Ala Ser Ser
165

(2) INFORMATION FOR SEQ ID NO:355:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 159 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..159
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566694

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:355:

Met Lys Met Ala Asn Thr Val Arg Thr Gly Lys Gly Thr Val Arg
1 5 10 15
Arg Lys Lys Lys Ala Val His Lys Thr Asn Thr Thr Asp Asp Lys Arg
20 25 30
Leu Gln Ser Thr Leu Lys Arg Ile Gly Val Asn Ser Ile Pro Ala Ile
35 40 45
Glu Glu Val Asn Ile Phe Lys Asp Asp Val Val Ile Gln Phe Ile Asn
50 55 60
Pro Lys Val Gln Ala Ser Ile Ala Ala Asn Thr Trp Val Val Ser Gly
65 70 75 80
Ser Pro Gln Thr Lys Lys Leu Gln Asp Ile Leu Pro Gln Ile Ile Ser

Met	Pro	Lys	Arg	Glu	Thr	Lys	Lys	Ile	Lys	Pro	Ser	Gln	Glu	Val	Ile
1			5						10				15		
Lys	Glu	Gly	Pro	Phe	Leu	Val	Thr	Ile	His	Leu	Lys	Gly	Ile	Tyr	Met
			20					25					30		
Ser	Asn	Tyr	Thr	Asn	Ser	Pro	Cys	Ala	Ala	Cys	Lys	Phe	Leu	Arg	Arg
		35					40					45			
Lys	Cys	Thr	Ser	Asp	Cys	Val	Phe	Ala	Pro	Tyr	Phe	Pro	Pro	Glu	Glu
	50					55				60					
Pro	Thr	Lys	Phe	Ala	Asn	Val	His	Arg	Ile	Phe	Gly	Ala	Ser	Asn	Val
					70					75				80	
Ser	Lys	Ile	Leu	His	Glu	Val	Xaa	Ser	Pro	Ser	Ala	Gly	Arg	Cys	Gly
			85						90				95		

Gln Leu Ala Gly Leu Arg Gly Gly Ser Thr Thr
100 105

(2) INFORMATION FOR SEQ ID NO:358:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 76 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..76
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566701

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:358:

```
Met Ser Asn Tyr Thr Asn Ser Pro Cys Ala Ala Cys Lys Phe Leu Arg
1          5          10          15
Arg Lys Cys Thr Ser Asp Cys Val Phe Ala Pro Tyr Phe Pro Pro Glu
20          25          30
Glu Pro Thr Lys Phe Ala Asn Val His Arg Ile Phe Gly Ala Ser Asn
35          40          45
Val Ser Lys Ile Leu His Glu Val Xaa Ser Pro Ser Ala Gly Arg Cys
50          55          60
Gly Gln Leu Ala Gly Leu Arg Gly Gly Ser Thr Thr
65          70          75
```

(2) INFORMATION FOR SEQ ID NO:359:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 77 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..77
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566702

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:359:

```
Met His Val Arg Leu Arg Ile Arg Thr Leu Phe Ser Ala Gly Gly Thr
1          5          10          15
Tyr Lys Val Cys Glu Arg Pro Pro Asp Ile Arg Gly Lys Gln Cys Glu
20          25          30
Gln Asp Pro Pro Arg Ser Gly Xaa Pro Ile Ser Gly Lys Met Arg Ser
35          40          45
Thr Arg Trp Leu Thr Arg Arg Lys His Asp Leu Lys Ile Gln Cys Met
50          55          60
Ala Ala Leu Glu Arg Ser Arg Cys Ser Lys Asp Arg Ser
65          70          75
```

(2) INFORMATION FOR SEQ ID NO:360:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 960 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..960
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566707

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:360:

```
accattaaac caggtctttaa gtacaaaact tcaaacaaaa ggtcaaaagc taattctttt      60
tttttgctaa gaaaaactaa ttcttctctc ttgcacctc caagtctcaa gcatcattag      120
ataaacaaat cctattcccg tcatggcagc aatgaccgcg gcagcagttc cagcaactgg      180
```


atctttccag	aaacaagacg	aggagtggcg	tgcggttctg	tctcctgagc	agtttagggg	240
tctcagacta	aaaggcacag	agtaagaagt	cctctagggt	ttttattttt	atttttctgt	300
ttacttgagc	agcaagaagt	ttacctgaac	atgttgtaa	tggttaattt	gggtatttag	360
taaacgagcg	aaaggagagt	ttacaagaa	gttcgaggaa	gggacttata	gttgtgctgg	420
ttgtggaact	gctctttata	aatcgaccac	taagtctgac	tccggttgcg	gttgccctgc	480
gttcttcgac	gccatccccc	gtgctattaa	acaaactgta	attogttcac	tctttctctc	540
tagcaaataa	catatttoga	gcatccatat	tcgtgaaact	cattgactat	aacattgact	600
attttagcca	aaccggcaaa	cccatttaag	gattgtaatt	acaataacta	atttgatgtt	660
tttaaatgta	tatagccaga	agcaggtgga	agaagaatgg	agataacatg	tcagatgtgt	720
gatggacatt	taggccaagt	tttcaaaagg	gaagggttact	ctactccaac	cgatcaacgt	780
caCtgcggtt	acagtgcttc	tctcaaatc	tctctgctg	gttctcccca	ataatcatat	840
cattgatcgg	accaatttat	ctcatgaaat	caagaatcta	ttctatgata	tcgtgtgagct	900
tgctaggttt	ctttcccata	ctcatgtaat	attatgattc	ctatgtgtgt	gtttttctct	960

(2) INFORMATION FOR SEQ ID NO:361:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 40 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..40
(D) OTHER INFORMATION: / Ceres Seq. ID 1566708

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:361:

Met	Ala	Ala	Met	Thr	Ala	Ala	Ala	Val	Pro	Ala	Thr	Gly	Ser	Phe	Gln
1			5					10					15		
Lys	Gln	Asp	Glu	Glu	Trp	Arg	Ala	Val	Leu	Ser	Pro	Glu	Gln	Phe	Arg
			20					25					30		
Val	Leu	Arg	Leu	Lys	Gly	Thr	Glu								
			35				40								

(2) INFORMATION FOR SEQ ID NO:362:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 45 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..45
(D) OTHER INFORMATION: / Ceres Seq. ID 1566709

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:362:

Met	Glu	Ile	Thr	Cys	Ala	Val	Cys	Asp	Gly	His	Leu	Gly	His	Val	Phe
1				5				10					15		
Lys	Gly	Glu	Gly	Tyr	Ser	Thr	Pro	Thr	Asp	Gln	Arg	His	Cys	Val	Asn
				20				25					30		
Ser	Val	Ser	Leu	Lys	Phe	Ser	Ser	Ala	Gly	Ser	Ser	Gln			
			35				40					45			

(2) INFORMATION FOR SEQ ID NO:363:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 66 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..66
(D) OTHER INFORMATION: / Ceres Seq. ID 1566710

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:363:

Met Phe Ser Lys Ala Lys Val Thr Leu Leu Gln Pro Ile Asn Val Thr
1 5 10 15
Ala Leu Thr Val Ser Leu Ser Asn Ser Leu Leu Leu Val Pro Pro Asn
20 25 30
Asn His Ile Ile Asp Arg Thr Thr Leu Ser His Glu Ile Lys Asn Leu
35 40 45
Phe Tyr Asp Leu Cys Glu Leu Ala Arg Phe Leu Ser His Thr His Val
50 55 60
Ile Leu
65

(2) INFORMATION FOR SEQ ID NO:364:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1279 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1279
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566711

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:364:

gttttgggtgt ttcttgcgtcg acgtgcgtat ctccaatctct attactcccc ttcttcaatg 60
atcataaaac ctacttcgat tctactcctt atcaactgaa tcaccgaaaa acctcacctt 120
ttttcttttt ccgatcatgg ggaatctgat cagtttgatc ttctgtgcgc ggagaaggca 180
gaggagcaat attctctcgg cgaatggaac ggctctcttt gaactccac cgaacagatt 240
tgtattcgcc gcgcgcgcac catatctgaa ccttaaccct aactacgttg accagtatcc 300
aggttaactgc ctctctcgcg cagtaactga gcgcgcgatg ctacgtgaca atttcaacca 360
tttgcatacac tatctctcca acagtaccac actactctat cctttgttcc acggcggtag 420
ataccctata ctgcgcgcctc ctacgtacgt ccaccagaaa gccgtcacga ttctgtaacga 480
tgttaactcg aagaagaaga ctttaacgct cataccgcac ccggagaatc cgaatcgact 540
tcttgtctcc ttcaactattg atgcattccat gcccggaagg atcacagttg ttttttttgc 600
tacagaagat gcagaatgta atcttagagc tacaaaaggaa gatactttgc ctccaatcac 660
ttttgatitc ggagaaggac ttggtcagaa gtccatacaa tcatctggaa cgggtataga 720
cttgacggcg tttaaaagatt ccgagctatt caaggagggtg gatacagatg tcttcccggt 780
ggcggttaag gcggaggcaa ctccagcgga agaaggaaa tctGgttcca ccaatgtgca 840
gattactcaa gtgggtgata ccaaggagaa agggagagatt aaaatagaag tgggtgaagca 900
gataactatg gtgaataaga ggaggtatga gctgcttgag atttatggga ttgagaacac 960
gggtgatggt tccgatgagg gaaaggaatg tgtgtgatgc ttgtctgaac caccgcatac 1020
aactgttctt cctctgcagc acatgtgtat gtgtagcggg tgcgcaaaag cgttaaggtt 1080
tcagacaaat ctgtgccagc ttgtcagaca aactgttgag atgcttttgc agattaacaa 1140
gaacggatga aatggagatg gagaatgaac aaattttagt aagcaatcga cttgtgtaat 1200
atatgccatg cttaattaag acgtaaaacg ttatggttca atatattata agtggaacat 1260
gagttcttaa atagcaatg

(2) INFORMATION FOR SEQ ID NO:365:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 337 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..337
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566712

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:365:

Met Gly Asn Leu Ile Ser Leu Ile Phe Cys Cys Gly Arg Arg Gln Arg
1 5 10 15
Ser Asn Ile Pro Pro Ala Met Glu Thr Ala Pro Leu Glu Leu Pro Pro
20 25 30

```

Asn Arg Phe Val Phe Ala Ala Ala Pro Pro Tyr Leu Asn Pro Asn Pro
      35      40      45
Asn Tyr Val Asp Gln Tyr Pro Gly Asn Cys Leu Pro Pro Val Thr
      50      55      60
Glu Pro Pro Met Leu Pro Tyr Asn Phe Asn His Leu His His Tyr Pro
      65      70      75      80
Pro Asn Ser Tyr Gln Leu Pro His Pro Leu Phe His Gly Gly Arg Tyr
      85      90      95
Pro Ile Leu Pro Pro Pro Thr Tyr Val His Gln Lys Ala Val Thr Ile
      100      105      110
Arg Asn Asp Val Asn Leu Lys Lys Lys Thr Leu Thr Leu Ile Pro Asp
      115      120      125
Pro Glu Asn Pro Asn Arg Leu Leu Val Ser Phe Thr Phe Asp Ala Ser
      130      135      140
Met Pro Gly Arg Ile Thr Val Val Phe Phe Ala Thr Glu Asp Ala Glu
      145      150      155      160
Cys Asn Leu Arg Ala Thr Lys Glu Asp Thr Leu Pro Pro Ile Thr Phe
      165      170      175
Asp Phe Gly Glu Gly Leu Gly Gln Lys Phe Ile Gln Ser Ser Gly Thr
      180      185      190
Gly Ile Asp Leu Thr Ala Phe Lys Asp Ser Glu Leu Phe Lys Glu Val
      195      200      205
Asp Thr Asp Val Phe Pro Leu Ala Val Lys Ala Glu Ala Thr Pro Ala
      210      215      220
Glu Glu Gly Lys Ser Gly Ser Thr Asn Val Gln Ile Thr Gln Val Val
      225      230      235      240
Tyr Thr Lys Glu Lys Gly Glu Ile Lys Ile Glu Val Val Lys Gln Ile
      245      250      255
Leu Trp Val Asn Lys Arg Arg Tyr Glu Leu Leu Glu Ile Tyr Gly Ile
      260      265      270
Glu Asn Thr Val Asp Gly Ser Asp Glu Gly Lys Glu Cys Val Val Cys
      275      280      285
Leu Ser Glu Pro Arg Asp Thr Thr Val Leu Pro Cys Arg His Met Cys
      290      295      300
Met Cys Ser Gly Cys Ala Lys Ala Leu Arg Phe Gln Thr Asn Leu Cys
      305      310      315      320
Pro Val Cys Arg Gln Pro Val Glu Met Leu Leu Glu Ile Asn Lys Asn
      325      330      335
Gly

```

(2) INFORMATION FOR SEQ ID NO:366:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 315 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..315

(D) OTHER INFORMATION: / Ceres Seq. ID 1566713

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:366:

```

Met Glu Thr Ala Pro Leu Glu Leu Pro Pro Asn Arg Phe Val Phe Ala
1      5      10      15
Ala Ala Pro Pro Tyr Leu Asn Pro Asn Pro Asn Tyr Val Asp Gln Tyr
      20      25      30
Pro Gly Asn Cys Leu Pro Pro Pro Val Thr Glu Pro Pro Met Leu Pro
      35      40      45
Tyr Asn Phe Asn His Leu His His Tyr Pro Pro Asn Ser Tyr Gln Leu
      50      55      60
Pro His Pro Leu Phe His Gly Gly Arg Tyr Pro Ile Leu Pro Pro Pro

```

65	70	75	80
Thr Tyr Val His	Gln Lys Ala Val Thr	Ile Arg Asn Asp Val	Asn Leu
	85	90	95
Lys Lys Lys Thr	Leu Thr Leu Ile Pro	Asp Pro Glu Asn Pro	Asn Arg
	100	105	110
Leu Leu Val Ser	Phe Thr Phe Asp Ala	Ser Met Pro Gly Arg	Ile Thr
	115	120	125
Val Val Phe Phe	Ala Thr Glu Asp Ala	Glu Cys Asn Leu Arg	Ala Thr
	130	135	140
Lys Glu Asp Thr	Leu Pro Pro Ile Thr	Phe Asp Phe Gly Glu	Gly Leu
	145	150	155
Gly Gln Lys Phe	Ile Gln Ser Ser Gly Thr	Gly Ile Asp Leu Thr	Ala
	165	170	175
Phe Lys Asp Ser	Glu Leu Phe Lys Glu	Val Asp Thr Asp Val	Phe Pro
	180	185	190
Leu Ala Val Lys	Ala Glu Ala Thr Pro	Ala Glu Glu Gly Lys	Ser Gly
	195	200	205
Ser Thr Asn Val	Gln Ile Thr Gln Val	Val Tyr Thr Lys Glu	Lys Gly
	210	215	220
Glu Ile Lys Ile	Glu Val Val Lys Gln	Ile Leu Trp Val Asn	Lys Arg
	225	230	235
Arg Tyr Glu Leu	Leu Glu Ile Tyr Gly Ile	Glu Asn Thr Val Asp	Gly
	245	250	255
Ser Asp Glu Gly	Lys Glu Cys Val Val Cys	Leu Ser Glu Pro Arg	Asp
	260	265	270
Thr Thr Val Leu	Pro Cys Arg His Met Cys	Met Cys Ser Gly Cys	Ala
	275	280	285
Lys Ala Leu Arg	Phe Gln Thr Asn Leu Cys	Pro Val Cys Arg Gln	Pro
	290	295	300
Val Glu Met Leu	Leu Glu Ile Asn Lys Asn	Gly	
	305	310	315

(2) INFORMATION FOR SEQ ID NO:367:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 270 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..270
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566714

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:367:

Met Leu Pro Tyr	Asn Phe Asn His Leu	His His Tyr Pro Pro	Asn Ser
1	5	10	15
Tyr Gln Leu Pro	His Pro Leu Phe His	Gly Gly Arg Tyr Pro	Ile Leu
	20	25	30
Pro Pro Pro Thr	Tyr Val His Gln Lys	Ala Val Thr Ile Arg	Asn Asp
	35	40	45
Val Asn Leu Lys	Lys Lys Thr Leu Thr	Leu Ile Pro Asp Pro	Glu Asn
	50	55	60
Pro Asn Arg Leu	Leu Val Ser Phe Thr Phe	Asp Ala Ser Met Pro	Gly
	65	70	75
Arg Ile Thr Val	Val Phe Phe Ala Thr	Glu Asp Ala Glu Cys	Asn Leu
	85	90	95
Arg Ala Thr Lys	Glu Asp Thr Leu Pro	Pro Ile Thr Phe Asp	Phe Gly
	100	105	110
Glu Gly Leu Gly	Gln Lys Phe Ile Gln	Ser Ser Gly Thr Gly	Ile Asp
	115	120	125
Leu Thr Ala Phe	Lys Asp Ser Glu Leu	Phe Lys Glu Val Asp	Thr Asp
	130	135	140

Val	Phe	Pro	Leu	Ala	Val	Lys	Ala	Glu	Ala	Thr	Pro	Ala	Glu	Glu	Gly
145					150					155					160
Lys	Ser	Gly	Ser	Thr	Asn	Val	Gln	Ile	Thr	Gln	Val	Val	Tyr	Thr	Lys
				165					170						175
Glu	Lys	Gly	Glu	Ile	Lys	Ile	Glu	Val	Val	Lys	Gln	Ile	Leu	Trp	Val
			180					185					190		
Asn	Lys	Arg	Arg	Tyr	Glu	Leu	Leu	Glu	Ile	Tyr	Gly	Ile	Glu	Asn	Thr
			195					200					205		
Val	Asp	Gly	Ser	Asp	Glu	Gly	Lys	Glu	Cys	Val	Val	Cys	Leu	Ser	Glu
			210				215					220			
Pro	Arg	Asp	Thr	Thr	Val	Leu	Pro	Cys	Arg	His	Met	Cys	Met	Cys	Ser
225					230					235					240
Gly	Cys	Ala	Lys	Ala	Leu	Arg	Phe	Gln	Thr	Asn	Leu	Cys	Pro	Val	Cys
			245						250					255	
Arg	Gln	Pro	Val	Glu	Met	Leu	Leu	Glu	Ile	Asn	Lys	Asn	Gly		
			260										270		

(2) INFORMATION FOR SEQ ID NO:368:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1537 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1537
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566715

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:368:

aatcaacacaca	cacaaacaca	cacacacaca	gcctttttcc	ttcgttgatc	gattgttaag	60
ctcgatccaa	tggcggataa	caccgataat	cggagatcct	tatggggagt	tccggagaag	120
cttcagcttc	acatagcgat	gctgacgttg	caattcggtt	acgcgggatt	ccacgtgggtg	180
tctcagctgc	ctcttaacat	gggaatcagc	aaactcgtct	tccctgttta	tcgtaacatc	240
atgccttgc	ttcttctct	tccttctcgt	tacttctctg	aaaagaagga	gagaccagcg	300
attactctca	actttctcat	ccagttcttc	tttttggcac	tcataggaat	aacagcgaac	360
caaggatttt	acttgttggg	actggacaac	acttcaccaa	catttgcttc	ctccatgcaa	420
aactctgttc	cgccatttac	ctttctcatg	gctgctcttc	tcaggattga	gaaagtaaga	480
ataaacagaa	gagacgggat	ctccaaaatc	ttaggaaacg	ctctttgtgt	cgccggagct	540
tcctgcatca	ccctctataa	aggtccaacc	atctacactc	cggctagcca	ccctccagct	600
catctactca	ccacaaactc	cgccgtctta	gcgcgcctag	gaaacgcgcg	gcctaaaaac	660
tggacccctg	gttgcatcta	ccctaactgg	cactgtctct	cgttggtcagg	ctggcttgtt	720
ttccaagctc	cggtttctaa	gtcttatcca	gcgaggtctc	cggtttacctc	ttacacttgt	780
ttctctggaa	tactcaagtt	ctgtgatcatt	gctgctttct	gtgaaagaga	ttctcaggct	840
tgggtttttc	tcctcgggtg	ggagcttttc	accatcctct	acgcgcggaat	cgtagcgtct	900
ggaatcgcgt	ttgcggttca	gatttgggtg	attgacagag	gggggtccagt	cttcgttgctg	960
gtttaccagc	ctgttcagac	tcttctgtgt	gcgatcatgg	ctctctattgc	gttaggcgaa	1020
gaattttatt	tgggggggat	tattggagcg	gtcttgatca	tagcgggact	ttActctgta	1080
ttgtacggta	agagcgaaga	gaggaataat	gcagcgcgtg	agaaggcaga	gattccagctc	1140
tcgcgggagc	atggtattga	acgtgcacct	gtttctcgca	actccatcaa	gtcgtccatc	1200
acaacaccac	tactccatca	gtcaacggag	aatgtttgac	tactttggac	aaatcaactct	1260
ccagcttaata	attacaagt	ccattaccaca	attaaaaggg	aacaatgtgtg	tgcgctttgtg	1320
ttttatgact	tttgtgtctg	ctttttttct	tagtggtttc	tcttcttttt	tttttctaaa	1380
aaattattaa	ttaccttaaga	aaggtttttg	aagaaaggaa	aaaaaatgg	tggatgagac	1440
atcattgttc	atgaggatga	tgatgatgat	gatagtgatg	aagaagacta	tgtgggagct	1500
ttgattggag	acttttctat	atataatc	tggctgg			

(2) INFORMATION FOR SEQ ID NO:369:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 389 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..389

(D) OTHER INFORMATION: / Ceres Seq. ID 1566716

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:369:

Met Ala Asp Asn Thr Asp Asn Arg Arg Ser Leu Trp Gly Val Pro Glu
1 5 10 15
Lys Leu Gln Leu His Ile Ala Met Leu Thr Leu Gln Phe Gly Tyr Ala
20 25 30
Gly Phe His Val Val Ser Arg Ala Ala Leu Asn Met Gly Ile Ser Lys
35 40 45
Leu Val Phe Pro Val Tyr Arg Asn Ile Ile Ala Leu Leu Leu Leu
50 55 60
Pro Phe Ala Tyr Phe Leu Glu Lys Lys Glu Arg Pro Ala Ile Thr Leu
65 70 75 80
Asn Phe Leu Ile Gln Phe Phe Phe Leu Ala Leu Ile Gly Ile Thr Ala
85 90 95
Asn Gln Gly Phe Tyr Leu Leu Gly Leu Asp Asn Thr Ser Pro Thr Phe
100 105 110
Ala Ser Ser Met Gln Asn Ser Val Pro Ala Ile Thr Phe Leu Met Ala
115 120 125
Ala Leu Leu Arg Ile Glu Lys Val Arg Ile Asn Arg Arg Asp Gly Ile
130 135 140
Ser Lys Ile Leu Gly Thr Ala Leu Cys Val Ala Gly Ala Ser Val Ile
145 150 155 160
Thr Leu Tyr Lys Gly Pro Thr Ile Tyr Thr Pro Ala Ser His Leu His
165 170 175
Ala His Leu Leu Thr Thr Asn Ser Ala Val Leu Ala Pro Leu Gly Asn
180 185 190
Ala Ala Pro Lys Asn Trp Thr Leu Gly Cys Ile Tyr Leu Ile Gly His
195 200 205
Cys Leu Ser Trp Ser Gly Trp Leu Val Phe Gln Ala Pro Val Leu Lys
210 215 220
Ser Tyr Pro Ala Arg Leu Ser Val Thr Ser Tyr Thr Cys Phe Phe Gly
225 230 235 240
Ile Ile Gln Phe Leu Ile Ile Ala Ala Phe Cys Glu Arg Asp Ser Gln
245 250 255
Ala Trp Val Phe His Ser Gly Trp Glu Leu Phe Thr Ile Leu Tyr Ala
260 265 270
Gly Ile Val Ala Ser Gly Ile Ala Phe Ala Val Gln Ile Trp Cys Ile
275 280 285
Asp Arg Gly Gly Pro Val Phe Val Ala Val Tyr Gln Pro Val Gln Thr
290 295 300
Leu Val Val Ala Ile Met Ala Ser Ile Ala Leu Gly Glu Glu Phe Tyr
305 310 315 320
Leu Gly Gly Ile Ile Gly Ala Val Leu Ile Ile Ala Gly Leu Tyr Phe
325 330 335
Val Leu Tyr Gly Lys Ser Glu Glu Arg Lys Phe Ala Ala Leu Glu Lys
340 345 350
Ala Glu Ile Gln Ser Ser Ala Glu His Gly Ile Glu Arg Ala Pro Val
355 360 365
Ser Arg Asn Ser Ile Lys Ser Ser Ile Thr Thr Pro Leu Leu His Gln
370 375 380
Ser Thr Asp Asn Val
385

(2) INFORMATION FOR SEQ ID NO:370:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 366 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..366

(D) OTHER INFORMATION: / Ceres Seq. ID 1566717

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:370:

Met	Leu	Thr	Leu	Gln	Phe	Gly	Tyr	Ala	Gly	Phe	His	Val	Val	Ser	Arg
1			5						10					15	
Ala	Ala	Leu	Asn	Met	Gly	Ile	Ser	Lys	Leu	Val	Phe	Pro	Val	Tyr	Arg
			20					25					30		
Asn	Ile	Ile	Ala	Leu	Leu	Leu	Leu	Pro	Phe	Ala	Tyr	Phe	Leu	Glu	
		35					40				45				
Lys	Lys	Glu	Arg	Pro	Ala	Ile	Thr	Leu	Asn	Phe	Leu	Ile	Gln	Phe	Phe
		50					55				60				
Phe	Leu	Ala	Leu	Ile	Gly	Ile	Thr	Ala	Asn	Gln	Gly	Phe	Tyr	Leu	Leu
					70					75				80	
Gly	Leu	Asp	Asn	Thr	Ser	Pro	Thr	Phe	Ala	Ser	Ser	Met	Gln	Asn	Ser
			85						90				95		
Val	Pro	Ala	Ile	Thr	Phe	Leu	Met	Ala	Ala	Leu	Leu	Arg	Ile	Glu	Lys
			100					105					110		
Val	Arg	Ile	Asn	Arg	Arg	Asp	Gly	Ile	Ser	Lys	Ile	Leu	Gly	Thr	Ala
			115				120					125			
Leu	Cys	Val	Ala	Gly	Ala	Ser	Val	Ile	Thr	Leu	Tyr	Lys	Gly	Pro	Thr
		130					135					140			
Ile	Tyr	Thr	Pro	Ala	Ser	His	Leu	His	Ala	His	Leu	Leu	Thr	Thr	Asn
					150					155					160
Ser	Ala	Val	Leu	Ala	Pro	Leu	Gly	Asn	Ala	Ala	Pro	Lys	Asn	Trp	Thr
			165						170					175	
Leu	Gly	Cys	Ile	Tyr	Leu	Ile	Gly	His	Cys	Leu	Ser	Trp	Ser	Gly	Trp
			180					185					190		
Leu	Val	Phe	Gln	Ala	Pro	Val	Leu	Lys	Ser	Tyr	Pro	Ala	Arg	Leu	Ser
			195				200					205			
Val	Thr	Ser	Tyr	Thr	Cys	Phe	Phe	Gly	Ile	Ile	Gln	Phe	Leu	Ile	Ile
			210				215					220			
Ala	Ala	Phe	Cys	Glu	Arg	Asp	Ser	Gln	Ala	Trp	Val	Phe	His	Ser	Gly
				230						235					240
Trp	Glu	Leu	Phe	Thr	Ile	Leu	Tyr	Ala	Gly	Ile	Val	Ala	Ser	Gly	Ile
				245					250					255	
Ala	Phe	Ala	Val	Gln	Ile	Trp	Cys	Ile	Asp	Arg	Gly	Gly	Pro	Val	Phe
			260					265					270		
Val	Ala	Val	Tyr	Gln	Pro	Val	Gln	Thr	Leu	Val	Val	Ala	Ile	Met	Ala
			275				280					285			
Ser	Ile	Ala	Leu	Gly	Glu	Glu	Phe	Tyr	Leu	Gly	Gly	Ile	Ile	Gly	Ala
					295						300				
Val	Leu	Ile	Ile	Ala	Gly	Leu	Tyr	Phe	Val	Leu	Tyr	Gly	Lys	Ser	Glu
				310						315					320
Glu	Arg	Lys	Phe	Ala	Ala	Leu	Glu	Lys	Ala	Glu	Ile	Gln	Ser	Ser	Ala
				325					330					335	
Glu	His	Gly	Ile	Glu	Arg	Ala	Pro	Val	Ser	Arg	Asn	Ser	Ile	Lys	Ser
			340					345					350		
Ser	Ile	Thr	Thr	Pro	Leu	Leu	His	Gln	Ser	Thr	Asp	Asn	Val		
			355				360					365			

(2) INFORMATION FOR SEQ ID NO:371:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 346 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..346

(D) OTHER INFORMATION: / Ceres Seq. ID 1566718

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:371:

Met Gly Ile Ser Lys Leu Val Phe Pro Val Tyr Arg Asn Ile Ile Ala
1 5 10 15
Leu Leu Leu Leu Leu Pro Phe Ala Tyr Phe Leu Glu Lys Lys Glu Arg
20 25 30
Pro Ala Ile Thr Leu Asn Phe Leu Ile Gln Phe Phe Phe Leu Ala Leu
35 40 45
Ile Gly Ile Thr Ala Asn Gln Gly Phe Tyr Leu Leu Gly Leu Asp Asn
50 55 60
Thr Ser Pro Thr Phe Ala Ser Ser Met Gln Asn Ser Val Pro Ala Ile
65 70 75 80
Thr Phe Leu Met Ala Ala Leu Leu Arg Ile Glu Lys Val Arg Ile Asn
85 90 95
Arg Arg Asp Gly Ile Ser Lys Ile Leu Gly Thr Ala Leu Cys Val Ala
100 105 110
Gly Ala Ser Val Ile Thr Leu Tyr Lys Gly Pro Thr Ile Tyr Thr Pro
115 120 125
Ala Ser His Leu His Ala His Leu Leu Thr Thr Asn Ser Ala Val Leu
130 135 140
Ala Pro Leu Gly Asn Ala Ala Pro Lys Asn Trp Thr Leu Gly Cys Ile
145 150 155 160
Tyr Leu Ile Gly His Cys Leu Ser Trp Ser Gly Trp Leu Val Phe Gln
165 170 175
Ala Pro Val Leu Lys Ser Tyr Pro Ala Arg Leu Ser Val Thr Ser Tyr
180 185 190
Thr Cys Phe Phe Gly Ile Ile Gln Phe Leu Ile Ile Ala Ala Phe Cys
195 200 205
Glu Arg Asp Ser Gln Ala Trp Val Phe His Ser Gly Trp Glu Leu Phe
210 215 220
Thr Ile Leu Tyr Ala Gly Ile Val Ala Ser Gly Ile Ala Phe Ala Val
225 230 235 240
Gln Ile Trp Cys Ile Asp Arg Gly Gly Pro Val Phe Val Ala Val Tyr
245 250 255
Gln Pro Val Gln Thr Leu Val Val Ala Ile Met Ala Ser Ile Ala Leu
260 265 270
Gly Glu Glu Phe Tyr Leu Gly Gly Ile Ile Gly Ala Val Leu Ile Ile
275 280 285
Ala Gly Leu Tyr Phe Val Leu Tyr Gly Lys Ser Glu Glu Arg Lys Phe
290 295 300
Ala Ala Leu Glu Lys Ala Glu Ile Gln Ser Ser Ala Glu His Gly Ile
305 310 315 320
Glu Arg Ala Pro Val Ser Arg Asn Ser Ile Lys Ser Ser Ile Thr Thr
325 330 335
Pro Leu Leu His Gln Ser Thr Asp Asn Val
340 345

(2) INFORMATION FOR SEQ ID NO:372:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1009 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1009

(D) OTHER INFORMATION: / Ceres Seq. ID 1566719

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:372:

catctttctaa gaaagaaaca aagaaagact tcacatttta ccattatttg ctctgagctc 60
agtaggagag ttcaagaaac aatggcgaag atgcaattat caatctttat cgctgtcgtt 120


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gcgcttatcg tctgctctgc atctgctaaa accgcaagcc ctccagctcc agtgctgcc 180
ccgacaccag ctccagacc agccccggaa aatgtgaatc tcaccgagct ttttaagtta 240
gctggctcgt tccacacatt cctgcactac cttctctcga ctggagtcac tgagactttc 300
caaaaccaag ctaacaacac tgagggaagc atcacaatct ttgtccctaa agatgatgct 360
ttcaagctc agaagaatcc tctttgttca aatctcacaa aggatcagct taagcagctt 420
gttctcttcc atgctcttcc tcattactat tcgctttcgg aattcaagaa cttgagccaa 480
tctggctccag tgagcacctt tgctgggtgt caatactcct tgaatttcac tgatgtttct 540
ggcacgggta ggattgattc tttatggacc aggactaaag tcagcagcag tgttttctcc 600
actgaccctg ttgcgggttta ccaattgaac cgcgtgcttc tacccgaagc aatctttggt 660
actgatgtcc ctccaatgcc tgctccagct cctgctccta tcgttagtgc tCcttcggat 720
ctctcttcag ttgctgattc tgaaggagct tcttcaccaa agtcctcaca caagaactcc 780
ggacaaaagc tgctactttg accaatctcc atggttattt ccggtttggt gcatctgttc 840
ttgtgatcat atggtttttg agattgagtt atgtttttta gttacaatgt gaagattgt 900
attactcat ttgaattgtc tttttgattt ttgaaccoca ttttttatta tacattttta 960
tcattattat tgtttgtcat tacgattttg tgaattgaaa ttgttcttc

```

(2) INFORMATION FOR SEQ ID NO:373:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 281 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..281

(D) OTHER INFORMATION: / Ceres Seq. ID 1566720

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:373:

```

His Leu Leu Arg Lys Lys Gln Arg Lys Thr Ser His Phe Thr Ile Ile
1 5 10 15
Cys Ser Glu Leu Ser Arg Arg Val Gln Glu Thr Met Ala Lys Met Gln
20 25 30
Leu Ser Ile Phe Ile Ala Val Val Ala Leu Ile Val Cys Ser Ala Ser
35 40 45
Ala Lys Thr Ala Ser Pro Pro Ala Pro Val Leu Pro Pro Thr Pro Ala
50 55 60
Pro Ala Pro Ala Pro Glu Asn Val Asn Leu Thr Glu Leu Leu Ser Val
65 70 75 80
Ala Gly Pro Phe His Thr Phe Leu Asp Tyr Leu Leu Ser Thr Gly Val
85 90 95
Ile Glu Thr Phe Gln Asn Gln Ala Asn Asn Thr Glu Glu Gly Ile Thr
100 105 110
Ile Phe Val Pro Lys Asp Asp Ala Phe Lys Ala Gln Lys Asn Pro Pro
115 120 125
Leu Ser Asn Leu Thr Lys Asp Gln Leu Lys Gln Leu Val Leu Phe His
130 135 140
Ala Leu Pro His Tyr Tyr Ser Leu Ser Glu Phe Lys Asn Leu Ser Gln
145 150 155 160
Ser Gly Pro Val Ser Thr Phe Ala Gly Gly Gln Tyr Ser Leu Lys Phe
165 170 175
Thr Asp Val Ser Gly Thr Val Arg Ile Asp Ser Leu Trp Thr Arg Thr
180 185 190
Lys Val Ser Ser Ser Val Phe Ser Thr Asp Pro Val Ala Val Tyr Gln
195 200 205
Leu Asn Arg Val Leu Leu Pro Glu Ala Ile Phe Gly Thr Asp Val Pro
210 215 220
Pro Met Pro Ala Pro Ala Pro Ala Pro Ile Val Ser Ala Pro Ser Asp
225 230 235 240
Ser Pro Ser Val Ala Asp Ser Glu Gly Ala Ser Ser Pro Lys Ser Ser
245 250 255
His Lys Asn Ser Gly Gln Lys Leu Leu Leu Ala Pro Ile Ser Met Val
260 265 270

```

Ile Ser Gly Leu Val Ala Leu Phe Leu
275 280

(2) INFORMATION FOR SEQ ID NO:374:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 254 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..254
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566721

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:374:

```
Met Ala Lys Met Gln Leu Ser Ile Phe Ile Ala Val Val Ala Leu Ile
1      5      10      15
Val Cys Ser Ala Ser Ala Lys Thr Ala Ser Pro Pro Ala Pro Val Leu
20      25      30
Pro Pro Thr Pro Ala Pro Ala Pro Ala Pro Glu Asn Val Asn Leu Thr
35      40      45
Glu Leu Leu Ser Val Ala Gly Pro Phe His Thr Phe Leu Asp Tyr Leu
50      55      60
Leu Ser Thr Gly Val Ile Glu Thr Phe Gln Asn Gln Ala Asn Asn Thr
65      70      75      80
Glu Glu Gly Ile Thr Ile Phe Val Pro Lys Asp Asp Ala Phe Lys Ala
85      90      95
Gln Lys Asn Pro Pro Leu Ser Asn Leu Thr Lys Asp Gln Leu Lys Gln
100     105     110
Leu Val Leu Phe His Ala Leu Pro His Tyr Tyr Ser Leu Ser Glu Phe
115     120     125
Lys Asn Leu Ser Gln Ser Gly Pro Val Ser Thr Phe Ala Gly Gly Gln
130     135     140
Tyr Ser Leu Lys Phe Thr Asp Val Ser Gly Thr Val Arg Ile Asp Ser
145     150     155     160
Leu Trp Thr Arg Thr Lys Val Ser Ser Ser Val Phe Ser Thr Asp Pro
165     170     175
Val Ala Val Tyr Gln Leu Asn Arg Val Leu Leu Pro Glu Ala Ile Phe
180     185     190
Gly Thr Asp Val Pro Pro Met Pro Ala Pro Ala Pro Ala Pro Ile Val
195     200     205
Ser Ala Pro Ser Asp Ser Pro Ser Val Ala Asp Ser Glu Gly Ala Ser
210     215     220
Ser Pro Lys Ser Ser His Lys Asn Ser Gly Gln Lys Leu Leu Leu Ala
225     230     235     240
Pro Ile Ser Met Val Ile Ser Gly Leu Val Ala Leu Phe Leu
245     250
```

(2) INFORMATION FOR SEQ ID NO:375:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 251 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..251
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566722

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:375:

```
Met Gln Leu Ser Ile Phe Ile Ala Val Val Ala Leu Ile Val Cys Ser
1      5      10      15
Ala Ser Ala Lys Thr Ala Ser Pro Pro Ala Pro Val Leu Pro Pro Thr
```

	20		25		30				
Pro Ala	Pro Ala	Pro Ala	Pro Glu	Asn Val	Asn Leu	Thr Glu	Leu Leu	Leu	
	35		40		45				
Ser Val	Ala Gly	Pro Phe	His Thr	Phe Leu	Asp Tyr	Leu Leu	Ser Thr		
	50		55		60				
Gly Val	Ile Glu	Thr Phe	Gln Asn	Gln Ala	Asn Asn	Thr Glu	Glu Gly		
	65		70		75		80		
Ile Thr	Ile Phe	Val Pro	Lys Asp	Asp Ala	Phe Lys	Ala Gln	Lys Asn		
		85		90		95			
Pro Pro	Leu Ser	Asn Leu	Thr Lys	Asp Gln	Leu Lys	Gln Leu	Val Leu		
	100		105		110				
Phe His	Ala Leu	Pro His	Tyr Tyr	Ser Leu	Ser Glu	Phe Lys	Asn Leu		
	115		120		125				
Ser Gln	Ser Gly	Pro Val	Ser Thr	Phe Ala	Gly Gly	Gln Tyr	Ser Leu		
	130		135		140				
Lys Phe	Thr Asp	Val Ser	Gly Thr	Val Arg	Ile Asp	Ser Leu	Trp Thr		
	145		150		155		160		
Arg Thr	Lys Val	Ser Ser	Ser Val	Phe Ser	Thr Asp	Pro Val	Ala Val		
		165		170		175			
Tyr Gln	Leu Asn	Arg Val	Leu Leu	Pro Glu	Ala Ile	Phe Gly	Thr Asp		
	180		185		190				
Val Pro	Pro Met	Pro Ala	Pro Ala	Pro Ala	Pro Ile	Val Ser	Ala Pro		
	195		200		205				
Ser Asp	Ser Pro	Ser Val	Ala Asp	Ser Glu	Gly Ala	Ser Ser	Pro Lys		
	210		215		220				
Ser Ser	His Lys	Asn Ser	Gly Gln	Lys Leu	Leu Leu	Ala Pro	Ile Ser		
	225		230		235		240		
Met Val	Ile Ser	Gly Leu	Val Ala	Leu Phe	Leu				
		245		250					

(2) INFORMATION FOR SEQ ID NO:376:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 877 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..877
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566727

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:376:

agattaggat	taaattaggg	cataaccctt	atcggagatt	tgaagccatg	ggaagaagaa	60
aaatcgagat	caagcgaatc	gagaacaaaa	gcagtcgaca	agtcactttc	tccaaacgac	120
gcaatggtct	catcgacaaa	gctcgcacaac	tttcgattct	ctgtgaatcc	tcctgcctgt	180
ttgtcgtcgt	atctgcctcc	ggaaaactct	atgactcttc	ctccggtgac	gagatagaag	240
cgctgttcaa	gccggagaaa	ctcctaatgt	ttgaactcga	tcttgaagaa	aaaattcaga	300
attatcttcc	acacaaggag	ttactagaaa	cagtcocaa	caagcttgaa	gaaccaaatg	360
tcgataatgt	aagtgttagat	tctctaattt	ctctggagga	acaacttgag	actgtctctg	420
ccgtaagttag	agctaggaga	gcagaaactga	tgatggagta	tatcgagctc	cttaaaagaaa	480
aggagaaatt	gctgagagaa	gagaaccagg	ttctggctag	ccagatggga	aagaatacgt	540
tgctggcaac	agatgatgag	agaggaaatgt	ttccgggga	tagctccggc	aacaaaatac	600
ccgagactct	cccgctgctc	aattagccac	catcatcaac	ggctgagttt	tcaccttaaa	660
ctcaaagcct	gattcataat	taagagaata	aatttgtata	ttataaaaa	ctgtgtaatc	720
tcaaaccttt	tatcttctct	taagtgggaa	tttaaggta	aaaaaagaa	gagaaagtat	780
ggatcagtgt	tgtaacctct	tcggagacaa	gatcagagtt	tgtgtgtttg	tgctgtgaatg	840
tacggattgg	atttttaaa	ttgtgctttc	tttcttcc			

(2) INFORMATION FOR SEQ ID NO:377:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 207 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:

(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..207
 (D) OTHER INFORMATION: / Ceres Seq. ID 1566728
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:377:
Ile Arg Ile Lys Leu Gly His Asn Pro Tyr Arg Arg Phe Glu Ala Met
1 5 10 15
Gly Arg Arg Lys Ile Glu Ile Lys Arg Ile Glu Asn Lys Ser Ser Arg
 20 25 30
Gln Val Thr Phe Ser Lys Arg Arg Asn Gly Leu Ile Asp Lys Ala Arg
 35 40 45
Gln Leu Ser Ile Leu Cys Glu Ser Ser Val Ala Val Val Val Ser
 50 55 60
Ala Ser Gly Lys Leu Tyr Asp Ser Ser Ser Gly Asp Glu Ile Glu Ala
65 70 75 80
Leu Phe Lys Pro Glu Lys Pro Gln Cys Phe Glu Leu Asp Leu Glu Glu
 85 90 95
Lys Ile Gln Asn Tyr Leu Pro His Lys Glu Leu Leu Glu Thr Val Gln
 100 105 110
Ser Lys Leu Glu Glu Pro Asn Val Asp Asn Val Ser Val Asp Ser Leu
 115 120 125
Ile Ser Leu Glu Glu Gln Leu Glu Thr Ala Leu Ser Val Ser Arg Ala
130 135 140
Arg Lys Ala Glu Leu Met Met Glu Tyr Ile Glu Ser Leu Lys Glu Lys
145 150 155 160
Glu Lys Leu Leu Arg Glu Glu Asn Gln Val Leu Ala Ser Gln Met Gly
 165 170 175
Lys Asn Thr Leu Leu Ala Thr Asp Asp Glu Arg Gly Met Phe Pro Gly
 180 185 190
Ser Ser Ser Gly Asn Lys Ile Pro Glu Thr Leu Pro Leu Leu Asn
 195 200 205

(2) INFORMATION FOR SEQ ID NO:378:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 192 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..192
 (D) OTHER INFORMATION: / Ceres Seq. ID 1566729
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:378:
Met Gly Arg Arg Lys Ile Glu Ile Lys Arg Ile Glu Asn Lys Ser Ser
1 5 10 15
Arg Gln Val Thr Phe Ser Lys Arg Arg Asn Gly Leu Ile Asp Lys Ala
 20 25 30
Arg Gln Leu Ser Ile Leu Cys Glu Ser Ser Val Ala Val Val Val
 35 40 45
Ser Ala Ser Gly Lys Leu Tyr Asp Ser Ser Ser Gly Asp Glu Ile Glu
50 55 60
Ala Leu Phe Lys Pro Glu Lys Pro Gln Cys Phe Glu Leu Asp Leu Glu
65 70 75 80
Glu Lys Ile Gln Asn Tyr Leu Pro His Lys Glu Leu Leu Glu Thr Val
 85 90 95
Gln Ser Lys Leu Glu Glu Pro Asn Val Asp Asn Val Ser Val Asp Ser
 100 105 110
Leu Ile Ser Leu Glu Glu Gln Leu Glu Thr Ala Leu Ser Val Ser Arg
115 120 125

Ala	Arg	Lys	Ala	Glu	Leu	Met	Met	Glu	Tyr	Ile	Glu	Ser	Leu	Lys	Glu
130						135					140				
Lys	Glu	Lys	Leu	Leu	Arg	Glu	Glu	Asn	Gln	Val	Leu	Ala	Ser	Gln	Met
145					150					155					160
Gly	Lys	Asn	Thr	Leu	Leu	Ala	Thr	Asp	Asp	Glu	Arg	Gly	Met	Phe	Pro
			165					170						175	
Gly	Ser	Ser	Ser	Gly	Asn	Lys	Ile	Pro	Glu	Thr	Leu	Pro	Leu	Leu	Asn
			180					185					190		

(2) INFORMATION FOR SEQ ID NO:379:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2022 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..2022

(D) OTHER INFORMATION: / Ceres Seq. ID 1566737

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:379:

acagtaacaa	tctctctctc	gcaccttctt	aaagctgtct	ctatttcttc	gcttccctct	60
tctcttcaact	cacaaaaacat	tttgttctaa	tcccgcaact	gctaaaaaca	aacctttttg	120
tcaaaaaatct	ctccttttcg	tgggtgacaga	aatctattgc	aggaaatggc	agaagcagca	180
tacacagtag	catcacagac	tgaaaacact	ggagaggaga	aatcatcatc	atctccttca	240
ttacccgaaa	tcgcctttgg	tatcgacatt	gggtactctc	aatgcagtat	agctgtttgg	300
aacggttctc	aagttcacat	cttgaggaaac	acaagaaacc	agaagctcat	caaatcattt	360
gtcactttca	aagatgaagt	tctgtctggt	gggtgttaga	accagctcgc	acatgagcag	420
gaaatgcata	ccggagccgc	tactttcaac	atgaagcgcg	tcgttgtgtg	tgtagacact	480
gatctctgtg	ttcacgctag	caagaacctt	cctttcttgg	tcaaaactct	tgatatttga	540
gttagaccgt	ttattgcagc	tttgtgtgaac	aatgcttggg	gatcaacaac	accagaggaa	600
gttttagcta	tatttctggt	ggagttacgt	ctgatggctg	aagctcagtt	gaaacgtcct	660
gtgagaaagt	tagtgcttac	ggttccggtt	tcgttctcta	ggttcacgt	cacacggttc	720
gaaagagcgt	gcgctatggc	tggacttcat	gttctctgtt	tgatgccgga	accaactgct	780
attgcgttgc	tttatgcgca	acagcagcag	atgactacgc	atgataaact	gggaagcggg	840
agcgagaggg	ttgcggttat	attcaatatg	ggagctgggt	actgcgcatg	tcggtttact	900
gctactcgtg	gtggtgtttc	acagataaaa	gcttttagctg	gtagcccatc	tgggggtgaa	960
gacattttgc	agagcacact	tcgccatata	gctccaccta	atgaagaagc	ttcgggggtg	1020
ctctctgtgt	cggcaccaga	cgcgattcac	aggctaaccg	atcaagaaaa	tgtccaaaatt	1080
gaagtgcatt	tgggaaatgg	taacaagata	tccaaggctc	ttgatagctt	agagttttgag	1140
gaagtgaacc	agaaggtatt	tgaggaaatg	gagagacttg	ttgtgcagtg	cctgcgagat	1200
gcgagagctc	atgggtgtgt	tatcgatgat	ttgataatgg	tggaggggtg	ttcgtacatc	1260
ccgaaagtta	gaactattat	caagaacgta	tgcagaagag	atgagatata	caaaagcggtg	1320
aatcctttag	aagctgcggt	tagaggagct	gctttggaag	gtcgggtgac	ttcagggggt	1380
catgatccct	ttgggagcgt	agatctgtta	accatacaa	ccacacactc	tcgagttgga	1440
gcgaagagta	acggaacaaa	attcataccc	gtgattcctc	gtaacacgat	gggtccagcg	1500
cggaaagacc	tctttttcac	aacgggttca	gacaaccaga	aggagctctc	gatcattata	1560
tacgaagagag	aaggagagac	tgttgaagag	aatcatcttc	ttggttattt	caagctcgtt	1620
gggattccgc	cagcaccgaa	aggtgttcca	gagatcaatg	tttgatgag	catcgatgcg	1680
ctgaatgctt	tacgggtttt	cgcagctgtg	ttgatgccgg	gatcttcgac	tcggctgtgt	1740
cotgtgattg	aggtgaggtg	gcctacggtt	gatgatggac	atggttgtgt	tgctcaagct	1800
ttgaatgtga	aatatggagc	tactcttgat	ttgattactt	ttcagagaaa	gatgtaaagt	1860
taaaataaaa	tgggtgttgt	gatagatttt	agattagatg	taagatagca	ggatgctctg	1920
tatagaaaaa	agttttgtaa	gtttgtgtgt	gttttgggtg	ttgtcgttga	agtggttaac	1980
aatgttttat	tggttaatga	agtaataatg	ctttgcagat	tg		

(2) INFORMATION FOR SEQ ID NO:380:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 563 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..563
(D) OTHER INFORMATION: / Ceres Seq. ID 1566738

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:380:

Met	Ala	Glu	Ala	Ala	Tyr	Thr	Val	Ala	Ser	Asp	Ser	Glu	Asn	Thr	Gly	
1				5					10				15			
Glu	Glu	Lys	Ser	Ser	Ser	Ser	Pro	Ser	Leu	Pro	Glu	Ile	Ala	Leu	Gly	
		20						25				30				
Ile	Asp	Ile	Gly	Thr	Ser	Gln	Cys	Ser	Ile	Ala	Val	Trp	Asn	Gly	Ser	
		35					40					45				
Gln	Val	His	Ile	Leu	Arg	Asn	Thr	Arg	Asn	Gln	Lys	Leu	Ile	Lys	Ser	
		50				55					60					
Phe	Val	Thr	Phe	Lys	Asp	Glu	Val	Pro	Ala	Gly	Gly	Val	Ser	Asn	Gln	
65				70					75					80		
Leu	Ala	His	Glu	Gln	Glu	Met	Leu	Thr	Gly	Ala	Ala	Ile	Phe	Asn	Met	
			85						90				95			
Lys	Arg	Leu	Val	Gly	Arg	Val	Asp	Thr	Asp	Pro	Val	Val	His	Ala	Ser	
		100						105					110			
Lys	Asn	Leu	Pro	Phe	Leu	Val	Gln	Thr	Leu	Asp	Ile	Gly	Val	Arg	Pro	
		115					120					125				
Phe	Ile	Ala	Ala	Leu	Val	Asn	Asn	Ala	Trp	Arg	Ser	Thr	Thr	Pro	Glu	
	130				135							140				
Glu	Val	Leu	Ala	Ile	Phe	Leu	Val	Glu	Leu	Arg	Leu	Met	Ala	Glu	Ala	
145				150					155					160		
Gln	Leu	Lys	Arg	Pro	Val	Arg	Asn	Val	Val	Leu	Thr	Val	Pro	Val	Ser	
		165							170					175		
Phe	Ser	Arg	Phe	Gln	Leu	Thr	Arg	Phe	Glu	Arg	Ala	Cys	Ala	Met	Ala	
	180							185					190			
Gly	Leu	His	Val	Leu	Arg	Leu	Met	Pro	Glu	Pro	Thr	Ala	Ile	Ala	Leu	
	195						200					205				
Leu	Tyr	Ala	Gln	Gln	Gln	Gln	Met	Thr	Thr	His	Asp	Asn	Met	Gly	Ser	
	210					215					220					
Gly	Ser	Glu	Arg	Leu	Ala	Val	Ile	Phe	Asn	Met	Gly	Ala	Gly	Tyr	Cys	
225				230					235					240		
Asp	Val	Ala	Val	Thr	Ala	Thr	Ala	Gly	Gly	Val	Ser	Gln	Ile	Lys	Ala	
		245							250					255		
Leu	Ala	Gly	Ser	Pro	Ile	Gly	Gly	Glu	Asp	Ile	Leu	Gln	Ser	Thr	Ile	
		260					265						270			
Arg	His	Ile	Ala	Pro	Pro	Asn	Glu	Glu	Ala	Ser	Gly	Leu	Leu	Arg	Val	
	275						280						285			
Ala	Ala	Gln	Asp	Ala	Ile	His	Arg	Leu	Thr	Asp	Gln	Glu	Asn	Val	Gln	
	290					295					300					
Ile	Glu	Val	Asp	Leu	Gly	Asn	Gly	Asn	Lys	Ile	Ser	Lys	Val	Leu	Asp	
305				310					315					320		
Arg	Leu	Glu	Phe	Glu	Glu	Val	Asn	Gln	Lys	Val	Phe	Glu	Glu	Cys	Glu	
		325							330					335		
Arg	Leu	Val	Val	Gln	Cys	Leu	Arg	Asp	Ala	Arg	Val	Asn	Gly	Gly	Asp	
	340						345						350			
Ile	Asp	Asp	Leu	Ile	Met	Val	Gly	Gly	Cys	Ser	Tyr	Ile	Pro	Lys	Val	
	355						360					365				
Arg	Thr	Ile	Ile	Lys	Asn	Val	Cys	Lys	Lys	Asp	Glu	Ile	Tyr	Lys	Gly	
	370					375					380					
Val	Asn	Pro	Leu	Glu	Ala	Ala	Val	Arg	Gly	Ala	Ala	Leu	Glu	Gly	Ala	
385				390					395					400		
Val	Thr	Ser	Gly	Ile	His	Asp	Pro	Phe	Gly	Ser	Leu	Asp	Leu	Leu	Thr	
		405							410					415		
Ile	Gln	Ala	Thr	Pro	Leu	Ala	Val	Gly	Ala	Arg	Ala	Asn	Gly	Asn	Lys	
		420					425						430			

Phe	Ile	Pro	Val	Ile	Pro	Arg	Asn	Thr	Met	Val	Pro	Ala	Arg	Lys	Asp	
	435						440					445				
Leu	Phe	Phe	Thr	Thr	Val	Gln	Asp	Asn	Gln	Lys	Glu	Ala	Leu	Ile	Ile	
	450					455					460					
Ile	Tyr	Glu	Gly	Glu	Gly	Glu	Thr	Val	Glu	Glu	Asn	His	Leu	Leu	Gly	
465					470				475						480	
Tyr	Phe	Lys	Leu	Val	Gly	Ile	Pro	Pro	Ala	Pro	Lys	Gly	Val	Pro	Glu	
			485						490					495		
Ile	Asn	Val	Cys	Met	Asp	Ile	Asp	Ala	Ser	Asn	Ala	Leu	Arg	Val	Phe	
		500					505						510			
Ala	Ala	Val	Leu	Met	Pro	Gly	Ser	Ser	Thr	Pro	Val	Val	Pro	Val	Ile	
		515				520						525				
Glu	Val	Arg	Met	Pro	Thr	Val	Asp	Asp	Gly	His	Gly	Trp	Cys	Ala	Gln	
	530					535					540					
Ala	Leu	Asn	Val	Lys	Tyr	Gly	Ala	Thr	Leu	Asp	Leu	Ile	Thr	Phe	Gln	
545				550					555						560	
Arg	Lys	Met														

(2) INFORMATION FOR SEQ ID NO:381:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 477 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..477

(D) OTHER INFORMATION: / Ceres Seq. ID 1566739

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:381:

Met	Leu	Thr	Gly	Ala	Ala	Ile	Phe	Asn	Met	Lys	Arg	Leu	Val	Gly	Arg	
1			5						10				15			
Val	Asp	Thr	Asp	Pro	Val	Val	His	Ala	Ser	Lys	Asn	Leu	Pro	Phe	Leu	
			20					25					30			
Val	Gln	Thr	Leu	Asp	Ile	Gly	Val	Arg	Pro	Phe	Ile	Ala	Ala	Leu	Val	
		35				40						45				
Asn	Asn	Ala	Trp	Arg	Ser	Thr	Thr	Pro	Glu	Glu	Val	Leu	Ala	Ile	Phe	
		50			55						60					
Leu	Val	Glu	Leu	Arg	Leu	Met	Ala	Glu	Ala	Gln	Leu	Lys	Arg	Pro	Val	
65				70				75					80			
Arg	Asn	Val	Val	Leu	Thr	Val	Pro	Val	Ser	Phe	Ser	Arg	Phe	Gln	Leu	
		85						90					95			
Thr	Arg	Phe	Glu	Arg	Ala	Cys	Ala	Met	Ala	Gly	Leu	His	Val	Leu	Arg	
		100				105						110				
Leu	Met	Pro	Glu	Pro	Thr	Ala	Ile	Ala	Leu	Leu	Tyr	Ala	Gln	Gln	Gln	
		115				120						125				
Gln	Met	Thr	Thr	His	Asp	Asn	Met	Gly	Ser	Gly	Ser	Glu	Arg	Leu	Ala	
		130				135						140				
Val	Ile	Phe	Asn	Met	Gly	Ala	Gly	Tyr	Cys	Asp	Val	Ala	Val	Thr	Ala	
145				150					155					160		
Thr	Ala	Gly	Gly	Val	Ser	Gln	Ile	Lys	Ala	Leu	Ala	Gly	Ser	Pro	Ile	
			165						170				175			
Gly	Gly	Glu	Asp	Ile	Leu	Gln	Ser	Thr	Ile	Arg	His	Ile	Ala	Pro	Pro	
		180						185					190			
Asn	Glu	Glu	Ala	Ser	Gly	Leu	Leu	Arg	Val	Ala	Ala	Gln	Asp	Ala	Ile	
		195				200						205				
His	Arg	Leu	Thr	Asp	Gln	Glu	Asn	Val	Gln	Ile	Glu	Val	Asp	Leu	Gly	
		210				215						220				
Asn	Gly	Asn	Lys	Ile	Ser	Lys	Val	Leu	Asp	Arg	Leu	Glu	Phe	Glu	Glu	
225				230					235					240		
Val	Asn	Gln	Lys	Val	Phe	Glu	Glu	Cys	Glu	Arg	Leu	Val	Val	Gln	Cys	

	245		250		255
Leu Arg Asp Ala Arg Val Asn Gly Gly Asp Ile Asp Asp Leu Ile Met	260		265		270
Val Gly Gly Cys Ser Tyr Ile Pro Lys Val Arg Thr Ile Ile Lys Asn	275		280		285
Val Cys Lys Lys Asp Glu Ile Tyr Lys Gly Val Asn Pro Leu Glu Ala	290		295		300
Ala Val Arg Gly Ala Ala Leu Glu Gly Ala Val Thr Ser Gly Ile His	305		310		315
Asp Pro Phe Gly Ser Leu Asp Leu Leu Thr Thr Ile Gln Ala Thr Pro Leu			325		330
Ala Val Gly Ala Arg Ala Asn Gly Asn Lys Phe Ile Pro Val Ile Pro			340		345
Arg Asn Thr Met Val Pro Ala Arg Lys Asp Leu Phe Phe Thr Thr Val			355		360
Gln Asp Asn Gln Lys Glu Ala Leu Ile Ile Ile Tyr Glu Gly Glu Gly			370		375
Glu Thr Val Glu Glu Asn His Leu Leu Gly Tyr Phe Lys Leu Val Gly			385		390
Ile Pro Pro Ala Pro Lys Gly Val Pro Glu Ile Asn Val Cys Met Asp			405		410
Ile Asp Ala Ser Asn Ala Leu Arg Val Phe Ala Ala Val Leu Met Pro			420		425
Gly Ser Ser Thr Pro Val Val Pro Val Ile Glu Val Arg Met Pro Thr			435		440
Val Asp Asp Gly His Gly Trp Cys Ala Gln Ala Leu Asn Val Lys Tyr			450		455
Gly Ala Thr Leu Asp Leu Ile Thr Phe Gln Arg Lys Met			465		470
					475

(2) INFORMATION FOR SEQ ID NO:382:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 468 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..468
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566740

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:382:

Met Lys Arg Leu Val Gly Arg Val Asp Thr Asp Pro Val Val His Ala					
1	5		10		15
Ser Lys Asn Leu Pro Phe Leu Val Gln Thr Leu Asp Ile Gly Val Arg					
	20		25		30
Pro Phe Ile Ala Ala Leu Val Asn Asn Ala Trp Arg Ser Thr Thr Pro					
	35		40		45
Glu Glu Val Leu Ala Ile Phe Leu Val Glu Leu Arg Leu Met Ala Glu					
	50		55		60
Ala Gln Leu Lys Arg Pro Val Arg Asn Val Val Leu Thr Val Pro Val					
	65		70		75
Ser Phe Ser Arg Phe Gln Leu Thr Arg Phe Glu Arg Ala Cys Ala Met					
	85		90		95
Ala Gly Leu His Val Leu Arg Leu Met Pro Glu Pro Thr Ala Ile Ala					
	100		105		110
Leu Leu Tyr Ala Gln Gln Gln Gln Met Thr Thr His Asp Asn Met Gly					
	115		120		125
Ser Gly Ser Glu Arg Leu Ala Val Ile Phe Asn Met Gly Ala Gly Tyr					
	130		135		140
Cys Asp Val Ala Val Thr Ala Thr Ala Gly Gly Val Ser Gln Ile Lys					
145	150		155		160

Ala Leu Ala Gly Ser Pro Ile Gly Gly Glu Asp Ile Leu Gln Ser Thr
165 170 175
Ile Arg His Ile Ala Pro Pro Asn Glu Glu Ala Ser Gly Leu Leu Arg
180 185 190
Val Ala Ala Gln Asp Ala Ile His Arg Leu Thr Asp Gln Glu Asn Val
195 200 205
Gln Ile Glu Val Asp Leu Gly Asn Gly Asn Lys Ile Ser Lys Val Leu
210 215 220
Asp Arg Leu Glu Phe Glu Glu Val Asn Gln Lys Val Phe Glu Glu Cys
225 230 235 240
Glu Arg Leu Val Val Gln Cys Leu Arg Asp Ala Arg Val Asn Gly Gly
245 250 255
Asp Ile Asp Asp Leu Ile Met Val Gly Gly Cys Ser Tyr Ile Pro Lys
260 265 270
Val Arg Thr Ile Ile Lys Asn Val Cys Lys Lys Asp Glu Ile Tyr Lys
275 280 285
Gly Val Asn Pro Leu Glu Ala Ala Val Arg Gly Ala Ala Leu Glu Gly
290 295 300
Ala Val Thr Ser Gly Ile His Asp Pro Phe Gly Ser Leu Asp Leu Leu
305 310 315 320
Thr Ile Gln Ala Thr Pro Leu Ala Val Gly Ala Arg Ala Asn Gly Asn
325 330 335
Lys Phe Ile Pro Val Ile Pro Arg Asn Thr Met Val Pro Ala Arg Lys
340 345 350
Asp Leu Phe Phe Thr Thr Val Gln Asp Asn Gln Lys Glu Ala Leu Ile
355 360 365
Ile Ile Tyr Glu Gly Glu Gly Glu Thr Val Glu Glu Asn His Leu Leu
370 375 380
Gly Tyr Phe Lys Leu Val Gly Ile Pro Pro Ala Pro Lys Gly Val Pro
385 390 395 400
Glu Ile Asn Val Cys Met Asp Ile Asp Ala Ser Asn Ala Leu Arg Val
405 410 415
Phe Ala Ala Val Leu Met Pro Gly Ser Ser Thr Pro Val Val Pro Val
420 425 430
Ile Glu Val Arg Met Pro Thr Val Asp Asp Gly His Gly Trp Cys Ala
435 440 445
Gln Ala Leu Asn Val Lys Tyr Gly Ala Thr Leu Asp Leu Ile Thr Phe
450 455 460
Gln Arg Lys Met
465

(2) INFORMATION FOR SEQ ID NO:383:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1957 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1957
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566745

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:383:

atagtgtctg	tctaattaat	atattgttcc	aaagaaaaat	atgtatctac	gtcttgcctc	60
taaacctctt	ttttcacatc	acaagcatct	taaaattttc	taaatcacctc	ttttgcgcat	120
gagacatgtc	tttttcgagg	gtttggtttc	gatctctttg	gtcatcttgg	agttgagcta	180
tgctgtttgc	ccaatctcat	cgatcaatg	ggtctgtctg	tattctcaac	gtttcatctt	240
tgaggccaac	aagcagggtta	tagtgatcaa	cgacatgttc	cctggaccga	tccttaattgc	300
aacagcaaac	gatatcattg	tcgttaaacat	tttcaacaat	ttgcccgaac	ccttccctcat	360
gacttggaat	ggattgcaat	tcgcggaagaa	ctcgtgggcaa	gatggagttc	gagggcacaaa	420
ctgtcccata	ctaccgggga	caaattggac	gtaccgtttt	caggtgaagg	atcaaatggg	480
aagttaacttt	tattttccga	cccttctact	tcagaaaagct	gccggaggat	acggtgctat	540

tagaatctat	ccccagaac	ttgtccagt	cccattocct	aagcccgaag	aagaatacga	600
catctctgatt	ggagatgggt	tttatctcga	ccatacagtt	atgagagctt	cacttgacgc	660
tggtcacagt	ttgcacaaatc	ctgatggat	tctttttaac	ggcggtggcc	ctgaagagac	720
cttcttttga	tttgaaacag	gcaaaacata	taggctaaga	atatcaaacg	tgggtctcaa	780
aacatgctta	aactctcagRa	rTScaagnc	acgatatgnt	tctagtttag	acagagggtta	840
cgatatgttca	aaaacgtggt	tactcgagcc	tggacatcca	cgtaggccaa	tcaactctca	900
ttcttctcac	tgccaaaaac	gacccgggtg	gaatttacgc	gttactactac	atattcgcca	960
cagctcgggt	cactgatctc	tacottggcg	gtatagcttt	aattcgatat	cccggtctcc	1020
cacttgaccc	agtcggacaa	ggtccactcg	cactcgcttt	gcaagatatt	gggtctctac	1080
ttgaacaagc	cotttccatt	agaatggacc	tgaacgttgg	agcagcaaga	tgcgaacctc	1140
aaggttctga	ccaactatgga	cgaataaacg	taaccagaac	gataatatta	cataacagac	1200
ttatgttatac	gtcgggcacaa	ctacggtata	cgattaaacg	gctttcgctt	gtctaacccg	1260
agaactccgtt	aaagctcggt	gatcattttc	agctaaatga	cacgataatc	cctggcagct	1320
tcccggttta	tccatccaac	aaaacaccga	ctcttggaa	ttcagtggtc	gatattcatt	1380
acaaagattt	catccacatc	gtgttccaga	accctctatt	tggattggag	agttatcaca	1440
togatgttga	caattttctc	gttgcggat	atgggatttg	agcttggctc	gaaagcaaaa	1500
aagctggata	taacttagta	gatgccgttt	cacgggtcaac	agttcaggtt	tatccattat	1560
cgtggacagc	aattattgata	gctatggata	atcaaggaat	gtggaaacgtg	agatcacaga	1620
aagcagagca	atgggtatctt	ggtcaagagc	tttatatgag	agttaaaggt	gaaggagaa	1680
aagatccttc	gactattccg	gttagagatg	aaaatccgat	accggggaat	gtcatccggt	1740
gtggcaaaagt	tcgataataa	ttaattgtct	gaaataataa	aaacctagaa	aagtctattt	1800
taattagcaa	aactaaagaa	cggtttaaag	gaatgatcac	agagtattag	gatctgtggt	1860
gatctagggt	tttgtggttt	gattgcgatt	cgatcaactt	gtgtaattgc	agaagacgga	1920
tggttaattta	aagagatgat	cttaggggtt	gtggtctt			

(2) INFORMATION FOR SEQ ID NO:384:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 236 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..236

(D) OTHER INFORMATION: / Ceres Seq. ID 1566746

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:384:

Met	Arg	His	Val	Phe	Val	Glu	Val	Leu	Val	Leu	Ile	Ser	Leu	Val	Ile
1			5					10						15	
Leu	Glu	Leu	Ser	Tyr	Ala	Phe	Ala	Pro	Ile	Ser	Ser	Tyr	Gln	Trp	Val
			20					25					30		
Val	Ser	Tyr	Ser	Gln	Arg	Phe	Ile	Leu	Gly	Gly	Asn	Lys	Gln	Val	Ile
			35				40				45				
Val	Ile	Asn	Asp	Met	Phe	Pro	Gly	Pro	Ile	Leu	Asn	Ala	Thr	Ala	Asn
			50			55					60				
Asp	Ile	Ile	Val	Val	Asn	Ile	Phe	Asn	Asn	Leu	Pro	Glu	Pro	Phe	Leu
			65			70				75				80	
Met	Thr	Trp	Asn	Gly	Leu	Gln	Leu	Arg	Lys	Asn	Ser	Trp	Gln	Asp	Gly
			85					90						95	
Val	Arg	Gly	Thr	Asn	Cys	Pro	Ile	Leu	Pro	Gly	Thr	Asn	Trp	Thr	Tyr
			100					105					110		
Arg	Phe	Gln	Val	Lys	Asp	Gln	Ile	Gly	Ser	Tyr	Phe	Tyr	Phe	Pro	Thr
			115				120					125			
Leu	Leu	Leu	Gln	Lys	Ala	Ala	Gly	Gly	Tyr	Gly	Ala	Ile	Arg	Ile	Tyr
			130				135				140				
Pro	Pro	Glu	Leu	Val	Pro	Val	Pro	Phe	Pro	Lys	Pro	Asp	Glu	Glu	Tyr
			145			150				155				160	
Asp	Ile	Leu	Ile	Gly	Asp	Trp	Phe	Tyr	Leu	Asp	His	Thr	Val	Met	Arg
			165					170						175	
Ala	Ser	Leu	Asp	Ala	Gly	His	Ser	Leu	Pro	Asn	Pro	Asp	Gly	Ile	Leu
			180					185					190		
Phe	Asn	Gly	Arg	Gly	Pro	Glu	Glu	Thr	Phe	Phe	Ala	Phe	Glu	Pro	Gly

(B) TYPE: amino acid

(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..217
(D) OTHER INFORMATION: / Ceres Seq. ID 1566748
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:387:
Met Asp Leu Asn Val Gly Ala Ala Arg Ser Asn Pro Gln Gly Ser Tyr
1 5 10 15
His Tyr Gly Arg Ile Asn Val Thr Arg Thr Ile Ile Leu His Asn Asp
20 25 30
Val Met Leu Ser Ser Gly Lys Leu Arg Tyr Thr Ile Asn Gly Val Ser
35 40 45
Phe Val Tyr Pro Glu Thr Pro Leu Lys Leu Val Asp His Phe Gln Leu
50 55 60
Asn Asp Thr Ile Ile Pro Gly Met Phe Pro Val Tyr Pro Ser Asn Lys
65 70 75 80
Thr Pro Thr Leu Gly Thr Ser Val Val Asp Ile His Tyr Lys Asp Phe
85 90 95
Ile His Ile Val Phe Gln Asn Pro Leu Phe Gly Leu Glu Ser Tyr His
100 105 110
Ile Asp Gly Tyr Asn Phe Phe Val Val Gly Tyr Gly Phe Gly Ala Trp
115 120 125
Ser Glu Ser Lys Lys Ala Gly Tyr Asn Leu Val Asp Ala Val Ser Arg
130 135 140
Ser Thr Val Gln Val Tyr Pro Tyr Ser Trp Thr Ala Ile Leu Ile Ala
145 150 155 160
Met Asp Asn Gln Gly Met Trp Asn Val Arg Ser Gln Lys Ala Glu Gln
165 170 175
Trp Tyr Leu Gly Gln Glu Leu Tyr Met Arg Val Lys Gly Glu Gly Glu
180 185 190
Glu Asp Pro Ser Thr Ile Pro Val Arg Asp Glu Asn Pro Ile Pro Gly
195 200 205
Asn Val Ile Arg Cys Gly Lys Val Arg
210 215

(2) INFORMATION FOR SEQ ID NO:387:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1206 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1206
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566749

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:387:

tatgaaattg	tagataaatg	gatcaaatcg	ttaactgtgga	tgagtttcaa	gagctggcca	60
aacaggccct	ccctaagatg	tactatgatt	tctacaatgg	aggagcagag	gatacaacaca	120
ctctcaatga	aaatgtccaa	gctttccgta	gaatcatggt	taggcctagg	gttctgtgtg	180
atgtgagcaa	catagatatg	tctacaagta	tattgggtta	cccaatctca	gctcccatca	240
tgattgctcc	aacagcaatg	cataagttgg	ctcatcctaa	aggagaaatc	gccacagcga	300
aagctgcagc	tcggtgtaac	actatcatga	tagtaccatt	catgtctact	tgacattattg	360
aggaggttgc	ttccagttgt	aacgctgttc	ggttttctca	aatatatgtg	tacaagagac	420
gtgatgtaac	agctcagatt	gtgaaaagag	ctgaaaaaac	tggattccaag	gctatagttc	480
taactgttga	tgttcccaga	ctgtgttaga	gggaagcaga	tataaagaac	aaaatgatat	540
ccccacagct	gaagaatttt	gaaggccttag	tttcaaccga	agtcgcagct	aatgaaggtt	600
cagggtttga	agcctttgcc	tctagtgcatt	ttgatgtctc	gttaagctgg	aaggatattg	660
aatggttaag	atctattaca	aagttgccaa	ttctgggtcaa	agggttactc	acacgtgaag	720
acgctcttaa	ggctgtgtga	gccggtgtag	atggaaatag	ggatccaac	cacggggctc	780

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gccagctcga ctattccccc gctacgataa ctgttttaga agaggttggt catgtgttga      840
aaggtaggat tccggttttg ctgtatggag gagtaagacg aggaacagat gttttcaaaG      900
cgSctggcgc tcggagcaca agctgttctt ataggaggcg ctatagtcta tgggcttgca      960
gctaagggtg aaagatggagt gaaaaaagtg attgatatgc tgaaaaatga gtttgagatt      1020
actatggccc tttctggctg tccaaccatt gatgacgtaa ccagaaaacca tgttaggaca      1080
gagaatgaga gaattaaatc tatgctctga tctctaaaacc aacagatcta gtctcagaga      1140
cttaatcaga cagttggaca acagtatgaa atactgtcaa tgcacataaa taaaagctc      1200
tatttc
```

(2) INFORMATION FOR SEQ ID NO:388:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 315 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..315

(D) OTHER INFORMATION: / Ceres Seq. ID 1566750

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:388:

```
Met Asp Gln Ile Val Asn Val Asp Glu Phe Gln Glu Leu Ala Lys Gln
1      5      10      15
Ala Leu Pro Lys Met Tyr Tyr Asp Phe Tyr Asn Gly Gly Ala Glu Asp
20      25      30
Gln His Thr Leu Asn Glu Asn Val Gln Ala Phe Arg Arg Ile Met Phe
35      40      45
Arg Pro Arg Val Leu Val Asp Val Ser Asn Ile Asp Met Ser Thr Ser
50      55      60
Ile Leu Gly Tyr Pro Ile Ser Ala Pro Ile Met Ile Ala Pro Thr Ala
65      70      75      80
Met His Lys Leu Ala His Pro Lys Gly Glu Ile Ala Thr Ala Lys Ala
85      90      95
Ala Ala Ala Cys Asn Thr Ile Met Ile Val Pro Phe Met Ser Thr Cys
100     105     110
Thr Ile Glu Glu Val Ala Ser Ser Cys Asn Ala Val Arg Phe Leu Gln
115     120     125
Ile Tyr Val Tyr Lys Arg Arg Asp Val Thr Ala Gln Ile Val Lys Arg
130     135     140
Ala Glu Lys Ala Gly Phe Lys Ala Ile Val Leu Thr Val Asp Val Pro
145     150     155     160
Arg Leu Gly Arg Arg Glu Ala Asp Ile Lys Asn Lys Met Ile Ser Pro
165     170     175
Gln Leu Lys Asn Phe Glu Gly Leu Val Ser Thr Glu Val Arg Pro Asn
180     185     190
Glu Gly Ser Gly Val Glu Ala Phe Ala Ser Ser Ala Phe Asp Ala Ser
195     200     205
Leu Ser Trp Lys Asp Ile Glu Trp Leu Arg Ser Ile Thr Lys Leu Pro
210     215     220
Ile Leu Val Lys Gly Leu Leu Thr Arg Glu Asp Ala Leu Lys Ala Val
225     230     235     240
Glu Ala Gly Val Asp Gly Ile Val Val Ser Asn His Gly Ala Arg Gln
245     250     255
Leu Asp Tyr Ser Pro Ala Thr Ile Thr Val Leu Glu Glu Val Val His
260     265     270
Val Val Lys Gly Arg Ile Pro Val Leu Leu Asp Gly Gly Val Arg Arg
275     280     285
Gly Thr Asp Val Phe Lys Ala Xaa Gly Ala Arg Ser Thr Ser Cys Ser
290     295     300
Tyr Arg Glu Ala Tyr Ser Leu Trp Ala Cys Ser
305     310     315
```

(2) INFORMATION FOR SEQ ID NO:389:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 295 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..295
 (D) OTHER INFORMATION: / Ceres Seq. ID 1566751

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:389:

Met	Tyr	Tyr	Asp	Phe	Tyr	Asn	Gly	Gly	Ala	Glu	Asp	Gln	His	Thr	Leu
1				5				10					15		
Asn	Glu	Asn	Val	Gln	Ala	Phe	Arg	Arg	Ile	Met	Phe	Arg	Pro	Arg	Val
			20					25					30		
Leu	Val	Asp	Val	Ser	Asn	Ile	Asp	Met	Ser	Thr	Ser	Ile	Leu	Gly	Tyr
			35					40				45			
Pro	Ile	Ser	Ala	Pro	Ile	Met	Ile	Ala	Pro	Thr	Ala	Met	His	Lys	Leu
			50				55					60			
Ala	His	Pro	Lys	Gly	Glu	Ile	Ala	Thr	Ala	Lys	Ala	Ala	Ala	Cys	
65				70				75						80	
Asn	Thr	Ile	Met	Ile	Val	Pro	Phe	Met	Ser	Thr	Cys	Thr	Ile	Glu	Glu
				85				90					95		
Val	Ala	Ser	Ser	Cys	Asn	Ala	Val	Arg	Phe	Leu	Gln	Ile	Tyr	Val	Tyr
				100				105					110		
Lys	Arg	Arg	Asp	Val	Thr	Ala	Gln	Ile	Val	Lys	Arg	Ala	Glu	Lys	Ala
				115				120				125			
Gly	Phe	Lys	Ala	Ile	Val	Leu	Thr	Val	Asp	Val	Pro	Arg	Leu	Gly	Arg
				130				135				140			
Arg	Glu	Ala	Asp	Ile	Lys	Asn	Lys	Met	Ile	Ser	Pro	Gln	Leu	Lys	Asn
145				150						155				160	
Phe	Glu	Gly	Leu	Val	Ser	Thr	Glu	Val	Arg	Pro	Asn	Glu	Gly	Ser	Gly
				165				170					175		
Val	Glu	Ala	Phe	Ala	Ser	Ser	Ala	Phe	Asp	Ala	Ser	Leu	Ser	Trp	Lys
				180				185					190		
Asp	Ile	Glu	Trp	Leu	Arg	Ser	Ile	Thr	Lys	Leu	Pro	Ile	Leu	Val	Lys
				195				200				205			
Gly	Leu	Leu	Thr	Arg	Glu	Asp	Ala	Leu	Lys	Ala	Val	Glu	Ala	Gly	Val
				210				215				220			
Asp	Gly	Ile	Val	Val	Ser	Asn	His	Gly	Ala	Arg	Gln	Leu	Asp	Tyr	Ser
225				230						235				240	
Pro	Ala	Thr	Ile	Thr	Val	Leu	Glu	Glu	Val	Val	His	Val	Val	Lys	Gly
				245				250					255		
Arg	Ile	Pro	Val	Leu	Leu	Asp	Gly	Gly	Val	Arg	Arg	Gly	Thr	Asp	Val
				260				265					270		
Phe	Lys	Ala	Xaa	Gly	Ala	Arg	Ser	Thr	Ser	Cys	Ser	Tyr	Arg	Glu	Ala
				275				280				285			
Tyr	Ser	Leu	Trp	Ala	Cys	Ser									
				290				295							

(2) INFORMATION FOR SEQ ID NO:390:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 269 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..269
 (D) OTHER INFORMATION: / Ceres Seq. ID 1566752

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:390:

Met Phe Arg Pro Arg Val Leu Val Asp Val Ser Asn Ile Asp Met Ser
1 5 10 15
Thr Ser Ile Leu Gly Tyr Pro Ile Ser Ala Pro Ile Met Ile Ala Pro
20 25 30
Thr Ala Met His Lys Leu Ala His Pro Lys Gly Glu Ile Ala Thr Ala
35 40 45
Lys Ala Ala Ala Ala Cys Asn Thr Ile Met Ile Val Pro Phe Met Ser
50 55 60
Thr Cys Thr Ile Glu Glu Val Ala Ser Ser Cys Asn Ala Val Arg Phe
65 70 75 80
Leu Gln Ile Tyr Val Tyr Lys Arg Arg Asp Val Thr Ala Gln Ile Val
85 90 95
Lys Arg Ala Glu Lys Ala Gly Phe Lys Ala Ile Val Leu Thr Val Asp
100 105 110
Val Pro Arg Leu Gly Arg Arg Glu Ala Asp Ile Lys Asn Lys Met Ile
115 120 125
Ser Pro Gln Leu Lys Asn Phe Glu Gly Leu Val Ser Thr Glu Val Arg
130 135 140
Pro Asn Glu Gly Ser Gly Val Glu Ala Phe Ala Ser Ser Ala Phe Asp
145 150 155 160
Ala Ser Leu Ser Trp Lys Asp Ile Glu Trp Leu Arg Ser Ile Thr Lys
165 170 175
Leu Pro Ile Leu Val Lys Gly Leu Leu Thr Arg Glu Asp Ala Leu Lys
180 185 190
Ala Val Glu Ala Gly Val Asp Gly Ile Val Val Ser Asn His Gly Ala
195 200 205
Arg Gln Leu Asp Tyr Ser Pro Ala Thr Ile Thr Val Leu Glu Glu Val
210 215 220
Val His Val Val Lys Gly Arg Ile Pro Val Leu Leu Asp Gly Gly Val
225 230 235 240
Arg Arg Gly Thr Asp Val Phe Lys Ala Xaa Gly Ala Arg Ser Thr Ser
245 250 255
Cys Ser Tyr Arg Glu Ala Tyr Ser Leu Trp Ala Cys Ser
260 265

(2) INFORMATION FOR SEQ ID NO:391:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1178 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1178

(D) OTHER INFORMATION: / Ceres Seq. ID 1566763

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:391:

taatttgggg	tcagggggtgg	gagttaccctc	gactttatgat	gacattttctc	aatacaagagg	60
aggctacaga	gatgccttaca	gtttgcacaca	gagtgcaaca	acaggggacgc	gatcgctttg	120
gtccagacag	ccctttggagc	agtttgttgt	agcgggagag	aattggtgctg	ttggtgagga	180
gtccaggaat	agatcgaatc	cgatcaatat	agacaacaac	gctttttcta	atggtgatgc	240
agaggctaag	cttcttcagt	cgttcaggca	ctgtatttcta	aagctttatta	aacttgaagg	300
atccgagctgg	ttgtttggac	aaagcagatgg	agttgatgaa	gaactgattg	acggggtagc	360
tgccagagag	aagtttatct	atgaagctga	agctcgagaa	ataaaccaagg	tggttcacat	420
ggggagagcaa	ctaattttcat	cggtttcctaa	ctgtggagat	ggttgcggtt	ggagagctga	480
tttgatttgtg	agcctttggag	tttggtgcat	tcaacgtgtc	cttgacttgt	ctctcatgga	540
gagtcggcct	gaagctttgg	gaaagtacac	ttactttctc	aacgcgcctac	agggagtgat	600
tgatccggcg	ttctcaaagg	tgccggacacc	aatgacacgc	tgctttttgcc	ttcagattcc	660
agcgagcaco	cagagagcga	gtccgacttc	agctaacgga	atgttacctc	cggtcgcaaa	720
accggtctaaa	ggcaaatgca	caaccgcagt	cacactttct	gatctaata	aaagcgttga	780
aattggcaatc	tcttgtagaa	aaggccgaac	cggtacagct	gcaggttgatg	tggtcttccc	840
aaaggggaaa	gagaatttgg	cttcgggtttt	gaagcgggtat	aaacgtcggt	tatcgaataa	900

accagtaggt atgaatcagg atggaccgg ttcaagaaaa aacgtgactg cgtacggatc 960
attgggttga agaagaagaa cattgtgaga aatctcatga tcaaagtac gtcgagagg 1020
aagccgaaga atcaaaaactc tcgcttttga ttgctctct gcttcgttaa ttgtgtatta 1080
agaaaagaag aaaaaaatg gatttttgtt gcttcagaat ttttcgctct ttttttctta 1140
ttttggtgtt aatgttatgt ttatatcat atatcttc

(2) INFORMATION FOR SEQ ID NO:392:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 322 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..322

(D) OTHER INFORMATION: / Ceres Seq. ID 1566764

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:392:

Asn	Leu	Gly	Ser	Gly	Val	Gly	Val	Pro	Ser	Thr	Tyr	Asp	Asp	Ile	Ser
1			5					10						15	
Gln	Ser	Arg	Gly	Gly	Tyr	Arg	Asp	Ala	Tyr	Ser	Leu	Pro	Gln	Ser	Ala
			20					25					30		
Thr	Thr	Gly	Thr	Gly	Ser	Leu	Trp	Ser	Arg	Gln	Pro	Phe	Glu	Gln	Phe
			35					40				45			
Val	Val	Ala	Glu	Arg	Asn	Gly	Ala	Val	Gly	Glu	Glu	Leu	Arg	Asn	Arg
			50				55				60				
Ser	Asn	Pro	Ile	Asn	Ile	Asp	Asn	Asn	Ala	Ser	Ser	Asn	Val	Asp	Ala
			65				70				75			80	
Glu	Ala	Lys	Leu	Leu	Gln	Ser	Phe	Arg	His	Cys	Ile	Leu	Lys	Leu	Ile
			85						90				95		
Lys	Leu	Glu	Gly	Ser	Glu	Trp	Leu	Phe	Gly	Gln	Ser	Asp	Gly	Val	Asp
			100					105					110		
Glu	Glu	Leu	Ile	Asp	Arg	Val	Ala	Ala	Arg	Glu	Lys	Phe	Ile	Tyr	Glu
			115				120					125			
Ala	Glu	Ala	Arg	Glu	Ile	Asn	Gln	Val	Gly	His	Met	Gly	Glu	Gln	Leu
			130				135					140			
Ile	Ser	Ser	Val	Pro	Asn	Cys	Gly	Asp	Gly	Cys	Val	Trp	Arg	Ala	Asp
			145				150				155			160	
Leu	Ile	Val	Ser	Phe	Gly	Val	Trp	Cys	Ile	His	Xaa	Val	Leu	Asp	Leu
			165						170				175		
Ser	Leu	Met	Glu	Ser	Arg	Pro	Glu	Leu	Trp	Gly	Lys	Tyr	Thr	Tyr	Val
			180					185					190		
Leu	Asn	Arg	Leu	Gln	Gly	Val	Ile	Asp	Pro	Ala	Phe	Ser	Lys	Leu	Arg
			195					200				205			
Thr	Pro	Met	Thr	Pro	Cys	Phe	Cys	Leu	Gln	Ile	Pro	Ala	Ser	His	Gln
			210				215				220				
Arg	Ala	Ser	Pro	Thr	Ser	Ala	Asn	Gly	Met	Leu	Pro	Pro	Ala	Ala	Lys
			225				230				235			240	
Pro	Ala	Lys	Gly	Lys	Cys	Thr	Thr	Ala	Val	Thr	Leu	Leu	Asp	Leu	Ile
			245						250				255		
Lys	Asp	Val	Glu	Met	Ala	Ile	Ser	Cys	Arg	Lys	Gly	Arg	Thr	Gly	Thr
			260					265					270		
Ala	Ala	Gly	Asp	Val	Ala	Phe	Pro	Lys	Gly	Lys	Glu	Asn	Leu	Ala	Ser
			275					280				285			
Val	Leu	Lys	Arg	Tyr	Lys	Arg	Arg	Leu	Ser	Asn	Lys	Pro	Val	Gly	Met
			290				295				300				
Asn	Gln	Asp	Gly	Pro	Gly	Ser	Arg	Lys	Asn	Val	Thr	Ala	Tyr	Gly	Ser
			305				310				315			320	
Leu	Gly														

(2) INFORMATION FOR SEQ ID NO:393:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 183 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..183
(D) OTHER INFORMATION: / Ceres Seq. ID 1566765
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:393:
Met Gly Glu Gln Leu Ile Ser Ser Val Pro Asn Cys Gly Asp Gly Cys
1 5 10 15
Val Trp Arg Ala Asp Leu Ile Val Ser Phe Gly Val Trp Cys Ile His
20 25 30
Xaa Val Leu Asp Leu Ser Leu Met Glu Ser Arg Pro Glu Leu Trp Gly
35 40 45
Lys Tyr Thr Tyr Val Leu Asn Arg Leu Gln Gly Val Ile Asp Pro Ala
50 55 60
Phe Ser Lys Leu Arg Thr Pro Met Thr Pro Cys Phe Cys Leu Gln Ile
65 70 75 80
Pro Ala Ser His Gln Arg Ala Ser Pro Thr Ser Ala Asn Gly Met Leu
85 90 95
Pro Pro Ala Ala Lys Pro Ala Lys Gly Lys Cys Thr Thr Ala Val Thr
100 105 110
Leu Leu Asp Leu Ile Lys Asp Val Glu Met Ala Ile Ser Cys Arg Lys
115 120 125
Gly Arg Thr Gly Thr Ala Ala Gly Asp Val Ala Phe Pro Lys Gly Lys
130 135 140
Glu Asn Leu Ala Ser Val Leu Lys Arg Tyr Lys Arg Arg Leu Ser Asn
145 150 155 160
Lys Pro Val Gly Met Asn Gln Asp Gly Pro Gly Ser Arg Lys Asn Val
165 170 175
Thr Ala Tyr Gly Ser Leu Gly
180

(2) INFORMATION FOR SEQ ID NO:394:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1514 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..1514
(D) OTHER INFORMATION: / Ceres Seq. ID 1566766

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:394:

atttctctac	caccgttgat	gttaggggtt	cggctgtatt	ctcaccgctg	ctgacgggaga	60
cggcccgaaat	ccgcaatttta	atcttcgagg	tctgatttta	gtgaagaaca	agattcaata	120
gtgatatgca	gattctcatgt	ctcccaattt	cgattctctc	gatcactcct	cgaacctcaa	180
ttccactctt	accatcactc	tcctcaaatc	ctcgccgcgat	tttcaacctc	acttcaactc	240
agagcccaaa	tcactgtttc	ttcaaaagat	tacataaatc	tcagactgtg	ttcagcaatc	300
cgattttggc	tgccatgaaa	agagaagaag	atgttgaagt	cgatgattcg	ttttatatga	360
gaaagtgtgt	ggagctagca	aaaagagcaa	ttgggtgtac	aagtcctaata	cctatggtga	420
gttggtgtcat	gttcaaaagt	ggtgacattg	ttggccaagg	gtttcatccc	aaagctggtc	480
agcctcatcg	tgaggtgttt	gtctcttagag	atgctggaga	gttagctgag	aatgctactg	540
cttatgttag	tttggaaaca	tgtaatcatt	accggaagaac	accgcccgtg	acagaagcat	600
tgattaaggc	taaggtgaga	agagttgtta	ttgggatggt	tgatccgaat	ccaattgttt	660
tttcttcggg	tattagtctg	tfgaaagatg	ctggaaatcga	tgttactgtg	agtgttgaaag	720
aagagttatg	caagaagaatg	aatgagggat	tcattccatcg	aatgttaaca	gggaagcctt	780
ttctcgccct	caggtattct	atgtctgtca	atggtgtgtt	gctagacaag	attgggcaag	840
gggcttcgga	tagtggtgga	tactactcga	agctatttga	ggaatatgat	gcgataatac	900

ttttctctc	gttatcggt	gaactctcga	gcattttctc	acaagaagct	attaatgttt	960
cgatccaacc	tattcagatc	atagtagcta	gcaatgcaca	acagtctcat	atccttgctt	1020
cttccacac	tggtgaagaa	tcgggtccaa	aagttgtagt	tttcaccgca	aaggaatcgg	1080
ttgcagaatc	cgggaatcgt	agtagcgggg	tcgaaaccgt	agtattggaa	aagmtaaaat	1140
tggtattcat	tttgattat	tgttacaacc	gtggactatg	cagtgctctg	ttagatttga	1200
gggggaacgt	caaagacott	gaagtctctc	tgagagatgg	atttgagcag	aaactattgc	1260
agaaagtaat	tattgaggtc	ttgcgggaat	ggagcacaaa	agatgagaga	cagatcgctt	1320
cgatgaagt	gttgaatcaa	aagcatgtga	aagatttgca	gtctaagcaa	ttaggtggaa	1380
gcgttttct	agagggctat	ttttgatgtt	ttcatgtatg	aatgaataca	agtcagtata	1440
tttaccttt	ttaaagcata	gtattattaa	ggttttacag	atcctattat	taatagattg	1500
ataacagatt	tttg					

(2) INFORMATION FOR SEQ ID NO:395:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 426 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..426

(D) OTHER INFORMATION: / Ceres Seq. ID 1566767

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:395:

Met	Gln	Ile	Ser	Cys	Leu	Pro	Ile	Ser	Ile	Pro	Ser	Ile	Thr	Pro	Arg
1				5					10					15	
Thr	Ser	Ile	Pro	Leu	Leu	Pro	Ser	Leu	Ser	Ser	Asn	Pro	Arg	Arg	Ile
			20					25					30		
Phe	Asn	Leu	Thr	Ser	Leu	Gln	Ser	Pro	Asn	His	Cys	Phe	Phe	Lys	Arg
		35					40					45			
Leu	His	Lys	Ser	Gln	Thr	Gly	Phe	Ser	Asn	Pro	Val	Leu	Ala	Ala	Met
		50				55					60				
Lys	Arg	Glu	Glu	Asp	Val	Glu	Val	Asp	Asp	Ser	Phe	Tyr	Met	Arg	Lys
65				70					75					80	
Cys	Val	Glu	Leu	Ala	Lys	Arg	Ala	Ile	Gly	Cys	Thr	Ser	Pro	Asn	Pro
			85						90					95	
Met	Val	Gly	Cys	Val	Ile	Val	Lys	Asp	Gly	Asp	Ile	Val	Gly	Gln	Gly
		100						105					110		
Phe	His	Pro	Lys	Ala	Gly	Gln	Pro	His	Ala	Glu	Val	Phe	Ala	Leu	Arg
		115					120					125			
Asp	Ala	Gly	Glu	Leu	Ala	Glu	Asn	Ala	Thr	Ala	Tyr	Val	Ser	Leu	Glu
		130				135					140				
Pro	Cys	Asn	His	Tyr	Gly	Arg	Thr	Pro	Pro	Cys	Thr	Glu	Ala	Leu	Ile
145				150						155				160	
Lys	Ala	Lys	Val	Arg	Arg	Val	Val	Ile	Gly	Met	Val	Asp	Pro	Asn	Pro
				165					170					175	
Ile	Val	Phe	Ser	Ser	Gly	Ile	Ser	Arg	Leu	Lys	Asp	Ala	Gly	Ile	Asp
			180					185					190		
Val	Thr	Val	Ser	Val	Glu	Glu	Glu	Leu	Cys	Lys	Lys	Met	Asn	Glu	Gly
			195					200				205			
Phe	Ile	His	Arg	Met	Leu	Thr	Gly	Lys	Pro	Phe	Leu	Ala	Leu	Arg	Tyr
			210			215					220				
Ser	Met	Ser	Val	Asn	Gly	Cys	Leu	Leu	Asp	Lys	Ile	Gly	Gln	Gly	Ala
225				230					235					240	
Ser	Asp	Ser	Gly	Gly	Tyr	Tyr	Ser	Lys	Leu	Leu	Gln	Glu	Tyr	Asp	Ala
			245						250					255	
Ile	Ile	Leu	Ser	Ser	Ser	Leu	Ser	Asp	Glu	Leu	Ser	Ser	Ile	Ser	Ser
			260					265					270		
Gln	Glu	Ala	Ile	Asn	Val	Ser	Ile	Gln	Pro	Ile	Gln	Ile	Ile	Val	Ala
			275					280				285			
Ser	Asn	Ala	Gln	Gln	Ser	His	Ile	Leu	Ala	Ser	Ser	His	Thr	Val	Glu
290						295						300			

Glu Ser Gly Pro Lys Val Val Val Phe Thr Ala Lys Glu Ser Val Ala
305 310 315 320
Glu Ser Gly Ile Ser Ser Ser Gly Val Glu Thr Val Val Leu Glu Lys
325 330 335
Xaa Asn Leu Asp Ser Ile Leu Asp Tyr Cys Tyr Asn Arg Gly Leu Cys
340 345 350
Ser Val Leu Leu Asp Leu Arg Gly Asn Val Lys Asp Leu Glu Val Leu
355 360 365
Leu Arg Asp Gly Phe Glu Gln Lys Leu Leu Gln Lys Val Ile Ile Glu
370 375 380
Val Leu Pro Glu Trp Ser Thr Lys Asp Glu Arg Gln Ile Ala Ser Met
385 390 395 400
Lys Trp Leu Glu Ser Lys His Val Lys Asp Leu Gln Ser Lys Gln Leu
405 410 415
Gly Gly Ser Val Leu Leu Glu Gly Tyr Phe
420 425

(2) INFORMATION FOR SEQ ID NO:396:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 363 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..363

(D) OTHER INFORMATION: / Ceres Seq. ID 1566768

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:396:

Met Lys Arg Glu Glu Asp Val Glu Val Asp Asp Ser Phe Tyr Met Arg
1 5 10 15
Lys Cys Val Glu Leu Ala Lys Arg Ala Ile Gly Cys Thr Ser Pro Asn
20 25 30
Pro Met Val Gly Cys Val Ile Val Lys Asp Gly Asp Ile Val Gly Gln
35 40 45
Gly Phe His Pro Lys Ala Gly Gln Pro His Ala Glu Val Phe Ala Leu
50 55 60
Arg Asp Ala Gly Glu Leu Ala Glu Asn Ala Thr Ala Tyr Val Ser Leu
65 70 75 80
Glu Pro Cys Asn His Tyr Gly Arg Thr Pro Pro Cys Thr Glu Ala Leu
85 90 95
Ile Lys Ala Lys Val Arg Arg Val Val Ile Gly Met Val Asp Pro Asn
100 105 110
Pro Ile Val Phe Ser Ser Gly Ile Ser Arg Leu Lys Asp Ala Gly Ile
115 120 125
Asp Val Thr Val Ser Val Glu Glu Leu Cys Lys Lys Met Asn Glu
130 135 140
Gly Phe Ile His Arg Met Leu Thr Gly Lys Pro Phe Leu Ala Leu Arg
145 150 155 160
Tyr Ser Met Ser Val Asn Gly Cys Leu Leu Asp Lys Ile Gly Gln Gly
165 170 175
Ala Ser Asp Ser Gly Gly Tyr Tyr Ser Lys Leu Leu Gln Glu Tyr Asp
180 185 190
Ala Ile Ile Leu Ser Ser Ser Leu Ser Asp Glu Leu Ser Ser Ile Ser
195 200 205
Ser Gln Glu Ala Ile Asn Val Ser Ile Gln Pro Ile Gln Ile Ile Val
210 215 220
Ala Ser Asn Ala Gln Gln Ser His Ile Leu Ala Ser Ser His Thr Val
225 230 235 240
Glu Glu Ser Gly Pro Lys Val Val Val Phe Thr Ala Lys Glu Ser Val
245 250 255
Ala Glu Ser Gly Ile Ser Ser Ser Gly Val Glu Thr Val Val Leu Glu

	260		265		270
Lys Xaa Asn Leu Asp Ser Ile Leu Asp Tyr Cys Tyr Asn Arg Gly Leu					
	275		280		285
Cys Ser Val Leu Leu Asp Leu Arg Gly Asn Val Lys Asp Leu Glu Val					
	290		295		300
Leu Leu Arg Asp Gly Phe Glu Gln Lys Leu Leu Gln Lys Val Ile Ile					
305		310		315	320
Glu Val Leu Pro Glu Trp Ser Thr Lys Asp Glu Arg Gln Ile Ala Ser					
	325		330		335
Met Lys Trp Leu Glu Ser Lys His Val Lys Asp Leu Gln Ser Lys Gln					
	340		345		350
Leu Gly Gly Ser Val Leu Leu Glu Gly Tyr Phe					
	355		360		

(2) INFORMATION FOR SEQ ID NO:397:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 349 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..349

(D) OTHER INFORMATION: / Ceres Seq. ID 1566769

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:397:

Met Arg Lys Cys Val Glu Leu Ala Lys Arg Ala Ile Gly Cys Thr Ser	
1	5
Pro Asn Pro Met Val Gly Cys Val Ile Val Lys Asp Gly Asp Ile Val	
	20
Gly Gln Gly Phe His Pro Lys Ala Gly Gln Pro His Ala Glu Val Phe	
	35
Ala Leu Arg Asp Ala Gly Glu Leu Ala Glu Asn Ala Thr Ala Tyr Val	
50	55
Ser Leu Glu Pro Cys Asn His Tyr Gly Arg Thr Pro Pro Cys Thr Glu	
65	70
Ala Leu Ile Lys Ala Lys Val Arg Arg Val Ile Gly Met Val Asp	
	85
Pro Asn Pro Ile Val Phe Ser Ser Gly Ile Ser Arg Leu Lys Asp Ala	
	100
Gly Ile Asp Val Thr Val Ser Val Glu Glu Glu Leu Cys Lys Lys Met	
	115
Asn Glu Gly Phe Ile His Arg Met Leu Thr Gly Lys Pro Phe Leu Ala	
130	135
Leu Arg Tyr Ser Met Ser Val Asn Gly Cys Leu Leu Asp Lys Ile Gly	
145	150
Gln Gly Ala Ser Asp Ser Gly Gly Tyr Tyr Ser Lys Leu Leu Gln Glu	
	165
Tyr Asp Ala Ile Ile Leu Ser Ser Ser Leu Ser Asp Glu Leu Ser Ser	
	180
Ile Ser Ser Gln Glu Ala Ile Asn Val Ser Ile Gln Pro Ile Gln Ile	
	195
Ile Val Ala Ser Asn Ala Gln Gln Ser His Ile Leu Ala Ser Ser His	
	210
Thr Val Glu Glu Ser Gly Pro Lys Val Val Val Phe Thr Ala Lys Glu	
225	230
Ser Val Ala Glu Ser Gly Ile Ser Ser Ser Gly Val Glu Thr Val Val	
	245
Leu Glu Lys Xaa Asn Leu Asp Ser Ile Leu Asp Tyr Cys Tyr Asn Arg	
	260
Gly Leu Cys Ser Val Leu Leu Asp Leu Arg Gly Asn Val Lys Asp Leu	
	275
	280
	285

Glu Val Leu Leu Arg Asp Gly Phe Glu Gln Lys Leu Leu Gln Lys Val
290 295 300
Ile Ile Glu Val Leu Pro Glu Trp Ser Thr Lys Asp Glu Arg Gln Ile
305 310 315 320
Ala Ser Met Lys Trp Leu Glu Ser Lys His Val Lys Asp Leu Gln Ser
325 330 335
Lys Gln Leu Gly Gly Ser Val Leu Glu Gly Tyr Phe
340 345

(2) INFORMATION FOR SEQ ID NO:398:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1571 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1571

(D) OTHER INFORMATION: / Ceres Seq. ID 1566785

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:398:

atcatctctc	tcacttcac	aaaactcaaa	aaaatgtctc	ccattccaaa	accactcttc	60
ttctttctct	tcctcaaatc	KtgCtatctc	ttctcaactc	actctctctt	cacctccac	120
tcacatctct	ccctatctcc	accaccacaa	actctcaccg	cttcaccacc	tcctctctct	180
cccggaaaaa	cccatctccg	tcgtctccac	catcaaacct	ccgatcaaga	ttcaaaatac	240
caatggctct	aatcatctca	ctccccatag	gaacaccacc	acaagctcaa	caaatgggtc	300
ttgacactgg	aagccaaact	tcttggatcc	aatgtcatcg	taaaaagctt	ccctccaaac	360
caaaaacatc	atttgatcca	tctctttctt	ctcttttctc	aactttgcct	tgctcaacac	420
ctctttgtaa	accagagaatt	cccgatttta	cccttctctc	ttcttgtgac	ttcaacagggt	480
tatgtcacta	ctcttacttc	tacgtctgatg	gaacctctgc	tgagggtgat	ctcgtcaaac	540
aaaaaatcac	tttctcaaat	accgaaatta	ccctctcttt	gatactaggt	tcgctcacag	600
agctctctga	tgataggggc	attttgggaa	tgaacogtgg	tcgtctctct	tttgtttctc	660
aagctaagat	ttcgaagttc	tcttattgca	tcctcccaaa	atcaaacccg	cccggtttta	720
ctccaacccg	ttcgtttttac	cttggtgata	accggaatc	acacggtttc	aaatacgttt	780
ctttgttgac	ttttctcgaa	agtcacacgaa	tgccgaatct	tgatctctct	gcttaccactg	840
ttctatgat	tgggattaga	tttggtttga	agaagcttaa	catttccggt	tcggtttttc	900
gacccgatgc	agggcggtcg	ggtcaaacaa	tggttgatcc	gggatccgag	tttactcatt	960
tagtagacgc	agcttacgat	aaagtaagag	cagagataat	gacacgtgta	ggacgaagat	1020
taaaagaagg	ttacgtctac	ggtggaacag	ctgacatgtg	tttcgatgga	aacgtggcga	1080
tgatccacag	gttgatagga	gatctttgtg	ttgtgttcc	tagaggagtt	gagatatttg	1140
ttcccaagaa	gagggttttg	gttaacgtag	gaggtgggat	tcattgcggt	ggaatccgag	1200
ggtcgagat	ctgtggagct	gctagtaata	taatcgggaa	cggtccatcag	caaaatcttt	1260
gggttgagtt	cgatgtgacc	aatagaagag	tggtgtttgc	taaagctgat	ttgacagag	1320
tagtgtgagg	aaaagggttc	tgctacggtt	acaaacaaag	gtcttatggt	ggactcgttt	1380
aaagatcgtc	gttcgatgat	gttaatcggg	cggtacatat	taaaatagca	gttttgtatg	1440
aaggaacttt	tattaggggc	ctgaaacaat	gtcctacaaa	taattaaaag	gtttcaactg	1500
agatttttat	gttgatccgt	ttgtatatta	tatggttcat	attaactgtt	tacataaaaa	1560
tatcttttat	t					

(2) INFORMATION FOR SEQ ID NO:399:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 441 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..441

(D) OTHER INFORMATION: / Ceres Seq. ID 1566786

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:399:

His Leu Ser His Phe His Lys Thr Gln Lys Asn Val Ser His Ser Lys
1 5 10 15

Thr Thr Leu Leu Leu Leu Leu Pro Gln Leu Xaa Leu Ser Leu Ser Thr
20 25 30
Ser Leu Ser Leu His Leu Pro Leu Thr Ser Leu Pro Ile Ser Thr Thr
35 40 45
Thr Asn Ser His Arg Phe Thr Thr Ser Leu Leu Ser Arg Lys Asn Pro
50 55 60
Ser Pro Ser Ser Pro Pro Tyr Asn Phe Arg Ser Arg Phe Lys Tyr Ser
65 70 75 80
Met Ala Leu Ile Ile Ser Leu Pro Ile Gly Thr Pro Pro Gln Ala Gln
85 90 95
Gln Met Val Leu Asp Thr Gly Ser Gln Leu Ser Trp Ile Gln Cys His
100 105 110
Arg Lys Lys Leu Pro Pro Lys Pro Lys Thr Ser Phe Asp Pro Ser Leu
115 120 125
Ser Ser Ser Phe Ser Thr Leu Pro Cys Ser His Pro Leu Cys Lys Pro
130 135 140
Arg Ile Pro Asp Phe Thr Leu Pro Thr Ser Cys Asp Ser Asn Arg Leu
145 150 155 160
Cys His Tyr Ser Tyr Phe Tyr Ala Asp Gly Thr Phe Ala Glu Gly Asn
165 170 175
Leu Val Lys Glu Lys Ile Thr Phe Ser Asn Thr Glu Ile Thr Pro Pro
180 185 190
Leu Ile Leu Gly Cys Ala Thr Glu Ser Ser Asp Asp Arg Gly Ile Leu
195 200 205
Gly Met Asn Arg Gly Arg Leu Ser Phe Val Ser Gln Ala Lys Ile Ser
210 215 220
Lys Phe Ser Tyr Cys Ile Pro Pro Lys Ser Asn Arg Pro Gly Phe Thr
225 230 235 240
Pro Thr Gly Ser Phe Tyr Leu Gly Asp Asn Pro Asn Ser His Gly Phe
245 250 255
Lys Tyr Val Ser Leu Leu Thr Phe Pro Glu Ser Gln Arg Met Pro Asn
260 265 270
Leu Asp Pro Leu Ala Tyr Thr Val Pro Met Ile Gly Ile Arg Phe Gly
275 280 285
Leu Lys Lys Leu Asn Ile Ser Gly Ser Val Phe Arg Pro Asp Ala Gly
290 295 300
Gly Ser Gly Gln Thr Met Val Asp Ser Gly Ser Glu Phe Thr His Leu
305 310 315 320
Val Asp Ala Ala Tyr Asp Lys Val Arg Ala Glu Ile Met Thr Arg Val
325 330 335
Gly Arg Arg Leu Lys Lys Gly Tyr Val Tyr Gly Gly Thr Ala Asp Met
340 345 350
Cys Phe Asp Gly Asn Val Ala Met Ile Pro Arg Leu Ile Gly Asp Leu
355 360 365
Val Phe Val Phe Thr Arg Gly Val Glu Ile Phe Val Pro Lys Glu Arg
370 375 380
Val Leu Val Asn Val Gly Gly Ile His Cys Val Gly Ile Gly Arg
385 390 395 400
Ser Ser Met Leu Gly Ala Ala Ser Asn Ile Ile Gly Asn Val His Gln
405 410 415
Gln Asn Leu Trp Val Glu Phe Asp Val Thr Asn Arg Arg Val Gly Phe
420 425 430
Ala Lys Ala Asp Cys Ser Arg Val Val
435 440

(2) INFORMATION FOR SEQ ID NO:400:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 361 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide

(D) OTHER INFORMATION: / Ceres Seq. ID 1566787

(B) LOCATION: 1..344

Figure 1

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:401:
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(2) INFORMATION FOR SEQ ID NO:402:

(A) LENGTH: 1816 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1816

(D) OTHER INFORMATION: / Ceres Seq. ID 1566797

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:402:

atgtttatag	ttactacaag	agtcactgag	aaataaatta	tacaaaatat	gtctaattgaa	60
aattctgtaa	tgtcattgat	atcgcatctc	tggtcattctc	tgtcttcaag	atgtatcaat	120
tgcgttgtaa	ggtttattcc	ttttcgggtg	cttgcaagcg	aagttaacca	acaaaggcgg	180


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accagtacaa tggcctgtgt ttgggataac tcccgagttc ttcttctcatg ttccagatgat 240
gtttggatggt gtcaccccgat gtttgacgaa aagccgagga acgttttctt accaacgaat 300
ctgtgtttagt ggaattctac gacccatgac tagtgttctt gcaaacatcg aatacatgct 360
caaaacaaat ttcaagaact ttccataaagg agagttttac aaagagagat tccgtgactt 420
actcgaagat ggtattttca atgcggatga tgaatcttgg aaagaacaga gacggatcat 480
cataacagaa atgcattcca ctccgtctctt ggaatcatct ttccagacga cgagagattt 540
gatagagagg aagcttttaa aagtatgga gagtttctcc aagtcacaa aagcttttga 600
tcttcaagag attcttttct ggttaacatt tgataatat tgcatcgagg gttctggaga 660
tgatccgggg acttttggat atgatcttcc tcaagttcca ttccgcaaa cggtttgaaga 720
agcaacagag tctactctgt ttccgttctat gatccgcct ttgtgttga aaccaatgaa 780
gttttttcat atagggtatg agaaagggct tagggaagcg gttgagacgg ttcaaacatt 840
tatcgacaag atggtttgtg aacgaatcgc gatgcttaag gaccaaggaa cattagcgaa 900
tagcaaatcc gatgtctctt cgaggctaat acagatcgaa agtcacaaaa gaggcgatga 960
aaatgatoga ttcaaccgca agtttttccg acagttctgc tcaagcttca tcttagccgg 1020
acgagacacg agttcccgct cgcttacttg gttcttctg ttgataacaa aacccccgga 1080
agtcaaaacc aagatccttc acgaaatcag agaaatcttg agccaaagag agaagaacaa 1140
ctacaagctt gatgaacccg gagaacacga gagttctctg cacttcacag tcaagaactt 1200
aaacgatatg gtttatctac aagcagcatt gtcagaatct cttagactct atccaccaat 1260
tccaatggaa atgaacaacg cgaccgagga agatgtgttt ccggatggaa ctttcttgag 1320
aaaaaggctca aggttttact tctcagtcta tgcaatggga aggatggaat cgatttgggg 1380
aaaaagctgt gaaatgttca aaccgaaaag atggatacaa ggaggggcaat acgtgagtga 1440
tgatcagttt aaatcgtctg tgttcaatgc aggtccaaga cttgttttag gaaaacatt 1500
tgcttacttg cagatgaaaa tgggtggctgc ttcgatcttg ctgaatctac aaatcaaggt 1560
tgatcaagat catgtttgtt ttcccgagat aacaacgact ttgtatatga aacatggtct 1620
taagtgacgg attacaccca gatctctaga agagaagaag caagatctat aaatatagaa 1680
gaaacaaaca gctaaactgt gaagtgttga ctgaaatata cataaataat ctttgttagt 1740
aaatgttaca gtgtgtgtat tatgtgtaat tcagatcaaa tgttatatac aaagaaaaaa 1800
Attgcaatca taaggc

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(2) INFORMATION FOR SEQ ID NO:403:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 477 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..477

(D) OTHER INFORMATION: / Ceres Seq. ID 1566798

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:403:

```

Met Phe Gly Trp Val Thr Arg Cys Leu Thr Lys Ser Arg Gly Thr Phe
1 5 10 15
Pro Tyr Gln Arg Ile Trp Phe Ser Gly Ser Tyr Gly Ala Met Thr Ser
20 25 30
Val Pro Ala Asn Ile Glu Tyr Met Leu Lys Thr Asn Phe Lys Asn Phe
35 40 45
Pro Lys Gly Glu Phe Tyr Lys Glu Arg Phe Arg Asp Leu Leu Glu Asp
50 55 60
Gly Ile Phe Asn Ala Asp Asp Glu Ser Trp Lys Glu Gln Arg Arg Ile
65 70 75 80
Ile Ile Thr Glu Met His Ser Thr Arg Phe Val Asp His Ser Phe Gln
85 90 95
Thr Thr Arg Asp Leu Ile Glu Arg Lys Leu Leu Lys Val Met Glu Ser
100 105 110
Phe Ser Lys Ser Gln Glu Ala Phe Asp Leu Gln Glu Ile Leu Leu Arg
115 120 125
Leu Thr Phe Asp Asn Ile Cys Ile Ala Gly Leu Gly Asp Asp Pro Gly
130 135 140
Thr Leu Asp Asp Asp Leu Pro His Val Pro Phe Ala Lys Ala Phe Glu
145 150 155 160
Glu Ala Thr Glu Ser Thr Leu Phe Arg Phe Met Ile Pro Pro Phe Val

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Met	Thr	Ser	Val	Pro	Ala	Asn	Ile	Glu	Tyr	Met	Leu	Lys	Thr	Asn	Phe
1				5				10					15		
Lys	Asn	Phe	Pro	Lys	Gly	Glu	Phe	Tyr	Lys	Glu	Arg	Phe	Arg	Asp	Leu
			20					25					30		
Leu	Glu	Asp	Gly	Ile	Phe	Asn	Ala	Asp	Asp	Glu	Ser	Trp	Lys	Glu	Gln
		35					40					45			
Arg	Arg	Ile	Ile	Ile	Thr	Glu	Met	His	Ser	Thr	Arg	Phe	Val	Asp	His
	50					55					60				
Ser	Phe	Gln	Thr	Thr	Arg	Asp	Leu	Ile	Glu	Arg	Lys	Leu	Leu	Lys	Val
65					70					75				80	

Met	Glu	Ser	Phe	Ser	Lys	Ser	Gln	Glu	Ala	Phe	Asp	Leu	Gln	Glu	Ile	
				85					90					95		
Leu	Leu	Arg	Leu	Thr	Phe	Asp	Asn	Ile	Cys	Ile	Ala	Gly	Leu	Gly	Asp	
			100					105					110			
Asp	Pro	Gly	Thr	Leu	Asp	Asp	Asp	Leu	Pro	His	Val	Pro	Phe	Ala	Lys	
		115					120					125				
Ala	Phe	Glu	Glu	Ala	Thr	Glu	Ser	Thr	Leu	Phe	Arg	Phe	Met	Ile	Pro	
		130				135					140					
Pro	Phe	Val	Trp	Lys	Pro	Met	Lys	Phe	Phe	Asp	Ile	Gly	Tyr	Glu	Lys	
		145			150					155					160	
Gly	Leu	Arg	Glu	Ala	Val	Glu	Thr	Val	His	Asn	Phe	Ile	Asp	Lys	Met	
			165					170						175		
Val	Val	Glu	Arg	Ile	Ala	Met	Leu	Lys	Asp	Gln	Gly	Thr	Leu	Ala	Asn	
			180					185					190			
Ser	Lys	Ser	Asp	Val	Leu	Ser	Arg	Leu	Ile	Gln	Ile	Glu	Ser	His	Lys	
		195					200						205			
Arg	Gly	Asp	Glu	Asn	Asp	Arg	Phe	Thr	Ala	Lys	Phe	Phe	Arg	Gln	Phe	
		210			215						220					
Cys	Ser	Ser	Phe	Ile	Leu	Ala	Gly	Arg	Asp	Thr	Ser	Ser	Val	Ala	Leu	
		225			230				235						240	
Thr	Trp	Phe	Phe	Trp	Leu	Ile	Thr	Lys	His	Pro	Glu	Val	Glu	Thr	Lys	
			245					250						255		
Ile	Leu	His	Glu	Ile	Arg	Glu	Ile	Leu	Ser	Gln	Arg	Glu	Lys	Asn	Asn	
		260					265						270			
Tyr	Lys	Leu	Asp	Glu	Thr	Gly	Glu	Thr	Glu	Ser	Ser	Arg	His	Phe	Thr	
		275					280					285				
Val	Lys	Glu	Leu	Asn	Asp	Met	Val	Tyr	Leu	Gln	Ala	Ala	Leu	Ser	Glu	
		290			295						300					
Ser	Leu	Arg	Leu	Tyr	Pro	Pro	Ile	Pro	Met	Glu	Met	Lys	Gln	Ala	Thr	
		305			310				315						320	
Glu	Glu	Asp	Val	Phe	Pro	Asp	Gly	Thr	Phe	Leu	Arg	Lys	Gly	Ser	Arg	
			325					330						335		
Val	Tyr	Phe	Ser	Val	Tyr	Ala	Met	Gly	Arg	Met	Glu	Ser	Ile	Trp	Gly	
			340				345						350			
Lys	Asp	Cys	Glu	Met	Phe	Lys	Pro	Glu	Arg	Trp	Ile	Gln	Gly	Gly	Gln	
		355					360					365				
Tyr	Val	Ser	Asp	Asp	Gln	Phe	Lys	Tyr	Val	Val	Phe	Asn	Ala	Gly	Pro	
		370			375						380					
Arg	Leu	Cys	Leu	Gly	Lys	Thr	Phe	Ala	Tyr	Leu	Gln	Met	Lys	Met	Val	
		385			390				395					400		
Ala	Ala	Ser	Ile	Leu	Leu	Asn	Tyr	Ser	Ile	Lys	Val	Asp	Gln	Asp	His	
			405					410					415			
Val	Val	Val	Pro	Arg	Val	Thr	Thr	Thr	Leu	Tyr	Met	Lys	His	Gly	Leu	
		420					425						430			
Lys	Val	Arg	Ile	Thr	Pro	Arg	Ser	Leu	Glu	Glu	Lys	Lys	Gln	Asp	Ser	
		435				440						445				

(2) INFORMATION FOR SEQ ID NO:405:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 438 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..438

(D) OTHER INFORMATION: / Ceres Seq. ID 1566800

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:405:

Met Leu Lys Thr Asn Phe Lys Asn Phe Pro Lys Gly Glu Phe Tyr Lys

1	5	10	15
Glu Arg Phe Arg	Asp Leu Leu Glu Asp	Gly Ile Phe Asn Ala Asp Asp	
	20	25	30
Glu Ser Trp Lys	Glu Gln Arg Arg Ile Ile Thr Glu Met His Ser		
	35	40	45
Thr Arg Phe Val Asp His Ser	Phe Gln Thr Thr Arg Asp Leu Ile Glu		
	50	55	60
Arg Lys Leu Leu Lys Val Met Glu Ser Phe Ser Lys Ser Gln Glu Ala			
	65	70	75
Phe Asp Leu Gln Glu Ile Leu Leu Arg Leu Thr Phe Asp Asn Ile Cys			
	85	90	95
Ile Ala Gly Leu Gly Asp Asp Pro Gly Thr Leu Asp Asp Asp Leu Pro			
	100	105	110
His Val Pro Phe Ala Lys Ala Phe Glu Glu Ala Thr Glu Ser Thr Leu			
	115	120	125
Phe Arg Phe Met Ile Pro Pro Phe Val Trp Lys Pro Met Lys Phe Phe			
	130	135	140
Asp Ile Gly Tyr Glu Lys Gly Leu Arg Glu Ala Val Glu Thr Val His			
	145	150	155
Asn Phe Ile Asp Lys Met Val Val Glu Arg Ile Ala Met Leu Lys Asp			
	165	170	175
Gln Gly Thr Leu Ala Asn Ser Lys Ser Asp Val Leu Ser Arg Leu Ile			
	180	185	190
Gln Ile Glu Ser His Lys Arg Gly Asp Glu Asn Asp Arg Phe Thr Ala			
	195	200	205
Lys Phe Phe Arg Gln Phe Cys Ser Ser Phe Ile Leu Ala Gly Arg Asp			
	210	215	220
Thr Ser Ser Val Ala Leu Thr Trp Phe Phe Trp Leu Ile Thr Lys His			
	225	230	235
Pro Glu Val Glu Thr Lys Ile Leu His Glu Ile Arg Glu Ile Leu Ser			
	245	250	255
Gln Arg Glu Lys Asn Asn Tyr Lys Leu Asp Glu Thr Gly Glu Thr Glu			
	260	265	270
Ser Ser Arg His Phe Thr Val Lys Glu Leu Asn Asp Met Val Tyr Leu			
	275	280	285
Gln Ala Ala Leu Ser Glu Ser Leu Arg Leu Tyr Pro Pro Ile Pro Met			
	290	295	300
Glu Met Lys Gln Ala Thr Glu Glu Asp Val Phe Pro Asp Gly Thr Phe			
	305	310	315
Leu Arg Lys Gly Ser Arg Val Tyr Phe Ser Val Tyr Ala Met Gly Arg			
	325	330	335
Met Glu Ser Ile Trp Gly Lys Asp Cys Glu Met Phe Lys Pro Glu Arg			
	340	345	350
Trp Ile Gln Gly Gly Gln Tyr Val Ser Asp Asp Gln Phe Lys Tyr Val			
	355	360	365
Val Phe Asn Ala Gly Pro Arg Leu Cys Leu Gly Lys Thr Phe Ala Tyr			
	370	375	380
Leu Gln Met Lys Met Val Ala Ala Ser Ile Leu Leu Asn Tyr Ser Ile			
	385	390	395
Lys Val Asp Gln Asp His Val Val Val Pro Arg Val Thr Thr Thr Leu			
	405	410	415
Tyr Met Lys His Gly Leu Lys Val Arg Ile Thr Pro Arg Ser Leu Glu			
	420	425	430
Glu Lys Lys Gln Asp Ser			
	435		

(2) INFORMATION FOR SEQ ID NO:406:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1370 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1370

(D) OTHER INFORMATION: / Ceres Seq. ID 1566823

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:406:

aaaaagggaaa	aaagaaaaaag	aagaagagga	gctaaaaaaa	cgacgtcgta	gaaggagatt	60
cttgccatgg	ccacacatag	tctctccttc	tctctcagag	tctcttctct	ctcttctctt	120
actctctcag	agagaattaa	agggcaagg	gtgggaatca	actacggcca	aatagccaac	180
aaactcccat	ctccgggaag	agtcgcccgt	ctccttcgat	cactaaacat	cacaagagta	240
aaactctcag	acgcagatcc	aaacgtcctc	tctctctctc	caaaactcaa	agtagatttc	300
atgatcggtt	taggcaacga	tatatctcaa	aacatgtcaa	cagatccaac	caaaagctcaa	360
gattgggttac	aaacaaagat	tgaaccacat	atctcaaaaa	caagaaatac	ctcaatagtt	420
gtcgccaacg	aaatcttcaa	aaccaatgat	catgtcctca	tccaaagcct	attacggcct	480
atgaaatcgg	tttaacgtgc	tttaaccaat	cttgggttag	agaacaagt	aaccgtaact	540
tcagctcatt	cttttagacat	tcttttcaaa	tcttatcctc	cttcttcagg	atcattcaaa	600
gaagaggttta	ttcaatatct	tcaaccactt	cttgattttc	attctcaaat	cgaatcacct	660
ttcttgataa	atgttatatc	cttttttgct	tataaagata	gtcctaaga	agttccattat	720
gagtatgttt	tgtttcaacc	taatacaagg	atggttgatc	caaacactaa	tcttcattat	780
gacaacatgt	tgtttgctca	agttgatgcg	ctttactctg	ccattaaagc	tttgggacat	840
accgatatcg	agggttcggat	atcggaacac	gggtggcctt	ctaaaggaga	tgagaatgag	900
attggaGctt	cgccggagaa	cgccgctttg	tataatggga	attgttgtaa	gttgatgacg	960
cagaggaaga	gaactccggc	gaagcaatct	gttctattg	atgtttatgt	gtttgctctg	1020
tttaatgaga	atctttaaacc	gggtccgggt	tctgagagga	attatggact	tttttatccg	1080
gatggtaaac	cggtttacaa	tgctgggtatg	caagggtatt	tacctgatat	tatctatact	1140
tcaagggcaa	ctacaattaa	gattttgaat	ttgtggagag	tcgtgatggg	ttgtgctgtg	1200
gcttggttca	tactcagat	ggcgacaaag	atgaggatga	gataaGcttc	gctgtgtgct	1260
ttgtctgtcc	ttgtaggatt	ttgtttttta	tatgttagtt	gattataggt	gagggtataca	1320
attctttgtc	atgtattgga	ttcacaaaaa	taaaaaaaat	taatttatct		

(2) INFORMATION FOR SEQ ID NO:407:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 392 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..392

(D) OTHER INFORMATION: / Ceres Seq. ID 1566824

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:407:

Met	Ala	Thr	His	Ser	Leu	Ser	Phe	Phe	Phe	Arg	Val	Leu	Leu	Leu	Leu
1				5					10				15		
Phe	Leu	Thr	Leu	Ser	Glu	Arg	Ile	Lys	Gly	Gln	Gly	Val	Gly	Ile	Asn
				20				25					30		
Tyr	Gly	Gln	Ile	Ala	Asn	Asn	Leu	Pro	Ser	Pro	Ala	Arg	Val	Ala	Val
				35				40				45			
Leu	Leu	Arg	Ser	Leu	Asn	Ile	Thr	Arg	Val	Lys	Leu	Thr	Asp	Ala	Asp
				50				55				60			
Pro	Asn	Val	Leu	Phe	Ser	Phe	Ser	Asn	Ser	Gln	Val	Asp	Phe	Met	Ile
				70				75					80		
Gly	Leu	Gly	Asn	Glu	Tyr	Leu	Gln	Asn	Met	Ser	Thr	Asp	Pro	Thr	Lys
				85				90				95			
Ala	Gln	Asp	Trp	Leu	Gln	Gln	Arg	Leu	Glu	Pro	His	Ile	Ser	Lys	Thr
				100				105				110			
Arg	Ile	Thr	Ser	Ile	Val	Val	Gly	Asn	Glu	Ile	Phe	Lys	Thr	Asn	Asp
				115				120				125			
His	Val	Leu	Ile	Gln	Ser	Leu	Leu	Pro	Ala	Met	Lys	Ser	Val	Tyr	Ala
				130				135				140			
Ala	Leu	Thr	Asn	Leu	Gly	Leu	Glu	Lys	Gln	Val	Thr	Val	Thr	Ser	Ala
				145				150				155			160

His Ser Leu Asp Ile Leu Ser Thr Ser Tyr Pro Pro Ser Ser Gly Ser
165 170 175
Phe Lys Glu Glu Phe Ile Gln Tyr Leu Gln Pro Leu Leu Asp Phe His
180 185 190
Ser Gln Ile Glu Ser Pro Phe Leu Ile Asn Ala Tyr Pro Phe Ala
195 200 205
Tyr Lys Asp Ser Pro Lys Glu Val Pro Leu Glu Tyr Val Leu Phe Gln
210 215 220
Pro Asn Gln Gly Met Val Asp Pro Asn Thr Asn Leu His Tyr Asp Asn
225 230 235
Met Leu Phe Ala Gln Val Asp Ala Leu Tyr Ser Ala Ile Lys Thr Leu
245 250 255
Gly His Thr Asp Ile Glu Val Arg Ile Ser Glu Thr Gly Trp Pro Ser
260 265 270
Lys Gly Asp Glu Asn Glu Ile Gly Ala Ser Pro Glu Asn Ala Ala Leu
275 280 285
Tyr Asn Gly Asn Leu Leu Lys Leu Ile Gln Gln Arg Lys Gly Thr Pro
290 295 300
Ala Lys Gln Ser Val Pro Ile Asp Val Tyr Val Phe Ala Leu Phe Asn
305 310 315
Glu Asn Leu Lys Pro Gly Pro Val Ser Glu Arg Asn Tyr Gly Leu Phe
325 330 335
Tyr Pro Asp Gly Lys Pro Val Tyr Asn Val Gly Met Gln Gly Tyr Leu
340 345 350
Pro Asp Ile Tyr Thr Ser Arg Ala Thr Thr Ile Lys Ile Leu Asn
355 360 365
Leu Trp Arg Val Val Met Gly Leu Ala Val Ala Trp Phe Ile Leu Asp
370 375 380
Met Gly Asp Lys Met Arg Met Arg
385 390

(2) INFORMATION FOR SEQ ID NO:408:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 314 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..314

(D) OTHER INFORMATION: / Ceres Seq. ID 1566825

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:408:

Met Ile Gly Leu Gly Asn Glu Tyr Leu Gln Asn Met Ser Thr Asp Pro
1 5 10 15
Thr Lys Ala Gln Asp Trp Leu Gln Gln Arg Leu Glu Pro His Ile Ser
20 25 30
Lys Thr Arg Ile Thr Ser Ile Val Val Gly Asn Glu Ile Phe Lys Thr
35 40 45
Asn Asp His Val Leu Ile Gln Ser Leu Leu Pro Ala Met Lys Ser Val
50 55 60
Tyr Ala Ala Leu Thr Asn Leu Gly Leu Glu Lys Gln Val Thr Val Thr
65 70 75 80
Ser Ala His Ser Leu Asp Ile Leu Ser Thr Ser Tyr Pro Pro Ser Ser
85 90 95
Gly Ser Phe Lys Glu Glu Phe Ile Gln Tyr Leu Gln Pro Leu Leu Asp
100 105 110
Phe His Ser Gln Ile Glu Ser Pro Phe Leu Ile Asn Ala Tyr Pro Phe
115 120 125
Phe Ala Tyr Lys Asp Ser Pro Lys Glu Val Pro Leu Glu Tyr Val Leu
130 135 140
Phe Gln Pro Asn Gln Gly Met Val Asp Pro Asn Thr Asn Leu His Tyr

145 150 155 160
Asp Asn Met Leu Phe Ala Gln Val Asp Ala Leu Tyr Ser Ala Ile Lys
165 170 175
Thr Leu Gly His Thr Asp Ile Glu Val Arg Ile Ser Glu Thr Gly Trp
180 185 190
Pro Ser Lys Gly Asp Glu Asn Glu Ile Gly Ala Ser Pro Glu Asn Ala
195 200 205
Ala Leu Tyr Asn Gly Asn Leu Lys Leu Ile Gln Gln Arg Lys Gly
210 215 220
Thr Pro Ala Lys Gln Ser Val Pro Ile Asp Val Tyr Val Phe Ala Leu
225 230 235 240
Phe Asn Glu Asn Leu Lys Pro Gly Pro Val Ser Glu Arg Asn Tyr Gly
245 250 255
Leu Phe Tyr Pro Asp Gly Lys Pro Val Tyr Asn Val Gly Met Gln Gly
260 265 270
Tyr Leu Pro Asp Ile Ile Tyr Thr Ser Arg Ala Thr Thr Ile Lys Ile
275 280 285
Leu Asn Leu Trp Arg Val Val Met Gly Leu Ala Val Ala Trp Phe Ile
290 295 300
Leu Asp Met Gly Asp Lys Met Arg Met Arg
305 310

(2) INFORMATION FOR SEQ ID NO:409:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 303 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..303
(D) OTHER INFORMATION: / Ceres Seq. ID 1566826

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:409:

Met Ser Thr Asp Pro Thr Lys Ala Gln Asp Trp Leu Gln Gln Arg Leu
1 5 10 15
Glu Pro His Ile Ser Lys Thr Arg Ile Thr Ser Ile Val Val Gly Asn
20 25 30
Glu Ile Phe Lys Thr Asn Asp His Val Leu Ile Gln Ser Leu Leu Pro
35 40 45
Ala Met Lys Ser Val Tyr Ala Ala Leu Thr Asn Leu Gly Leu Glu Lys
50 55 60
Gln Val Thr Val Thr Ser Ala His Ser Leu Asp Ile Leu Ser Thr Ser
65 70 75 80
Tyr Pro Pro Ser Ser Gly Ser Phe Lys Glu Glu Phe Ile Gln Tyr Leu
85 90 95
Gln Pro Leu Leu Asp Phe His Ser Gln Ile Glu Ser Pro Phe Leu Ile
100 105 110
Asn Ala Tyr Pro Phe Phe Ala Tyr Lys Asp Ser Pro Lys Glu Val Pro
115 120 125
Leu Glu Tyr Val Leu Phe Gln Pro Asn Gln Gly Met Val Asp Pro Asn
130 135 140
Thr Asn Leu His Tyr Asp Asn Met Leu Phe Ala Gln Val Asp Ala Leu
145 150 155 160
Tyr Ser Ala Ile Lys Thr Leu Gly His Thr Asp Ile Glu Val Arg Ile
165 170 175
Ser Glu Thr Gly Trp Pro Ser Lys Gly Asp Glu Asn Glu Ile Gly Ala
180 185 190
Ser Pro Glu Asn Ala Ala Leu Tyr Asn Gly Asn Leu Leu Lys Leu Ile
195 200 205
Gln Gln Arg Lys Gly Thr Pro Ala Lys Gln Ser Val Pro Ile Asp Val
210 215 220

(2) INFORMATION FOR SEO ID NO:410:

(A) LENGTH: 1530 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(D) TOPOLOGY: linear
MOLECULE TYPE: DNA (c

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1530

(D) OTHER INFORMATION: / Ceres Seq. ID 1566827

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:410:

gtatattttt	ttgacagcgc	gattacagaaa	tttggaaaag	atcagcttttt	ttttcttcgg	60
ttcttaacctt	ttaaagggtgc	tgaaaattttg	ggaaatcactg	atacaattttg	tttaatatgat	120
ttctctgattt	aggggtttctc	tgcatgcctc	ttagaatcagc	aagtgtaaag	caattaccat	180
ggtgacatcgc	aagcagatgc	atttctctctc	ctgtgggtgtg	gtgataactc	cgacgatacc	240
ctctccatcc	gagaaattccc	acggaaattct	tctccaaaagc	gtgctgcgtc	ttctctgcga	300
gcgcagaagcg	gcgaaagagac	tatgaagaag	aaaaaagaag	agaagaagaa	gaattttgggt	360
cccgagtagta	tcgtcccgatg	ctggaacgag	gaagatgagc	tctctatctt	aaaggagta	420
gttgattacaa	gagctaaagc	aggattccaat	cccaaaattg	attgggagtg	gtttttacagt	480
ttctccggtaa	gttctatcgt	tcgcaaaatt	ctccaggagc	aggtttttgag	taagatcagc	540
aagttgtaaaa	ggagattttca	tgttctattg	gagaaaatca	gtgaagggaa	tgatccgaaa	600
tttactagatt	ctagtgatttc	tgaagccctg	gtgtttttct	cgatgatttg	gggaacaggt	660
gaattttgta	atgatgatgg	tactgataag	gagatgggtga	aggagcacga	tgtaaaacgga	720
aattggcgacg	ctgaaaatgg	gatgcctcga	atagccacag	agaacagagc	tgggggagagc	780
tgtttaaagg	agcatgagga	aagcttaaat	gagaattggg	cagaggagat	aagagacaac	840
gacgacagat	ctcgaaaagc	acacgacgtc	gcagagcgga	gcgagagaga	gattgtgtaag	900
gagcatgagg	aaccttttaa	tgagaattggt	gcagagaata	taagagacaa	taaccgggac	960
actcaaatagt	cacagcagag	cgagagcagc	agtgaggaga	tgttgtaagga	gcgatgaggaa	1020
gttgGctaat	actgaacttg	taatatgagaa	tggggcagc	aaaaaacacg	agacacggac	1080
tactgtgtga	aaagagagac	atgatgagca	tgatgatgat	gagttatgcg	ctgtgcagga	1140
tgcttttgtag	gcgttaattg	cgcaagtggt	aagtggtttt	caaaagaagc	tcgacgtgga	1200
gaagctgatg	aacctttgaa	tcgaaaaaag	agaagagttg	atgtgatgat	ggaaacgtgt	1260
atgtgttgtag	gaagaagaagt	tgtaatatcaa	gaagctttga	ttttcccgca	aggaatcgctg	1320
ggcagcgaat	gatgatttaga	tgaataacct	aagccgcttg	agcattttgt	gttaaattagg	1380
ttcttagttaa	gcctaatagc	ttgctctgtt	cagtgtaatat	ctttggaatg	tctcttttgt	1440
ctgttttggc	aagttgtttg	aagacattcc	agtttttaac	gaagtatcca	gaagagccat	1500
ccatgaccat	ttctggaatt	aaataaatttc				

(2) INFORMATION FOR SEQ ID NO:411:

(1) SEQUENCE CHARACTERIST

(A) LENGTH: 235 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..235

(D) OTHER INFORMATION: / Ceres Seq. ID 1566828

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:411:

Met Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Asn Leu Gly Pro Pro Leu

1	5	10	15
Ile Val Arg Ile Trp Asn Glu Glu Asp Glu Leu Ser Ile Leu Lys Gly	20	25	30
Leu Val Asp Tyr Arg Ala Lys Thr Gly Phe Asn Pro Lys Ile Asp Trp	35	40	45
Asp Ala Phe Tyr Ser Phe Leu Gly Ser Ser Ile Val Ala Lys Phe Ser	50	55	60
Lys Glu Gln Val Leu Ser Lys Ile Arg Lys Leu Lys Arg Arg Phe His	65	70	75
Val His Trp Glu Lys Ile Ser Glu Gly Asn Asp Pro Lys Phe Thr Arg	80	85	90
Ser Ser Asp Ser Glu Ala Phe Gly Phe Ser Ser Met Ile Trp Gly Gln	95	100	105
Gly Glu Phe Gly Asn Asp Asp Gly Met Asp Lys Glu Met Val Lys Glu	110	115	120
His Asp Val Asn Gly Asn Gly Ala Ala Glu Asn Gly Thr Ala Arg Ile	125	130	135
Ala Gln Glu Asn Glu Ser Gly Glu Glu Met Leu Lys Glu His Glu Glu	140	145	150
Thr Leu Asn Glu Asn Gly Ala Glu Glu Ile Arg Asp Asn Asp Glu Thr	155	160	165
Ala Arg Lys Ala Gln Gln Leu Glu Ser Glu Ser Glu Glu Glu Met Leu	170	175	180
Lys Glu His Glu Glu Pro Phe Asn Glu Asn Gly Ala Glu Asn Ile Arg	185	190	195
Asp Asn Asn Gly Thr Thr Gln Ile Ala Gln Gln Ser Glu Ser Glu Ser	200	205	210
Glu Glu Met Leu Lys Glu His Glu Glu Val Gly	215	220	225
	230	235	

(2) INFORMATION FOR SEQ ID NO:412:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 128 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..128

(D) OTHER INFORMATION: / Ceres Seq. ID 1566829

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:412:

Met Ile Trp Gly Gln Gly Glu Phe Gly Asn Asp Asp Gly Met Asp Lys	1	5	10	15
Glu Met Val Lys Glu His Asp Val Asn Gly Asn Gly Ala Ala Glu Asn	20	25	30	35
Gly Thr Ala Arg Ile Ala Gln Glu Asn Glu Ser Gly Glu Glu Met Leu	40	45	50	55
Lys Glu His Glu Glu Thr Leu Asn Glu Asn Gly Ala Glu Glu Ile Arg	60	65	70	75
Asp Asn Asp Glu Thr Ala Arg Lys Ala Gln Gln Leu Glu Ser Glu Ser	80	85	90	95
Glu Glu Glu Met Leu Lys Glu His Glu Glu Pro Phe Asn Glu Asn Gly	100	105	110	115
Ala Glu Asn Ile Arg Asp Asn Asn Gly Thr Thr Gln Ile Ala Gln Gln	120	125		
Ser Glu Ser Glu Ser Glu Glu Met Leu Lys Glu His Glu Glu Val Gly				

(2) INFORMATION FOR SEQ ID NO:413:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1824 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..1824
(D) OTHER INFORMATION: / Ceres Seq. ID 1566838
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:413:

attctctttt	ctctctcttc	tctctcacac	aacacaaaca	actcttgaga	gagagaaaca	60
aattcttcc	ttgacacttc	tctccaaatc	ctcatctcat	tctctatctc	aaacatttgc	120
tcactctcac	gatgagccat	aaccacaaac	aacctcacgc	gccagtcocg	gtccatgtca	180
caaacgcgga	gccaaactct	aaccacaaac	acctcccaaa	ctttctatta	tcgctgtctc	240
tcaaatcagt	aaaactcggg	taccactaac	tgatctccaa	cgctctctac	atcctctctc	300
ttctctctct	cgcgcgcaac	atcgctaaac	tctctctctt	caccatcaac	gacctctctc	360
tcctctacaa	cacactcgtg	ttccatttcc	tctccgccac	actcgccacc	gacctcttgc	420
tctctctctc	caccgcttac	ttaccacccc	gtcctgcgcg	tgtcttctct	ctcgactttc	480
cgtgttacaa	accagaccct	tcactgatct	gcactcgtga	aacattccatg	gacagatctc	540
aacgtgttag	catcttcaca	gaAgacaaat	TagtcttccA	acaaaagatc	ctcgaaaAga	600
tcgggtctag	gtcagaaaaa	ttacttccct	gaagctcttc	ttcgtgttcc	tcctaactct	660
tgtatggtag	aagcgagaaa	agaggcgaaa	acagtattgt	tcggagctat	tgacgcgggt	720
cttgagagaa	cctcgtgtga	acataaagat	attggaatcc	ttgtggtgaa	ttgtagcttg	780
tttaatccaa	caccgtcaat	ttctgctatg	attgtgaata	agtataaagt	tagagggcaac	840
attttgagct	ataattcttg	tgggaatgga	tgtagtgtgc	gccttatctc	catgtatctc	900
gctaaaacaga	tgtcttcagg	gcaaccacaa	tcatacgcac	tgtgtgtgag	cacagagaac	960
ataaccctaa	actggtactt	aggcaacgac	cgatacaatgc	ttctatctaa	ttgtattctc	1020
cgatgtggcg	gagcgcgggt	acttctctcg	aaccgctcct	ctgatcgcag	cogttcaaaa	1080
tatcagctca	tccataccgt	cgttaccacc	aaaggagctg	atgacaacgc	attcggtctg	1140
gtttaccac	gagaagacaa	caacgcagaa	gaaccgcgca	agatcggagt	ctcactctct	1200
aaaaactcta	tggcaatagc	cggagaagct	ctcaagacaa	acatcacaa	ctctcgacca	1260
ctagtctctac	caatgtccga	acaacttctc	tttttcgcga	ctcttgtggc	cggaaaagtc	1320
ttcaaatgta	agaaaaataa	gccttaccat	ccctgacttca	agctagcttt	cgagcatttc	1380
tgtatccacg	ctggaggtag	agccgtgctt	gacgagattg	agaagaacct	gatttatctc	1440
gaatggcaca	tggagccatc	gaggatgacg	ttgaaccggg	ttgtaaacac	ttcgagttag	1500
tcacttttgt	atgagcttgc	gtatagttaa	gctaaaggaa	ggattaagag	aggagatagg	1560
acttggcaga	tgtcttttgg	atcgggtttt	aagtgttaaca	gtcgggtttg	gaaagctttg	1620
agaacgattg	atccaatgga	cgagaagact	aatccatgga	ttgatgagat	tgatgacttt	1680
cctgttcaag	ttctaggat	cactccatt	acatcgtcgt	agtgttttta	aattcttttg	1740
gagaactaat	ttgttatggt	ttattaaatg	taataactta	tgtgatgtga	tattttttta	1800
ttatcttaat	atatatgatt	gccg				

(2) INFORMATION FOR SEQ ID NO:414:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 352 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..352
(D) OTHER INFORMATION: / Ceres Seq. ID 1566839
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:414:

Met	Glu	Glu	Ala	Arg	Lys	Glu	Ala	Glu	Thr	Val	Met	Phe	Gly	Ala	Ile
1			5						10				15		
Asp	Ala	Val	Leu	Glu	Lys	Thr	Gly	Val	Lys	Pro	Lys	Asp	Ile	Gly	Ile
			20						25				30		
Leu	Val	Val	Asn	Cys	Ser	Leu	Phe	Asn	Pro	Thr	Pro	Ser	Leu	Ser	Ala
			35						40				45		
Met	Ile	Val	Asn	Lys	Tyr	Lys	Leu	Arg	Gly	Asn	Ile	Leu	Ser	Tyr	Asn
			50				55				60				

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Leu Gly Gly Met Gly Cys Ser Ala Gly Leu Ile Ser Ile Asp Leu Ala
65 70 75 80
Lys Gln Met Leu Gln Val Gln Pro Asn Ser Tyr Ala Leu Val Val Ser
85 90 95
Thr Glu Asn Ile Thr Leu Asn Trp Tyr Leu Gly Asn Asp Arg Ser Met
100 105 110
Leu Leu Ser Asn Cys Ile Phe Arg Met Gly Gly Ala Ala Val Leu Leu
115 120 125
Ser Asn Arg Ser Ser Asp Arg Ser Arg Ser Lys Tyr Gln Leu Ile His
130 135 140
Thr Val Arg Thr His Lys Gly Ala Asp Asp Asn Ala Phe Gly Cys Val
145 150 155 160
Tyr Gln Arg Glu Asp Asn Asn Ala Glu Glu Thr Gly Lys Ile Gly Val
165 170 175
Ser Leu Ser Lys Asn Leu Met Ala Ile Ala Gly Glu Ala Leu Lys Thr
180 185 190
Asn Ile Thr Thr Leu Gly Pro Leu Val Leu Pro Met Ser Glu Gln Leu
195 200 205
Leu Phe Phe Ala Thr Leu Val Ala Arg Lys Val Phe Lys Val Lys Lys
210 215 220
Ile Lys Pro Tyr Ile Pro Asp Phe Lys Leu Ala Phe Glu His Phe Cys
225 230 235 240
Ile His Ala Gly Gly Arg Ala Val Leu Asp Glu Ile Glu Lys Asn Leu
245 250 255
Asp Leu Ser Glu Trp His Met Glu Pro Ser Arg Met Thr Leu Asn Arg
260 265 270
Phe Gly Asn Thr Ser Ser Ser Ser Leu Trp Tyr Glu Leu Ala Tyr Ser
275 280 285
Glu Ala Lys Gly Arg Ile Lys Arg Gly Asp Arg Thr Trp Gln Ile Ala
290 295 300
Phe Gly Ser Gly Phe Lys Cys Asn Ser Ala Val Trp Lys Ala Leu Arg
305 310 315 320
Thr Ile Asp Pro Met Asp Glu Lys Thr Asn Pro Trp Ile Asp Glu Ile
325 330 335
Asp Asp Phe Pro Val Gln Val Pro Arg Ile Thr Pro Ile Thr Ser Ser
340 345 350

(2) INFORMATION FOR SEQ ID NO:415:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 341 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..341
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566840

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:415:

Met Phe Gly Ala Ile Asp Ala Val Leu Glu Lys Thr Gly Val Lys Pro
1 5 10 15
Lys Asp Ile Gly Ile Leu Val Val Asn Cys Ser Leu Phe Asn Pro Thr
20 25 30
Pro Ser Leu Ser Ala Met Ile Val Asn Lys Tyr Lys Leu Arg Gly Asn
35 40 45
Ile Leu Ser Tyr Asn Leu Gly Gly Met Gly Cys Ser Ala Gly Leu Ile
50 55 60
Ser Ile Asp Leu Ala Lys Gln Met Leu Gln Val Gln Pro Asn Ser Tyr
65 70 75 80
Ala Leu Val Val Ser Thr Glu Asn Ile Thr Leu Asn Trp Tyr Leu Gly

2008年12月10日

(i) SEQUENCE CHARACTERISTICS:

- ```
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
```

- (D) OTHER INFORMATION: / Ceres Seq. ID 1566841

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 1   | Met | Ile | Val | Asn | 5   | Tyr | Lys | Leu | Arg | Gly | 10  | Asn | Ile | Leu | Ser | Tyr | Asn | 15  |
| 1   | Leu | Gly | Gly | Met | 20  | Gly | Cys | Ser | Ala | Gly | 25  | Ile | Ser | Ile | Asp | 30  | Leu | Ala |
| Lys | Gln | Met | 20  | Gln | Val | Gln | Pro | 40  | Asn | Ser | Tyr | Ala | 45  | Leu | Val | Val | Ser |     |
| Thr | Glu | Asn | Ile | Thr | Leu | Asn | 55  | Trp | Tyr | Leu | Gly | 60  | Asn | Asp | Arg | Ser | Met |     |
| Leu | Leu | Ser | Asn | Cys | Ile | Phe | Arg | Met | Gly | Gly | 75  | Ala | Ala | Val | Leu | Leu | 80  |     |
| 65  | Ser | Asn | Arg | Ser | 85  | Asp | Arg | Ser | Arg | Ser | 90  | Lys | Tyr | Gln | Leu | Ile | His |     |
| Thr | Val | Arg | 100 | Thr | His | Lys | Gly | Ala | 105 | Asp | Asp | Asn | Ala | Phe | Gly | Cys | Val |     |
| Tyr | Gln | Arg | 115 | Glu | Asp | Asn | Asn | Ala | 120 | Glu | Glu | Thr | Gly | Lys | 125 | Ile | Gly | Val |

Ser Leu Ser Lys Asn Leu Met Ala Ile Ala Gly Glu Ala Leu Lys Thr  
130 135 140  
Asn Ile Thr Thr Leu Gly Pro Leu Val Leu Pro Met Ser Glu Gln Leu  
145 150 155 160  
Leu Phe Phe Ala Thr Leu Val Ala Arg Lys Val Phe Lys Val Lys Lys  
165 170 175  
Ile Lys Pro Tyr Ile Pro Asp Phe Lys Leu Ala Phe Glu His Phe Cys  
180 185 190  
Ile His Ala Gly Gly Arg Ala Val Leu Asp Glu Ile Glu Lys Asn Leu  
195 200 205  
Asp Leu Ser Glu Trp His Met Glu Pro Ser Arg Met Thr Leu Asn Arg  
210 215 220  
Phe Gly Asn Thr Ser Ser Ser Ser Leu Trp Tyr Glu Leu Ala Tyr Ser  
225 230 235 240  
Glu Ala Lys Gly Arg Ile Lys Arg Gly Asp Arg Thr Trp Gln Ile Ala  
245 250 255  
Phe Gly Ser Gly Phe Lys Cys Asn Ser Ala Val Trp Lys Ala Leu Arg  
260 265 270  
Thr Ile Asp Pro Met Asp Glu Lys Thr Asn Pro Trp Ile Asp Glu Ile  
275 280 285  
Asp Asp Phe Pro Val Gln Val Pro Arg Ile Thr Pro Ile Thr Ser Ser  
290 295 300

(2) INFORMATION FOR SEQ ID NO:417:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 998 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..998
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566909

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:417:

|             |             |             |            |             |            |     |
|-------------|-------------|-------------|------------|-------------|------------|-----|
| aatattcattt | ccattttogat | tcgattcctc  | ctttgtgtgg | gagggcctttg | ttcggtcaac | 60  |
| ttatgtgttc  | tggtttttgtc | tccttttttat | tgattaggga | ccgatctatc  | aaggcttcaa | 120 |
| gggcaaacag  | aaatgggacca | cgacaagaca  | ggatgcctga | gcccacctga  | aggtcccaag | 180 |
| ctatgtacta  | acaactgcgg  | tttctttgga  | agcgctgcc  | caatgaacat  | gtgttctaag | 240 |
| tgtcacaagg  | atatgttgtt  | ccaacaggag  | cagggcgcta | agtttgcata  | tcgagtgtct | 300 |
| ggaacatcgt  | catccagcaa  | catcataaag  | gaaaccttta | ccgctgcgtt  | ggtcgatatt | 360 |
| gaaaccaaatt | ccgttgagcc  | gatgactgtt  | tcgtacagc  | catcctctgt  | ccaagtctgt | 420 |
| cgagagtgat  | tagcaccaga  | agaagctcgc  | aaaccaaagg | gaccaagccg  | atgtactact | 480 |
| tgcaataaagc | gggttgccct  | gactggattc  | aaatgtcgtc | gtgggagcct  | ctctgtcgga | 540 |
| acacacccgct | atgcagacat  | acatgactgc  | tccttcaatt | accatgctgc  | tgccgaagag | 600 |
| gcgatagcta  | aggcaaacct  | ggttgtgaaa  | gcagagaagc | ttgacaaaaa  | ctgaaaaact | 660 |
| aagtaaacact | ctctgtgttc  | atcaggtggc  | ctggtgtttc | cttctcctgt  | ctgtgtctgg | 720 |
| ttcaagtatt  | ctcatgttaa  | aaagggttta  | tataaaggtg | aatgaaagcg  | tgcttgcatt | 780 |
| ttagcgtctt  | ccatctctct  | gcaatatttg  | tggtgtggaa | ctttctatta  | cttgtgtttg | 840 |
| caagcagaga  | aacgtgctct  | taaaaaaaat  | gctttgtgtg | tttatctctc  | tactattttt | 900 |
| gagcactgtg  | ttatgtgttc  | ctgtttggtc  | tgatcatat  | tgagattgtc  | tctgtagcta | 960 |
| catgaagcct  | atttaaaaaa  | ggcctgtgtt  | tgctcttc   |             |            |     |

(2) INFORMATION FOR SEQ ID NO:418:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 173 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..173

(D) OTHER INFORMATION: / Ceres Seq. ID 1566910

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:418:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |   |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|---|
| Met | Asp | His | Asp | Lys | Thr | Gly | Cys | Gln | Ser | Pro | Pro | Glu | Gly | Pro | Lys | 1 |
|     |     |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |   |
| Leu | Cys | Thr | Asn | Asn | Cys | Gly | Phe | Phe | Gly | Ser | Ala | Ala | Thr | Met | Asn |   |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     |     | 30  |     |   |
| Met | Cys | Ser | Lys | Cys | His | Lys | Asp | Met | Leu | Phe | Gln | Gln | Glu | Gln | Gly |   |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |   |
| Ala | Lys | Phe | Ala | Ser | Ala | Val | Ser | Gly | Thr | Ser | Ser | Ser | Ser | Asn | Ile |   |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |   |
| Ile | Lys | Glu | Thr | Phe | Thr | Ala | Ala | Leu | Val | Asp | Ile | Glu | Thr | Lys | Ser |   |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |   |
| Val | Glu | Pro | Met | Thr | Val | Ser | Val | Gln | Pro | Ser | Ser | Val | Gln | Val | Val |   |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |   |
| Ala | Glu | Val | Val | Ala | Pro | Glu | Glu | Ala | Ala | Lys | Pro | Lys | Gly | Pro | Ser |   |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     |     | 110 |     |   |
| Arg | Cys | Thr | Thr | Cys | Asn | Lys | Arg | Val | Gly | Leu | Thr | Gly | Phe | Lys | Cys |   |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     |     | 125 |     |     |   |
| Arg | Cys | Gly | Ser | Leu | Phe | Cys | Gly | Thr | His | Arg | Tyr | Ala | Asp | Ile | His |   |
|     |     |     | 130 |     |     | 135 |     |     |     |     | 140 |     |     |     |     |   |
| Asp | Cys | Ser | Phe | Asn | Tyr | His | Ala | Ala | Ala | Gln | Glu | Ala | Ile | Ala | Lys |   |
| 145 |     |     |     | 150 |     |     |     |     |     | 155 |     |     |     |     | 160 |   |
| Ala | Asn | Pro | Val | Val | Lys | Ala | Glu | Lys | Leu | Asp | Lys | Ile |     |     |     |   |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     |     |   |

(2) INFORMATION FOR SEQ ID NO:419:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 143 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..143

(D) OTHER INFORMATION: / Ceres Seq. ID 1566911

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:419:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |   |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|---|
| Met | Asn | Met | Cys | Ser | Lys | Cys | His | Lys | Asp | Met | Leu | Phe | Gln | Gln | Glu | 1 |
|     |     |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |   |
| Gln | Gly | Ala | Lys | Phe | Ala | Ser | Ala | Val | Ser | Gly | Thr | Ser | Ser | Ser | Ser |   |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |   |
| Asn | Ile | Ile | Lys | Glu | Thr | Phe | Thr | Ala | Ala | Leu | Val | Asp | Ile | Glu | Thr |   |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |   |
| Lys | Ser | Val | Glu | Pro | Met | Thr | Val | Ser | Val | Gln | Pro | Ser | Ser | Val | Gln |   |
|     |     |     | 50  |     |     | 55  |     |     |     |     | 60  |     |     |     |     |   |
| Val | Val | Ala | Glu | Val | Val | Ala | Pro | Glu | Glu | Ala | Ala | Lys | Pro | Lys | Gly |   |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |   |
| Pro | Ser | Arg | Cys | Thr | Thr | Cys | Asn | Lys | Arg | Val | Gly | Leu | Thr | Gly | Phe |   |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |   |
| Lys | Cys | Arg | Cys | Gly | Ser | Leu | Phe | Cys | Gly | Thr | His | Arg | Tyr | Ala | Asp |   |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |   |
| Ile | His | Asp | Cys | Ser | Phe | Asn | Tyr | His | Ala | Ala | Ala | Gln | Glu | Ala | Ile |   |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |   |
| Ala | Lys | Ala | Asn | Pro | Val | Val | Lys | Ala | Glu | Lys | Leu | Asp | Lys | Ile |     |   |
|     |     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |   |

(2) INFORMATION FOR SEQ ID NO:420:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 141 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..141  
(D) OTHER INFORMATION: / Ceres Seq. ID 1566912  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:420:  
Met Cys Ser Lys Cys His Lys Asp Met Leu Phe Gln Gln Glu Gln Gly  
1 5 10 15  
Ala Lys Phe Ala Ser Ala Val Ser Gly Thr Ser Ser Ser Ser Asn Ile  
20 25 30  
Ile Lys Glu Thr Phe Thr Ala Ala Leu Val Asp Ile Glu Thr Lys Ser  
35 40 45  
Val Glu Pro Met Thr Val Ser Val Gln Pro Ser Ser Val Gln Val Val  
50 55 60  
Ala Glu Val Val Ala Pro Glu Glu Ala Ala Lys Pro Lys Gly Pro Ser  
65 70 75 80  
Arg Cys Thr Thr Cys Asn Lys Arg Val Gly Leu Thr Gly Phe Lys Cys  
85 90 95  
Arg Cys Gly Ser Leu Phe Cys Gly Thr His Arg Tyr Ala Asp Ile His  
100 105 110  
Asp Cys Ser Phe Asn Tyr His Ala Ala Gln Glu Ala Ile Ala Lys  
115 120 125  
Ala Asn Pro Val Val Lys Ala Glu Lys Leu Asp Lys Ile  
130 135 140

(2) INFORMATION FOR SEQ ID NO:421:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 574 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..574

(D) OTHER INFORMATION: / Ceres Seq. ID 1566913

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:421:

aaacgcagaaa ttaRaaacccc cttttgcctc aaaaAccctg atttcaaatc tccccaaagca 60  
caacaatggc gaatacaatg agatgcaga gggggaagag attgagagca ataagaagag 120  
aaatagtga gaaggaatca ttactcttaa cgagagaaga cgccaaatcc gccgctattg 180  
aagccgcact cgctgctccg aagttaccag ttogtcaagc cccagtttct ccgtttatgg 240  
aagttgcgac gccttctctc gagtctgcat ctgcctccac tacaatgcc aaaaatagtg 300  
atgagaaat ggaatgatgag aagaaaaaca agtcgctaaa acctattggg aagaagtga 360  
agaagaagtt taagctgggg atgaagaatc gtgctagtaa ggggtgcctt cgaggcaaac 420  
gaaactaaaa ctggtcttgg cttcttcta ctgggtttgt ttctacttg cataatttat 480  
gttctctctt aattttgggg ttcttcaatg tcttagaata tagcatcttt tgtactgtgt 540  
tttttccatg agtttcagta ctatagaaac cctg

(2) INFORMATION FOR SEQ ID NO:422:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 120 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..120

(D) OTHER INFORMATION: / Ceres Seq. ID 1566914

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:422:

Met Ala Lys Ser Met Arg Cys Lys Arg Val Lys Arg Leu Arg Ala Ile  
1 5 10 15

Arg Arg Glu Ile Val Glu Lys Glu Ser Phe Thr Leu Thr Arg Glu Asp  
20 25 30  
Ala Lys Ser Ala Ala Ile Glu Ala Ala Leu Ala Ala Pro Lys Leu Pro  
35 40 45  
Val Arg Gln Ala Pro Val Ser Phe Met Glu Val Ala Thr Pro Ser  
50 55 60  
Ser Glu Ser Ala Ser Ala Ser Thr Thr Ile Ala Lys Asn Ser Asp Glu  
65 70 75 80  
Glu Met Asp Asp Glu Lys Lys Asn Lys Ser Leu Lys Pro Ile Gly Lys  
85 90 95  
Lys Leu Lys Lys Lys Phe Lys Leu Gly Met Lys Asn Arg Arg Ser Lys  
100 105 110  
Gly Val Leu Arg Gly Lys Arg Asn  
115 120

(2) INFORMATION FOR SEQ ID NO:423:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 116 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..116

(D) OTHER INFORMATION: / Ceres Seq. ID 1566915

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:423:

Met Arg Cys Lys Arg Val Lys Arg Leu Arg Ala Ile Arg Arg Glu Ile  
1 5 10 15  
Val Glu Lys Glu Ser Phe Thr Leu Thr Arg Glu Asp Ala Lys Ser Ala  
20 25 30  
Ala Ile Glu Ala Ala Leu Ala Ala Pro Lys Leu Pro Val Arg Gln Ala  
35 40 45  
Pro Val Ser Pro Phe Met Glu Val Ala Thr Pro Ser Ser Glu Ser Ala  
50 55 60  
Ser Ala Ser Thr Thr Ile Ala Lys Asn Ser Asp Glu Glu Met Asp Asp  
65 70 75 80  
Glu Lys Lys Asn Lys Ser Leu Lys Pro Ile Gly Lys Lys Leu Lys Lys  
85 90 95  
Lys Phe Lys Leu Gly Met Lys Asn Arg Arg Ser Lys Gly Val Leu Arg  
100 105 110  
Gly Lys Arg Asn  
115

(2) INFORMATION FOR SEQ ID NO:424:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 63 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..63

(D) OTHER INFORMATION: / Ceres Seq. ID 1566916

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:424:

Met Glu Val Ala Thr Pro Ser Ser Glu Ser Ala Ser Ala Ser Thr Thr  
1 5 10 15  
Ile Ala Lys Asn Ser Asp Glu Glu Met Asp Asp Glu Lys Lys Asn Lys  
20 25 30  
Ser Leu Lys Pro Ile Gly Lys Lys Leu Lys Lys Lys Phe Lys Leu Gly  
35 40 45  
Met Lys Asn Arg Arg Ser Lys Gly Val Leu Arg Gly Lys Arg Asn



50

55

60

(2) INFORMATION FOR SEQ ID NO:425:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1793 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1793

(D) OTHER INFORMATION: / Ceres Seq. ID 1566917

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:425:

|             |            |            |            |            |             |      |
|-------------|------------|------------|------------|------------|-------------|------|
| aacatctctaa | tcgaaaaaac | aatctatctt | ttgggtccct | aaaaaagctc | cttcttttat  | 60   |
| cttgttttct  | aagtattctt | tttgtatgag | tttcaaagct | tatcattatc | tcactcttct  | 120  |
| tcctatagcta | tgactacttt | aacgaagatt | caagtgtacc | cacaagctct | ggagcacogt  | 180  |
| ctctctctca  | gagatccgat | acgggtcggg | tcaagattga | cttgtagaga | acgtagtaat  | 240  |
| aggggtttat  | tgcatcgggt | tgagaaaaaa | gttgaagaaa | agagaaaaat | tgagaaaatt  | 300  |
| aagggaaatg  | ggctgtggga | ttctttgaaa | cttgggtttt | taggggttag | taaatttaggg | 360  |
| ttcttctcta  | aaagttagta | taatcagaaa | gttgaaaact | tggagatggt | ttctctctcg  | 420  |
| gtttgtgttc  | aaattgcgag | atacattgtg | acgatgacaa | gtactggagc | tattcttttg  | 480  |
| atttgggttc  | aattatcagg | tgagatagat | tcgatgaact | cattgtgttg | gtatagttgg  | 540  |
| cttgggtgaa  | tctcatctgg | accatgactc | ggtgctaaca | tggttttgga | agatcattat  | 600  |
| cgagccggtc  | cacggaatgt | tgttataacc | ggaagcacta | ggggactagg | gaaagctctt  | 660  |
| gctagagagt  | ttcttctctc | tgagacacga | gtcattgtca | catctcgcag | ttctgaaatc  | 720  |
| gttgatagta  | ctctcaaaag | gctagagcaa | aatctcaaa  | agattatgag | taacgctagc  | 780  |
| gagtcagcta  | gaagaaacct | gagtgatgct | aaggtagtgt | gtattgcctg | tgatgtttgc  | 840  |
| aaaccogaag  | acgtttagaa | ctctgtcgat | ttcgtgtgaa | aagagcttgg | ttccatcaac  | 900  |
| atatggataa  | acaatgctgg | tactaacaaa | ggttttagac | cgtactctca | attcacggaa  | 960  |
| gaagatatca  | cacagattgt | ctccacaact | ttgattggat | caattctatg | tacacagagg  | 1020 |
| gctatagatg  | tgatgagcag | acagcacagt | ggtggacaca | tttttaacct | ggatgggtct  | 1080 |
| ggctctggag  | gttcaagtac | ttctctcact | gccgtatatg | gttcaacaaa | atgtggactct | 1140 |
| agggcatttc  | atgggtctct | agtgaagaaa | agccaaaaaa | caaacgttgg | cttccacact  | 1200 |
| gcactccctg  | gcattgttct | gacagaactt | cttctcagtg | gttcgagcat | taaaaaaaag  | 1260 |
| cagatgttta  | acataactct | tgagcttctc | gagacagtag | ctagaacttt | ggtaccacga  | 1320 |
| atgcgagttg  | tgaaaagttc | gggaaaagcc | gtcaattacc | taactctctc | tcggatatgt  | 1380 |
| ttagctattg  | tcacttctct | gctaaggaga | ggccgatggt | ttgatgacca | aggacgggag  | 1440 |
| ttatatcgag  | cagaagcaga | tagactaagg | aactggggag | agaacaggag | gaggttgtcg  | 1500 |
| ttaacagacg  | cgatggagat | gtatacacag | aatacttggg | ttctgttttt | ctctctttct  | 1560 |
| gttgttttgc  | ctttcatcat | cttacaaga  | acaacacctc | gtcttttttc | aggcacataa  | 1620 |
| caaacatctt  | ctctcgatgt | gttttaagaa | aattgtaaac | gtatcagtta | tgataaaaaa  | 1680 |
| acatatatat  | aacagaacog | atttgttcac | gtaaacaact | cttatagttg | tagaatgtgt  | 1740 |
| cgttgttgaa  | aacaatgaaa | aaaatagatt | gtaataaact | tttatcagat | tgt         |      |

(2) INFORMATION FOR SEQ ID NO:426:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 496 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..496

(D) OTHER INFORMATION: / Ceres Seq. ID 1566918

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:426:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Thr | Thr | Leu | Thr | Lys | Ile | Gln | Val | Tyr | Pro | Gln | Val | Leu | Glu | His |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Arg | Leu | Phe | Phe | Arg | Asp | Pro | Ile | Arg | Val | Gly | Ser | Arg | Leu | Thr | Cys |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Arg | Glu | Arg | Ser | Asn | Arg | Val | Tyr | Val | His | Arg | Cys | Glu | Lys | Lys | Val |
|     |     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Glu | Arg | Lys | Arg | Lys | Val | Glu | Lys | Phe | Lys | Gly | Asn | Gly | Ser | Trp | Asp |  |
| 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |  |
| Ser | Leu | Lys | Ser | Gly | Phe | Leu | Gly | Phe | Ser | Lys | Leu | Gly | Phe | Leu | Ser |  |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |  |
| Lys | Asp | Glu | Tyr | Asn | Gln | Lys | Val | Glu | Asn | Leu | Glu | Met | Val | Phe | Ser |  |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |  |
| Ser | Val | Ala | Val | Gln | Ile | Ala | Arg | Tyr | Ile | Val | Thr | Met | Thr | Ser | Thr |  |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |
| Gly | Ala | Ile | Leu | Leu | Ile | Gly | Phe | Gln | Leu | Ser | Gly | Gly | Asp | Ser | Ser |  |
|     |     | 115 |     |     |     |     |     | 120 |     |     |     | 125 |     |     |     |  |
| Met | Asn | Ser | Leu | Val | Trp | Lys | Ser | Trp | Leu | Gly | Gly | Ile | Ile | Ile | Gly |  |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |  |
| Thr | Met | Thr | Gly | Ala | Asn | Met | Val | Leu | Glu | Asp | His | Tyr | Arg | Ala | Gly |  |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |  |
| Pro | Arg | Asn | Val | Val | Ile | Thr | Gly | Ser | Thr | Arg | Gly | Leu | Gly | Lys | Ala |  |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |  |
| Leu | Ala | Arg | Glu | Phe | Leu | Leu | Ser | Gly | Asp | Arg | Val | Ile | Val | Thr | Ser |  |
|     |     |     | 180 |     |     |     |     |     | 185 |     |     |     | 190 |     |     |  |
| Arg | Ser | Ser | Glu | Ser | Val | Asp | Met | Thr | Val | Lys | Glu | Leu | Glu | Gln | Asn |  |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |  |
| Leu | Lys | Glu | Ile | Met | Ser | Asn | Ala | Ser | Glu | Ser | Ala | Arg | Lys | Lys | Leu |  |
|     |     | 210 |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |  |
| Ser | Asp | Ala | Lys | Val | Val | Gly | Ile | Ala | Cys | Asp | Val | Cys | Lys | Pro | Glu |  |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |  |
| Asp | Val | Glu | Lys | Leu | Ser | Asn | Phe | Ala | Val | Lys | Glu | Leu | Gly | Ser | Ile |  |
|     |     |     | 245 |     |     |     |     |     | 250 |     |     |     |     | 255 |     |  |
| Asn | Ile | Trp | Ile | Asn | Asn | Ala | Gly | Thr | Asn | Lys | Gly | Phe | Arg | Pro | Leu |  |
|     |     | 260 |     |     |     |     |     | 265 |     |     |     |     | 270 |     |     |  |
| Leu | Lys | Phe | Thr | Glu | Glu | Asp | Ile | Thr | Gln | Ile | Val | Ser | Thr | Asn | Leu |  |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |  |
| Ile | Gly | Ser | Ile | Leu | Cys | Thr | Arg | Gly | Ala | Ile | Asp | Val | Met | Ser | Arg |  |
|     |     | 290 |     |     |     |     | 295 |     |     |     | 300 |     |     |     |     |  |
| Gln | His | Ser | Gly | Gly | His | Ile | Phe | Asn | Met | Asp | Gly | Ala | Gly | Ser | Gly |  |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |  |
| Gly | Ser | Ser | Thr | Pro | Leu | Thr | Ala | Val | Tyr | Gly | Ser | Thr | Lys | Cys | Gly |  |
|     |     |     | 325 |     |     |     |     |     | 330 |     |     |     |     | 335 |     |  |
| Leu | Arg | Gln | Phe | His | Gly | Ser | Ile | Val | Lys | Glu | Ser | Gln | Lys | Thr | Asn |  |
|     |     |     | 340 |     |     |     |     |     | 345 |     |     |     | 350 |     |     |  |
| Val | Gly | Leu | His | Thr | Ala | Ser | Pro | Gly | Met | Val | Leu | Thr | Glu | Leu | Leu |  |
|     |     | 355 |     |     |     |     | 360 |     |     |     |     | 365 |     |     |     |  |
| Leu | Ser | Gly | Ser | Ser | Ile | Lys | Asn | Lys | Gln | Met | Phe | Asn | Ile | Ile | Cys |  |
|     |     | 370 |     |     |     | 375 |     |     |     |     | 380 |     |     |     |     |  |
| Glu | Leu | Pro | Glu | Thr | Val | Ala | Arg | Thr | Leu | Val | Pro | Arg | Met | Arg | Val |  |
| 385 |     |     |     |     | 390 |     |     |     |     | 395 |     |     |     |     | 400 |  |
| Val | Lys | Gly | Ser | Gly | Lys | Ala | Val | Asn | Tyr | Leu | Thr | Pro | Pro | Arg | Ile |  |
|     |     |     | 405 |     |     |     |     |     | 410 |     |     |     |     | 415 |     |  |
| Leu | Leu | Ala | Ile | Val | Thr | Ser | Trp | Leu | Arg | Arg | Gly | Arg | Trp | Phe | Asp |  |
|     |     |     | 420 |     |     |     |     | 425 |     |     |     |     | 430 |     |     |  |
| Asp | Gln | Gly | Arg | Ala | Leu | Tyr | Ala | Ala | Glu | Ala | Asp | Arg | Leu | Arg | Asn |  |
|     |     | 435 |     |     |     |     | 440 |     |     |     |     | 445 |     |     |     |  |
| Trp | Ala | Glu | Asn | Arg | Thr | Arg | Leu | Ser | Leu | Thr | Asp | Ala | Met | Glu | Met |  |
|     |     | 450 |     |     |     | 455 |     |     |     |     | 460 |     |     |     |     |  |
| Tyr | Thr | Glu | Asn | Thr | Trp | Val | Ser | Val | Phe | Ser | Leu | Ser | Val | Val | Cys |  |
| 465 |     |     |     |     | 470 |     |     |     |     | 475 |     |     |     |     | 480 |  |
| Ala | Phe | Ile | Ile | Leu | Gln | Ser | Thr | Thr | Pro | Ser | Ser | Phe | Pro | Gly | Thr |  |
|     |     |     | 485 |     |     |     |     |     | 490 |     |     |     |     | 495 |     |  |

- (2) INFORMATION FOR SEQ ID NO:427:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 404 amino acids

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Val | Phe | Ser | Ser | Val | Ala | Val | Gln | Ile | Ala | Arg | Tyr | Ile | Val | Thr |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Met | Thr | Ser | Thr | Gly | Ala | Ile | Leu | Leu | Ile | Gly | Phe | Gln | Leu | Ser | Gly |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Gly | Asp | Ser | Ser | Met | Asn | Ser | Leu | Val | Trp | Tyr | Ser | Trp | Leu | Gly | Gly |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ile | Ile | Ile | Gly | Thr | Met | Thr | Gly | Ala | Asn | Met | Val | Leu | Glu | Asp | His |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Tyr | Arg | Ala | Gly | Pro | Arg | Asn | Val | Val | Ile | Thr | Gly | Ser | Thr | Arg | Gly |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Leu | Gly | Lys | Ala | Leu | Ala | Arg | Glu | Phe | Leu | Leu | Ser | Gly | Asp | Arg | Val |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Ile | Val | Thr | Ser | Arg | Ser | Ser | Glu | Ser | Val | Asp | Met | Thr | Val | Lys | Glu |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Leu | Glu | Gln | Asn | Leu | Lys | Glu | Ile | Met | Ser | Asn | Ala | Ser | Glu | Ser | Ala |
|     |     | 115 |     |     |     | 120 |     |     |     |     |     | 125 |     |     |     |
| Arg | Lys | Lys | Leu | Ser | Asp | Ala | Lys | Val | Val | Gly | Ile | Ala | Cys | Asp | Val |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Cys | Lys | Pro | Glu | Asp | Val | Glu | Lys | Leu | Ser | Asn | Phe | Ala | Val | Lys | Glu |
| 145 |     |     |     | 150 |     |     |     |     |     | 155 |     |     |     | 160 |     |
| Leu | Gly | Ser | Ile | Asn | Ile | Trp | Ile | Asn | Asn | Ala | Gly | Thr | Asn | Lys | Gly |
|     |     |     |     | 165 |     |     |     | 170 |     |     |     |     |     | 175 |     |
| Phe | Arg | Pro | Leu | Leu | Lys | Phe | Thr | Glu | Glu | Asp | Ile | Thr | Gln | Ile | Val |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Ser | Thr | Asn | Leu | Ile | Gly | Ser | Ile | Leu | Cys | Thr | Arg | Gly | Ala | Ile | Asp |
|     |     | 195 |     |     |     | 200 |     |     |     |     |     | 205 |     |     |     |
| Val | Met | Ser | Arg | Gln | His | Ser | Gly | Gly | His | Ile | Phe | Asn | Met | Asp | Gly |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Ala | Gly | Ser | Gly | Gly | Ser | Ser | Thr | Pro | Leu | Thr | Ala | Val | Tyr | Gly | Ser |
| 225 |     |     |     | 230 |     |     |     |     |     | 235 |     |     |     | 240 |     |
| Thr | Lys | Cys | Gly | Leu | Arg | Gln | Phe | His | Gly | Ser | Ile | Val | Lys | Glu | Ser |
|     |     |     |     | 245 |     |     |     | 250 |     |     |     |     | 255 |     |     |
| Gln | Lys | Thr | Asn | Val | Gly | Leu | His | Thr | Ala | Ser | Pro | Gly | Met | Val | Leu |
|     |     | 260 |     |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Thr | Glu | Leu | Leu | Leu | Ser | Gly | Ser | Ser | Ile | Lys | Asn | Lys | Gln | Met | Phe |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Asn | Ile | Ile | Cys | Glu | Leu | Pro | Glu | Thr | Val | Ala | Arg | Thr | Leu | Val | Pro |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Arg | Met | Arg | Val | Val | Lys | Gly | Ser | Gly | Lys | Ala | Val | Asn | Tyr | Leu | Thr |
| 305 |     |     |     | 310 |     |     |     |     |     | 315 |     |     |     | 320 |     |
| Pro | Pro | Arg | Ile | Leu | Leu | Ala | Ile | Val | Thr | Ser | Trp | Leu | Arg | Arg | Gly |
|     |     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |     |
| Arg | Trp | Phe | Asp | Asp | Gln | Gly | Arg | Ala | Leu | Tyr | Ala | Ala | Glu | Ala | Asp |
|     |     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |
| Arg | Leu | Arg | Asn | Trp | Ala | Glu |     |     |     |     |     |     |     |     |     |

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 388 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ix) FEATURE:

(B) LOCATION: 1..388

SEQUENCE DESCRIPTION: SEQ ID NO:428:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Thr | Ser | Thr | Gly | Ala | Ile | Leu | Leu | Ile | Gly | Phe | Gln | Leu | Ser | Gly |
| 1   | Gly | Asp | Ser | Ser | Met | Asn | Ser | Leu | Val | Trp | Tyr | Ser | Trp | Leu | Gly |
|     |     |     |     | 20  |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ile | Ile | Ile | Gly | Thr | Met |     | Thr | Gly | Ala | Asn | Met | Val | Leu | Glu | Asp |
|     |     | 35  |     |     |     |     |     | 40  |     |     |     |     | 45  |     | His |
| Tyr | Arg | Ala | Gly | Pro | Arg | Asn | Val | Val | Ile | Thr | Gly | Ser | Thr | Arg | Gly |
|     | 50  |     |     |     |     | 55  |     |     |     |     |     | 60  |     |     |     |
| Leu | Gly | Lys | Ala | Leu | Ala | Arg | Glu | Phe | Leu | Leu | Ser | Gly | Asp | Arg | Val |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Ile | Val | Thr | Ser | Arg | Ser | Ser | Glu | Ser | Val | Asp | Met | Thr | Val | Lys | Glu |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Leu | Glu | Gln | Asn | Leu | Lys | Glu | Ile | Met | Ser | Asn | Ala | Ser | Glu | Ser | Ala |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Arg | Gly | Lys | Leu | Ser | Asp | Ala | Lys | Val | Val | Gly | Ile | Ala | Cys | Asp | Val |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Cys | Lys | Pro | Glu | Asp | Val | Glu | Lys | Leu | Ser | Asn | Phe | Ala | Val | Lys | Glu |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Leu | Gly | Ser | Ile | Asn | Ile | Trp | Ile | Asn | Asn | Ala | Gly | Thr | Asn | Lys | Gly |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |     |
| Phe | Arg | Pro | Leu | Leu | Lys | Phe | Thr | Glu | Glu | Asp | Ile | Thr | Gln | Ile | Val |
|     |     |     |     | 165 |     |     |     | 170 |     |     |     |     | 175 |     |     |
| Ser | Thr | Asn | Leu | Ile | Gly | Ser | Ile | Leu | Cys | Thr | Arg | Gly | Ala | Ile | Asp |
|     |     | 180 |     |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Val | Met | Ser | Arg | Gln | His | Ser | Gly | Gly | His | Ile | Phe | Asn | Met | Asp | Gly |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Ala | Gly | Ser | Gly | Gly | Ser | Ser | Thr | Pro | Leu | Thr | Ala | Val | Tyr | Gly | Ser |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Thr | Lys | Cys | Gly | Leu | Arg | Gln | Phe | His | Gly | Ser | Ile | Val | Lys | Glu | Ser |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     | 240 |     |
| Gln | Lys | Thr | Asn | Val | Gly | Leu | His | Thr | Ala | Ser | Pro | Gly | Met | Val | Leu |
|     |     |     | 245 |     |     |     |     |     | 250 |     |     |     | 255 |     |     |
| Thr | Glu | Leu | Leu | Leu | Ser | Gly | Ser | Ser | Ile | Lys | Asn | Lys | Gln | Met | Phe |
|     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |     |
| Asn | Ile | Ile | Cys | Glu | Leu | Pro | Glu | Thr | Val | Ala | Arg | Thr | Leu | Val | Pro |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Arg | Met | Arg | Val | Val | Lys | Gly | Ser | Gly | Lys | Ala | Val | Asn | Tyr | Leu | Thr |
|     | 290 |     |     |     |     | 295 |     |     |     | 300 |     |     |     |     |     |
| Pro | Pro | Arg | Ile | Leu | Leu | Ala | Ile | Val | Thr | Ser | Trp | Leu | Arg | Arg | Gly |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     | 320 |     |
| Arg | Trp | Phe | Asp | Asp | Gln | Gly | Arg | Ala | Leu | Tyr | Ala | Ala | Glu | Ala | Asp |
|     |     |     | 325 |     |     |     |     |     | 330 |     |     |     | 335 |     |     |
| Arg | Leu | Arg | Asn | Trp | Ala | Glu | Asn | Arg | Thr | Arg | Leu | Ser | Leu | Thr | Asp |
|     |     |     | 340 |     |     |     |     |     | 345 |     |     |     | 350 |     |     |
| Ala | Met | Glu | Met | Tyr | Thr | Glu | Asn | Thr | Trp | Val | Ser | Val | Phe | Ser | Leu |
|     |     | 3   |     |     |     |     |     |     |     |     |     |     |     |     |     |

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(2) INFORMATION FOR SEQ ID NO:429:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 681 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..681

(D) OTHER INFORMATION: / Ceres Seq. ID 1566921

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:429:

|            |             |            |            |            |            |     |
|------------|-------------|------------|------------|------------|------------|-----|
| acataatcat | cgctattctc  | tctctctctc | tctctctctc | tctctctcgc | tctcatattt | 60  |
| gcagttgaca | atttgtttctc | tttgggaaat | tagagatgca | ggcatcaaga | gcgcgactgt | 120 |
| ttaaagaata | caaagaggta  | cagcgagaga | aagtagcaga | tcctgatatt | caattgatct | 180 |
| gtgacgatac | caacataattc | aaatggaccg | ctcttatcaa | aggaccttcg | gagactcctt | 240 |
| acgaaggcgg | tgtttttcag  | cttgcttttt | ctgttctctg | accttatcct | ttgcaacctc | 300 |
| ctcaagttcg | attcttgacc  | aagatatccc | atcctaattg | tcatttcaag | acaggagaaa | 360 |
| tatgtctcga | cattttgaag  | aatgcttggg | gtcctgcttg | gacgcttcag | tctgtgtgta | 420 |
| gagctatcat | agcattgatg  | gctcatctcg | agcgggacac | tcctcttaac | tgcgactcag | 480 |
| ggaatctctc | aagatctggg  | gatgtgagag | ggttcaattc | aatggcaca  | atgtatacac | 540 |
| gcctcgccgc | tatgctcaag  | aaaggatgat | gatgatgatg | atcctcttgc | tttttttttg | 600 |
| tttttttttt | tgaatytgt   | aatgatattg | attCtgcgag | agtgaataca | ttattaacga | 660 |
| gaagaaCgat | gattctctt   | t          |            |            |            |     |

(2) INFORMATION FOR SEQ ID NO:430:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 157 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..157

(D) OTHER INFORMATION: / Ceres Seq. ID 1566922

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:430:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Gln | Ala | Ser | Arg | Ala | Arg | Leu | Phe | Lys | Glu | Tyr | Lys | Glu | Val | Gln |  |
| 1   |     |     | 5   |     |     |     | 10  |     |     | 15  |     |     |     |     |     |  |
| Arg | Glu | Lys | Val | Ala | Asp | Pro | Asp | Ile | Gln | Leu | Ile | Cys | Asp | Asp | Thr |  |
|     |     |     | 20  |     |     |     | 25  |     |     |     |     | 30  |     |     |     |  |
| Asn | Ile | Phe | Lys | Trp | Thr | Ala | Leu | Ile | Lys | Gly | Pro | Ser | Glu | Thr | Pro |  |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Tyr | Glu | Gly | Gly | Val | Phe | Gln | Leu | Ala | Phe | Ser | Val | Pro | Glu | Pro | Tyr |  |
|     |     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |  |
| Pro | Leu | Gln | Pro | Pro | Gln | Val | Arg | Phe | Leu | Thr | Lys | Ile | Phe | His | Pro |  |
|     |     |     | 65  |     |     |     | 70  |     |     |     | 75  |     |     | 80  |     |  |
| Asn | Val | His | Phe | Lys | Thr | Gly | Glu | Ile | Cys | Leu | Asp | Ile | Leu | Lys | Asn |  |
|     |     |     | 85  |     |     |     | 90  |     |     |     |     |     | 95  |     |     |  |
| Ala | Trp | Ser | Pro | Ala | Trp | Thr | Leu | Gln | Ser | Val | Cys | Arg | Ala | Ile | Ile |  |
|     |     |     | 100 |     |     |     | 105 |     |     |     |     |     | 110 |     |     |  |
| Ala | Leu | Met | Ala | His | Pro | Glu | Pro | Asp | Ser | Pro | Leu | Asn | Cys | Asp | Ser |  |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |  |
| Gly | Asn | Leu | Leu | Arg | Ser | Gly | Asp | Val | Arg | Gly | Phe | Asn | Ser | Met | Ala |  |
|     |     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |  |
| Gln | Met | Tyr | Thr | Arg | Leu | Ala | Ala | Met | Pro | Lys | Lys | Gly |     |     |     |  |
|     |     |     | 145 |     |     |     | 150 |     |     |     | 155 |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:431:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 429 base pairs  
(B) TYPE: nucleic acid

(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
(A) NAME/KEY: -  
(B) LOCATION: 1..429  
(D) OTHER INFORMATION: / Ceres Seq. ID 1566936  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:431:  
aaaWacaaa aaaaaaatgc tttaaagat aaagccgggtg gttctcatgt cgttcttgct 60  
tctgtttcca ttgtgttctt cggggtttag agaaggccat ggagtactc acacgacca 120  
aaatttcotta aacaagggttg aagagagat tccaacgac atggattatc cggaaccagg 180  
tccagaccgg aacaacgac caacaaaacc cggttatggt ttctctccc caccgccacc 240  
gccactgtca ccgccaccg caccgaatat gaactaagaa tcatgatgaa gcaaaaatat 300  
gtaatatcgt taaatcatgc tcgtgagaag aactagtatt catgtgaagc aaaaagaaaa 360  
cttaaatatg atgattctat gatattgact atcaaagtaa tcaatcaaat ataaaagagt 420  
aaaatttgg

(2) INFORMATION FOR SEQ ID NO:432:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 91 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..91  
(D) OTHER INFORMATION: / Ceres Seq. ID 1566937  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:432:  
Xaa Thr Asn Lys Lys Met Leu Ser Lys Ile Lys Pro Val Val Leu Met  
1 5 10 15  
Ser Phe Leu Leu Phe Pro Leu Cys Ser Ser Gly Phe Arg Glu Gly  
20 25 30  
His Gly Val Thr His Thr Asp Gln Asn Ser Leu Asn Lys Val Glu Glu  
35 40 45  
Ser Ile Pro Thr Ile Met Asp Tyr Pro Glu Pro Gly Pro Asp Pro Lys  
50 55 60  
His Asp Pro Thr Lys Pro Gly Tyr Gly Phe Pro Pro Pro Pro Pro  
65 70 75 80  
Pro Leu Ser Pro Pro Pro Pro Asn Met Asn  
85 90

(2) INFORMATION FOR SEQ ID NO:433:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 86 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..86  
(D) OTHER INFORMATION: / Ceres Seq. ID 1566938  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:433:  
Met Leu Ser Lys Ile Lys Pro Val Val Leu Met Ser Phe Leu Leu Leu  
1 5 10 15  
Phe Pro Leu Cys Ser Ser Gly Phe Arg Glu Gly His Gly Val Thr His  
20 25 30  
Thr Asp Gln Asn Ser Leu Asn Lys Val Glu Glu Ser Ile Pro Thr Ile  
35 40 45  
Met Asp Tyr Pro Glu Pro Gly Pro Asp Pro Lys His Asp Pro Thr Lys  
50 55 60  
Pro Gly Tyr Gly Phe Pro Pro Pro Pro Pro Pro Leu Ser Pro Pro

65 70 75 80  
Pro Pro Pro Asn Met Asn  
85

(2) INFORMATION FOR SEQ ID NO:434:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 76 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..76  
(D) OTHER INFORMATION: / Ceres Seq. ID 1566939

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:434:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ser | Phe | Leu | Leu | Phe | Pro | Leu | Cys | Ser | Ser | Gly | Phe | Arg | Glu |
| 1   |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Gly | His | Gly | Val | Thr | His | Thr | Asp | Gln | Asn | Ser | Leu | Asn | Lys | Val |
|     |     |     | 20  |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Glu | Ser | Ile | Pro | Thr | Ile | Met | Asp | Tyr | Pro | Glu | Pro | Gly | Pro | Asp |
|     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Lys | His | Asp | Pro | Thr | Lys | Pro | Gly | Tyr | Gly | Phe | Pro | Pro | Pro | Pro |
|     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Pro | Pro | Leu | Ser | Pro | Pro | Pro | Pro | Pro | Asn | Met | Asn |     |     |     |
| 65  |     |     | 70  |     |     |     | 75  |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:435:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 716 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..716  
(D) OTHER INFORMATION: / Ceres Seq. ID 1566946

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:435:

|             |             |            |            |            |             |     |
|-------------|-------------|------------|------------|------------|-------------|-----|
| cccttgatca  | gatagtga    | gagattctct | atattgcaga | tcatctccgc | agtttgctaa  | 60  |
| atcgccggga  | aatttactga  | atttggagct | agtcattgct | tcagatccgt | acaaaatgat  | 120 |
| gtccaaagcc  | gacaaaaatga | caaagctcac | gcttactaga | tggagtgcgt | attggagagg  | 180 |
| tgctactagt  | aacacaaata  | cacaaaaaaa | aaaaaacag  | aaagtaacat | gagatctctc  | 240 |
| ttattagcgc  | tgtgcctggt  | tcttgcttta | cactgcggtg | aagcagccgt | gtcttgcaac  | 300 |
| acgggtgattg | cggatcttta  | cccttgctta | tcctactgtg | ctcaggggcg | accggtccca  | 360 |
| accctctgct  | gcaacggctc  | cacaacactc | aagagtcagg | ctcaaacctc | tgtggaccgt  | 420 |
| caggggGctc  | gtcgttgcat  | caaatctgct | attggaggac | tcactctctc | tcctagaacc  | 480 |
| atccaaaatg  | ctttgggaatt | gccttctaaa | tgtgggtgct | atctccctta | caagttcagc  | 540 |
| ctttccactg  | actgcgacag  | tatccagtga | gacaagcaga | aaatctctaa | ggaagctact  | 600 |
| acaagaacta  | taataaccta  | ataattaata | aatgaggcca | ttggtttgct | agttgctaatt | 660 |
| tgatcagtga  | tgtattgtca  | ttttgaatgt | tctaataatc | gcaggcactt | atctcc      |     |

(2) INFORMATION FOR SEQ ID NO:436:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 113 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..113  
(D) OTHER INFORMATION: / Ceres Seq. ID 1566947

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:436:

Met Arg Ser Leu Leu Leu Ala Val Cys Leu Val Leu Ala Leu His Cys  
1 5 10 15  
Gly Glu Ala Ala Val Ser Cys Asn Thr Val Ile Ala Asp Leu Tyr Pro  
20 25 30  
Cys Leu Ser Tyr Val Thr Gln Gly Gly Pro Val Pro Thr Leu Cys Cys  
35 40 45  
Asn Gly Leu Thr Thr Leu Lys Ser Gln Ala Gln Thr Ser Val Asp Arg  
50 55 60  
Gln Gly Val Cys Arg Cys Ile Lys Ser Ala Ile Gly Gly Leu Thr Leu  
65 70 75 80  
Ser Pro Arg Thr Ile Gln Asn Ala Leu Glu Leu Pro Ser Lys Cys Gly  
85 90 95  
Val Asp Leu Pro Tyr Lys Phe Ser Pro Ser Thr Asp Cys Asp Ser Ile  
100 105 110  
Gln

(2) INFORMATION FOR SEQ ID NO:437:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2928 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..2928
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566955

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:437:

|             |             |             |            |             |             |      |
|-------------|-------------|-------------|------------|-------------|-------------|------|
| aaaaactcct  | aaaccaaatt  | ataattgtta  | gtaagttaag | taacagagaa  | caaaataata  | 60   |
| ctcgtaacct  | ttgtttccaa  | actataacgt  | aacttttgtt | catcatcttc  | acagttttctg | 120  |
| ttctctgttc  | taagatttct  | aaatttttgt  | tttttttttt | ctttttttct  | tcgattatttt | 180  |
| ttgattttct  | gatggaattc  | cgcaaacctc  | ttaagtctca | tagctcgat   | aaacagatta  | 240  |
| taagcacogg  | aatcaaaac   | gagaagacaa  | agaagaagaa | gaaactggcg  | aatcttgacg  | 300  |
| atggcgacat  | tgctaaaaat  | cagagctctg  | ggtctagtct | cgatggaaac  | agctataagt  | 360  |
| tctggcaaga  | cattgcaaca  | gatgattata  | caaagagcgg | gagtttcgat  | ttccgcgaat  | 420  |
| acogtgagga  | gatcacactc  | gatgtaaacg  | aagaacaaga | ggaacacag   | gagtccaaga  | 480  |
| acaacaacaa  | tttgtccggg  | tctaaagaaa  | cgagagcttc | tttcaaaaa   | aacagttcag  | 540  |
| gaactaataa  | tatgtctcgt  | tctgtacgtt  | cttgatcatc | ttcgactctg  | ttttcatcgg  | 600  |
| ccacaatcgc  | gttaaattta  | gagcagcagt  | tggaggatga | aggagaggtg  | gttgtaagat  | 660  |
| gttcacatcg  | gaggaaaaac  | gagcttgttt  | cgagggcgaa | ggcgagatcg  | aggttgatag  | 720  |
| atccgcacaa  | agaagaggaa  | caacaatact  | cgagctggat | cgggacatcg  | gatcagttaa  | 780  |
| gatcaggttt  | atctgggaga  | caactctgat  | atattgatga | agaagatgat  | tcttcggctg  | 840  |
| aagaagatgt  | tccagtggaa  | tatcgaagt   | tgaaaatgga | cgcgataacg  | ttgcttcaat  | 900  |
| ggatgagctt  | aatcgcactc  | gtagtggcgt  | tagtgttgag | tctagcgctt  | catacttga   | 960  |
| gAaaaatgct  | actctatgga  | gccttcatct  | gtggaaaatg | gaagtggctt  | tctgtgtctt  | 1020 |
| catctgcggg  | aggctgggtt  | ccggatgcgg  | aatcacgaat | atcgtctctt  | ttatcgaaag  | 1080 |
| aaacttctta  | ttgaggaaac  | gggttcttta  | ctctgtatac | ggtgtgaaga  | ctcgtgttca  | 1140 |
| gaactgtctc  | ttgctttggc  | tctgtctcgt  | cctctggcat | ttctgtctcg  | acaagaaagt  | 1200 |
| agaaaaggaa  | acacaaagcg  | acgttcttct  | tctcgtatct | aaaatattag  | tgtgtttctt  | 1260 |
| gttgagcagc  | gtcttatggc  | tgatcaagac  | actgggtgtg | aaagttttag  | catctcgttt  | 1320 |
| ccagcttagt  | acctactttg  | atcggattca  | agaagctctg | tttcatcatt  | acttgatcga  | 1380 |
| gcagttatct  | tgacctccaa  | tgcttgagtt  | aagcaggatt | gaggagaagg  | aagatcggaac | 1440 |
| gcaagatgag  | atctacaagg  | tgcaaaaagg  | aggagctgat | ttatccaccg  | aaactttgtc  | 1500 |
| cgctgcggtt  | ctccaggaaa  | aaagtggaa   | tacaatgaac | atgaagttct  | ctccaatcat  | 1560 |
| tccgaagacg  | gggtggtgata | acggaatcac  | aatggatgat | ttacacaaga  | tgaatcagaa  | 1620 |
| aaactgttca  | gcttgggaaca | tgaagagact  | gtgagaagt  | gtgagaataa  | tttccctgac  | 1680 |
| tacgttggac  | gaacaagcgc  | ttcaaaaacac | gatgtgaagt | gaatccactc  | gacagatacg  | 1740 |
| gagcgaaaaa  | gaagcttaag  | cagctgcaag  | gaagattttc | aagaacgtag  | ctcaacctgg  | 1800 |
| cacaaaaacac | atatacctgg  | aggactttgt  | gaagtttttg | cgagtagacg  | aggcgatgaa  | 1860 |
| gacaatgtgt  | ctcttcgaag  | gcgccttagt  | gacaaaaaag | attactaat   | cagccttgaa  | 1920 |
| gaactggctg  | gtaaatgctt  | tcagagagag  | aagagcactt | gccttaaacac | tacaatgacac | 1980 |



|            |             |             |            |             |             |      |
|------------|-------------|-------------|------------|-------------|-------------|------|
| caaaacagca | gtgaacaaac  | tccatcacat  | gattagtttt | ctcactgcc   | ttgtcatcat  | 2040 |
| agtcataatg | ctgatccctc  | ttgaaatcgc  | tacttccaag | tatcttttat  | ttttaacttc  | 2100 |
| acaagttatg | ctcttagcct  | tcattgtttg  | gaactctctc | aagaccgcct  | tcagatcaat  | 2160 |
| catctctctc | ttcatcattc  | acccttaaga  | tgttggtgat | cggttactca  | tcgacactgt  | 2220 |
| agagatggtg | gtggaggaaa  | tgaacattct  | cacaaacagt | ttcttgagag  | ctgacaactc  | 2280 |
| gaagatttgt | tatccaaaata | ttcttctatg  | gcagaaagcg | atccacaatt  | acaaccgtag  | 2340 |
| tcgggatatg | ggagatgaag  | ttacatgctg  | tgtccacatt | actactcctc  | ctgaaaagat  | 2400 |
| tgctgcaatc | aaacaaagaa  | tatcaagcta  | cattgatagc | aagccagagt  | attggtatcc  | 2460 |
| aaaagctgat | atcatttgtaa | aggatgtgga  | agatttgaac | attgtgagga  | tagcaatatg  | 2520 |
| gctgtgtcat | aaaatttaacc | atcaaaaacat | gggagagaga | tttacaagaa  | gagcggttgt  | 2580 |
| gatcgaggaa | gtaatcaaaa  | tcctctcoga  | actcgacatt | caataccoggt | ttcatccact  | 2640 |
| tgatatcaat | gttaaaaacca | tgccaacagt  | tgtctcgagc | agagttccac  | acggtgtggtc | 2700 |
| acaaaaccct | gattcaaggt  | aattatagag  | atgatgtgaa | ttgtgtttatc | tttaactctta | 2760 |
| agtggtgttt | agtatgaggt  | ttgatttgtg  | tatttttttt | ttcttttttt  | gtaaacoggt  | 2820 |
| tggtgtatat | atatgaaggt  | gaaagcaaat  | agtgggatca | taaaccttgtg | ttatagaaac  | 2880 |
| tttatgaaaa | tagaaactaa  | tgatattttt  | agtaatgatt | tttttttt    |             |      |

(2) INFORMATION FOR SEQ ID NO:438:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 607 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..607

(D) OTHER INFORMATION: / Ceres Seq. ID 1566956

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:438:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Asp | Glu | Leu | Asn | Arg | Thr | Arg | Ser | Gly | Val | Ser | Val | Glu | Ser | Ser |
| 1   |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Ala | Ser | Tyr | Leu | Glu | Lys | Asn | Ala | Thr | Leu | Trp | Ser | Leu | His | Leu | Trp |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Lys | Trp | Glu | Val | Val | Leu | Leu | Val | Leu | Ile | Cys | Gly | Arg | Leu | Val | Ser |
|     |     | 35  |     |     |     |     |     | 40  |     |     |     | 45  |     |     |     |
| Gly | Cys | Gly | Ile | Arg | Ile | Ile | Val | Phe | Phe | Ile | Glu | Arg | Asn | Phe | Leu |
|     |     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |
| Leu | Arg | Lys | Arg | Val | Leu | Tyr | Phe | Val | Tyr | Gly | Val | Lys | Thr | Ala | Val |
|     |     | 65  |     |     |     |     | 70  |     |     |     | 75  |     |     | 80  |     |
| Gln | Asn | Cys | Leu | Trp | Leu | Gly | Leu | Val | Leu | Val | Ala | Trp | His | Phe | Leu |
|     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Phe | Asp | Lys | Lys | Val | Glu | Arg | Glu | Thr | Gln | Ser | Asp | Val | Leu | Leu | Leu |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Val | Ser | Lys | Ile | Leu | Val | Cys | Phe | Leu | Leu | Ser | Thr | Val | Leu | Trp | Leu |
|     |     | 115 |     |     |     |     |     | 120 |     |     |     |     | 125 |     |     |
| Ile | Lys | Thr | Leu | Val | Val | Lys | Val | Leu | Ala | Ser | Ser | Phe | His | Val | Ser |
|     |     | 130 |     |     |     |     | 135 |     |     |     | 140 |     |     |     |     |
| Thr | Tyr | Phe | Asp | Arg | Ile | Gln | Glu | Ala | Leu | Phe | His | His | Tyr | Leu | Ile |
|     |     | 145 |     |     |     |     | 150 |     |     | 155 |     |     |     | 160 |     |
| Glu | Thr | Leu | Ser | Val | Pro | Pro | Met | Leu | Glu | Leu | Ser | Arg | Ile | Glu | Glu |
|     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |     |
| Glu | Glu | Asp | Arg | Thr | Gln | Asp | Glu | Ile | Tyr | Lys | Val | Gln | Lys | Gly | Gly |
|     |     | 180 |     |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Ala | Asp | Leu | Ser | Pro | Glu | Leu | Cys | Ser | Ala | Ala | Phe | Pro | Gln | Glu | Lys |
|     |     | 195 |     |     |     |     |     | 200 |     |     |     | 205 |     |     |     |
| Ser | Gly | Ser | Thr | Met | Asn | Met | Lys | Phe | Ser | Pro | Ile | Ile | Pro | Lys | Thr |
|     |     | 210 |     |     |     |     | 215 |     |     |     | 220 |     |     |     |     |
| Gly | Gly | Asp | Asn | Gly | Ile | Thr | Met | Asp | Asp | Leu | His | Lys | Met | Asn | Gln |
|     |     | 225 |     |     |     |     | 230 |     |     |     | 235 |     |     | 240 |     |
| Lys | Asn | Val | Ser | Ala | Trp | Asn | Met | Lys | Arg | Leu | Met | Lys | Ile | Val | Arg |
|     |     | 245 |     |     |     |     |     | 250 |     |     |     |     | 255 |     |     |
| Asn | Ile | Ser | Leu | Thr | Thr | Leu | Asp | Glu | Gln | Ala | Leu | Gln | Asn | Thr | Cys |

260 265 270  
Glu Asp Glu Ser Thr Arg Gln Ile Arg Ser Glu Lys Glu Ala Lys Ala  
275 280 285  
Ala Ala Arg Lys Ile Phe Lys Asn Val Ala Gln Pro Gly Thr Lys His  
290 295 300  
Ile Tyr Leu Glu Asp Leu Met Arg Phe Leu Arg Val Asp Glu Ala Met  
305 310 315 320  
Lys Thr Met Cys Leu Phe Glu Gly Ala Leu Val Thr Lys Lys Ile Thr  
325 330 335  
Lys Ser Ala Leu Lys Asn Trp Leu Val Asn Ala Phe Arg Glu Arg Arg  
340 345 350  
Ala Leu Ala Leu Thr Leu Asn Asp Thr Lys Thr Ala Val Asn Lys Leu  
355 360 365  
His His Met Ile Ser Phe Leu Thr Ala Ile Val Ile Val Ile Trp  
370 375 380  
Leu Ile Leu Leu Glu Ile Ala Thr Ser Lys Tyr Leu Leu Phe Leu Thr  
385 390 395 400  
Ser Gln Val Val Leu Leu Ala Phe Met Phe Gly Asn Ser Leu Lys Thr  
405 410 415  
Val Phe Glu Ser Ile Ile Phe Leu Phe Ile Ile His Pro Tyr Asp Val  
420 425 430  
Gly Asp Arg Leu Leu Ile Asp Thr Val Glu Met Val Val Glu Glu Met  
435 440 445  
Asn Ile Leu Thr Thr Val Phe Leu Arg Ala Asp Asn Leu Lys Ile Val  
450 455 460  
Tyr Pro Asn Ile Leu Leu Trp Gln Lys Ala Ile His Asn Tyr Asn Arg  
465 470 475 480  
Ser Pro Asp Met Gly Asp Glu Val Thr Cys Cys Val His Ile Thr Thr  
485 490 495  
Pro Pro Glu Lys Ile Ala Ala Ile Lys Gln Arg Ile Ser Ser Tyr Ile  
500 505 510  
Asp Ser Lys Pro Glu Tyr Trp Tyr Pro Lys Ala Asp Ile Val Lys  
515 520 525  
Asp Val Glu Asp Leu Asn Ile Val Arg Ile Ala Ile Trp Leu Cys His  
530 535 540  
Lys Ile Asn His Gln Asn Met Gly Glu Arg Phe Thr Arg Arg Ala Leu  
545 550 555 560  
Leu Ile Glu Glu Val Ile Lys Ile Leu Leu Glu Leu Asp Ile Gln Tyr  
565 570 575  
Arg Phe His Pro Leu Asp Ile Asn Val Lys Thr Met Pro Thr Val Val  
580 585 590  
Ser Ser Arg Val Pro Pro Gly Trp Ser Gln Asn Pro Asp Ser Arg  
595 600 605

(2) INFORMATION FOR SEQ ID NO:439:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 440 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide  
(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..440  
(D) OTHER INFORMATION: / Ceres Seq. ID 1566957

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:439:

Met Leu Glu Leu Ser Arg Ile Glu Glu Glu Asp Arg Thr Gln Asp  
1 5 10 15  
Glu Ile Tyr Lys Val Gln Lys Gly Gly Ala Asp Leu Ser Pro Glu Leu  
20 25 30  
Cys Ser Ala Ala Phe Pro Gln Glu Lys Ser Gly Ser Thr Met Asn Met  
35 40 45

Lys Phe Ser Pro Ile Ile Pro Lys Thr Gly Gly Asp Asn Gly Ile Thr  
50 55 60  
Met Asp Asp Leu His Lys Met Asn Gln Lys Asn Val Ser Ala Trp Asn  
65 70 75 80  
Met Lys Arg Leu Met Lys Ile Val Arg Asn Ile Ser Leu Thr Thr Leu  
85 90 95  
Asp Glu Gln Ala Leu Gln Asn Thr Cys Glu Asp Glu Ser Thr Arg Gln  
100 105 110  
Ile Arg Ser Glu Lys Glu Ala Lys Ala Ala Arg Lys Ile Phe Lys  
115 120 125  
Asn Val Ala Gln Pro Gly Thr Lys His Ile Tyr Leu Glu Asp Leu Met  
130 135 140  
Arg Phe Leu Arg Val Asp Glu Ala Met Lys Thr Met Cys Leu Phe Glu  
145 150 155 160  
Gly Ala Leu Val Thr Lys Lys Ile Thr Lys Ser Ala Leu Lys Asn Trp  
165 170 175  
Leu Val Asn Ala Phe Arg Glu Arg Arg Ala Leu Ala Leu Thr Leu Asn  
180 185 190  
Asp Thr Lys Thr Ala Val Asn Lys Leu His His Met Ile Ser Phe Leu  
195 200 205  
Thr Ala Ile Val Ile Ile Val Ile Trp Leu Ile Leu Leu Glu Ile Ala  
210 215 220  
Thr Ser Lys Tyr Leu Leu Phe Leu Thr Ser Gln Val Val Leu Leu Ala  
225 230 235 240  
Phe Met Phe Gly Asn Ser Leu Lys Thr Val Phe Glu Ser Ile Ile Phe  
245 250 255  
Leu Phe Ile Ile His Pro Tyr Asp Val Gly Asp Arg Leu Leu Ile Asp  
260 265 270  
Thr Val Glu Met Val Val Glu Glu Met Asn Ile Leu Thr Thr Val Phe  
275 280 285  
Leu Arg Ala Asp Asn Leu Lys Ile Val Tyr Pro Asn Ile Leu Leu Trp  
290 295 300  
Gln Lys Ala Ile His Asn Tyr Asn Arg Ser Pro Asp Met Gly Asp Glu  
305 310 315 320  
Val Thr Cys Cys Val His Ile Thr Thr Pro Pro Glu Lys Ile Ala Ala  
325 330 335  
Ile Lys Gln Arg Ile Ser Ser Tyr Ile Asp Ser Lys Pro Glu Tyr Trp  
340 345 350  
Tyr Pro Lys Ala Asp Ile Ile Val Lys Asp Val Glu Asp Leu Asn Ile  
355 360 365  
Val Arg Ile Ala Ile Trp Leu Cys His Lys Ile Asn His Gln Asn Met  
370 375 380  
Gly Glu Arg Phe Thr Arg Arg Ala Leu Leu Ile Glu Glu Val Ile Lys  
385 390 395 400  
Ile Leu Leu Glu Leu Asp Ile Gln Tyr Arg Phe His Pro Leu Asp Ile  
405 410 415  
Asn Val Lys Thr Met Pro Thr Val Val Ser Ser Arg Val Pro Pro Gly  
420 425 430  
Trp Ser Gln Asn Pro Asp Ser Arg  
435 440

(2) INFORMATION FOR SEQ ID NO:440:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 395 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..395
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566958

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:440:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Asn | Met | Lys | Phe | Ser | Pro | Ile | Ile | Pro | Lys | Thr | Gly | Gly | Asp | Asn |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Gly | Ile | Thr | Met | Asp | Asp | Leu | His | Lys | Met | Asn | Gln | Lys | Asn | Val | Ser |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ala | Trp | Asn | Met | Lys | Arg | Leu | Met | Lys | Ile | Val | Arg | Asn | Ile | Ser | Leu |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Thr | Thr | Leu | Asp | Glu | Gln | Ala | Leu | Gln | Asn | Thr | Cys | Glu | Asp | Glu | Ser |
|     |     |     | 50  |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Thr | Arg | Gln | Ile | Arg | Ser | Glu | Lys | Glu | Ala | Lys | Ala | Ala | Ala | Arg | Lys |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Ile | Phe | Lys | Asn | Val | Ala | Gln | Pro | Gly | Thr | Lys | His | Ile | Tyr | Leu | Glu |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Asp | Leu | Met | Arg | Phe | Leu | Arg | Val | Asp | Glu | Ala | Met | Lys | Thr | Met | Cys |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Leu | Phe | Glu | Gly | Ala | Leu | Val | Thr | Lys | Lys | Ile | Thr | Lys | Ser | Ala | Leu |
|     |     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |
| Lys | Asn | Trp | Leu | Val | Asn | Ala | Phe | Arg | Glu | Arg | Arg | Ala | Leu | Ala | Leu |
|     |     |     | 130 |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Thr | Leu | Asn | Asp | Thr | Lys | Thr | Ala | Val | Asn | Lys | Leu | His | His | Met | Ile |
| 145 |     |     |     |     | 150 |     |     |     | 155 |     |     |     |     | 160 |     |
| Ser | Phe | Leu | Thr | Ala | Ile | Val | Ile | Ile | Val | Ile | Trp | Leu | Ile | Leu | Leu |
|     |     |     |     |     | 165 |     |     |     | 170 |     |     |     |     | 175 |     |
| Glu | Ile | Ala | Thr | Ser | Lys | Tyr | Leu | Leu | Phe | Leu | Thr | Ser | Gln | Val | Val |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Leu | Leu | Ala | Phe | Met | Phe | Gly | Asn | Ser | Leu | Lys | Thr | Val | Phe | Glu | Ser |
|     |     |     | 195 |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Ile | Ile | Phe | Leu | Phe | Ile | Ile | His | Pro | Tyr | Asp | Val | Gly | Asp | Arg | Leu |
|     |     |     | 210 |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Leu | Ile | Asp | Thr | Val | Glu | Met | Val | Val | Glu | Glu | Met | Asn | Ile | Leu | Thr |
| 225 |     |     |     |     | 230 |     |     |     | 235 |     |     |     |     | 240 |     |
| Thr | Val | Phe | Leu | Arg | Ala | Asp | Asn | Leu | Lys | Ile | Val | Tyr | Pro | Asn | Ile |
|     |     |     |     | 245 |     |     |     | 250 |     |     |     |     |     | 255 |     |
| Leu | Leu | Trp | Gln | Lys | Ala | Ile | His | Asn | Tyr | Asn | Arg | Ser | Pro | Asp | Met |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Gly | Asp | Glu | Val | Thr | Cys | Cys | Val | His | Ile | Thr | Thr | Pro | Pro | Glu | Lys |
|     |     |     | 275 |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Ile | Ala | Ala | Ile | Lys | Gln | Arg | Ile | Ser | Ser | Tyr | Ile | Asp | Ser | Lys | Pro |
|     |     |     | 290 |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Glu | Tyr | Trp | Tyr | Pro | Lys | Ala | Asp | Ile | Ile | Val | Lys | Asp | Val | Glu | Asp |
| 305 |     |     |     |     | 310 |     |     |     | 315 |     |     |     |     | 320 |     |
| Leu | Asn | Ile | Val | Arg | Ile | Ala | Ile | Trp | Leu | Cys | His | Lys | Ile | Asn | His |
|     |     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |     |
| Gln | Asn | Met | Gly | Glu | Arg | Phe | Thr | Arg | Arg | Ala | Leu | Leu | Ile | Glu | Glu |
|     |     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |
| Val | Ile | Lys | Ile | Leu | Leu | Glu | Leu | Asp | Ile | Gln | Tyr | Arg | Phe | His | Pro |
|     |     |     | 355 |     |     |     | 360 |     |     |     |     | 365 |     |     |     |
| Leu | Asp | Ile | Asn | Val | Lys | Thr | Met | Pro | Thr | Val | Val | Ser | Ser | Arg | Val |
|     |     |     | 370 |     |     | 375 |     |     |     |     | 380 |     |     |     |     |
| Pro | Pro | Gly | Trp | Ser | Gln | Asn | Pro | Asp | Ser | Arg |     |     |     |     |     |
| 385 |     |     |     |     | 390 |     |     |     | 395 |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:441:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1463 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1463

(D) OTHER INFORMATION: / Ceres Seq. ID 1566971

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:441:

|             |             |             |             |             |             |      |
|-------------|-------------|-------------|-------------|-------------|-------------|------|
| aaaaaccgat  | tcattttaaac | aacaaaaaac  | cacttacaga  | gttcgttcgc  | cggcgcgcgGc | 60   |
| gagtcacgt   | catcaatgtc  | aaacatcggt  | gttcctagaca | acggcggtgg  | tctaatcaaa  | 120  |
| gccggacaa   | gcggcgagcg  | tgatccacac  | accgtaatcc  | cgaaactgtct | ctacaaaacct | 180  |
| ctctcttcca  | aaaaattcat  | ccaccatca   | ccactcacca  | ctctctccga  | cgaatcgac   | 240  |
| ctcaactcgc  | cgcgcgtacg  | cgcgccaaat  | gaccgtggct  | acatcataaa  | ctccgacct   | 300  |
| caacgcgaaa  | ctcgggtcaca | cctattcact  | tcctctctcc  | acatagctcc  | ctctctctcc  | 360  |
| ctctctctcc  | tcaccgaagc  | accactctca  | atcccttcgc  | tccaacgaac  | caacgacgaa  | 420  |
| ctcgcttcgc  | aagatttcgc  | attctctctc  | ctctatatag  | ctcatctcca  | atctcttggt  | 480  |
| catctctatg  | aagctagtcg  | tcagccgtgat | tcaactctct  | caaagactca  | gtgtagctct  | 540  |
| gttggttgatt | gtggtttctc  | cttcaactca  | gctgttcctg  | ttcttcacaa  | tttcaactctc | 600  |
| aatcacgcga  | ttaagaggat  | tgatttagga  | ggaaaagcgt  | ttactaatta  | cttgaggaaa  | 660  |
| ttggtttctt  | atagatctat  | taattgttat  | gatgaaactt  | ttttagttga  | tgatgctaaa  | 720  |
| gagaagcttt  | gttttgtttc  | acttgatctt  | cttcgtgata  | tccgccttgc  | tagaatagg   | 780  |
| aaactcttta  | tcaagtctac  | ttatgttctt  | octgatgggt  | ttacacatac  | caaaaggcat  | 840  |
| gttaaagacc  | ctcaagctgc  | taagagggtt  | cttagtttgt  | cagagaaaga  | gtctgttggt  | 900  |
| gtgatggata  | aggttgggga  | gagaaagaag  | gctgacatga  | acaaaaatga  | gattgattta  | 960  |
| acgaatgagc  | gttttcttgt  | acctgagacg  | ttattccagc  | ctgcagattt  | agggatgaat  | 1020 |
| caggcgggac  | ttgcagagtg  | cattgtccga  | gctataaact  | catgccaatt  | ttacttgcaa  | 1080 |
| ccagttttgt  | atcaaaagcat | tatcttaact  | ggtggaagta  | cattatttcc  | acaacttaag  | 1140 |
| gagagactag  | aaggagagct  | tcgaccactt  | gtccagatgc  | actttgatgt  | gaagataaca  | 1200 |
| actcagagg   | accctcaact  | aggtgtatgg  | agaggttggt  | cacttttggt  | ttccagcccg  | 1260 |
| gatttcagag  | ccatgtgtgt  | caccaaggct  | gagtacgaag  | aacttgatgc  | agctcggtgt  | 1320 |
| cgtagacgat  | tccttcaatt  | aggctaacca  | aaacaatatc  | acatgagttg  | gttgtaagtt  | 1380 |
| gaaactcttc  | acattatttg  | tcgtatatgt  | taatgcatgt  | attgtttttc  | ttcttctctc  | 1440 |
| aatttgaaaa  | acttcaaacc  | gtc         |             |             |             |      |

(2) INFORMATION FOR SEQ ID NO:442:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 421 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..421

(D) OTHER INFORMATION: / Ceres Seq. ID 1566972

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:442:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ser | Asn | Ile | Val | Val | Leu | Asp | Asn | Gly | Gly | Gly | Leu | Ile | Lys | Ala |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Gly | Gln | Gly | Gly | Glu | Arg | Asp | Pro | Thr | Thr | Val | Ile | Pro | Asn | Cys | Leu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Tyr | Lys | Pro | Leu | Ser | Ser | Lys | Lys | Phe | Ile | His | Pro | Ser | Pro | Leu | Thr |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Thr | Leu | Ser | Asp | Glu | Ile | Asp | Leu | Thr | Ser | Ala | Ala | Val | Arg | Arg | Pro |
|     |     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |
| Ile | Asp | Arg | Gly | Tyr | Leu | Ile | Asn | Ser | Asp | Leu | Gln | Arg | Glu | Ile | Trp |
|     |     |     |     |     |     |     | 70  |     |     |     | 75  |     |     | 80  |     |
| Ser | His | Leu | Phe | Thr | Ser | Leu | Leu | His | Ile | Ala | Pro | Ser | Ser | Ser | Ser |
|     |     |     |     |     |     |     | 85  |     |     |     | 90  |     |     | 95  |     |
| Leu | Leu | Leu | Thr | Glu | Ala | Pro | Leu | Ser | Ile | Pro | Ser | Val | Gln | Arg | Thr |
|     |     |     |     |     |     |     | 100 |     |     |     |     |     | 110 |     |     |
| Thr | Asp | Glu | Leu | Val | Phe | Glu | Asp | Phe | Gly | Phe | Ser | Ser | Leu | Tyr | Ile |
|     |     |     |     |     |     |     | 115 |     |     |     |     |     | 125 |     |     |
| Ala | His | Pro | Gln | Ser | Leu | Val | His | Leu | Tyr | Glu | Ala | Ser | Arg | Gln | Pro |
|     |     |     |     |     |     |     | 130 |     |     |     |     |     | 140 |     |     |
| Asp | Ser | Ile | Leu | Ser | Lys | Thr | Gln | Cys | Ser | Leu | Val | Val | Asp | Cys | Gly |
|     |     |     |     |     |     |     | 145 |     |     |     |     |     | 155 |     | 160 |
| Phe | Ser | Phe | Thr | His | Ala | Val | Pro | Val | Leu | His | Asn | Phe | Thr | Leu | Asn |
|     |     |     |     |     |     |     | 165 |     |     |     |     |     | 170 |     | 175 |

His Ala Ile Lys Arg Ile Asp Leu Gly Gly Lys Ala Phe Thr Asn Tyr  
180 185 190  
Leu Lys Glu Leu Val Ser Tyr Arg Ser Ile Asn Val Met Asp Glu Thr  
195 200 205  
Phe Leu Val Asp Asp Ala Lys Glu Lys Leu Cys Phe Val Ser Leu Asp  
210 215 220  
Leu Leu Arg Asp Leu Arg Leu Ala Arg Asn Gly Asn Thr Leu Ile Lys  
225 230 235 240  
Ser Thr Tyr Val Leu Pro Asp Gly Val Thr His Thr Lys Gly Tyr Val  
245 250 255  
Lys Asp Pro Gln Ala Ala Lys Arg Phe Leu Ser Leu Ser Glu Lys Glu  
260 265 270  
Ser Val Val Val Met Asp Lys Val Gly Glu Arg Lys Lys Ala Asp Met  
275 280 285  
Asn Lys Asn Glu Ile Asp Leu Thr Asn Glu Arg Phe Leu Val Pro Glu  
290 295 300  
Thr Leu Phe Gln Pro Ala Asp Leu Gly Met Asn Gln Ala Gly Leu Ala  
305 310 315 320  
Glu Cys Ile Val Arg Ala Ile Asn Ser Cys His Ser Tyr Leu Gln Pro  
325 330 335  
Val Leu Tyr Gln Ser Ile Ile Leu Thr Gly Gly Ser Thr Leu Phe Pro  
340 345 350  
Gln Leu Lys Glu Arg Leu Glu Gly Glu Leu Arg Pro Leu Val Pro Asp  
355 360 365  
His Phe Asp Val Lys Ile Thr Thr Gln Glu Asp Pro Ile Leu Gly Val  
370 375 380  
Trp Arg Gly Gly Ser Leu Leu Ala Ser Ser Pro Asp Phe Glu Ser Met  
385 390 395 400  
Cys Val Thr Lys Ala Glu Tyr Glu Glu Leu Gly Ser Ala Arg Cys Arg  
405 410 415  
Arg Arg Phe Phe His  
420

(2) INFORMATION FOR SEQ ID NO:443:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 217 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..217
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566973

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:443:

Met Asp Glu Thr Phe Leu Val Asp Asp Ala Lys Glu Lys Leu Cys Phe  
1 5 10 15  
Val Ser Leu Asp Leu Leu Arg Asp Leu Arg Leu Ala Arg Asn Gly Asn  
20 25 30  
Thr Leu Ile Lys Ser Thr Tyr Val Leu Pro Asp Gly Val Thr His Thr  
35 40 45  
Lys Gly Tyr Val Lys Asp Pro Gln Ala Ala Lys Arg Phe Leu Ser Leu  
50 55 60  
Ser Glu Lys Glu Ser Val Val Val Met Asp Lys Val Gly Glu Arg Lys  
65 70 75 80  
Lys Ala Asp Met Asn Lys Asn Glu Ile Asp Leu Thr Asn Glu Arg Phe  
85 90 95  
Leu Val Pro Glu Thr Leu Phe Gln Pro Ala Asp Leu Gly Met Asn Gln  
100 105 110  
Ala Gly Leu Ala Glu Cys Ile Val Arg Ala Ile Asn Ser Cys His Ser  
115 120 125  
Tyr Leu Gln Pro Val Leu Tyr Gln Ser Ile Ile Leu Thr Gly Gly Ser

|                                                                 |                             |     |
|-----------------------------------------------------------------|-----------------------------|-----|
| 130                                                             | 135                         | 140 |
| Thr Leu Phe Pro Gln Leu Lys Glu Arg                             | Leu Gly Glu Leu Arg Pro     |     |
| 145                                                             | 150                         | 155 |
| Leu Val Pro Asp His Phe Asp Val Lys Ile Thr Thr Gln Glu Asp Pro |                             |     |
|                                                                 | 165                         | 170 |
| Ile Leu Gly Val Trp Arg Gly Gly Ser                             | Leu Leu Ala Ser Ser Pro Asp |     |
|                                                                 | 180                         | 185 |
| Phe Glu Ser Met Cys Val Thr Lys Ala                             | Glu Tyr Glu Glu Leu Gly Ser |     |
|                                                                 | 195                         | 200 |
| Ala Arg Cys Arg Arg Arg Phe Phe His                             |                             | 205 |
|                                                                 | 210                         | 215 |

(2) INFORMATION FOR SEQ ID NO:444:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1143 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1143
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566985

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:444:

|             |             |            |             |            |             |      |
|-------------|-------------|------------|-------------|------------|-------------|------|
| attctctagg  | cttttttata  | ttctgaaagt | tttgattttt  | tgtatcttgt | tttgtttctc  | 60   |
| aatcatcaat  | ttgtgtagt   | agctcactag | caaacatagg  | aggggaggtt | gaataatag   | 120  |
| tggaggttga  | ctgtgaatga  | gagcaaatc  | gttgaatctg  | cgttgcaatc | tgagctcaga  | 180  |
| gtcgatggtc  | gtggcccttta | tgattaccgc | aagcttacta  | tttaagtttg | caaggaatat  | 240  |
| ggcagctcac  | aagttcaact  | gggtcagact | catgtaatgg  | cttttgtgac | tgctcagcta  | 300  |
| gtacaacctt  | acaaagacag  | acctagttaa | gggtcctctc  | ctatctctac | cgagttttct  | 360  |
| ccaatggctg  | tccatcggtt  | tggagccagg | catcctgggtg | aatctgctgt | tgagcttggc  | 420  |
| cgtattatag  | acogtgcctc  | acagaaaagc | cgtgcagtag  | atacagagtc | gctttgtgtt  | 480  |
| ctagccgaaa  | agctgggtttg | gtctgtgtgc | attgatcttc  | acatttttga | caatggagggg | 540  |
| aaottgggtg  | atgctgtctaa | tgttgctgcc | ttagccgcac  | tcatgacttt | caggagacct  | 600  |
| gattgcaactg | taggagggga  | caacagtcac | gacgtgatca  | tacatccacc | cgaagaaaagg | 660  |
| Gaaccacttc  | ctttgataat  | acatcatctc | ccaatagcct  | tcacgttttg | attttttaat  | 720  |
| aaaggcagta  | tcttgggtgt  | ggaccacaat | tacgttgaag  | agactgttat | gtgtgggaga  | 780  |
| atgactgtga  | cagtcaatgc  | caatggcgat | atatgcgcaa  | tcacaaaacc | aggagaagaa  | 840  |
| ggcgtgaacc  | agagtgtaat  | ccttcattgc | ctgcgtcttg  | cttcttcaag | agcttctgca  | 900  |
| acaacaaaga  | taattagaga  | tgcagttgaa | gcatacaacc  | gtgagaggag | ctcacagaag  | 960  |
| gtggagcggc  | atcatacttt  | ggctaagtct | gaagttttgg  | gacctattgt | agttgtgtag  | 1020 |
| gaagagacat  | aaataaaaca  | tttgtctgtg | tgtctcgaatg | taataaaaga | tttagttgtg  | 1080 |
| agaatatctta | tcagcaacac  | taagctataa | aaacgtcgat  | atgatcaaga | catgttgaga  | 1140 |

(2) INFORMATION FOR SEQ ID NO:445:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 307 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..307
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566986

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:445:

|                                                                 |    |
|-----------------------------------------------------------------|----|
| Met Glu Gly Arg Leu Asn Asn Met Trp Arg Leu Thr Val Asn Glu Ser |    |
| 1                                                               | 5  |
| Lys Phe Val Glu Ser Ala Leu Gln Ser Glu Leu Arg Val Asp Gly Arg |    |
| 20                                                              | 25 |
| Gly Leu Tyr Asp Tyr Arg Lys Leu Thr Ile Lys Phe Gly Lys Glu Tyr |    |
| 35                                                              | 40 |
|                                                                 | 45 |

Gly Ser Ser Gln Val Gln Leu Gly Gln Thr His Val Met Ala Phe Val  
50 55 60  
Thr Ala Gln Leu Val Gln Pro Tyr Lys Asp Arg Pro Ser Glu Gly Ser  
65 70 75 80  
Phe Ser Ile Phe Thr Glu Phe Ser Pro Met Ala Asp Pro Ser Phe Glu  
85 90 95  
Pro Gly His Pro Gly Glu Ser Ala Val Glu Leu Gly Arg Ile Ile Asp  
100 105 110  
Arg Ala Leu Arg Glu Ser Arg Ala Val Asp Thr Glu Ser Leu Cys Val  
115 120 125  
Leu Ala Gly Lys Leu Val Trp Ser Val Arg Ile Asp Leu His Ile Leu  
130 135 140  
Asp Asn Gly Gly Asn Leu Val Asp Ala Ala Asn Val Ala Ala Leu Ala  
145 150 155 160  
Ala Leu Met Thr Phe Arg Arg Pro Asp Cys Thr Val Gly Gly Asp Asn  
165 170 175  
Ser Gln Asp Val Ile Ile His Pro Pro Glu Glu Arg Glu Pro Leu Pro  
180 185 190  
Leu Ile Ile His His Leu Pro Ile Ala Phe Thr Phe Gly Phe Phe Asn  
195 200 205  
Lys Gly Ser Ile Leu Val Met Asp Pro Thr Tyr Val Glu Glu Ala Val  
210 215 220  
Met Cys Gly Arg Met Thr Val Thr Val Asn Ala Asn Gly Asp Ile Cys  
225 230 235 240  
Ala Ile Gln Lys Pro Gly Glu Glu Gly Val Asn Gln Ser Val Ile Leu  
245 250 255  
His Cys Leu Arg Leu Ala Ser Ser Arg Ala Ser Ala Thr Thr Lys Ile  
260 265 270  
Ile Arg Asp Ala Val Glu Ala Tyr Asn Arg Glu Arg Ser Ser Gln Lys  
275 280 285  
Val Glu Arg His His Thr Leu Ala Lys Ser Glu Val Leu Gly Pro Ile  
290 295 300  
Val Val Val  
305

(2) INFORMATION FOR SEQ ID NO:446:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 300 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..300
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566987

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:446:

Met Trp Arg Leu Thr Val Asn Glu Ser Lys Phe Val Glu Ser Ala Leu  
1 5 10  
Gln Ser Glu Leu Arg Val Asp Gly Arg Gly Leu Tyr Asp Tyr Arg Lys  
20 25 30  
Leu Thr Ile Lys Phe Gly Lys Glu Tyr Gly Ser Ser Gln Val Gln Leu  
35 40 45  
Gly Gln Thr His Val Met Ala Phe Val Thr Ala Gln Leu Val Gln Pro  
50 55 60  
Tyr Lys Asp Arg Pro Ser Glu Gly Ser Phe Ser Ile Phe Thr Glu Phe  
65 70 75 80  
Ser Pro Met Ala Asp Pro Ser Phe Glu Pro Gly His Pro Gly Glu Ser  
85 90 95  
Ala Val Glu Leu Gly Arg Ile Ile Asp Arg Ala Leu Arg Glu Ser Arg  
100 105 110  
Ala Val Asp Thr Glu Ser Leu Cys Val Leu Ala Gly Lys Leu Val Trp



(2) INFORMATION FOR SEQ ID NO:447:

(A) LENGTH: 247 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

MOLECULE TYPE: peptid

(A) NAME/KEY: peptide

(B) LOCATION: 1..247

(D) OTHER INFORMATION: / Ceres Seq. ID 1566988

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:447:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Phe | Val | Thr | Ala | Gln | Leu | Val | Gln | Pro | Tyr | Lys | Asp | Arg | Pro |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ser | Glu | Gly | Ser | Phe | Ser | Ile | Phe | Thr | Glu | Phe | Ser | Pro | Met | Ala | Asp |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Pro | Ser | Phe | Glu | Pro | Gly | His | Pro | Gly | Glu | Ser | Ala | Val | Glu | Leu | Gly |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Arg | Ile | Ile | Asp | Arg | Ala | Leu | Arg | Glu | Ser | Arg | Ala | Val | Asp | Thr | Glu |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ser | Leu | Cys | Val | Leu | Ala | Gly | Lys | Leu | Val | Trp | Ser | Val | Arg | Ile | Asp |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Leu | His | Ile | Leu | Asp | Asn | Gly | Gly | Asn | Leu | Val | Asp | Ala | Ala | Asn | Val |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Ala | Ala | Leu | Ala | Ala | Leu | Met | Thr | Phe | Arg | Arg | Pro | Asp | Cys | Thr | Val |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Gly | Gly | Asp | Asn | Ser | Gln | Asp | Val | Ile | Ile | His | Pro | Pro | Glu | Glu | Arg |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Glu | Pro | Leu | Pro | Leu | Ile | Ile | His | His | Leu | Pro | Ile | Ala | Phe | Thr | Phe |
|     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Gly | Phe | Phe | Asn | Lys | Gly | Ser | Ile | Leu | Val | Met | Asp | Pro | Thr | Tyr | Val |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |     |
| Glu | Glu | Ala | Val | Met | Cys | Gly | Arg | Met | Thr | Val | Thr | Val | Asn | Ala | Asn |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Gly | Asp | Ile | Cys | Ala | Ile | Gln | Lys | Pro | Gly | Glu | Glu | Gly | Val | Asn | Gln |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Ser | Val | Ile | Leu | His | Cys | Leu | Arg | Leu | Ala | Ser | Ser | Arg | Ala | Ser | Ala |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Thr | Lys | Ile | Ile | Arg | Asp | Ala | Val | Glu | Ala | Tyr | Asn | Arg | Glu | Arg |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Ser | Ser | Gln | Lys | Val | Glu | Arg | His | His | Thr | Leu | Ala | Lys | Ser | Glu | Val |
|     | 225 |     |     |     | 230 |     |     |     |     | 235 |     |     |     | 240 |     |
| Leu | Gly | Pro | Ile | Val | Val | Val |     |     |     |     |     |     |     |     |     |
|     |     |     |     | 245 |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:448:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1130 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1130
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566989

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:448:

|             |             |            |            |            |             |      |
|-------------|-------------|------------|------------|------------|-------------|------|
| attttttctcc | taccgtcgaa  | ctaaatccta | gggcacaggt | gaaatcgccg | agtgacgtct  | 60   |
| agccaccgca  | cgcctctctt  | ctccggttat | ctcgtacta  | atcagactat | tcacacagcta | 120  |
| tgctcacaggt | agacagcaga  | aattcatcag | cagccaagcg | tgctagaact | gacggggggc  | 180  |
| gtagagaaga  | tgattggatc  | tgcccaagtt | gtggcaatgt | caacttttca | ttcaggacaa  | 240  |
| cttgcaaat   | gcgttaattgc | actcagccta | gacctgcaga | tcataatgga | aagtcctgctc | 300  |
| ccaaacctat  | gcaacatcaa  | caaggtttct | catcaccccg | ggcatactta | ggatctgggg  | 360  |
| gtccccctcc  | agtatatatg  | ggcgggtcac | catatggatc | tcctctcttt | aatggatcgt  | 420  |
| ctatgcctcc  | tatgaagctg  | ccattttctg | gggggtcgcc | ttaccatttt | aactataata  | 480  |
| gcgaatgcc   | tgccggagct  | cattacagac | cattacatat | gtctggacca | ccaccatacc  | 540  |
| atggcggtac  | tatgatggga  | atgggtggta | tgatgggaat | gcctccacca | atagacaggt  | 600  |
| atggccttgg  | tatggcaatg  | ggctctggtt | ctgcgcgtcg | catgatgcca | agaccaaggt  | 660  |
| tttaccaga   | tgaaaaatca  | caaaagagag | attcaactcg | cgataatgat | tggtcatgtc  | 720  |
| cgaatttggt  | taattgtaaac | ttctcattca | gaactgtatg | taacatgagg | aagtgcacaa  | 780  |
| ctccaaagcc  | tggttctcag  | cagggtggaa | gctcagataa | aatatccaaa | caaaatgcac  | 840  |
| cggaaggag   | ctggaagtgt  | gataactgtg | gaaatataaa | ctaccatttc | aggagcaaat  | 900  |
| gcaacaggca  | aaactgtgga  | gctgataagc | ctggggatcg | gtcgaatgga | tctccgtccc  | 960  |
| gtgcaccaga  | agagaacgat  | caggtttgta | agatgtatct | atgtggtcac | aactgtttgt  | 1020 |
| taataaaatg  | tttgctctg   | aaactcgtaa | atgtaacaac | ctgtgtagat | tttatgcctt  | 1080 |
| gtgaaagcag  | aggttatatg  | tttatgaaaa | aattgactcc | gaTcactgtt |             |      |

(2) INFORMATION FOR SEQ ID NO:449:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 337 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..337
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566990

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:449:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ser | Gln | Val | Asp | Ser | Arg | Asn | Ser | Ser | Ala | Ala | Lys | Arg | Ala | Arg |
|     |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Thr | Asp | Gly | Gly | Arg | Arg | Glu | Asp | Asp | Trp | Ile | Cys | Pro | Ser | Cys | Gly |
|     |     |     |     | 20  |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Asn | Val | Asn | Phe | Ser | Phe | Arg | Thr | Thr | Cys | Asn | Met | Arg | Asn | Cys | Thr |
|     |     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |
| Gln | Pro | Arg | Pro | Ala | Asp | His | Asn | Gly | Lys | Ser | Ala | Pro | Lys | Pro | Met |
|     |     |     |     | 50  |     |     | 55  |     |     |     | 60  |     |     |     |     |
| Gln | His | Gln | Gln | Gly | Phe | Ser | Ser | Pro | Gly | Ala | Tyr | Leu | Gly | Ser | Gly |
|     |     |     |     | 65  |     |     | 70  |     |     | 75  |     |     |     | 80  |     |
| Gly | Pro | Pro | Pro | Gly | Tyr | Met | Gly | Gly | Ser | Pro | Tyr | Gly | Ser | Pro | Leu |
|     |     |     |     | 85  |     |     | 90  |     |     |     |     |     |     | 95  |     |

Phe Asn Gly Ser Ser Met Pro Pro Tyr Asp Val Pro Phe Ser Gly Gly  
100 105 110  
Ser Pro Tyr His Phe Asn Tyr Asn Ser Arg Met Pro Ala Gly Ala His  
115 120 125  
Tyr Arg Pro Leu His Met Ser Gly Pro Pro Pro Tyr His Gly Gly Ser  
130 135 140  
Met Met Gly Ser Gly Gly Met Tyr Gly Met Pro Pro Ile Asp Arg  
145 150 155 160  
Tyr Gly Leu Gly Met Ala Met Gly Pro Gly Ser Ala Ala Ala Met Met  
165 170 175  
Pro Arg Pro Arg Phe Tyr Pro Asp Glu Lys Ser Gln Lys Arg Asp Ser  
180 185 190  
Thr Arg Asp Asn Asp Trp Thr Cys Pro Asn Cys Gly Asn Val Asn Phe  
195 200 205  
Ser Phe Arg Thr Val Cys Asn Met Arg Lys Cys Asn Thr Pro Lys Pro  
210 215 220  
Gly Ser Gln Gln Gly Gly Ser Ser Asp Lys Ile Ser Lys Gln Asn Ala  
225 230 235 240  
Pro Glu Gly Ser Trp Lys Cys Asp Asn Cys Gly Asn Ile Asn Tyr Pro  
245 250 255  
Phe Arg Ser Lys Cys Asn Arg Gln Asn Cys Gly Ala Asp Lys Pro Gly  
260 265 270  
Asp Arg Ser Asn Gly Ser Pro Ser Arg Ala Pro Glu Glu Asn Asp Gln  
275 280 285  
Val Cys Lys Met Tyr Leu Cys Gly His Asn Cys Leu Leu Ile Lys Cys  
290 295 300  
Leu Pro Leu Lys Leu Val Asn Val Thr Thr Cys Val Asp Phe Met Pro  
305 310 315 320  
Cys Glu Ser Arg Gly Tyr Met Phe Met Lys Lys Leu Thr Pro Thr Thr  
325 330 335  
Phe

(2) INFORMATION FOR SEQ ID NO:450:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 294 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..294

(D) OTHER INFORMATION: / Ceres Seq. ID 1566991

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:450:

Met Arg Asn Cys Thr Gln Pro Arg Pro Ala Asp His Asn Gly Lys Ser  
1 5 10 15  
Ala Pro Lys Pro Met Gln His Gln Gly Phe Ser Ser Pro Gly Ala  
20 25 30  
Tyr Leu Gly Ser Gly Gly Pro Pro Val Tyr Met Gly Gly Ser Pro  
35 40 45  
Tyr Gly Ser Pro Leu Phe Asn Gly Ser Ser Met Pro Pro Tyr Asp Val  
50 55 60  
Pro Phe Ser Gly Gly Ser Pro Tyr His Phe Asn Tyr Asn Ser Arg Met  
65 70 75 80  
Pro Ala Gly Ala His Tyr Arg Pro Leu His Met Ser Gly Pro Pro Pro  
85 90 95  
Tyr His Gly Gly Ser Met Met Gly Ser Gly Gly Met Tyr Gly Met Pro  
100 105 110  
Pro Pro Ile Asp Arg Tyr Gly Leu Gly Met Ala Met Gly Pro Gly Ser  
115 120 125  
Ala Ala Ala Met Met Pro Arg Pro Arg Phe Tyr Pro Asp Glu Lys Ser

130 135 140  
Gln Lys Arg Asp Ser Thr Arg Asp Asn Asp Trp Thr Cys Pro Asn Cys  
145 150 155 160  
Gly Asn Val Asn Phe Ser Phe Arg Thr Val Cys Asn Met Arg Lys Cys  
165 170 175  
Asn Thr Pro Lys Pro Gly Ser Gln Gln Gly Gly Ser Ser Asp Lys Ile  
180 185 190  
Ser Lys Gln Asn Ala Pro Glu Gly Ser Trp Lys Cys Asp Asn Cys Gly  
195 200 205  
Asn Ile Asn Tyr Pro Phe Arg Ser Lys Cys Asn Arg Gln Asn Cys Gly  
210 215 220  
Ala Asp Lys Pro Gly Asp Arg Ser Asn Gly Ser Pro Ser Arg Ala Pro  
225 230 235 240  
Glu Glu Asn Asp Gln Val Cys Lys Met Tyr Leu Cys Gly His Asn Cys  
245 250 255  
Leu Leu Ile Lys Cys Leu Pro Leu Lys Leu Val Asn Val Thr Thr Cys  
260 265 270  
Val Asp Phe Met Pro Cys Glu Ser Arg Gly Tyr Met Phe Met Lys Lys  
275 280 285  
Leu Thr Pro Thr Thr Phe  
290

(2) INFORMATION FOR SEQ ID NO:451:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 274 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..274

(D) OTHER INFORMATION: / Ceres Seq. ID 1566992

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:451:

Met Gln His Gln Gln Gly Phe Ser Ser Pro Gly Ala Tyr Leu Gly Ser  
1 5 10 15  
Gly Gly Pro Pro Pro Val Tyr Met Gly Gly Ser Pro Tyr Gly Ser Pro  
20 25 30  
Leu Phe Asn Gly Ser Ser Met Pro Pro Tyr Asp Val Pro Phe Ser Gly  
35 40 45  
Gly Ser Pro Tyr His Phe Asn Tyr Asn Ser Arg Met Pro Ala Gly Ala  
50 55 60  
His Tyr Arg Pro Leu His Met Ser Gly Pro Pro Tyr His Gly Gly  
65 70 75 80  
Ser Met Met Gly Ser Gly Gly Met Tyr Gly Met Pro Pro Pro Ile Asp  
85 90 95  
Arg Tyr Gly Leu Gly Met Ala Met Gly Pro Gly Ser Ala Ala Ala Met  
100 105 110  
Met Pro Arg Pro Arg Phe Tyr Pro Asp Glu Lys Ser Gln Lys Arg Asp  
115 120 125  
Ser Thr Arg Asp Asn Asp Trp Thr Cys Pro Asn Cys Gly Asn Val Asn  
130 135 140  
Phe Ser Phe Arg Thr Val Cys Asn Met Arg Lys Cys Asn Thr Pro Lys  
145 150 155 160  
Pro Gly Ser Gln Gln Gly Gly Ser Ser Asp Lys Ile Ser Lys Gln Asn  
165 170 175  
Ala Pro Glu Gly Ser Trp Lys Cys Asp Asn Cys Gly Asn Ile Asn Tyr  
180 185 190  
Pro Phe Arg Ser Lys Cys Asn Arg Gln Asn Cys Gly Ala Asp Lys Pro  
195 200 205  
Gly Asp Arg Ser Asn Gly Ser Pro Ser Arg Ala Pro Glu Glu Asn Asp  
210 215 220

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Gln Val Cys Lys Met Tyr Leu Cys Gly His Asn Cys Leu Leu Ile Lys  
225 230 235 240  
Cys Leu Pro Leu Lys Leu Val Asn Val Thr Thr Cys Val Asp Phe Met  
245 250 255  
Pro Cys Glu Ser Arg Gly Tyr Met Phe Met Lys Lys Leu Thr Pro Thr  
260 265 270  
Thr Phe

(2) INFORMATION FOR SEQ ID NO:452:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1717 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1717

(D) OTHER INFORMATION: / Ceres Seq. ID 1566993

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:452:

|             |             |            |             |             |             |      |
|-------------|-------------|------------|-------------|-------------|-------------|------|
| aaaaaaggct  | tctctgtgtt  | gttctctgtg | tgttctctgt  | tggtcattct  | tctttctttt  | 60   |
| cacttctctt  | tcttcttcgc  | tcttctcttc | actgtcgggt  | tcoattttgc  | gcgaaaagtt  | 120  |
| cttcaacttt  | tccagctttt  | ttttgttctc | tgacagtttt  | ttttttgttt  | ggtacaaaat  | 180  |
| aaagatgcca  | gtaagtgtgg  | cactagtttt | gctgttgaca  | ttgagcagtg  | taattctgat  | 240  |
| taatgggaga  | agttacggcg  | tcggaaacat | atgcgatcgt  | ggtcggagaC  | cgagcggag   | 300  |
| accacacagt  | gtcaaaatca  | ctgatttttg | tgctgtggga  | gatgggaaaa  | cggtgaacac  | 360  |
| acttgcgttt  | caaaatgctg  | tcttttatct | aaagtctttc  | gctgataaag  | gtggtgtctc  | 420  |
| gctttatgtt  | cctccgggac  | Ggtggctcac | cggaagtttc  | aacctcacca  | gtcatctcac  | 480  |
| tctcttcttc  | gagaaagacg  | ccgtcatact | tgcttcacag  | gatccatcgc  | attggcaagt  | 540  |
| cacggatgcc  | ttaccgtcat  | atgggcgggg | tattgatcta  | ccagggaaga  | gatacatgat  | 600  |
| tttgataaac  | ggtagacatg  | tacatgatgt | agtagtaaca  | ggtagataac  | gtaccataga  | 660  |
| tgggcaaggc  | cttgttttgt  | gggactgggt | taattctcat  | tctttagagt  | acagtcgccc  | 720  |
| tcaacttctc  | gagtttgtct  | ctgcgcaaaa | tgtcattgta  | tcaaatctta  | cattcttgaa  | 780  |
| tgctccggct  | tatactatcc  | attcgtttta | ttgtcgcaat  | ttatatactc  | atagagtaac  | 840  |
| ggctaatact  | tgtccaagaat | ctccttatac | catcggattt  | gtccagagatt | cttctgaaaa  | 900  |
| tgtgtgtatc  | caagaatcta  | gtatcaacat | ggggatgatg  | gccattttct  | ttaaaaagtg  | 960  |
| tgtggatgaa  | tacggtttat  | cgtagtcaa  | acctactgct  | aatgtccaga  | taagaaatgt  | 1020 |
| ttacccttaga | gcagcttctg  | gttcctccat | ttccttttgt  | agtgaatagt  | ctggttggtat | 1080 |
| atctgatgtt  | gaggtcagtg  | atgctcacat | acacaactcg  | ttatccggga  | ttgcctttag  | 1140 |
| aaacacaaat  | ggaagatgtg  | gttatattaa | ggagattgat  | atttccaaac  | tccatattgt  | 1200 |
| taagtgttgt  | actgcatttc  | tagccaacgc | tagcttcggt  | actcatccgg  | atttctgttt  | 1260 |
| cgatgaaagt  | gcttaccocg  | ttgtgagtca | catcagggtta | catgacattg  | ttggagaaaa  | 1320 |
| cataagcact  | gctggaattt  | tctttggaac | gaagagtgct  | ctttcaactt  | cgatttttgt  | 1380 |
| atcgaaatca  | tctctgtcga  | ttaaaaactc | ggcttctcct  | gctgattctt  | ggcaagtcct  | 1440 |
| atattgtgac  | gggtcttcgg  | aattcgtagt | ccctgaacgc  | tgcttgagtc  | tgaagagttt  | 1500 |
| tgatagttac  | tatggttagag | ctgaggccct | atgaaaccaa  | acttcattag  | gaatgatgat  | 1560 |
| tcatattttg  | ttaaagagaga | gcaaatgggt | ctgattcttt  | tctttccccc  | aaaaataaac  | 1620 |
| cacagttgtg  | agaattattta | cctgttcctt | gttggtgttg  | ttgtccctgt  | tatttgacag  | 1680 |
| ttgtgagatt  | aatatattct  | gtacagggtc | atttctt     |             |             |      |

(2) INFORMATION FOR SEQ ID NO:453:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 510 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..510

(D) OTHER INFORMATION: / Ceres Seq. ID 1566994

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:453:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Lys | Lys | Ala | Ser | Leu | Cys | Cys | Ser | Leu | Cys | Cys | Ser | Leu | Trp | Ser | Phe |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Phe | Phe | Leu | Phe | Thr | Ser | Ser | Ser | Ser | Ser | Leu | Phe | Phe | Ser | Leu | Ser |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Gly | Ser | Ile | Trp | Arg | Glu | Lys | Phe | Phe | Thr | Phe | Ser | Ser | Phe | Phe | Leu |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     |     | 45  |     |     |
| Phe | Ser | Asp | Ser | Phe | Phe | Phe | Val | Trp | Leu | Gln | Ile | Lys | Met | Pro | Val |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Ser | Val | Ala | Leu | Val | Leu | Leu | Leu | Thr | Leu | Ser | Ser | Val | Ile | Leu | Ile |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Asn | Gly | Arg | Ser | Tyr | Gly | Val | Gly | Asn | Ile | Cys | Asp | Arg | Gly | Arg | Arg |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Pro | Ser | Glu | Arg | Pro | His | Ser | Val | Lys | Ile | Thr | Asp | Phe | Gly | Ala | Val |
|     |     |     |     | 100 |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Gly | Asp | Gly | Lys | Thr | Leu | Asn | Thr | Leu | Ala | Phe | Gln | Asn | Ala | Val | Phe |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Tyr | Leu | Lys | Ser | Phe | Ala | Asp | Lys | Gly | Gly | Ala | Gln | Leu | Tyr | Val | Pro |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Pro | Gly | Arg | Trp | Leu | Thr | Gly | Ser | Phe | Asn | Leu | Thr | Ser | His | Leu | Thr |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |     |
| Leu | Phe | Leu | Glu | Lys | Asp | Ala | Val | Ile | Leu | Ala | Ser | Gln | Asp | Pro | Ser |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| His | Trp | Gln | Val | Thr | Asp | Ala | Leu | Pro | Ser | Tyr | Gly | Arg | Gly | Ile | Asp |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Leu | Pro | Gly | Lys | Arg | Tyr | Met | Ser | Leu | Ile | Asn | Gly | Asp | Met | Leu | His |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Asp | Val | Val | Val | Thr | Gly | Asp | Asn | Gly | Thr | Ile | Asp | Gly | Gln | Gly | Leu |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Val | Trp | Trp | Asp | Arg | Phe | Asn | Ser | His | Ser | Leu | Glu | Tyr | Ser | Arg | Pro |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     | 240 |     |
| His | Leu | Val | Glu | Phe | Val | Ser | Ala | Glu | Asn | Val | Ile | Val | Ser | Asn | Leu |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Thr | Phe | Leu | Asn | Ala | Pro | Ala | Tyr | Thr | Ile | His | Ser | Val | Tyr | Cys | Arg |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Asn | Leu | Tyr | Ile | His | Arg | Val | Thr | Ala | Asn | Thr | Cys | Pro | Glu | Ser | Pro |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Tyr | Thr | Ile | Gly | Ile | Val | Pro | Asp | Ser | Ser | Glu | Asn | Val | Cys | Ile | Gln |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Glu | Ser | Ser | Ile | Asn | Met | Gly | Tyr | Asp | Ala | Ile | Ser | Leu | Lys | Ser | Gly |
|     |     |     |     | 310 |     |     |     |     |     | 315 |     |     |     | 320 |     |
| Trp | Asp | Glu | Tyr | Gly | Leu | Ser | Tyr | Ala | Arg | Pro | Thr | Ala | Asn | Val | Gln |
|     |     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |     |
| Ile | Arg | Asn | Val | Tyr | Leu | Arg | Ala | Ala | Ser | Gly | Ser | Ser | Ile | Ser | Phe |
|     |     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |
| Gly | Ser | Glu | Met | Ser | Gly | Gly | Ile | Ser | Asp | Val | Glu | Val | Ser | Asp | Ala |
|     |     | 355 |     |     |     |     | 360 |     |     |     |     | 365 |     |     |     |
| His | Ile | His | Asn | Ser | Leu | Ser | Gly | Ile | Ala | Phe | Arg | Thr | Thr | Asn | Gly |
|     |     | 370 |     |     |     | 375 |     |     |     |     | 380 |     |     |     |     |
| Arg | Cys | Gly | Tyr | Ile | Lys | Glu | Ile | Asp | Ile | Ser | Asn | Ile | His | Met | Val |
| 385 |     |     |     |     | 390 |     |     |     |     | 395 |     |     |     | 400 |     |
| Asn | Val | Gly | Thr | Ala | Phe | Leu | Ala | Asn | Gly | Ser | Phe | Gly | Thr | His | Pro |
|     |     |     |     | 405 |     |     |     |     | 410 |     |     |     |     | 415 |     |
| Asp | Ser | Gly | Phe | Asp | Glu | Asn | Ala | Tyr | Pro | Leu | Val | Ser | His | Ile | Arg |
|     |     |     | 420 |     |     |     |     | 425 |     |     |     |     | 430 |     |     |
| Leu | His | Asp | Ile | Val | Gly | Glu | Asn | Ile | Ser | Thr | Ala | Gly | Tyr | Phe | Phe |
|     |     | 435 |     |     |     |     | 440 |     |     |     |     |     | 445 |     |     |
| Gly | Thr | Lys | Glu | Ser | Pro | Phe | Thr | Ser | Ile | Leu | Leu | Ser | Asn | Ile | Ser |
|     | 450 |     |     |     |     | 455 |     |     |     |     | 460 |     |     |     |     |
| Leu | Ser | Ile | Lys | Asn | Ser | Ala | Ser | Pro | Ala | Asp | Ser | Trp | Gln | Cys | Ser |
| 465 |     |     |     |     | 470 |     |     |     |     | 475 |     |     |     | 480 |     |
| Tyr | Val | Asp | Gly | Ser | Ser | Glu | Phe | Val | Val | Pro | Glu | Pro | Cys | Leu | Glu |

(2) INFORMATION FOR SEQ ID NO:454:

(1) SEQUENCE CHARACTERISTICS:

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:454:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Pro | Val | Ser | 5   | Ala | Leu | Val | Leu | Leu | Leu | Thr | Leu | Ser | Ser | Val |     |
| 1   | Ile | Leu | Ile | Asn | Gly | Arg | Ser | Tyr | Gly | Val | Gly | Asn | Ile | Cys | Asp | Arg |
|     |     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Gly | Arg | Arg | Pro | Ser | Glu | Arg | Pro | His | Ser | Val | Lys | Ile | Thr | Asp | Phe |     |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| Gly | Ala | Val | Gly | Asp | Gly | Lys | Thr | Leu | Asn | Thr | Leu | Ala | Phe | Gln | Asn |     |
|     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |
| Ala | Val | Phe | Tyr | Leu | Lys | Ser | Phe | Ala | Asp | Lys | Gly | Gly | Ala | Gln | Leu |     |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Tyr | Val | Pro | Pro | Gly | Arg | Trp | Leu | Thr | Gly | Ser | Phe | Asn | Leu | Thr | Ser |     |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| His | Leu | Thr | Leu | Phe | Leu | Glu | Lys | Asp | Ala | Val | Ile | Leu | Ala | Ser | Gln |     |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |     |
| Asp | Pro | Ser | His | Trp | Gln | Val | Thr | Asp | Ala | Leu | Pro | Ser | Tyr | Gly | Arg |     |
|     |     |     | 115 |     |     |     |     | 120 |     |     |     | 125 |     |     |     |     |
| Gly | Ile | Asp | Leu | Pro | Gly | Lys | Arg | Tyr | Met | Ser | Leu | Ile | Asn | Gly | Asp |     |
|     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |     |
| Met | Leu | His | Asp | Val | Val | Val | Thr | Gly | Asp | Asn | Gly | Thr | Ile | Asp | Gly | 160 |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     |     |     |
| Gln | Gly | Leu | Val | Trp | Trp | Asp | Arg | Phe | Asn | Ser | His | Ser | Leu | Glu | Tyr |     |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |     |
| Ser | Arg | Pro | His | Leu | Val | Glu | Phe | Val | Ser | Ala | Glu | Asn | Val | Ile | Val |     |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |     |
| Ser | Asn | Leu | Thr | Phe | Leu | Asn | Ala | Pro | Ala | Tyr | Thr | Ile | His | Ser | Val |     |
|     |     |     | 195 |     |     |     | 200 |     |     |     |     | 205 |     |     |     |     |
| Tyr | Cys | Arg | Asn | Leu | Tyr | Ile | His | Arg | Val | Thr | Ala | Asn | Thr | Cys | Pro |     |
|     |     |     | 210 |     |     | 215 |     |     |     |     | 220 |     |     |     |     |     |
| Glu | Ser | Pro | Tyr | Thr | Ile | Gly | Ile | Val | Pro | Asp | Ser | Ser | Glu | Asn | Val |     |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |     |
| Cys | Ile | Gln | Glu | Ser | Ser | Ile | Asn | Met | Gly | Tyr | Asp | Ala | Ile | Ser | Leu |     |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     | 255 |     |     |     |
| Lys | Ser | Gly | Trp | Asp | Glu | Tyr | Gly | Leu | Ser | Tyr | Ala | Arg | Pro | Thr | Ala |     |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |     |
| Asn | Val | Gln | Ile | Arg | Asn | Val | Tyr | Leu | Arg | Ala | Ala | Ser | Gly | Ser | Ser |     |
|     |     |     | 275 |     |     |     | 280 |     |     |     |     | 285 |     |     |     |     |
| Ile | Ser | Phe | Gly | Ser | Glu | Met | Ser | Gly | Gly | Ile | Ser | Asp | Val | Glu | Val |     |
|     |     |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |     |
| Ser | Asp | Ala | His | Ile | His | Asn | Ser | Leu | Ser | Gly | Ile | Ala | Phe | Arg | Thr |     |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |     |
| Thr | Asn | Gly | Arg | Cys | Gly | Tyr | Ile | Lys | Glu | Ile | Asp | Ile | Ser | Asn | Ile |     |
|     |     |     |     | 325 |     |     |     |     | 330 |     |     |     | </  |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| His | Ile | Arg | Leu | His | Asp | Ile | Val | Gly | Glu | Asn | Ile | Ser | Thr | Ala | Gly |  |
|     | 370 |     |     |     | 375 |     |     |     |     | 380 |     |     |     |     |     |  |
| Tyr | Phe | Phe | Gly | Thr | Lys | Glu | Ser | Pro | Phe | Thr | Ser | Ile | Leu | Leu | Ser |  |
|     | 385 |     |     |     | 390 |     |     |     |     | 395 |     |     |     |     | 400 |  |
| Asn | Ile | Ser | Leu | Ser | Ile | Lys | Asn | Ser | Ala | Ser | Pro | Ala | Asp | Ser | Trp |  |
|     |     |     | 405 |     |     |     |     |     | 410 |     |     |     |     |     | 415 |  |
| Gln | Cys | Ser | Tyr | Val | Asp | Gly | Ser | Ser | Glu | Phe | Val | Val | Pro | Glu | Pro |  |
|     |     |     | 420 |     |     |     |     |     | 425 |     |     |     |     |     | 430 |  |
| Cys | Leu | Glu | Leu | Lys | Ser | Phe | Asp | Ser | Tyr | Tyr | Gly | Arg | Ala | Glu | Ala |  |
|     |     | 435 |     |     |     |     | 440 |     |     |     |     |     |     |     | 445 |  |
| Leu |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:455:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 312 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..312
- (D) OTHER INFORMATION: / Ceres Seq. ID 1566996

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:455:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ser | Leu | Ile | Asn | Gly | Asp | Met | Leu | His | Asp | Val | Val | Thr | Gly |     |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Asp | Asn | Gly | Thr | Ile | Asp | Gly | Gln | Gly | Leu | Val | Trp | Trp | Asp | Arg | Phe |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Asn | Ser | His | Ser | Leu | Glu | Tyr | Ser | Arg | Pro | His | Leu | Val | Glu | Phe | Val |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |
| Ser | Ala | Glu | Asn | Val | Ile | Val | Ser | Asn | Leu | Thr | Phe | Leu | Asn | Ala | Pro |
|     |     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |
| Ala | Tyr | Thr | Ile | His | Ser | Val | Tyr | Cys | Arg | Asn | Leu | Tyr | Ile | His | Arg |
|     |     |     | 65  |     |     |     | 70  |     |     |     | 75  |     |     |     | 80  |
| Val | Thr | Ala | Asn | Thr | Cys | Pro | Glu | Ser | Pro | Tyr | Thr | Ile | Gly | Ile | Val |
|     |     |     |     | 85  |     |     |     |     |     | 90  |     |     |     | 95  |     |
| Pro | Asp | Ser | Ser | Glu | Asn | Val | Cys | Ile | Gln | Glu | Ser | Ser | Ile | Asn | Met |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     |     | 110 |     |
| Gly | Tyr | Asp | Ala | Ile | Ser | Leu | Lys | Ser | Gly | Trp | Asp | Glu | Tyr | Gly | Leu |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     |     | 125 |     |     |
| Ser | Tyr | Ala | Arg | Pro | Thr | Ala | Asn | Val | Gln | Ile | Arg | Asn | Val | Tyr | Leu |
|     |     |     | 130 |     |     |     | 135 |     |     |     | 140 |     |     |     |     |
| Arg | Ala | Ala | Ser | Gly | Ser | Ser | Ile | Ser | Phe | Gly | Ser | Glu | Met | Ser | Gly |
|     |     |     |     | 145 |     |     | 150 |     |     | 155 |     |     |     |     | 160 |
| Gly | Ile | Ser | Asp | Val | Glu | Val | Ser | Asp | Ala | His | Ile | His | Asn | Ser | Leu |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Ser | Gly | Ile | Ala | Phe | Arg | Thr | Thr | Asn | Gly | Arg | Cys | Gly | Tyr | Ile | Lys |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     |     | 190 |     |
| Glu | Ile | Asp | Ile | Ser | Asn | Ile | His | Met | Val | Asn | Val | Gly | Thr | Ala | Phe |
|     |     |     | 195 |     |     |     | 200 |     |     |     |     |     | 205 |     |     |
| Leu | Ala | Asn | Gly | Ser | Phe | Gly | Thr | His | Pro | Asp | Ser | Gly | Phe | Asp | Glu |
|     |     |     | 210 |     |     |     | 215 |     |     |     |     |     | 220 |     |     |
| Asn | Ala | Tyr | Pro | Leu | Val | Ser | His | Ile | Arg | Leu | His | Asp | Ile | Val | Gly |
|     |     |     | 225 |     |     |     | 230 |     |     |     | 235 |     |     |     | 240 |
| Glu | Asn | Ile | Ser | Thr | Ala | Gly | Tyr | Phe | Phe | Gly | Thr | Lys | Glu | Ser | Pro |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Phe | Thr | Ser | Ile | Leu | Leu | Ser | Asn | Ile | Ser | Leu | Ser | Ile | Lys | Asn | Ser |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     |     | 270 |     |
| Ala | Ser | Pro | Ala | Asp | Ser | Trp | Gln | Cys | Ser | Tyr | Val | Asp | Gly | Ser | Ser |
|     |     |     | 275 |     |     |     | 280 |     |     |     |     |     | 285 |     |     |
| Glu | Phe | Val | Val | Pro | Glu | Pro | Cys | Leu | Glu | Leu | Lys | Ser | Phe | Asp | Ser |



290  
Tyr Tyr Gly Arg Ala Glu Ala Leu  
305 310

295

300

(2) INFORMATION FOR SEQ ID NO:456:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 719 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..719  
(D) OTHER INFORMATION: / Ceres Seq. ID 1567007

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:456:

|             |            |             |             |            |             |     |
|-------------|------------|-------------|-------------|------------|-------------|-----|
| cttttcgcgt  | ggtcgaccaa | acctaaaaacc | ccccaaaaaga | gaaaaatcaa | agaccattcg  | 60  |
| ctatttcgct  | cgctactcag | ttgcagaaga  | agatgccgac  | actcacaaag | ctttattcca  | 120 |
| tggaagaagc  | cgcaactcac | aacaagcaag  | atgactgctg  | ggctgctatc | gacggcaagg  | 180 |
| tctatgatgt  | atcctcttat | atggatgagc  | atcctggagg  | agatgatgtg | cttcttgctg  | 240 |
| tcgcaggcaa  | agatgcaacg | gatgattttg  | aagacgcagg  | gcacagcaaa | gatgctaggg  | 300 |
| aacttatgga  | gaagtatttt | attggcgagc  | tagatgaatc  | ttctttaccg | gaaataacctg | 360 |
| agcttaagat  | ctacaagaag | gaccagccac  | aagactctgt  | tcagaagcgt | tttgacttga  | 420 |
| caaacgcagta | ttggggtggt | cctgtctcca  | ttatcccat   | ctctgtagcg | gttagtgtct  | 480 |
| tgttctctcg  | caagacttaa | taagttagtag | tctcttctct  | accttgatat | gctctgggat  | 540 |
| attgaattac  | ttggggaatc | aactttacac  | ccccattata  | gattttttga | ataacagata  | 600 |
| tgatagagag  | ataattgtta | tttttcatt   | ttatcagatt  | ttgagtttag | atcatgtttc  | 660 |
| ataacactta  | ttactcgata | tgattatatc  | atgattaatg  | gatggtttgg | tttgctggcg  |     |

(2) INFORMATION FOR SEQ ID NO:457:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 110 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..110  
(D) OTHER INFORMATION: / Ceres Seq. ID 1567008

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:457:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Leu | Phe | Ala | Trp | Ser | Thr | Lys | Pro | Lys | Thr | Pro | Lys | Lys | Arg | Lys | Ile |  |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |  |
| Lys | Asp | His | Ser | Leu | Phe | Arg | Ser | Leu | Leu | Ser | Cys | Arg | Arg | Arg | Cys |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Arg | His | Ser | Gln | Ser | Phe | Ile | Pro | Trp | Lys | Lys | Pro | Gln | Leu | Thr | Thr |  |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Ser | Lys | Met | Thr | Ala | Gly | Ser | Ser | Ser | Thr | Ala | Arg | Ser | Met | Met | Tyr |  |
|     |     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |  |
| Pro | Leu | Ile | Trp | Met | Ser | Ile | Leu | Glu | Glu | Met | Met | Cys | Phe | Leu | Leu |  |
|     |     |     | 65  |     |     |     | 70  |     |     | 75  |     |     |     | 80  |     |  |
| Ser | Gln | Ala | Lys | Met | Gln | Arg | Met | Ile | Leu | Lys | Thr | Gln | Gly | Thr | Ala |  |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |  |
| Lys | Met | Leu | Gly | Asn | Leu | Trp | Arg | Ser | Ile | Leu | Leu | Ala | Ser |     |     |  |
|     |     |     | 100 |     |     |     | 105 |     |     |     |     | 110 |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:458:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 135 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..135  
(D) OTHER INFORMATION: / Ceres Seq. ID 1567009

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:458:

Met Pro Thr Leu Thr Lys Leu Tyr Ser Met Glu Glu Ala Ala Thr His  
1 5 10 15  
Asn Lys Gln Asp Asp Cys Trp Val Val Ile Asp Gly Lys Val Tyr Asp  
20 25 30  
Val Ser Ser Tyr Met Asp Glu His Pro Gly Gly Asp Asp Val Leu Leu  
35 40 45  
Ala Val Ala Gly Lys Asp Ala Thr Asp Asp Phe Glu Asp Ala Gly His  
50 55 60  
Ser Lys Asp Ala Arg Glu Leu Met Glu Lys Tyr Phe Ile Gly Glu Leu  
65 70 75 80  
Asp Glu Ser Ser Leu Pro Glu Ile Pro Glu Leu Lys Ile Tyr Lys Lys  
85 90 95  
Asp Gln Pro Gln Asp Ser Val Gln Lys Leu Phe Asp Leu Thr Lys Gln  
100 105 110  
Tyr Trp Val Val Pro Val Ser Ile Ile Thr Ile Ser Val Ala Val Ser  
115 120 125  
Val Leu Phe Ser Arg Lys Thr  
130 135

(2) INFORMATION FOR SEQ ID NO:459:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 126 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..126  
(D) OTHER INFORMATION: / Ceres Seq. ID 1567010

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:459:

Met Glu Glu Ala Ala Thr His Asn Lys Gln Asp Asp Cys Trp Val Val  
1 5 10 15  
Ile Asp Gly Lys Val Tyr Asp Val Ser Ser Tyr Met Asp Glu His Pro  
20 25 30  
Gly Gly Asp Asp Val Leu Leu Ala Val Ala Gly Lys Asp Ala Thr Asp  
35 40 45  
Asp Phe Glu Asp Ala Gly His Ser Lys Asp Ala Arg Glu Leu Met Glu  
50 55 60  
Lys Tyr Phe Ile Gly Glu Leu Asp Glu Ser Ser Leu Pro Glu Ile Pro  
65 70 75 80  
Glu Leu Lys Ile Tyr Lys Lys Asp Gln Pro Gln Asp Ser Val Gln Lys  
85 90 95  
Leu Phe Asp Leu Thr Lys Gln Tyr Trp Val Val Pro Val Ser Ile Ile  
100 105 110  
Thr Ile Ser Val Ala Val Ser Val Leu Phe Ser Arg Lys Thr  
115 120 125

(2) INFORMATION FOR SEQ ID NO:460:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1124 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..1124  
(D) OTHER INFORMATION: / Ceres Seq. ID 1567015

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:460:

|             |             |            |             |             |            |      |
|-------------|-------------|------------|-------------|-------------|------------|------|
| acgacggaga  | gaaaacgtct  | tccaaagacg | aattgagcgc  | gtggaagaag  | aaaaaaaaa  | 60   |
| atcaaaatcc  | aatttgtatc  | tcaaagtagt | gaagaagaag  | gagaagcaat  | cgaattctc  | 120  |
| tgacgatgtt  | gttacaaccc  | caaagatcct | cttatcgatt  | atcgtaattc  | gtagaaaaag | 180  |
| aagcagagag  | aaaatgggag  | gcgaagatga | taaagataag  | aaatgggaatc | ctccaccacc | 240  |
| gcagcagaag  | coggactcaa  | ggccttggga | agtctctcgc  | gcttttgtaa  | tctgcgcaac | 300  |
| cgctactact  | tctgcgcgtt  | atcagctcgc | aagaaatctt  | gattgggtct  | ataccagagt | 360  |
| aactagaaca  | cogtggcgcg  | gaagaggaac | tttccgaaca  | tcttttcagg  | cgaagaatcg | 420  |
| gagaagggtac | aacaaacgga  | tgcaagagga | gtatgaggat  | gaattggaga  | gagtggcacg | 480  |
| tattaggcgt  | atgcaaacgc  | tttccaacag | agagagggaat | aaatttagaa  | ggggctacga | 540  |
| gaactggacg  | gaaaatgatc  | ctgGtgacac | gcaataccat  | cagcagtttc  | agcgacatga | 600  |
| ttggtactcg  | aaaactgagt  | cttcgcakag | aaaccaaagg  | accaatcacc  | aggagccttc | 660  |
| agaccagaga  | agagtatatc  | cactatcaca | ccattactct  | gttttagggc  | tcagcaggtc | 720  |
| cccgacaact  | ccatacacag  | aagctgagat | taagaaagca  | ttcagggaaa  | aggctttgga | 780  |
| attccatcca  | gaccaaatac  | aggataacaa | aattgtagct  | gaagcaaaat  | tcaaagaggt | 840  |
| gttactttca  | tatgaagcta  | taaaacagga | aataaaaagg  | aagtgtatct  | ttttggtaag | 900  |
| cgagatcaat  | ctctttttcca | tgcgctctaa | agaaattgga  | atattgtcta  | caatatcgat | 960  |
| ccagagtttt  | tttgggtgtc  | ttcccatctt | ataagtttat  | tttaatatgc  | tttgtgtttg | 1020 |
| ctttttttac  | tcagtttaag  | ttctttgttg | taatatgtaa  | taaaaccaat  | ccacagctta | 1080 |
| aatatgttga  | agagagagaat | ttgggacaga | tggtccattg  | attc        |            |      |

(2) INFORMATION FOR SEQ ID NO:461:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 294 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..294

(D) OTHER INFORMATION: / Ceres Seq. ID 1567016

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:461:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Arg | Arg | Arg | Glu | Asn | Val | Phe | Gln | Arg | Arg | Ile | Glu | Ala | Val | Glu | Glu |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Glu | Lys | Lys | Lys | Ser | Lys | Ser | Asn | Leu | Ile | Phe | Lys | Val | Val | Lys | Lys |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Glu | Glu | Lys | Gln | Ser | Lys | Phe | Ser | Asp | Asp | Val | Val | Thr | Thr | Pro | Lys |
|     |     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |
| Ile | Leu | Leu | Ser | Ile | Ile | Val | Ile | Arg | Arg | Lys | Arg | Ser | Arg | Glu | Lys |
|     |     |     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |
| Met | Gly | Gly | Glu | Asp | Asp | Lys | Asp | Lys | Lys | Trp | Asn | Pro | Pro | Pro | Pro |
|     |     |     | 70  |     |     |     |     |     |     | 75  |     |     |     | 80  |     |
| Gln | Gln | Lys | Pro | Asp | Ser | Arg | Pro | Trp | Glu | Val | Leu | Ala | Ala | Phe | Val |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Ile | Cys | Ala | Thr | Ala | Thr | Thr | Phe | Ala | Val | His | Gln | Leu | Arg | Arg | Asn |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     |     | 110 |     |
| Phe | Asp | Trp | Val | Tyr | Thr | Gln | Leu | Thr | Arg | Thr | Pro | Ser | Ala | Gly | Arg |
|     |     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |
| Gly | Thr | Phe | Arg | Thr | Ser | Phe | Gln | Glu | Glu | Ala | Trp | Arg | Arg | Tyr | Asn |
|     |     |     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |
| Lys | Arg | Met | Gln | Glu | Glu | Tyr | Glu | Asp | Glu | Leu | Glu | Arg | Val | Ala | Arg |
|     |     |     | 145 |     |     |     |     | 150 |     |     |     |     | 155 |     | 160 |
| Ile | Arg | Arg | Met | Gln | Ser | Val | Phe | Asn | Arg | Glu | Arg | Asn | Lys | Phe | Arg |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |     |
| Arg | Gly | Tyr | Glu | Asn | Trp | Thr | Glu | Asn | Asp | Pro | Gly | Ala | Gln | Gln | Tyr |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| His | Gln | Gln | Phe | Gln | Arg | His | Asp | Trp | Tyr | Trp | Lys | Thr | Glu | Ser | Ser |
|     |     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |
| Xaa | Arg | Asn | Gln | Arg | Thr | Asn | His | Gln | Glu | Pro | Ser | Asp | Gln | Arg | Arg |
|     |     |     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |
| Val | Tyr | Pro | Leu | Ser | His | His | Tyr | Ser | Val | Leu | Gly | Leu | Ser | Arg | Ser |

225 230 235 240  
Arg Ala Thr Pro Tyr Thr Glu Ala Glu Ile Lys Lys Ala Phe Arg Glu  
245 250 255  
Lys Ala Leu Glu Phe His Pro Asp Gln Asn Gln Asp Asn Lys Ile Val  
260 265 270  
Ala Glu Ala Lys Phe Lys Glu Val Leu Leu Ser Tyr Glu Ala Ile Lys  
275 280 285  
Gln Glu Ile Lys Glu Lys  
290

(2) INFORMATION FOR SEQ ID NO:462:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 230 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..230

(D) OTHER INFORMATION: / Ceres Seq. ID 1567017

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:462:

Met Gly Gly Glu Asp Asp Lys Asp Lys Lys Trp Asn Pro Pro Pro Pro  
1 5 10 15  
Gln Gln Lys Pro Asp Ser Arg Pro Trp Glu Val Leu Ala Ala Phe Val  
20 25 30  
Ile Cys Ala Thr Ala Thr Thr Phe Ala Val His Gln Leu Arg Arg Asn  
35 40 45  
Phe Asp Trp Val Tyr Thr Gln Leu Thr Arg Thr Pro Ser Ala Gly Arg  
50 55 60  
Gly Thr Phe Arg Thr Ser Phe Gln Glu Glu Ala Trp Arg Arg Tyr Asn  
65 70 75 80  
Lys Arg Met Gln Glu Glu Tyr Glu Asp Glu Leu Glu Arg Val Ala Arg  
85 90 95  
Ile Arg Arg Met Gln Ser Val Phe Asn Arg Glu Arg Asn Lys Phe Arg  
100 105 110  
Arg Gly Tyr Glu Asn Trp Thr Glu Asn Asp Pro Gly Ala Gln Gln Tyr  
115 120 125  
His Gln Gln Phe Gln Arg His Asp Trp Tyr Trp Lys Thr Glu Ser Ser  
130 135 140  
Xaa Arg Asn Gln Arg Thr Asn His Gln Glu Pro Ser Asp Gln Arg Arg  
145 150 155 160  
Val Tyr Pro Leu Ser His His Tyr Ser Val Leu Gly Leu Ser Arg Ser  
165 170 175  
Arg Ala Thr Pro Tyr Thr Glu Ala Glu Ile Lys Lys Ala Phe Arg Glu  
180 185 190  
Lys Ala Leu Glu Phe His Pro Asp Gln Asn Gln Asp Asn Lys Ile Val  
195 200 205  
Ala Glu Ala Lys Phe Lys Glu Val Leu Leu Ser Tyr Glu Ala Ile Lys  
210 215 220  
Gln Glu Ile Lys Glu Lys  
225 230

(2) INFORMATION FOR SEQ ID NO:463:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 148 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..148

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:463:

(2)

(i) SEQUENCE CHARACTERISTICS:

(B) TYPE: nucleic acid

(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME

(A) NAME/REF: —  
(B) LOCATION: 1

(D) OTHER INFORMATION

SEQUENCE DESCRIPTION: SEQ ID NO:464:

(XI) SEQUENCE DESCRIPTION: SEQ ID NO:404:  
aaacga tccttccttt gcttataaac cccaatcttc t

(2) INFORMATION FOR SEQ ID NO:465:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 145 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..145  
(D) OTHER INFORMATION: / Ceres Seq. ID 1567046  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:465:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Gly | His | Ala | Thr | Ser | Leu | Ser | His | Phe | Leu | Ile | Leu | Ser | Ser | Ser |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Arg | Phe | Ser | Arg | Leu | Gly | Ser | Leu | Thr | Arg | Leu | Leu | Ser | Lys | Pro | Thr |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Ser | Leu | Ser | Gly | Ser | Leu | Ser | Ser | Ile | Ser | Val | Thr | Gly | Gln | Gly | Phe |  |
|     |     |     | 35  |     |     |     |     | 40  |     |     |     | 45  |     |     |     |  |
| Arg | Cys | Cys | Cys | Ser | Ala | Ala | Thr | Asp | Asp | Thr | Ser | Pro | Ser | Val | Lys |  |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |
| Lys | Arg | Val | Val | Ser | Gly | Val | Gln | Pro | Thr | Gly | Ser | Ile | His | Leu | Gly |  |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |  |
| Asn | Tyr | Leu | Gly | Ala | Ile | Lys | Asn | Trp | Val | Ala | Phe | Gln | Asp | Thr | Tyr |  |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     | 95  |     |     |  |
| Glu | Thr | Leu | Phe | Ile | Ile | Val | Asp | His | His | Ala | Ile | Thr | Leu | Pro | Tyr |  |
|     |     |     |     | 100 |     |     |     |     | 105 |     |     |     | 110 |     |     |  |
| Asp | Thr | Arg | Gln | Leu | Gly | Lys | Ala | Thr | Thr | Asp | Thr | Ala | Ala | Leu | Tyr |  |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |  |
| Leu | Ala | Cys | Glu | Asn | Asp | Ser | Val | Gln | Arg | Glu | Ile | Thr | Gln | Gly | Gly |  |
|     |     |     | 130 |     |     | 135 |     |     |     |     | 140 |     |     |     |     |  |

Gly  
145

(2) INFORMATION FOR SEQ ID NO:466:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 148 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..148  
(D) OTHER INFORMATION: / Ceres Seq. ID 1567047  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:466:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Ser | Leu | Thr | Asp | Gly | Leu | Ser | Lys | Met | Ser | Lys | Ser | Ala | Pro | Ser |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     | 15  |     |     |  |
| Asp | Gln | Ser | Arg | Ile | Asn | Leu | Leu | Asp | Ser | Lys | Asp | Leu | Ile | Val | Asp |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Lys | Ile | Lys | Arg | Cys | Lys | Thr | Asp | Ser | Phe | Ala | Gly | Leu | Glu | Phe | Asp |  |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Asn | Ala | Glu | Arg | Pro | Glu | Cys | Asn | Asn | Leu | Leu | Ser | Ile | Tyr | Gln | Ile |  |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |
| Val | Ser | Gly | Lys | Thr | Lys | Glu | Glu | Val | Val | Glu | Glu | Cys | Lys | Asp | Met |  |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |  |
| Ser | Trp | Gly | Thr | Phe | Lys | Pro | Leu | Leu | Ala | Asp | Ala | Leu | Ile | Asp | His |  |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |  |
| Leu | Ser | Pro | Ile | Gln | Val | Arg | Tyr | Gln | Glu | Ile | Ile | Ala | Glu | Pro | Glu |  |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |
| Tyr | Leu | Asp | Lys | Ile | Leu | Ser | Glu | Gly | Ala | Asp | Arg | Ala | Glu | Glu | Leu |  |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |  |
| Gly | Ala | Val | Thr | Met | Arg | Asn | Met | Tyr | Gln | Ala | Met | Gly | Tyr | Tyr | Gln |  |
|     |     |     | 130 |     |     | 135 |     |     |     |     |     | 140 |     |     |     |  |

Arg Arg Arg Tyr

145

(2) INFORMATION FOR SEQ ID NO:467:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 139 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..139

(D) OTHER INFORMATION: / Ceres Seq. ID 1567048

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:467:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ser | Lys | Ser | Ala | Pro | Ser | Asp | Gln | Ser | Arg | Ile | Asn | Leu | Leu | Asp |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ser | Lys | Asp | Leu | Ile | Val | Asp | Lys | Ile | Lys | Arg | Cys | Lys | Thr | Asp | Ser |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     | 30  |     |     |     |
| Phe | Ala | Gly | Leu | Glu | Phe | Asp | Asn | Ala | Glu | Arg | Pro | Glu | Cys | Asn | Asn |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Leu | Leu | Ser | Ile | Tyr | Gln | Ile | Val | Ser | Gly | Lys | Thr | Lys | Glu | Glu | Val |
|     |     | 50  |     |     | 55  |     |     |     |     |     | 60  |     |     |     |     |
| Val | Glu | Glu | Cys | Lys | Asp | Met | Ser | Trp | Gly | Thr | Phe | Lys | Pro | Leu | Leu |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Ala | Asp | Ala | Leu | Ile | Asp | His | Leu | Ser | Pro | Ile | Gln | Val | Arg | Tyr | Gln |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Glu | Ile | Ile | Ala | Glu | Pro | Glu | Tyr | Leu | Asp | Lys | Ile | Leu | Ser | Glu | Gly |
|     |     |     | 100 |     |     |     |     |     | 105 |     |     |     | 110 |     |     |
| Ala | Asp | Arg | Ala | Glu | Glu | Leu | Gly | Ala | Val | Thr | Met | Arg | Asn | Met | Tyr |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     |     | 125 |     |     |
| Gln | Ala | Met | Gly | Tyr | Tyr | Gln | Arg | Arg | Arg | Tyr |     |     |     |     |     |
|     |     | 130 |     |     |     |     | 135 |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:468:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 465 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..465

(D) OTHER INFORMATION: / Ceres Seq. ID 1567082

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:468:

|            |             |            |            |             |             |     |
|------------|-------------|------------|------------|-------------|-------------|-----|
| agaaatctaa | tgggattggt  | gaggaagcta | cagaggaaga | gttgatggat  | gcaacagctc  | 60  |
| ttgctgattc | tacttggtat  | tttatatgtc | cacatactgg | tgttgcattg  | acggcgctga  | 120 |
| tgaagctgag | aaagtcagga  | gttattggag | cgaatgatcg | gactgtgggtg | gtgagtagac  | 180 |
| ctcatggatt | gaagtattaca | cagagtaaga | ttgattatca | ttctaagaac  | ataaaggaga  | 240 |
| tggcttgtag | attggcgaat  | ccaccagtg  | aggttaagcg | aaagtttggt  | tcagttatgtg | 300 |
| atgttctcaa | ggagctattt  | aagagcaatg | ataaataagc | tttggtgtgt  | tgttctctca  | 360 |
| aagctcttca | cgctcatatg  | tgatattgtt | ggctttgtta | ttagaggaag  | taatgaaatt  | 420 |
| tcgtttcttt | ggactgtgtg  | aataaaaacg | ctggGttggt | tccgt       |             |     |

(2) INFORMATION FOR SEQ ID NO:469:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 111 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..111

(D) OTHER INFORMATION: / Ceres Seq. ID 1567083

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:469:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Lys | Ser | Asn | Gly | Ile | Val | Glu | Glu | Ala | Thr | Glu | Glu | Glu | Leu | Met | Asp |
| 1   |     | 5   |     |     |     |     |     |     | 10  |     |     |     | 15  |     |     |
| Ala | Thr | Ala | Leu | Ala | Asp | Ser | Thr | Gly | Met | Phe | Ile | Cys | Pro | His | Thr |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     | 30  |     |     |     |
| Gly | Val | Ala | Leu | Thr | Ala | Leu | Met | Lys | Leu | Arg | Lys | Ser | Gly | Val | Ile |
|     |     | 35  |     |     |     |     | 40  |     |     |     | 45  |     |     |     |     |
| Gly | Ala | Asn | Asp | Arg | Thr | Val | Val | Val | Ser | Thr | Ala | His | Gly | Leu | Lys |
|     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Phe | Thr | Gln | Ser | Lys | Ile | Asp | Tyr | His | Ser | Lys | Asn | Ile | Lys | Glu | Met |
|     |     | 65  |     |     |     | 70  |     |     |     | 75  |     |     |     | 80  |     |
| Ala | Cys | Arg | Leu | Ala | Asn | Pro | Pro | Val | Lys | Val | Lys | Ala | Lys | Phe | Gly |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Ser | Val | Met | Asp | Val | Leu | Lys | Glu | Tyr | Leu | Lys | Ser | Asn | Asp | Lys |     |
|     |     | 100 |     |     |     |     | 105 |     |     |     |     |     | 110 |     |     |

(2) INFORMATION FOR SEQ ID NO:470:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 97 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..97

(D) OTHER INFORMATION: / Ceres Seq. ID 1567084

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:470:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Asp | Ala | Thr | Ala | Leu | Ala | Asp | Ser | Thr | Gly | Met | Phe | Ile | Cys | Pro |
| 1   |     | 5   |     |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| His | Thr | Gly | Val | Ala | Leu | Thr | Ala | Leu | Met | Lys | Leu | Arg | Lys | Ser | Gly |
|     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |     |
| Val | Ile | Gly | Ala | Asn | Asp | Arg | Thr | Val | Val | Val | Ser | Thr | Ala | His | Gly |
|     |     | 35  |     |     |     |     | 40  |     |     |     | 45  |     |     |     |     |
| Leu | Lys | Phe | Thr | Gln | Ser | Lys | Ile | Asp | Tyr | His | Ser | Lys | Asn | Ile | Lys |
|     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Glu | Met | Ala | Cys | Arg | Leu | Ala | Asn | Pro | Pro | Val | Lys | Val | Lys | Ala | Lys |
|     |     | 65  |     |     |     | 70  |     |     |     | 75  |     |     |     | 80  |     |
| Phe | Gly | Ser | Val | Met | Asp | Val | Leu | Lys | Glu | Tyr | Leu | Lys | Ser | Asn | Asp |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |

Lys

(2) INFORMATION FOR SEQ ID NO:471:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 86 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..86

(D) OTHER INFORMATION: / Ceres Seq. ID 1567085

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:471:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Phe | Ile | Cys | Pro | His | Thr | Gly | Val | Ala | Leu | Thr | Ala | Leu | Met | Lys |
| 1   |     |     | 5   |     |     |     |     |     |     | 10  |     |     |     | 15  |     |
| Leu | Arg | Lys | Ser | Gly | Val | Ile | Gly | Ala | Asn | Asp | Arg | Thr | Val | Val |     |
|     |     |     | 20  |     |     |     | 25  |     |     |     |     | 30  |     |     |     |
| Ser | Thr | Ala | His | Gly | Leu | Lys | Phe | Thr | Gln | Ser | Lys | Ile | Asp | Tyr | His |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |



Ser Lys Asn Ile Lys Glu Met Ala Cys Arg Leu Ala Asn Pro Pro Val  
50 55 60  
Lys Val Lys Ala Lys Phe Gly Ser Val Met Asp Val Leu Lys Glu Tyr  
65 70 75 80  
Leu Lys Ser Asn Asp Lys  
85

(2) INFORMATION FOR SEQ ID NO:472:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1216 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1216
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567088

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:472:

|             |            |             |             |             |            |      |
|-------------|------------|-------------|-------------|-------------|------------|------|
| ccgtagGaaa  | agaaaaaggg | cggctgatga  | agaagtgcga  | aacagttcgc  | acataaggcc | 60   |
| ctacaccttt  | agttactcag | aactcagaca  | tgcaactcaa  | gattttgatc  | cttccaacaa | 120  |
| gctttggggg  | ggaggatttg | gacctgtttt  | taagggaataa | ctgaacgacg  | gaagagagat | 180  |
| agccgtgaag  | caattgtcag | tgtcatccag  | gcaaggaaaag | ggccaatttg  | ttgcggagat | 240  |
| tgccactata  | tcacctgttc | agcatcgcaa  | ccttgtaaaa  | ttgtatggat  | gctgcattga | 300  |
| gggaaatcag  | cgcgatgttg | tatatgaata  | cctctcaaac  | aagagtcctag | atcaagctct | 360  |
| attcgaggaa  | aagagtttgc | agcttggttg  | gtcacagcgt  | ttcgagatat  | gcttgggagt | 420  |
| agcaaaaggt  | ttagcatata | tgcatagaga  | gtcaaatccc  | cgtatagtag  | atagggaagt | 480  |
| gaaggcaagc  | aatattcttc | tggactcgga  | tctggtcccc  | aaactctcag  | attttggggt | 540  |
| ggccaaacta  | tatgatgata | agaagaccga  | cataagttacc | cgagttgcag  | ggacgatagg | 600  |
| atatctgtca  | ccagagtagc | tgatgcttgg  | acatctttacg | gagaagacgg  | atgtgtttgc | 660  |
| cttttggtata | gtggccttgc | aaattgtcag  | cggaaggcct  | aactcctctc  | cagaattaga | 720  |
| tgatgacaaa  | caataccttc | tcgaatgggc  | atggagcccta | caccaagagc  | agcgtgatat | 780  |
| ggaagtagta  | tgaccggatc | tgacagaatt  | tgacaaggaa  | gaagtgaaac  | gtgtaatagg | 840  |
| agtagcgctt  | ttgtgcacac | aaacagatca  | tgcaatacga  | ccaactatgt  | cccagtggtg | 900  |
| aggtatgttg  | accggtgatg | tggagataac  | ggaagccaat  | gccaagccag  | ggtacgtctc | 960  |
| tgagagaaca  | tttgagaatg | caatgagcct  | catgagtgtg  | tcaacgagct  | cgagctggat | 1020 |
| attgctgtgaa | actccaaaag | attcttccaa  | gtcccaaggt  | gaagaacatg  | gacgacgaca | 1080 |
| ttgaaacttg  | aaaactttgt | gtttttctat  | tttttttctt  | tacataaaaa  | aaaagaagtc | 1140 |
| aatatagaaa  | tcgtttgttg | taaataaacac | atatacatat  | tcgtttgacc  | aaaattggat | 1200 |
| ttgactgttt  | ctcctcg    |             |             |             |            |      |

(2) INFORMATION FOR SEQ ID NO:473:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 360 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..360
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567089

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:473:

|                                                                 |  |
|-----------------------------------------------------------------|--|
| Arg Arg Lys Arg Lys Arg Ala Ala Asp Glu Glu Val Leu Asn Ser Leu |  |
| 1 5 10 15                                                       |  |
| His Ile Arg Pro Tyr Thr Phe Ser Tyr Ser Glu Leu Arg Thr Ala Thr |  |
| 20 25 30                                                        |  |
| Gln Asp Phe Asp Pro Ser Asn Lys Leu Gly Glu Gly Phe Gly Pro     |  |
| 35 40 45                                                        |  |
| Val Phe Lys Gly Lys Leu Asn Asp Gly Arg Glu Ile Ala Val Lys Gln |  |
| 50 55 60                                                        |  |
| Leu Ser Val Ala Ser Arg Gln Gly Lys Gly Gln Phe Val Ala Glu Ile |  |
| 65 70 75 80                                                     |  |

Ala Thr Ile Ser Pro Val Gln His Arg Asn Leu Val Lys Leu Tyr Gly  
85 90 95  
Cys Cys Ile Glu Gly Asn Gln Arg Met Leu Val Tyr Glu Tyr Leu Ser  
100 105 110  
Asn Lys Ser Leu Asp Gln Ala Leu Phe Glu Glu Lys Ser Leu Gln Leu  
115 120 125  
Gly Trp Ser Gln Arg Phe Glu Ile Cys Leu Gly Val Ala Lys Gly Leu  
130 135 140  
Ala Tyr Met His Glu Glu Ser Asn Pro Arg Ile Val His Arg Asp Val  
145 150 155 160  
Lys Ala Ser Asn Ile Leu Leu Asp Ser Asp Leu Val Pro Lys Leu Ser  
165 170 175  
Asp Phe Gly Leu Ala Lys Leu Tyr Asp Asp Lys Lys Thr His Ile Ser  
180 185 190  
Thr Arg Val Ala Gly Thr Ile Gly Tyr Leu Ser Pro Glu Tyr Val Met  
195 200 205  
Leu Gly His Leu Thr Glu Lys Thr Asp Val Phe Ala Phe Gly Ile Val  
210 215 220  
Ala Leu Glu Ile Val Ser Gly Arg Pro Asn Ser Ser Pro Glu Leu Asp  
225 230 235 240  
Asp Asp Lys Gln Tyr Leu Leu Glu Trp Ala Trp Ser Leu His Gln Glu  
245 250 255  
Gln Arg Asp Met Glu Val Val Asp Pro Asp Leu Thr Glu Phe Asp Lys  
260 265 270  
Glu Glu Val Lys Arg Val Ile Gly Val Ala Phe Leu Cys Thr Gln Thr  
275 280 285  
Asp His Ala Ile Arg Pro Thr Met Ser Arg Val Val Gly Met Leu Thr  
290 295 300  
Gly Asp Val Glu Ile Thr Glu Ala Asn Ala Lys Pro Gly Tyr Val Ser  
305 310 315 320  
Glu Arg Thr Phe Glu Asn Ala Met Ser Phe Met Ser Gly Ser Thr Ser  
325 330 335  
Ser Ser Trp Ile Leu Pro Glu Thr Pro Lys Asp Ser Ser Lys Ser Gln  
340 345 350  
Val Glu Glu His Gly Arg Arg His  
355 360

(2) INFORMATION FOR SEQ ID NO:474:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 256 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..256
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567090

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:474:

Met Leu Val Tyr Glu Tyr Leu Ser Asn Lys Ser Leu Asp Gln Ala Leu  
1 5 10 15  
Phe Glu Glu Lys Ser Leu Gln Leu Gly Trp Ser Gln Arg Phe Glu Ile  
20 25 30  
Cys Leu Gly Val Ala Lys Gly Leu Ala Tyr Met His Glu Glu Ser Asn  
35 40 45  
Pro Arg Ile Val His Arg Asp Val Lys Ala Ser Asn Ile Leu Leu Asp  
50 55 60  
Ser Asp Leu Val Pro Lys Leu Ser Asp Phe Gly Leu Ala Lys Leu Tyr  
65 70 75 80  
Asp Asp Lys Lys Thr His Ile Ser Thr Arg Val Ala Gly Thr Ile Gly  
85 90 95  
Tyr Leu Ser Pro Glu Tyr Val Met Leu Gly His Leu Thr Glu Lys Thr

|                                                                 |     |     |
|-----------------------------------------------------------------|-----|-----|
| 100                                                             | 105 | 110 |
| Asp Val Phe Ala Phe Gly Ile Val Ala Leu Glu Ile Val Ser Gly Arg |     |     |
| 115                                                             | 120 | 125 |
| Pro Asn Ser Ser Pro Glu Leu Asp Asp Lys Gln Tyr Leu Leu Glu     |     |     |
| 130                                                             | 135 | 140 |
| Trp Ala Trp Ser Leu His Gln Glu Gln Arg Asp Met Glu Val Val Asp |     |     |
| 145                                                             | 150 | 155 |
| Pro Asp Leu Thr Glu Phe Asp Lys Glu Glu Val Lys Arg Val Ile Gly |     |     |
| 165                                                             | 170 | 175 |
| Val Ala Phe Leu Cys Thr Gln Thr Asp His Ala Ile Arg Pro Thr Met |     |     |
| 180                                                             | 185 | 190 |
| Ser Arg Val Val Gly Met Leu Thr Gly Asp Val Glu Ile Thr Glu Ala |     |     |
| 195                                                             | 200 | 205 |
| Asn Ala Lys Pro Gly Tyr Val Ser Glu Arg Thr Phe Glu Asn Ala Met |     |     |
| 210                                                             | 215 | 220 |
| Ser Phe Met Ser Gly Ser Thr Ser Ser Ser Trp Ile Leu Pro Glu Thr |     |     |
| 225                                                             | 230 | 235 |
| Pro Lys Asp Ser Ser Lys Ser Gln Val Glu Glu His Gly Arg Arg His |     |     |
| 245                                                             | 250 | 255 |

(2) INFORMATION FOR SEQ ID NO:475:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 214 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..214

(D) OTHER INFORMATION: / Ceres Seq. ID 1567091

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:475:

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| Met His Glu Glu Ser Asn Pro Arg Ile Val His Arg Asp Val Lys Ala |     |
| 1                                                               | 5   |
| Ser Asn Ile Leu Leu Asp Ser Asp Leu Val Pro Lys Leu Ser Asp Phe |     |
| 20                                                              | 25  |
| Gly Leu Ala Lys Leu Tyr Asp Asp Lys Lys Thr His Ile Ser Thr Arg |     |
| 35                                                              | 40  |
| Val Ala Gly Thr Ile Gly Tyr Leu Ser Pro Glu Tyr Val Met Leu Gly |     |
| 50                                                              | 55  |
| His Leu Thr Glu Lys Thr Asp Val Phe Ala Phe Gly Ile Val Ala Leu |     |
| 65                                                              | 70  |
| Glu Ile Val Ser Gly Arg Pro Asn Ser Ser Pro Glu Leu Asp Asp Asp |     |
| 85                                                              | 90  |
| Lys Gln Tyr Leu Leu Glu Trp Ala Trp Ser Leu His Gln Glu Gln Arg |     |
| 100                                                             | 105 |
| Asp Met Glu Val Val Asp Pro Asp Leu Thr Glu Phe Asp Lys Glu Glu |     |
| 115                                                             | 120 |
| Val Lys Arg Val Ile Gly Val Ala Phe Leu Cys Thr Gln Thr Asp His |     |
| 130                                                             | 135 |
| Ala Ile Arg Pro Thr Met Ser Arg Val Val Gly Met Leu Thr Gly Asp |     |
| 145                                                             | 150 |
| Val Glu Ile Thr Glu Ala Asn Ala Lys Pro Gly Tyr Val Ser Glu Arg |     |
| 165                                                             | 170 |
| Thr Phe Glu Asn Ala Met Ser Phe Met Ser Gly Ser Thr Ser Ser     |     |
| 180                                                             | 185 |
| Trp Ile Leu Pro Glu Thr Pro Lys Asp Ser Ser Lys Ser Gln Val Glu |     |
| 195                                                             | 200 |
| Glu His Gly Arg Arg His                                         |     |
| 210                                                             |     |

(2) INFORMATION FOR SEQ ID NO:476:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1192 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1192
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567092

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:476:

```
aaaatctctc gctctgttac gccattttcg tgagtgaagaa gaagaaaccc taagagtctc 60
tcccacaaac ctcaaaccat ggccagggga ctcgattga agggcattat gcgcgccacc 120
accgacattg tcacggcccat gcctacgcgc atcgacaatt cgcacatcat cgtcacacgc 180
tcgcgtgaca aatcaatcat cctctggaaa ctcacaaagg acgagaagtc ttacgggtgt 240
gctcagcgta ggctcacagg tcactctcac ttctgtggaag atgttgtctt ctcactcgga 300
ggtcagtttg cactctccgg aagttgggac ggtgagctcc gtctctggga tctcgccacg 360
ggagaaacaa ctcgctcgatt cgttggtcac acgaaagatg tgctctctgt tgccttctct 420
actgataacc gtcagatcgt gtctgcttct cgtgatcgta cgattaagct ttggaacaca 480
cttggtgagt gcaagtatac catctctgaa ggtgatggtc acaaggaaatg ggtagttgt 540
gttaggttta gtcctaatac tcttgtacca actattgtat ctgcttcttg ggataaaaat 600
gtgaaagtgt ggaatctcca gaactgtaag ctgaggaact ctcttggttg tcaactctgt 660
tacctcaaca ctgttgtgtg ctgcctgatg ggttcgctat gcgccagtag tgggaaagat 720
gggtgtatct tggttggtgga tttggctgaa ggaagaagac ttactcgtct tgaggctgtg 780
tcgattatct acNtcgcttt gcttcagctc taacagatac ttggtgtgtg ctgctactga 840
gaatagcatt aggatttggt atcttgagag caagtctggt gttgaggact tgaaggttga 900
tctcaagctt gaggcagaga agaatagaag ttggtgttga actggttaac agaagaaggt 960
tatctactgc acaagcttga actggagtcg agatggaagc acattgttca gtggttacac 1020
tgatggagtt gtcagggtct ggggtatttg tcgttactag agatcacac aagatgaaga 1080
agaagtcaacg aaatctccgg aaaaaagtag ctgcttttaa tttttccaga Ctcgcgtcagt 1140
attgtattag tctctcgcaa acctctattt tggcaatttt tgtttaattt cc
```

(2) INFORMATION FOR SEQ ID NO:477:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 244 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..244
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567093

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:477:

```
Met Ala Glu Gly Leu Val Leu Lys Gly Ile Met Arg Ala His Thr Asp
1 5 10 15
Ile Val Thr Ala Ile Ala Thr Pro Ile Asp Asn Ser Asp Ile Ile Val
20 25 30
Thr Ala Ser Arg Asp Lys Ser Ile Ile Leu Trp Lys Leu Thr Lys Asp
35 40 45
Glu Lys Ser Tyr Gly Val Ala Gln Arg Arg Leu Thr Gly His Ser His
50 55 60
Phe Val Glu Asp Val Val Leu Ser Ser Asp Gly Gln Phe Ala Leu Ser
65 70 75 80
Gly Ser Trp Asp Gly Glu Leu Arg Leu Trp Asp Leu Ala Thr Gly Glu
85 90 95
Thr Thr Arg Arg Phe Val Gly His Thr Lys Asp Val Leu Ser Val Ala
100 105 110
Phe Ser Thr Asp Asn Arg Gln Ile Val Ser Ala Ser Arg Asp Arg Thr
115 120 125
Ile Lys Leu Trp Asn Thr Leu Gly Glu Cys Lys Tyr Thr Ile Ser Glu
```

(2) INFORMATION FOR SEQ ID NO:478:

(A) LENGTH: 234 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: lin

MOLECULE TYPE: peptide

## (A) NAME

(B) LOCATION: 1..234

(D) OTHER INFORMATION:

SEQUENCE DESCRIPTION: SEQ ID NO:478:

(XI) SEQUENCE DESCRIPTION: SEQ ID NO:478:  
Arg Ala His Thr Asp Ile Val Thr Ala Ile A

[illegible]

(2) INFORMATION FOR SEQ ID NO:479:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 123 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..123  
(D) OTHER INFORMATION: / Ceres Seq. ID 1567095  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:479:  
Met Val Arg Tyr Ala Pro Val Val Gly Lys Met Val Leu Ser Cys Cys  
1 5 10 15  
Gly Ile Trp Leu Lys Glu Arg Ser Phe Thr Arg Leu Arg Leu Val Arg  
20 25 30  
Leu Phe Xaa Ser Leu Cys Phe Ser Pro Asn Arg Tyr Trp Leu Cys Ala  
35 40 45  
Ala Thr Glu Asn Ser Ile Arg Ile Trp Asp Leu Glu Ser Lys Ser Val  
50 55 60  
Val Glu Asp Leu Lys Val Asp Leu Lys Ser Glu Ala Glu Lys Asn Glu  
65 70 75 80  
Gly Gly Val Gly Thr Gly Asn Gln Lys Lys Val Ile Tyr Cys Thr Ser  
85 90 95  
Leu Asn Trp Ser Ala Asp Gly Ser Thr Leu Phe Ser Gly Tyr Thr Asp  
100 105 110  
Gly Val Val Arg Val Trp Gly Ile Gly Arg Tyr  
115 120

(2) INFORMATION FOR SEQ ID NO:480:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1290 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1290

(D) OTHER INFORMATION: / Ceres Seq. ID 1567096

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:480:

|             |             |            |             |            |            |      |
|-------------|-------------|------------|-------------|------------|------------|------|
| atcttaccct  | aaaaaccaca  | tttcttaact | tcttcaataa  | aaaaaagaaa | agcttcacc  | 60   |
| tttaatttta  | ccctcaacc   | caaaacaaaa | accccttctc  | ccacgagggc | atacagaat  | 120  |
| atcaagacc   | caatctttct  | tctacttccc | caatctctag  | atgacaatct | aacgatacag | 180  |
| ttctctttag  | atcgattacc  | aaatacaaa  | gatcaatttt  | tcttacatga | acactctgtt | 240  |
| gtaattggac  | aggagaatct  | agaactgagt | cttttatgta  | cagagagcaa | cgttgatgat | 300  |
| ggagggcatg  | tgtgtgacga  | aactccgatt | gaattttcga  | ttcctcagat | gggtttttct | 360  |
| caatcggaga  | gtgaggagat  | tatcatggag | atgggtggaga | aggagaagca | gcatttgcca | 420  |
| agtgatgatt  | acatacaag   | acttagaagt | ggagatttgg  | atttgaatgt | tggagaagaa | 480  |
| gatgcctcca  | attggatttg  | gaaggcttgg | gaagtacacc  | agtttggacc | attgtgtttt | 540  |
| tgcttagcaa  | tgaactactt  | ggatcgattc | ttatcggttc  | atgatttggc | tagtggcaaa | 600  |
| ggttggtat   | tgacgtttgt  | ggctgtggct | tgtttatcat  | tgccagccaa | aattgaagaa | 660  |
| actgaagtt   | caatgttgat  | agacttctag | gttggagatc  | ctcagtttgt | gtttgagctt | 720  |
| aaatcagttc  | aaagataagg  | gcttttgggt | ttgaacagat  | tgaattggag | attgagagca | 780  |
| ataactccat  | gctcatatcat | aagatatctc | ctgagaaaga  | tgagttaaat | tgatcaagaa | 840  |
| ccatccaaga  | cattgatata  | tagatcatta | caagtgtatg  | ccagcacaca | caaaggtatt | 900  |
| gacttttttg  | agtttagacc  | ttctgaagtt | gctgtgctgt  | tgccactttc | tgtttctcgt | 960  |
| gaattgcaga  | gagtagactt  | tgacaactct | tcttctctct  | ctctttttct | actacttcaa | 1020 |
| aaaggagagag | tgaagaagat  | aggggaaatg | atagagagtg  | atggctcaga | cttattttca | 1080 |
| caaacaccca  | atgggggttt  | agaagtatcg | gcttgttgtt  | tcagctttta | gacccatgat | 1140 |
| tcttcttctt  | cttatcacat  | tctttcttaa | aaaaaaaact  | gtttttttct | tacattatta | 1200 |
| taatcagtat  | gagtgtctgt  | gagaggttga | aaaaagagga  | caataaatca | aagcaaaaa  | 1260 |
| tttaaaaaa   | caataaaagt  | tattatttt  |             |            |            |      |

(2) INFORMATION FOR SEQ ID NO:481:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 308 amino acids

(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..308  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1567097  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:481:  
Met Ala Glu Glu Asn Leu Glu Leu Ser Leu Leu Cys Thr Glu Ser Asn  
1                  5                  10                  15  
Val Asp Asp Glu Gly Met Ile Val Asp Glu Thr Pro Ile Glu Ile Ser  
                  20                  25                  30  
Ile Pro Gln Met Gly Phe Ser Gln Ser Glu Glu Ile Ile Met  
                  35                  40                  45  
Glu Met Val Glu Lys Glu Lys Gln His Leu Pro Ser Asp Asp Tyr Ile  
                  50                  55                  60  
Lys Arg Leu Arg Ser Gly Asp Leu Asp Leu Asn Val Gly Arg Arg Asp  
65                  70                  75                  80  
Ala Leu Asn Trp Ile Trp Lys Ala Cys Glu Val His Gln Phe Gly Pro  
                  85                  90                  95  
Leu Cys Phe Cys Leu Ala Met Asn Tyr Leu Asp Arg Phe Leu Ser Val  
                  100                 105                 110  
His Asp Leu Pro Ser Gly Lys Gly Trp Ile Leu Gln Leu Leu Ala Val  
                  115                 120                 125  
Ala Cys Leu Ser Leu Ala Ala Lys Ile Glu Glu Thr Glu Val Pro Met  
                  130                 135                 140  
Leu Ile Asp Leu Gln Val Gly Asp Pro Gln Phe Val Phe Glu Ala Lys  
145                 150                 155                 160  
Ser Val Gln Arg Met Glu Leu Leu Val Leu Asn Arg Leu Lys Trp Arg  
                  165                 170                 175  
Leu Arg Ala Ile Thr Pro Cys Ser Tyr Ile Arg Tyr Phe Leu Arg Lys  
                  180                 185                 190  
Met Ser Lys Cys Asp Gln Glu Pro Ser Asn Thr Leu Ile Ser Arg Ser  
                  195                 200                 205  
Leu Gln Val Ile Ala Ser Thr Lys Gly Ile Asp Phe Leu Glu Phe  
                  210                 215                 220  
Arg Pro Ser Glu Val Ala Ala Val Ala Leu Ser Val Ser Gly Glu  
225                 230                 235                 240  
Leu Gln Arg Val His Phe Asp Asn Ser Ser Phe Ser Pro Leu Phe Ser  
                  245                 250                 255  
Leu Leu Gln Lys Glu Arg Val Lys Lys Ile Gly Glu Met Ile Glu Ser  
                  260                 265                 270  
Asp Gly Ser Asp Leu Phe Ser Gln Thr Pro Asn Gly Val Leu Glu Val  
                  275                 280                 285  
Ser Ala Cys Cys Phe Ser Phe Lys Thr His Asp Ser Ser Ser Ser Tyr  
                  290                 295                 300  
Thr His Leu Ser  
305  
(2) INFORMATION FOR SEQ ID NO:482:  
    (i) SEQUENCE CHARACTERISTICS:  
        (A) LENGTH: 287 amino acids  
        (B) TYPE: amino acid  
        (C) STRANDEDNESS:  
        (D) TOPOLOGY: linear  
    (ii) MOLECULE TYPE: peptide  
    (ix) FEATURE:  
        (A) NAME/KEY: peptide  
        (B) LOCATION: 1..287  
        (D) OTHER INFORMATION: / Ceres Seq. ID 1567098  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:482:

```

Met Ile Val Asp Glu Thr Pro Ile Glu Ile Ser Ile Pro Gln Met Gly
1 5 10 15
Phe Ser Gln Ser Glu Ser Glu Glu Ile Met Glu Met Val Glu Lys
20 25 30
Glu Lys Gln His Leu Pro Ser Asp Asp Tyr Ile Lys Arg Leu Arg Ser
35 40 45
Gly Asp Leu Asp Leu Asn Val Gly Arg Arg Asp Ala Leu Asn Trp Ile
50 55 60
Trp Lys Ala Cys Glu Val His Gln Phe Gly Pro Leu Cys Phe Cys Leu
65 70 75 80
Ala Met Asn Tyr Leu Asp Arg Phe Leu Ser Val His Asp Leu Pro Ser
85 90 95
Gly Lys Gly Trp Trp Ile Leu Gln Leu Leu Ala Val Ala Cys Leu Ser Leu
100 105 110
Ala Ala Lys Ile Glu Glu Thr Glu Val Pro Met Leu Ile Asp Leu Gln
115 120 125
Val Gly Asp Pro Gln Phe Val Phe Glu Ala Lys Ser Val Gln Arg Met
130 135 140
Glu Leu Leu Val Leu Asn Arg Leu Lys Trp Arg Leu Arg Ala Ile Thr
145 150 155 160
Pro Cys Ser Tyr Ile Arg Tyr Phe Leu Arg Lys Met Ser Lys Cys Asp
165 170 175
Gln Glu Pro Ser Asn Thr Leu Ile Ser Arg Ser Leu Gln Val Ile Ala
180 185 190
Ser Thr Thr Lys Gly Ile Asp Phe Leu Glu Phe Arg Pro Ser Glu Val
195 200 205
Ala Ala Ala Val Ala Leu Ser Val Ser Gly Glu Leu Gln Arg Val His
210 215 220
Phe Asp Asn Ser Ser Phe Ser Pro Leu Phe Ser Leu Leu Gln Lys Glu
225 230 235 240
Arg Val Lys Lys Ile Gly Glu Met Ile Glu Ser Asp Gly Ser Asp Leu
245 250 255
Phe Ser Gln Thr Pro Asn Gly Val Leu Glu Val Ser Ala Cys Cys Phe
260 265 270
Ser Phe Lys Thr His Asp Ser Ser Ser Ser Tyr Thr His Leu Ser
275 280 285

```

(2) INFORMATION FOR SEQ ID NO:483:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 273 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..273

- (D) OTHER INFORMATION: / Ceres Seq. ID 1567099

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:483:

```

Met Gly Phe Ser Gln Ser Glu Ser Glu Glu Ile Ile Met Glu Met Val
1 5 10 15
Glu Lys Glu Lys Gln His Leu Pro Ser Asp Asp Tyr Ile Lys Arg Leu
20 25 30
Arg Ser Gly Asp Leu Asp Leu Asn Val Gly Arg Arg Asp Ala Leu Asn
35 40 45
Trp Ile Trp Lys Ala Cys Glu Val His Gln Phe Gly Pro Leu Cys Phe
50 55 60
Cys Leu Ala Met Asn Tyr Leu Asp Arg Phe Leu Ser Val His Asp Leu
65 70 75 80
Pro Ser Gly Lys Gly Trp Ile Leu Gln Leu Leu Ala Val Ala Cys Leu
85 90 95
Ser Leu Ala Ala Lys Ile Glu Glu Thr Glu Val Pro Met Leu Ile Asp

```



|                                                                 |     |     |
|-----------------------------------------------------------------|-----|-----|
| 100                                                             | 105 | 110 |
| Leu Gln Val Gly Asp Pro Gln Phe Val Phe Glu Ala Lys Ser Val Gln |     |     |
| 115                                                             | 120 | 125 |
| Arg Met Glu Leu Leu Val Leu Asn Arg Leu Lys Trp Arg Leu Arg Ala |     |     |
| 130                                                             | 135 | 140 |
| Ile Thr Pro Cys Ser Tyr Ile Arg Tyr Phe Leu Arg Lys Met Ser Lys |     |     |
| 145                                                             | 150 | 155 |
| Cys Asp Gln Glu Pro Ser Asn Thr Leu Ile Ser Arg Ser Leu Gln Val |     |     |
| 165                                                             | 170 | 175 |
| Ile Ala Ser Thr Thr Lys Gly Ile Asp Phe Leu Glu Phe Arg Pro Ser |     |     |
| 180                                                             | 185 | 190 |
| Glu Val Ala Ala Ala Val Ala Leu Ser Val Ser Gly Glu Leu Gln Arg |     |     |
| 195                                                             | 200 | 205 |
| Val His Phe Asp Asn Ser Ser Phe Ser Pro Leu Phe Ser Leu Leu Gln |     |     |
| 210                                                             | 215 | 220 |
| Lys Glu Arg Val Lys Lys Ile Gly Glu Met Ile Glu Ser Asp Gly Ser |     |     |
| 225                                                             | 230 | 235 |
| Asp Leu Phe Ser Gln Thr Pro Asn Gly Val Leu Glu Val Ser Ala Cys |     |     |
| 245                                                             | 250 | 255 |
| Cys Phe Ser Phe Lys Thr His Asp Ser Ser Ser Tyr Thr His Leu     |     |     |
| 260                                                             | 265 | 270 |
| Ser                                                             |     |     |

(2) INFORMATION FOR SEQ ID NO:484:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1164 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1164
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567116

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:484:

|             |             |             |            |             |             |      |
|-------------|-------------|-------------|------------|-------------|-------------|------|
| gagagaaaga  | gagagatatg  | atattattaa  | gtagtagtat | aagcctctca  | agaccagttt  | 60   |
| cttctcaaaag | cttctctccca | ctgctgcca   | cttcaacaag | gagatctcat  | tcctctgtca  | 120  |
| cagctcaagtg | ctgctgtttct | tccagaagtg  | tggtgaagaa | tcctgagtta  | aaatgttctt  | 180  |
| tggagaatct  | ctttgaaatc  | caggctttga  | gggaagtgtt | tggttcaggg  | tttgacagta  | 240  |
| ttttctctct  | ctctcaggca  | ggccagggtta | tagcgttgga | tcctctcatct | ggttatcaga  | 300  |
| acatttgcca  | actaggagtg  | gctgctgctg  | tgggagaaaa | caagctgact  | cttccatctg  | 360  |
| atggttgactc | ggaatcaatg  | atgatgatga  | tgatgagagg | catgactgct  | aagaactttg  | 420  |
| accctgttag  | gtactctgga  | agatgggttg  | aagtactctc | tcctaaagcg  | ggatttgcaq  | 480  |
| gtcaaggcca  | agaagactgt  | cattgcactc  | agggagtata | cacgtttgat  | atgaaggaa   | 540  |
| cagccattag  | agtagataca  | ttttgtgttc  | atggcagccc | tgatggatat  | ataacaggaa  | 600  |
| tcagagggaa  | agttcaatgc  | gtgggagcgg  | aagacctcga | gaaaaagcag  | actgacttag  | 660  |
| aaaaagcaaga | gatgattaaa  | gagaagtgtt  | tcctacagat | tcgccaccat  | ctttttatcc  | 720  |
| ccaagtgtcc  | ttatgatgtc  | atagccacag  | actacgacaa | ctacgcactt  | gtttctggag  | 780  |
| ctaaagacaa  | gggctttgtt  | caggtatact  | caaggacgcc | aaatccagga  | cttgagttca  | 840  |
| tcgcaaaagta | caagaactac  | ttggcacaat  | ttggctatga | cccggaaaaa  | ataaaggata  | 900  |
| caccacagga  | ctgtgaagtg  | actgatgctg  | agctagcagc | catgatgtcc  | atgccaggtta | 960  |
| tgagagcaaac | actgaccaac  | cagtttccag  | atcttggtat | aaAgaaagtc  | agtcacagtt  | 1020 |
| gatcccttcca | caagtgtgtt  | tgaacacctg  | aagaaacttg | taccgtctca  | tttcaaatag  | 1080 |
| agcaagcttc  | tttgctcaaa  | tcttatgta   | gactataatc | actgtccata  | tatacatatc  | 1140 |
| ttccagaatc  | aaaacactct  | tctg        |            |             |             |      |

(2) INFORMATION FOR SEQ ID NO:485:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..339  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1567117  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:485:  
Glu Lys Glu Arg Asp Met Ile Leu Leu Ser Ser Ser Ile Ser Leu Ser  
1                  5                  10                  15  
Arg Pro Val Ser Ser Gln Ser Phe Ser Pro Pro Ala Ala Thr Ser Thr  
                  20                  25                  30  
Arg Arg Ser His Ser Ser Val Thr Val Lys Cys Cys Cys Ser Ser Arg  
                  35                  40                  45  
Arg Leu Leu Lys Asn Pro Glu Leu Lys Cys Ser Leu Glu Asn Leu Phe  
50                  55                  60                  65  
Glu Ile Gln Ala Leu Arg Lys Cys Phe Val Ser Gly Phe Ala Ala Ile  
                  70                  75                  80  
Leu Leu Leu Ser Gln Ala Gly Gln Gly Ile Ala Leu Asp Leu Ser Ser  
                  85                  90                  95  
Gly Tyr Gln Asn Ile Cys Gln Leu Gly Ser Ala Ala Ala Val Gly Glu  
                  100                 105                 110  
Asn Lys Leu Thr Leu Pro Ser Asp Gly Asp Ser Glu Ser Met Met Met  
                 115                 120                 125  
Met Met Met Arg Gly Met Thr Ala Lys Asn Phe Asp Pro Val Arg Tyr  
130                 135                 140  
Ser Gly Arg Trp Phe Glu Val Ala Ser Leu Lys Arg Gly Phe Ala Gly  
145                 150                 155                 160  
Gln Gly Gln Glu Asp Cys His Cys Thr Gln Gly Val Tyr Thr Phe Asp  
                 165                 170                 175  
Met Lys Glu Ser Ala Ile Arg Val Asp Thr Phe Cys Val His Gly Ser  
                 180                 185                 190  
Pro Asp Gly Tyr Ile Thr Gly Ile Arg Gly Lys Val Gln Cys Val Gly  
                 195                 200                 205  
Ala Glu Asp Leu Glu Lys Ser Glu Thr Asp Leu Glu Lys Gln Glu Met  
210                 215                 220  
Ile Lys Glu Lys Cys Phe Leu Arg Phe Pro Thr Ile Pro Phe Ile Pro  
225                 230                 235  
Lys Leu Pro Tyr Asp Val Ile Ala Thr Asp Tyr Asp Asn Tyr Ala Leu  
                 245                 250                 255  
Val Ser Gly Ala Lys Asp Lys Gly Phe Val Gln Val Tyr Ser Arg Thr  
                 260                 265                 270  
Pro Asn Pro Gly Pro Glu Phe Ile Ala Lys Tyr Lys Asn Tyr Leu Ala  
                 275                 280                 285  
Gln Phe Gly Tyr Asp Pro Glu Lys Ile Lys Asp Thr Pro Gln Asp Cys  
290                 295                 300  
Glu Val Thr Asp Ala Glu Leu Ala Ala Met Met Ser Met Pro Gly Met  
305                 310                 315                 320  
Glu Gln Thr Leu Thr Asn Gln Phe Pro Asp Leu Gly Leu Lys Lys Val  
                 325                 330                 335  
Ser Pro Val

(2) INFORMATION FOR SEQ ID NO:486:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 334 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

- (ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..334  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1567118

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 1   | Met | Ile | Leu | Leu | 5   | Ser | Ser | Ile | Ser | Leu | Ser | Arg | Pro | Val | Ser | Ser |
| 1   | Gln | Ser | Phe | Ser | 20  | Pro | Pro | Ala | Ala | Thr | Ser | Thr | Arg | Arg | Ser | 15  |
|     | Ser | Val | Thr | Val | Lys | Cys | Cys | Cys | Ser | Ser | Ser | Arg | Arg | Leu | Leu | Lys |
|     |     |     | 35  |     |     |     |     | 40  |     |     |     |     |     | 45  |     | Asn |
| Pro | Glu | Leu | Lys | Cys | Ser | Leu | Glu | Asn | Leu | Phe | Glu | Ile | Gln | Ala | Leu |     |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |
| Arg | Lys | Cys | Phe | Val | Ser | Gly | Phe | Ala | Ala | Ile | Leu | Leu | Ser | Gln |     |     |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Ala | Gly | Gln | Gly | Ile | Ala | Leu | Asp | Leu | Ser | Ser | Gly | Tyr | Gln | Asn | Ile |     |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Cys | Gln | Leu | Gly | Ser | Ala | Ala | Ala | Val | Gly | Glu | Asn | Lys | Leu | Thr | Leu |     |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |     |
| Pro | Ser | Asp | Gly | Asp | Ser | Glu | Ser | Met | Met | Met | Met | Met | Met | Arg | Gly |     |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |     |
| Met | Thr | Ala | Lys | Asn | Phe | Asp | Pro | Val | Arg | Tyr | Ser | Gly | Arg | Trp | Phe |     |
|     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |     |
| Glu | Val | Ala | Ser | Leu | Lys | Arg | Gly | Phe | Ala | Gly | Gln | Gly | Gln | Glu | Asp |     |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |     |
| Cys | His | Cys | Thr | Gln | Gly | Val | Tyr | Thr | Phe | Asp | Met | Lys | Glu | Ser | Ala |     |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | 175 |     |
| Ile | Arg | Val | Asp | Thr | Phe | Cys | Val | His | Gly | Ser | Pro | Asp | Gly | Tyr | Ile |     |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |     |
| Thr | Gly | Ile | Arg | Gly | Lys | Val | Gln | Cys | Val | Gly | Ala | Glu | Asp | Leu | Glu |     |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |     |
| Lys | Ser | Glu | Thr | Asp | Leu | Glu | Lys | Gln | Glu | Met | Ile | Lys | Glu | Lys | Cys |     |
|     |     | 210 |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |     |
| Phe | Leu | Arg | Phe | Pro | Thr | Ile | Pro | Phe | Ile | Pro | Lys | Leu | Pro | Tyr | Asp |     |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |     |
| Val | Ile | Ala | Thr | Asp | Tyr | Asp | Asn | Tyr | Ala | Leu | Val | Ser | Gly | Ala | Lys |     |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |     |
| Asp | Lys | Gly | Phe | Val | Gln | Val | Tyr | Ser | Arg | Thr | Pro | Asn | Pro | Gly | Pro |     |
|     |     | 260 |     |     |     |     |     | 265 |     |     |     |     | 270 |     |     |     |
| Glu | Phe | Ile | Ala | Lys | Tyr | Lys | Asn | Tyr | Leu | Ala | Gln | Phe | Gly | Tyr | Asp |     |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |     |
| Pro | Glu | Lys | Ile | Lys | Asp | Thr | Pro | Gln | Asp | Cys | Glu | Val | Thr | Asp | Ala |     |
|     |     | 290 |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |     |
| Glu | Leu | Ala | Ala | Met | Met | Ser | Met | Pro | Gly | Met | Glu | Gln | Thr | Leu | Thr |     |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |     |
| Asn | Gln | Phe | Pro | Asp | Leu | Gly | Leu | Lys | Lys | Val | Ser | Pro | Val |     |     |     |
|     |     |     |     | 325 |     |     |     |     | 330 |     |     |     |     |     |     |     |

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 214 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ix) FEATURE:

(B) LOCATION: 1..214

SEQUENCE DESCRIPTION: SEQ ID NO:487:

|     |     |     |  |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |
|-----|-----|-----|--|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|
| 1   |     |     |  | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |  |  |
| Val | Arg | Tyr |  | Ser | Gly | Arg | Trp | Phe | Glu | Val | Ala | Ser | Leu | Lys | Arg | Gly |  |  |
|     |     |     |  | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |  |
| Phe | Ala | Gly |  | Gln | Gly | Gln | Glu | Asp | Cys | His | Cys | Thr | Gln | Gly | Val | Tyr |  |  |
|     |     | 35  |  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |  |

[illegible]

(2) INFORMATION FOR SEQ ID NO:488:

## (1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1223 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..1223  
(D) OTHER INFORMATION: / Ceres Seq. ID 1567120

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:488:

|             |              |              |              |              |             |      |
|-------------|--------------|--------------|--------------|--------------|-------------|------|
| gaccacataca | attcttGStaa  | tatctctctctc | tcaacttttoga | atataattctta | agataacaaga | 120  |
| gaccacataca | cttaaaqgtttg | gtgaagaataa  | aqaagacaaat  | acgaaggaaa   | gtggttggttg | 60   |
| ataagagatc  | tttcttcoggg  | aaagatactaa  | aagacccaacc  | ccatgaacct   | ctattcgacg  | 180  |
| ctactfgagct | gtggaagtgt   | ttctttctaca  | gagctctcat   | cgcgtgagtc   | atagcgaact  | 240  |
| tccttttctc  | ctaigtctact  | attatgactg   | tcactcggtta  | caagagccag   | accgatcttg  | 300  |
| ccgatgaatc  | tacacagtg    | acagcggctg   | cgctctcttg   | tatggcagtg   | gccttttggtg | 360  |
| cgatgatatt  | catctctctc   | ctactgacgc   | cggcctctct   | ttgtggcgat   | ataatctcgg  | 420  |
| cagtgacttt  | ttggctgtgtg  | ttgtgctcga   | aagtgcagctt  | ggtagagaca   | gtgagtgtac  | 480  |
| ttgtggtcta  | gtgcctcggg   | ggcatttcgt   | gtgtggcctt   | gtgcgaaggc   | ttccagctgt  | 540  |
| cttaacttaac | cccgtaacgt   | ggtgctgcata  | atggtctctc   | tgacgcttac   | agcatcgcca  | 600  |
| ccggtgtgtgc | acgcagagac   | atttgtacat   | tcgctttagt   | tcaacagctc   | ttctctgtca  | 660  |
| ctgatccocaa | gaggagtgctg  | cgtgactctc   | acgttctcgt   | attgtgtcca   | tttgcaattg  | 720  |
| gattttgagc  | gtctaatcgt   | caacttagcta  | accatccaat   | acaggcgata   | gggtacaacc  | 780  |
| ctgcacaaga  | ttctcggagct  | ggaatcattc   | acacaacaaga  | caaaagctgtg  | gacacattct  | 840  |
| ggatattcttg | ggttggtctcg  | ttctctgtgt   | cagcactctc   | cagctttctc   | ctacagttgt  | 900  |
| tggttgaggcg | tggtgcgatt   | aaggccctgc   | ggtctttcag   | gagccagcctg  | cacgtttaac  | 960  |
| tttgatagtc  | ttctcttcgta  | gtacatcaaa   | gagagaaaaaa  | gaaagacataa  | taagagagcg  | 1020 |
| tttgataattt | attcttggtta  | gacgttttga   | ccgaagtgtac  | gtgtagttact  | agtatctaat  | 1080 |
| ttctagctgt  | ggtgagagaga  | gatattttga   | agtgtcgctt   | gtggcgcaac   | tttgaattgc  | 1140 |
| tactctctatg | attaaatctc   | ttgtctactc   | ccctgacctt   | taagattgct   | ctattttaata | 1200 |
| gtactaaata  | ttctctaat    | atg          |              |              |             |      |

(2) INFORMATION FOR SEQ ID NO:489:

### (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 286 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..286

(D) OTHER INFORMATION: / Ceres Seq. ID 1567121

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:489:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Thr | Lys | Glu | Val | Val | Gly | Asp | Lys | Arg | Ser | Phe | Ser | Gly | Lys | Asp |
| 1   |     |     | 5   |     |     |     | 10  |     |     |     |     |     |     | 15  |     |
| Tyr | Gln | Asp | Pro | Pro | Pro | Glu | Pro | Leu | Phe | Asp | Ala | Thr | Glu | Leu | Gly |
|     |     |     | 20  |     |     |     | 25  |     |     |     |     |     | 30  |     |     |
| Lys | Trp | Ser | Phe | Tyr | Arg | Ala | Leu | Ile | Ala | Glu | Phe | Ile | Ala | Thr | Leu |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Leu | Phe | Leu | Tyr | Val | Thr | Ile | Met | Thr | Val | Ile | Gly | Tyr | Lys | Ser | Gln |
|     |     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |
| Thr | Asp | Pro | Ala | Leu | Asn | Pro | Asp | Gln | Cys | Thr | Gly | Val | Gly | Val | Leu |
|     |     |     |     |     |     |     | 70  |     |     |     | 75  |     |     | 80  |     |
| Gly | Ile | Ala | Trp | Ala | Phe | Gly | Gly | Met | Ile | Phe | Ile | Leu | Val | Tyr | Cys |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     | 95  |     |
| Thr | Ala | Gly | Ile | Ser | Gly | Gly | His | Ile | Asn | Pro | Ala | Val | Thr | Phe | Gly |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     | 110 |     |
| Leu | Leu | Leu | Ala | Arg | Lys | Val | Thr | Leu | Val | Arg | Ala | Val | Met | Tyr | Met |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     | 125 |     |
| Val | Ala | Gln | Cys | Leu | Gly | Ala | Ile | Cys | Gly | Val | Ala | Leu | Val | Lys | Ala |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     | 140 |     |
| Phe | Gln | Ser | Ala | Tyr | Phe | Thr | Arg | Tyr | Gly | Gly | Ala | Asn | Gly | Leu |     |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     | 155 |     |
| 145 |     |     |     |     |     |     |     |     |     |     |     |     |     | 160 |     |
| Ser | Asp | Gly | Tyr | Ser | Ile | Gly | Thr | Gly | Val | Ala | Ala | Glu | Ile | Ile | Gly |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     | 175 |     |
| Thr | Phe | Val | Leu | Val | Tyr | Thr | Val | Phe | Ser | Ala | Thr | Asp | Pro | Lys | Arg |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     | 190 |     |
| Ser | Ala | Arg | Asp | Ser | His | Val | Pro | Val | Leu | Ala | Pro | Leu | Pro | Ile | Gly |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     | 205 |     |
| Phe | Ala | Val | Phe | Ile | Val | His | Leu | Ala | Thr | Ile | Pro | Ile | Thr | Gly | Thr |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     | 220 |     |
| Gly | Ile | Asn | Pro | Ala | Arg | Ser | Leu | Gly | Ala | Ala | Ile | Ile | Tyr | Asn | Lys |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     | 235 |     |
| 225 |     |     |     |     |     |     |     |     |     |     |     |     |     | 240 |     |
| Asp | Lys | Ala | Trp | Asp | His | His | Trp | Ile | Phe | Trp | Val | Gly | Pro | Phe | Ala |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     | 255 |     |
| Gly | Ala | Ala | Ile | Ala | Ala | Phe | Tyr | His | Gln | Phe | Val | Leu | Arg | Ala | Gly |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     | 270 |     |
| Ala | Ile | Lys | Ala | Leu | Gly | Ser | Phe | Arg | Ser | Gln | Pro | His | Val |     |     |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     | 285 |     |

(2) INFORMATION FOR SEQ ID NO:490:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 231 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..231

(D) OTHER INFORMATION: / Ceres Seq. ID 1567122

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:490:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Thr | Val | Ile | Gly | Tyr | Lys | Ser | Gln | Thr | Asp | Pro | Ala | Leu | Asn | Pro |
| 1   |     |     |     |     |     |     |     |     |     |     |     |     |     | 10  |     |
| Asp | Gln | Cys | Thr | Gly | Val | Gly | Val | Leu | Gly | Ile | Ala | Trp | Ala | Phe | Gly |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     | 30  |     |
| Gly | Met | Ile | Phe | Ile | Leu | Val | Tyr | Cys | Thr | Ala | Gly | Ile | Ser | Gly | Gly |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     | 45  |     |
| His | Ile | Asn | Pro | Ala | Val | Thr | Phe | Gly | Leu | Leu | Leu | Ala | Arg | Lys | Val |

(2) INFORMATION FOR SEQ ID NO:491:

(A) LENGTH: 198 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: lin

MOLECULE TYPE: peptid

(A) NAME/KEY: peptide

{B) LOCATION: 1..198

(D) OTHER INFORMATION: / Ceres Seq. ID 1567123

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:491:

[illegible]

(2) INFORMATION FOR SEQ ID NO:492:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1174 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1174
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567128

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:492:

|             |            |             |             |              |             |      |
|-------------|------------|-------------|-------------|--------------|-------------|------|
| aaaatttgcg  | aaactaat   | tttcaatt    | ttcttctg    | atctctctga   | aagcttctct  | 60   |
| tcttctcttc  | accatgtctg | gttatcctcc  | atcaagccaa  | gggttaagggtt | acggcggttaa | 120  |
| tccaacacct  | cctcagccac | cgtacggatc  | aaccggcaat  | aacctctctc   | cgtgogggatc | 180  |
| atccggcagc  | aatctctctc | ctccgtacgg  | atcatcagcc  | tctcaccgt    | acgcagttcc  | 240  |
| ctacggagct  | cagccgcgtc | cttacgggtc  | accaccgtca  | gcaccgtacg   | cgtctctctc  | 300  |
| aggagaccat  | aataagccgc | acaaagagaa  | acctcacggc  | gcctctctacg  | gatctccatc  | 360  |
| tcccgggtgc  | tacgggtctc | atccatcgtc  | tggaccttcc  | gactacgggtg  | gttacggagg  | 420  |
| agcgccgagc  | cagttctggc | atggaggagg  | ttacggaggga | gcgcgcgagc   | agttctggaca | 480  |
| tggaggagggt | tacggagctc | ctcctccgca  | agcttcttat  | ggaagtccgt   | ttgcgtctct  | 540  |
| ggttcgcgtc  | cgttttctc  | ccggaacaga  | tccgaacatt  | gtggttctgt   | tccaagctgc  | 600  |
| ggatcgggac  | aatagtggat | tcactcgatg  | taaggagctt  | caaggagctc   | tatcttcgta  | 660  |
| taatcagagc  | ttcagcatal | gaactgttca  | tctcttatg   | tatctattca   | ccaacagcaa  | 720  |
| tgtcaggagc  | attggaccac | aagagtgtac  | ttcacttttc  | Tkkagtcttc   | agaattggag  | 780  |
| gtctatcttt  | gagaggtttg | ataaggacag  | aagcggtaga  | atagatacaa   | acgagctgag  | 840  |
| agatgcactc  | atgagccttg | ggttttctgt  | gtctctctgt  | attttggatc   | tgctggtttc  | 900  |
| aaagtgttgc  | aaaagcggag | gcagggaacag | ggctatcgaa  | tatgacaatt   | tcactcgagt  | 960  |
| ttgtttgact  | gtaaaagggc | tcaccgagaa  | gttcaaggag  | aggatgacgg   | cgtttatcag  | 1020 |
| ctcagctact  | ttcaattacg | agaaacttc   | gctcactgtt  | ttaccattcc   | tcgtcgtctt  | 1080 |
| agtgaattgt  | tttttttttt | ttgttgaccA  | aasagattgt  | tttctaactc   | tattttcttt  | 1140 |
| gtgagctttt  | ggatatttta | tttgttgtct  | tttt        |              |             |      |

(2) INFORMATION FOR SEQ ID NO:493:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 359 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..359
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567129

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:493:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Lys | Phe | Arg | Lys | Leu | Ile | Phe | Ser | Leu | Ser | Ser | Ser | Leu | Ile | Ser | Leu |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     | 15  |     |     |     |
| Lys | Ala | Ser | Leu | Leu | Leu | Leu | Thr | Met | Ser | Gly | Tyr | Pro | Pro | Ser | Ser |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     | 30  |     |     |     |
| Gln | Gly | Tyr | Gly | Tyr | Gly | Gly | Asn | Pro | Pro | Pro | Pro | Gln | Pro | Pro | Tyr |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Gly | Ser | Thr | Gly | Asn | Asn | Pro | Pro | Pro | Cys | Gly | Ser | Ser | Gly | Ser | Asn |
|     |     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |
| Pro | Pro | Pro | Pro | Tyr | Gly | Ser | Ser | Ala | Ser | Ser | Pro | Tyr | Ala | Val | Pro |
|     |     |     |     |     |     |     | 70  |     |     |     | 75  |     |     | 80  |     |
| Tyr | Gly | Ala | Gln | Pro | Ala | Pro | Tyr | Gly | Ala | Pro | Pro | Ser | Ala | Pro | Tyr |
|     |     |     |     |     |     |     | 85  |     |     |     | 90  |     |     | 95  |     |
| Ala | Ser | Pro | Pro | Gly | Asp | His | Asn | Lys | Pro | His | Lys | Glu | Lys | Pro | His |
|     |     |     |     |     |     |     | 100 |     |     |     | 105 |     |     | 110 |     |
| Gly | Ala | Ser | Tyr | Gly | Ser | Pro | Ser | Pro | Gly | Gly | Tyr | Gly | Ala | His | Pro |
|     |     |     |     |     |     |     | 115 |     |     |     | 120 |     |     | 125 |     |
| Ser | Ser | Gly | Pro | Ser | Asp | Tyr | Gly | Gly | Tyr | Gly | Gly | Ala | Pro | Gln | Gln |

|                                                                 |     |     |
|-----------------------------------------------------------------|-----|-----|
| 130                                                             | 135 | 140 |
| Ser Gly His Gly Gly Gly Tyr Gly Gly Ala Pro Gln Gln Ser Gly His | 150 | 160 |
| 145                                                             | 155 | 170 |
| Gly Gly Gly Tyr Gly Ala Pro Pro Pro Gln Ala Ser Tyr Gly Ser Pro | 165 | 175 |
| Phe Ala Ser Leu Val Pro Ser Ala Phe Pro Pro Gly Thr Asp Pro Asn | 180 | 190 |
| Ile Val Ala Cys Phe Gln Ala Ala Asp Arg Asp Asn Ser Gly Phe Ile | 195 | 205 |
| Asp Asp Lys Glu Leu Gln Gly Ala Leu Ser Ser Tyr Tyr Gln Ser Phe | 210 | 220 |
| Ser Ile Arg Thr Val His Leu Leu Met Tyr Leu Phe Thr Asn Ser Asn | 215 | 230 |
| 225                                                             | 235 | 240 |
| Val Arg Lys Ile Gly Pro Lys Glu Phe Thr Ser Leu Phe Xaa Ser Leu | 245 | 255 |
| Gln Asn Trp Arg Ser Ile Phe Glu Arg Phe Asp Lys Asp Arg Ser Gly | 260 | 270 |
| Arg Ile Asp Thr Asn Glu Leu Arg Asp Ala Leu Met Ser Leu Gly Phe | 275 | 285 |
| Ser Val Ser Pro Val Ile Leu Asp Leu Leu Val Ser Lys Phe Asp Lys | 290 | 300 |
| Ser Gly Gly Arg Asn Arg Ala Ile Glu Tyr Asp Asn Phe Ile Glu Cys | 295 | 310 |
| 305                                                             | 315 | 320 |
| Cys Leu Thr Val Lys Gly Leu Thr Glu Lys Phe Lys Glu Lys Asp Thr | 325 | 330 |
| Ala Leu Ser Gly Ser Ala Thr Phe Asn Tyr Glu Asn Phe Met Leu Thr | 335 | 345 |
| Val Leu Pro Phe Leu Val Ala                                     | 340 | 350 |
| 355                                                             |     |     |

(2) INFORMATION FOR SEQ ID NO:494:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 335 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..335
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567130

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:494:

|                                                                     |
|---------------------------------------------------------------------|
| Met Ser Gly Tyr Pro Pro Ser Ser Gln Gly Tyr Gly Tyr Gly Gly Asn     |
| 1 5 10 15                                                           |
| Pro Pro Pro Pro Gln Pro Pro Tyr Gly Ser Thr Gly Asn Asn Pro Pro     |
| 20 25 30                                                            |
| Pro Cys Gly Ser Ser Gly Ser Asn Pro Pro Pro Tyr Gly Ser Ser         |
| 35 40 45                                                            |
| Ala Ser Ser Pro Tyr Ala Val Pro Tyr Gly Ala Gln Pro Ala Pro Tyr     |
| 50 55 60                                                            |
| Gly Ala Pro Pro Ser Ala Pro Tyr Ala Ser Pro Pro Gly Asp His Asn     |
| 65 70 75 80                                                         |
| Lys Pro His Lys Glu Lys Pro His Gly Ala Ser Tyr Gly Ser Pro Ser     |
| 85 90 95                                                            |
| Pro Gly Gly Tyr Gly Ala His Pro Ser Ser Gly Pro Ser Asp Tyr Gly     |
| 100 105 110                                                         |
| Gly Tyr Gly Gly Ala Pro Gln Gln Ser Gly His Gly Gly Tyr Gly Tyr Gly |
| 115 120 125                                                         |
| Gly Ala Pro Gln Gln Ser Gly His Gly Gly Tyr Gly Ala Pro Pro         |
| 130 135 140                                                         |
| Pro Gln Ala Ser Tyr Gly Ser Pro Phe Ala Ser Leu Val Pro Ser Ala     |
| 145 150 155 160                                                     |



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Phe Pro Pro Gly Thr Asp Pro Asn Ile Val Ala Cys Phe Gln Ala Ala
 165 170 175
Asp Arg Asp Asn Ser Gly Phe Ile Asp Asp Lys Glu Leu Gln Gly Ala
 180 185 190
Leu Ser Ser Tyr Asn Gln Ser Phe Ser Ile Arg Thr Val His Leu Leu
 195 200 205
Met Tyr Leu Phe Thr Asn Ser Asn Val Arg Lys Ile Gly Pro Lys Glu
 210 215 220
Phe Thr Ser Leu Phe Xaa Ser Leu Gln Asn Trp Arg Ser Ile Phe Glu
 225 230 235
Arg Phe Asp Lys Asp Arg Ser Gly Arg Ile Asp Thr Asn Glu Leu Arg
 245 250 255
Asp Ala Leu Met Ser Leu Gly Phe Ser Val Ser Pro Val Ile Leu Asp
 260 265 270
Leu Leu Val Ser Lys Phe Asp Lys Ser Gly Gly Arg Asn Arg Ala Ile
 275 280 285
Glu Tyr Asp Asn Phe Ile Glu Cys Cys Leu Thr Val Lys Gly Leu Thr
 290 295 300
Glu Lys Phe Lys Glu Lys Asp Thr Ala Leu Ser Gly Ser Ala Thr Phe
 305 310 315 320
Asn Tyr Glu Asn Phe Met Leu Thr Val Leu Pro Phe Leu Val Ala
 325 330 335

```

(2) INFORMATION FOR SEQ ID NO:495:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1572 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1572
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567133

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:495:

```

ctctctctct ctctcacttc atctatggct tcttctcttc tgcagtctct ctctctctctg 60
ttttgccttg ctctgtttct tcttctcttc atcgctctct ccatcggcac caactatggc 120
caggctgccta acaaccttcc tccccctaaa aacgtcatcc ctctctctcaa gtctgtggga 180
gctacaaaag tcaagctcta tgacgcgcat ccacaagccc tacgtgcctt cgcgggctcc 240
ggcttcgagc tcaccgtggc cctcggtaac gagtacctgg ctcatgatgag gcacctatt 300
aaagcccaag gctgggtgaa ggagaacgtc caagcttacc tcccaaacac caagatcgtg 360
gcactcgtag tgggaacgaa agTcttcacc tcaaaccaag cagccctcac ggcagccctc 420
ttcccggtcta tgcaaacgat ccacgggtgt ctggtggatt gtggcctaaa caagcagatc 480
tttgtacgca cggctcactc actagccatc ttggatgtat ctaccctcc cgtgcgcaact 540
tccttcgccc ggcactctct cggctccttc actccatctc tggacttcca cgtcaagact 600
ggctccacca tctcatcaca cgcctacctc ttcttgcctc acgaagaaaa ccccaaacac 660
gtttctctcg actctgtact ctcccaacca aatcaaggct tcaccgctcc tggctctaatt 720
ttccactacg acaacatgct cttcgctcag gtccgacgac tctatcacgc tcttgacgct 780
gtccgcatca gctacaagaa agttcccatc gtctgtctcg agaccgggat gccttccaac 840
ggtagaccgc aagaagtcgg agccacctgc gacaatgctc gcaagtacaa ttgggaatctc 900
atcaagatga tgatgagcaa gaagatgagg acgctatttc gacttgagtg cgtactcaac 960
tactgtctct ttgtctctct taacgagaac atgaagcctg Gaccaaacctc cgagaggaaa 1020
tacggtctct tcaaccCtga cggaaactcc gtttactcac ttgggatcaa gacctcttcc 1080
actcatagta gtggtatggt tagcagcaac tccactgggt gtagttagcag tggcgggtggc 1140
ggtaaacact gtgctctctc cgcgggtggt ggcactatc agccagtcaac gggtaaccca 1200
tcaccggatt acatgtocat ttctctcgcc gggggaaaaa gcagattcgt tgagtgtgtg 1260
ttgttctctt tcttgctttt catcatcaag cttcggttgt aaaagctctc ccaactagatc 1320
tcgtgcgctt tgtactttta cggggttgat gacgtgatat agcccccaaa tttaatttaa 1380
ttagttttgt gttggtgttt tggtcggagg atgatttagg agacatacca tctttgttgt 1440
gccacattgc tctccaactc ttttcttttt tccattccat ctctctttta 1500
catagattat ttaaataatg aatcttagtt gattagattt ttctaaagaa gatgatgatt 1560
ttcgataaaa gc

```

(2) INFORMATION FOR SEQ ID NO:496:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 433 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide

- (B) LOCATION: 1..433

- (D) OTHER INFORMATION: / Ceres Seq. ID 1567134

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:496:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Ser | Leu | Ser | Leu | Thr | Ser | Ser | Met | Ala | Ser | Ser | Ser | Leu | Gln | Ser |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     | 15  |     |     |
| Leu | Phe | Ser | Leu | Phe | Cys | Leu | Ala | Leu | Phe | Ser | Leu | Pro | Leu | Ile | Val |
|     |     |     | 20  |     |     |     |     |     | 25  |     |     |     | 30  |     |     |
| Ser | Ser | Ile | Gly | Ile | Asn | Tyr | Gly | Gln | Val | Ala | Asn | Asn | Leu | Pro | Pro |
|     |     |     | 35  |     |     |     |     | 40  |     |     |     | 45  |     |     |     |
| Pro | Lys | Asn | Val | Ile | Pro | Leu | Leu | Lys | Ser | Val | Gly | Ala | Thr | Lys | Val |
|     |     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |
| Lys | Leu | Tyr | Asp | Ala | Asp | Pro | Gln | Ala | Leu | Arg | Ala | Phe | Ala | Gly | Ser |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Gly | Phe | Glu | Leu | Thr | Val | Ala | Leu | Gly | Asn | Glu | Tyr | Leu | Ala | Gln | Met |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Ser | Asp | Pro | Ile | Lys | Ala | Gln | Gly | Trp | Val | Lys | Glu | Asn | Val | Gln | Ala |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Tyr | Leu | Pro | Asn | Thr | Lys | Ile | Val | Ala | Ile | Val | Val | Gly | Asn | Glu | Val |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Leu | Thr | Ser | Asn | Gln | Ser | Ala | Leu | Thr | Ala | Ala | Leu | Phe | Pro | Ala | Met |
|     |     |     | 130 |     |     |     | 135 |     |     |     | 140 |     |     |     |     |
| Gln | Ser | Ile | His | Gly | Ala | Leu | Val | Asp | Cys | Gly | Leu | Asn | Lys | Gln | Ile |
| 145 |     |     |     |     | 150 |     |     |     | 155 |     |     |     |     | 160 |     |
| Phe | Val | Thr | Thr | Ala | His | Ser | Leu | Ala | Ile | Leu | Asp | Val | Ser | Tyr | Pro |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Pro | Ser | Ala | Thr | Ser | Phe | Arg | Arg | Asp | Leu | Leu | Gly | Ser | Leu | Thr | Pro |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     |     | 190 |     |
| Ile | Leu | Asp | Phe | His | Val | Lys | Thr | Gly | Ser | Pro | Ile | Leu | Ile | Asn | Ala |
|     |     |     | 195 |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Tyr | Pro | Phe | Phe | Ala | Tyr | Glu | Glu | Asn | Pro | Lys | His | Val | Ser | Leu | Asp |
|     |     |     | 210 |     |     |     | 215 |     |     |     | 220 |     |     |     |     |
| Phe | Val | Leu | Phe | Gln | Pro | Asn | Gln | Gly | Phe | Thr | Asp | Pro | Gly | Ser | Asn |
| 225 |     |     |     |     | 230 |     |     |     | 235 |     |     |     |     | 240 |     |
| Phe | His | Tyr | Asp | Asn | Met | Leu | Phe | Ala | Gln | Val | Asp | Ala | Val | Tyr | His |
|     |     |     | 245 |     |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Ala | Leu | Asp | Ala | Val | Gly | Ile | Ser | Tyr | Lys | Lys | Val | Pro | Ile | Val | Val |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Ser | Glu | Thr | Gly | Trp | Pro | Ser | Asn | Gly | Asp | Pro | Gln | Glu | Val | Gly | Ala |
|     |     |     | 275 |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Thr | Cys | Asp | Asn | Ala | Arg | Lys | Tyr | Asn | Gly | Asn | Leu | Ile | Lys | Met | Met |
|     |     |     | 290 |     |     |     | 295 |     |     |     | 300 |     |     |     |     |
| Met | Ser | Lys | Lys | Met | Arg | Thr | Pro | Ile | Arg | Pro | Glu | Cys | Asp | Leu | Thr |
| 305 |     |     |     |     | 310 |     |     |     | 315 |     |     |     |     | 320 |     |
| Ile | Phe | Val | Phe | Ala | Leu | Phe | Asn | Glu | Asn | Met | Lys | Pro | Gly | Pro | Thr |
|     |     |     | 325 |     |     |     |     |     | 330 |     |     |     |     | 335 |     |
| Ser | Glu | Arg | Asn | Tyr | Gly | Leu | Phe | Asn | Pro | Asp | Gly | Thr | Pro | Val | Tyr |
|     |     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |
| Ser | Leu | Gly | Ile | Lys | Thr | Ser | Ser | Thr | His | Ser | Ser | Gly | Ser | Gly | Ser |
|     |     |     | 355 |     |     |     |     | 360 |     |     |     | 365 |     |     |     |
| Ser | Asn | Ser | Thr | Gly | Gly | Ser | Ser | Ser | Gly | Gly | Gly | Gly | Asn | Thr | Gly |
|     |     |     | 370 |     |     |     | 375 |     |     |     |     | 380 |     |     |     |
| Gly | Ser | Ser | Ser | Gly | Gly | Gly | Ile | Tyr | Gln | Pro | Val | Thr | Gly | Asn | Pro |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 385 |     |     |     | 390 |     |     |     |     | 395 |     |     |     | 400 |
| Ser | Pro | Asp | Tyr | Met | Ser | Ile | Ser | Ser | Ala | Gly | Gly | Lys | Gly |
|     |     |     |     | 405 |     |     |     |     | 410 |     |     |     | 415 |
| Val | Glu | Cys | Val | Leu | Phe | Phe | Phe | Leu | Leu | Cys | Ile | Ile | Lys |
|     |     |     | 420 |     |     |     |     | 425 |     |     |     |     | 430 |
| Leu |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:497:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 425 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..425

(D) OTHER INFORMATION: / Ceres Seq. ID 1567135

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:497:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Ser | Ser | Ser | Leu | Gln | Ser | Leu | Phe | Ser | Leu | Phe | Cys | Leu | Ala |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     | 15  |     |     |
| Leu | Phe | Ser | Leu | Pro | Leu | Ile | Val | Ser | Ser | Ile | Gly | Ile | Asn | Tyr | Gly |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Gln | Val | Ala | Asn | Asn | Leu | Pro | Pro | Pro | Lys | Asn | Val | Ile | Pro | Leu | Leu |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Lys | Ser | Val | Gly | Ala | Thr | Lys | Val | Lys | Leu | Tyr | Asp | Ala | Asp | Pro | Gln |
|     |     |     | 50  |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Ala | Leu | Arg | Ala | Phe | Ala | Gly | Ser | Gly | Phe | Glu | Leu | Thr | Val | Ala | Leu |
|     |     |     | 65  |     | 70  |     |     |     | 75  |     |     |     | 80  |     |     |
| Gly | Asn | Glu | Tyr | Leu | Ala | Gln | Met | Ser | Asp | Pro | Ile | Lys | Ala | Gln | Gly |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Trp | Val | Lys | Glu | Asn | Val | Gln | Ala | Tyr | Leu | Pro | Asn | Thr | Lys | Ile | Val |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Ala | Ile | Val | Val | Gly | Asn | Glu | Val | Leu | Thr | Ser | Asn | Gln | Ser | Ala | Leu |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Thr | Ala | Ala | Leu | Phe | Pro | Ala | Met | Gln | Ser | Ile | His | Gly | Ala | Leu | Val |
|     |     |     | 130 |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Asp | Cys | Gly | Leu | Asn | Lys | Gln | Ile | Phe | Val | Thr | Thr | Ala | His | Ser | Leu |
|     |     |     | 145 |     | 150 |     |     |     |     | 155 |     |     |     | 160 |     |
| Ala | Ile | Leu | Asp | Val | Ser | Tyr | Pro | Pro | Ser | Ala | Thr | Ser | Phe | Arg | Arg |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Asp | Leu | Leu | Gly | Ser | Leu | Thr | Pro | Ile | Leu | Asp | Phe | His | Val | Lys | Thr |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Gly | Ser | Pro | Ile | Leu | Ile | Asn | Ala | Tyr | Pro | Phe | Phe | Ala | Tyr | Glu | Glu |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Asn | Pro | Lys | His | Val | Ser | Leu | Asp | Phe | Val | Leu | Phe | Gln | Pro | Asn | Gln |
|     |     | 210 |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Gly | Phe | Thr | Asp | Pro | Gly | Ser | Asn | Phe | His | Tyr | Asp | Asn | Met | Leu | Phe |
|     |     | 225 |     |     | 230 |     |     |     |     | 235 |     |     |     | 240 |     |
| Ala | Gln | Val | Asp | Ala | Val | Tyr | His | Ala | Leu | Asp | Ala | Val | Gly | Ile | Ser |
|     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |     |
| Tyr | Lys | Lys | Val | Pro | Ile | Val | Val | Ser | Glu | Thr | Gly | Trp | Pro | Ser | Asn |
|     |     |     | 260 |     |     |     | 265 |     |     |     |     | 270 |     |     |     |
| Gly | Asp | Pro | Gln | Glu | Val | Gly | Ala | Thr | Cys | Asp | Asn | Ala | Arg | Lys | Tyr |
|     |     | 275 |     |     |     | 280 |     |     |     |     | 285 |     |     |     |     |
| Asn | Gly | Asn | Leu | Ile | Lys | Met | Met | Met | Ser | Lys | Lys | Met | Arg | Thr | Pro |
|     |     | 290 |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Ile | Arg | Pro | Glu | Cys | Asp | Leu | Thr | Ile | Phe | Val | Phe | Ala | Leu | Phe | Asn |
|     |     | 305 |     |     | 310 |     |     |     | 315 |     |     |     |     | 320 |     |
| Glu | Asn | Met | Lys | Pro | Gly | Pro | Thr | Ser | Glu | Arg | Asn | Tyr | Gly | Leu | Phe |
|     |     |     | 325 |     |     |     |     |     | 330 |     |     |     |     | 335 |     |

Asn Pro Asp Gly Thr Pro Val Tyr Ser Leu Gly Ile Lys Thr Ser Ser  
340 345 350  
Thr His Ser Ser Gly Ser Gly Ser Ser Asn Ser Thr Gly Gly Ser Ser  
355 360 365  
Ser Gly Gly Gly Gly Asn Thr Gly Gly Ser Ser Ser Gly Gly Gly Ile  
370 375 380  
Tyr Gln Pro Val Thr Gly Asn Pro Ser Pro Asp Tyr Met Ser Ile Ser  
385 390 395 400  
Ser Ala Gly Gly Lys Gly Arg Phe Val Glu Cys Val Leu Phe Phe Phe  
405 410 415  
Leu Leu Cys Ile Ile Lys Leu Arg Leu  
420 425

(2) INFORMATION FOR SEQ ID NO:498:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 338 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..338

(D) OTHER INFORMATION: / Ceres Seq. ID 1567136

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:498:

Met Ser Asp Pro Ile Lys Ala Gln Gly Trp Val Lys Glu Asn Val Gln  
1 5 10 15  
Ala Tyr Leu Pro Asn Thr Lys Ile Val Ala Ile Val Val Gly Asn Glu  
20 25 30  
Val Leu Thr Ser Asn Gln Ser Ala Leu Thr Ala Ala Leu Phe Pro Ala  
35 40 45  
Met Gln Ser Ile His Gly Ala Leu Val Asp Cys Gly Leu Asn Lys Gln  
50 55 60  
Ile Phe Val Thr Thr Ala His Ser Leu Ala Ile Leu Asp Val Ser Tyr  
65 70 75 80  
Pro Pro Ser Ala Thr Ser Phe Arg Arg Asp Leu Leu Gly Ser Leu Thr  
85 90 95  
Pro Ile Leu Asp Phe His Val Lys Thr Gly Ser Pro Ile Leu Ile Asn  
100 105 110  
Ala Tyr Pro Phe Phe Ala Tyr Glu Glu Asn Pro Lys His Val Ser Leu  
115 120 125  
Asp Phe Val Leu Phe Gln Pro Asn Gln Gly Phe Thr Asp Pro Gly Ser  
130 135 140  
Asn Phe His Tyr Asp Asn Met Leu Phe Ala Gln Val Asp Ala Val Tyr  
145 150 155 160  
His Ala Leu Asp Ala Val Gly Ile Ser Tyr Lys Lys Val Pro Ile Val  
165 170 175  
Val Ser Glu Thr Gly Trp Pro Ser Asn Gly Asp Pro Gln Glu Val Gly  
180 185 190  
Ala Thr Cys Asp Asn Ala Arg Lys Tyr Asn Gly Asn Leu Ile Lys Met  
195 200 205  
Met Met Ser Lys Lys Met Arg Thr Pro Ile Arg Pro Glu Cys Asp Leu  
210 215 220  
Thr Ile Phe Val Phe Ala Leu Phe Asn Glu Asn Met Lys Pro Gly Pro  
225 230 235 240  
Thr Ser Glu Arg Asn Tyr Gly Leu Phe Asn Pro Asp Gly Thr Pro Val  
245 250 255  
Tyr Ser Leu Gly Ile Lys Thr Ser Ser Thr His Ser Ser Gly Ser Gly  
260 265 270  
Ser Ser Asn Ser Thr Gly Gly Ser Ser Ser Gly Gly Gly Asn Thr  
275 280 285  
Gly Gly Ser Ser Ser Gly Gly Ile Tyr Gln Pro Val Thr Gly Asn

(2) INFORMATION FOR SEO ID NO:499:

(A) LENGTH: 440 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ix) FEATURE:

(D) OTHER INFORMATION: / Ceres Seq. ID 1567149

|             |             |             |             |             |             |     |
|-------------|-------------|-------------|-------------|-------------|-------------|-----|
| atcataaacc  | caaaacaata  | acaaaataatt | gggttctaatt | gtgaagtgatt | attatgtgatt | 60  |
| ctctgtgac   | tttgtgtgctt | ctctctctct  | gtcttcaact  | agaagatgaa  | ccataagaact | 120 |
| caaaacccctt | ctctagtctct | tgtaaacgatt | acggcggttg  | atgtggcggt  | ggaggtatgta | 180 |
| ctatgtgctt  | taagaagaag  | tgtatgcgtt  | atctgttaaa  | tataataaag  | acacatcat   | 240 |
| tttataataa  | tatagtcatc  | atgatgttgtt | tgtattttct  | attgttatag  | ctatagatta  | 300 |
| tggatgcatt  | aggatccttt  | tgtcttgatt  | cgattttgtg  | cagtttttgc  | tgcataatat  | 360 |
| atgtgttgta  | tgaataaatg  | agggaaacct  | actgttttct  | ctatttgtatg | tttgtgtaag  | 420 |
| aagttctcag  | ttaaatttatg |             |             |             |             |     |

(2) INFORMATION FOR SEO ID NO:500:

(A) LENGTH: 74 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ix) FEATURE:

(D) OTHER INFORMATION: / Ceres Seq. ID 1567150

[illegible]

(2) INFORMATION FOR SEQ ID NO:501:

(A) LENGTH: 65 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ix) FEATURE:

(D) OTHER INFORMATION: / Ceres Seq. ID 1567151

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:501:

Met Gly Phe Ile Gly Lys Ser Val Leu Val Ser Leu Val Ala Leu Trp  
1 5 10 15  
Cys Phe Thr Ser Ser Val Phe Thr Glu Glu Val Asn His Lys Thr Gln  
20 25 30  
Thr Pro Ser Leu Ala Pro Gly Lys Asp Thr Ala Val Glu Val Ala Val  
35 40 45  
Glu Asp Val Leu Trp Ile Val Arg Arg Ser Val Ser Leu Ile Val Lys  
50 55 60

Ile  
65

(2) INFORMATION FOR SEQ ID NO:502:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1560 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1560

(D) OTHER INFORMATION: / Ceres Seq. ID 1567164

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:502:

|             |             |            |             |            |             |      |
|-------------|-------------|------------|-------------|------------|-------------|------|
| aaaagctctgt | ttattcaaga  | ttattccgat | aatgcagtc   | ctctccaccc | cacacaccat  | 60   |
| ctctctctct  | ctccccagaa  | cctctccgtc | tcgtctttct  | ccctctcttc | actcccttgc  | 120  |
| tttccccact  | cgattaccgt  | ctcttttcta | ttctttctca  | acgtcgatcc | cccccgatgc  | 180  |
| cgccgatgat  | ttcattgtcg  | gtgactgtct | cgctctacgag | gacggcgctc | tcgaagaccc  | 240  |
| ttaccttgat  | aaggaggtca  | ctcaggttgc | gaagcaggag  | cgcaagaaga | atcgccgtgg  | 300  |
| cggggctaag  | agatttagat  | aatccgagat | tgagcccgag  | aacctcgtgc | cgaggggaatg | 360  |
| gagggtatatt | caggcggagg  | tgaatctgac | gaagaaggac  | aagcgcaaaa | tagcgcagga  | 420  |
| gatggagttc  | ggggttcggg  | tggagaagaa | gaggcaagg   | ctaattccgc | tagggaaagt  | 480  |
| tgacttgaa   | gactttctca  | cgtacaagga | agccaagtgt  | gctcaattga | ggcctgtcat  | 540  |
| ctctgataaa  | cggggaatt   | tctccgacga | cagtggagcg  | tcaagcgatg | gagagaccgc  | 600  |
| tgtatcatct  | ccacgcgagc  | gagtggtccc | taagaacctc  | agatgggcag | tttacggaaa  | 660  |
| gggatttcgac | cagtttgcca  | agttcttcaa | tagcgacaag  | tacgatccca | gcgacaagaa  | 720  |
| atcccgacggc | cctcgaaagc  | tgctttcaaa | agaagagaag  | tttatgtcta | atagccggaa  | 780  |
| tcctgaccta  | gcggttgcca  | catcaaaaaa | atggcttctc  | cttcacacac | tggcagcatg  | 840  |
| tggagagttt  | tatctggttg  | attccttgct | aaagcacaat  | cttgatatca | atgcacccga  | 900  |
| tgtggggcgc  | ttgacagtat  | ttcaccgagc | aatcatttgt  | aagaagcagg | ctattactaa  | 960  |
| ctacctgctg  | agggaaatcgg | caaatccatt | tggttttgat  | gacgaagggt | cgaccttgat  | 1020 |
| gcactatgct  | gtgcaaacag  | catcagctcc | cacaataaaa  | cttctctcat | tgtataaacg  | 1080 |
| tgataaaac   | gctcaggaca  | ggcagcgggt | gactccactg  | cacgttgtag | tacaggccagc | 1140 |
| agaaagctac  | attgtaaagc  | ttcttttgat | aaaaggggcg  | gacatagaag | tgaagaacaa  | 1200 |
| ggatgggtta  | actccgcttg  | ggctttgcct | ctaccttgga  | agagagatga | ggacgtatgc  | 1260 |
| agggtgatgaa | gctgttgaaa  | gagtttccac | ttagcagaca  | caagaagaga | tttgtaacaa  | 1320 |
| cagCatgaag  | atatttgata  | gtcctttcaa | tttcagcttg  | agatacactc | acttatgaga  | 1380 |
| acctgagaaa  | aggagatgga  | ggtaaaagtg | atgattaggg  | catttgaacc | tcggagtcgg  | 1440 |
| atgtgggtcca | ctgtctcact  | tccttaaat  | tggtttgctg  | ttagtcttat | ccatcgattt  | 1500 |
| tggatattta  | tcacaaactg  | atccattctt | aaagaaaata  | tctgaaaata | aataaaaagt  | 1560 |

(2) INFORMATION FOR SEQ ID NO:503:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 430 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..430

(D) OTHER INFORMATION: / Ceres Seq. ID 1567165

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:503:

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..420

(D) OTHER INFORMATION: / Ceres Seq. ID 1567166

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:504:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Gln | Ser | Leu | Ser | Thr | Pro | His | Thr | Ile | Ser | Leu | Leu | Leu | Pro | Arg |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Thr | Ser | Pro | Ser | Arg | Leu | Ser | Pro | Ser | Ser | Gln | Thr | Ser | Ile | Leu | Pro |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Thr | Arg | Leu | Arg | Ser | Leu | Ser | Tyr | Ser | Ser | Gln | Thr | Ser | Ile | Leu | Pro |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Asp | Ala | Gly | Asp | Asp | Phe | Ile | Val | Gly | Asp | Cys | Leu | Val | Tyr | Glu | Asp |
|     |     |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Gly | Val | Phe | Glu | Asp | Pro | Tyr | Leu | Asp | Lys | Glu | Val | Thr | Gln | Val | Ala |
| 65  |     |     |     |     |     | 70  |     |     | 75  |     |     |     |     | 80  |     |
| Lys | Gln | Glu | Arg | Lys | Lys | Asn | Arg | Arg | Gly | Gly | Ala | Lys | Arg | Leu | Asp |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Glu | Ser | Glu | Ile | Glu | Pro | Glu | Asn | Leu | Val | Pro | Glu | Glu | Trp | Arg | Asp |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Ile | Gln | Ala | Glu | Val | Asn | Leu | Thr | Lys | Lys | Asp | Lys | Arg | Lys | Ile | Ala |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     |     | 125 |     |     |
| Gln | Glu | Met | Glu | Phe | Gly | Val | Arg | Val | Glu | Lys | Lys | Arg | Gln | Gly | Leu |
|     |     |     | 130 |     |     |     | 135 |     |     |     |     |     | 140 |     |     |
| Ile | Pro | Leu | Arg | Lys | Val | Asp | Leu | Asn | Asp | Phe | Leu | Thr | Tyr | Lys | Glu |
| 145 |     |     |     |     | 150 |     |     |     | 155 |     |     |     |     | 160 |     |
| Ala | Lys | Leu | Ala | Gln | Leu | Arg | Pro | Val | Ile | Leu | Asp | Lys | Pro | Gly | Asn |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Phe | Ser | Asp | Asp | Ser | Gly | Ala | Ser | Ser | Asp | Gly | Glu | Thr | Ala | Val | Ser |
|     |     |     | 180 |     |     |     | 185 |     |     |     |     |     | 190 |     |     |
| Ser | Pro | Ser | Glu | Arg | Val | Ala | Pro | Lys | Asn | Pro | Arg | Trp | Ala | Val | Tyr |
|     |     |     | 195 |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Gly | Lys | Gly | Phe | Asp | His | Val | Ala | Lys | Phe | Phe | Asn | Ser | Asp | Lys | Tyr |
|     |     |     | 210 |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Asp | Pro | Ser | Asp | Lys | Lys | Ser | Asp | Gly | Pro | Arg | Lys | Leu | Leu | Ser | Lys |
| 225 |     |     |     |     | 230 |     |     |     | 235 |     |     |     |     | 240 |     |
| Glu | Glu | Lys | Phe | Met | Leu | Asn | Ser | Arg | Asn | Pro | Asp | Leu | Ala | Val | Ala |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Thr | Ser | Lys | Lys | Trp | Leu | Pro | Leu | His | Thr | Leu | Ala | Ala | Cys | Gly | Glu |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Phe | Tyr | Leu | Val | Asp | Ser | Leu | Leu | Lys | His | Asn | Leu | Asp | Ile | Asn | Ala |
|     |     |     | 275 |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Thr | Asp | Val | Gly | Gly | Leu | Thr | Val | Leu | His | Arg | Ala | Ile | Ile | Gly | Lys |
|     |     |     | 290 |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Lys | Gln | Ala | Ile | Thr | Asn | Tyr | Leu | Leu | Arg | Glu | Ser | Ala | Asn | Pro | Phe |
|     |     |     |     | 310 |     |     |     |     |     | 315 |     |     |     | 320 |     |
| Val | Leu | Asp | Asp | Glu | Gly | Ala | Thr | Leu | Met | His | Tyr | Ala | Val | Gln | Thr |
|     |     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |     |
| Ala | Ser | Ala | Pro | Thr | Ile | Lys | Leu | Leu | Leu | Leu | Tyr | Asn | Ala | Asp | Ile |
|     |     |     | 340 |     |     |     | 345 |     |     |     |     |     | 350 |     |     |
| Asn | Ala | Gln | Asp | Arg | Asp | Gly | Trp | Thr | Pro | Leu | His | Val | Ala | Val | Gln |
|     |     |     | 355 |     |     |     | 360 |     |     |     |     | 365 |     |     |     |
| Ala | Arg | Arg | Ser | Asp | Ile | Val | Lys | Leu | Leu | Ile | Lys | Gly | Ala | Asp |     |
|     |     |     | 370 |     |     | 375 |     |     |     | 380 |     |     |     |     |     |
| Ile | Glu | Val | Lys | Asn | Lys | Asp | Gly | Leu | Thr | Pro | Leu | Gly | Leu | Cys | Leu |
| 385 |     |     |     | 390 |     |     |     |     |     | 395 |     |     |     | 400 |     |
| Tyr | Leu | Gly | Glu | Ile | Arg | Thr | Tyr | Ala | Gly | Asp | Glu | Ala | Val | Glu |     |
|     |     |     | 405 |     |     |     |     | 410 |     |     |     |     | 415 |     |     |
| Arg | Val | Ser | Thr |     |     |     |     |     |     |     |     |     |     |     |     |
|     |     |     | 420 |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:505:

(i) SEQUENCE CHARACTERISTICS:



(A) LENGTH: 290 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..290  
(D) OTHER INFORMATION: / Ceres Seq. ID 1567167  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:505:  
Met Glu Phe Gly Val Arg Val Glu Lys Lys Arg Gln Gly Leu Ile Pro  
1 5 10 15  
Leu Arg Lys Val Asp Leu Asn Asp Phe Leu Thr Tyr Lys Glu Ala Lys  
20 25 30  
Leu Ala Gln Leu Arg Pro Val Ile Leu Asp Lys Pro Gly Asn Phe Ser  
35 40 45  
Asp Asp Ser Gly Ala Ser Ser Asp Gly Glu Thr Ala Val Ser Ser Pro  
50 55 60  
Ser Glu Arg Val Ala Pro Lys Asn Pro Arg Trp Ala Val Tyr Gly Lys  
65 70 75 80  
Gly Phe Asp His Val Ala Lys Phe Phe Asn Ser Asp Lys Tyr Asp Pro  
85 90 95  
Ser Asp Lys Lys Ser Asp Gly Pro Arg Lys Leu Leu Ser Lys Glu Glu  
100 105 110  
Lys Phe Met Leu Asn Ser Arg Asn Pro Asp Leu Ala Val Ala Thr Ser  
115 120 125  
Lys Lys Trp Leu Pro Leu His Thr Leu Ala Ala Cys Gly Glu Phe Tyr  
130 135 140  
Leu Val Asp Ser Leu Leu Lys His Asn Leu Asp Ile Asn Ala Thr Asp  
145 150 155 160  
Val Gly Gly Leu Thr Val Leu His Arg Ala Ile Ile Gly Lys Lys Gln  
165 170 175  
Ala Ile Thr Asn Tyr Leu Leu Arg Glu Ser Ala Asn Pro Phe Val Leu  
180 185 190  
Asp Asp Glu Gly Ala Thr Leu Met His Tyr Ala Val Gln Thr Ala Ser  
195 200 205  
Ala Pro Thr Ile Lys Leu Leu Leu Leu Tyr Asn Ala Asp Ile Asn Ala  
210 215 220  
Gln Asp Arg Asp Gly Trp Thr Pro Leu His Val Ala Val Gln Ala Arg  
225 230 235 240  
Arg Ser Asp Ile Val Lys Leu Leu Leu Ile Lys Gly Ala Asp Ile Glu  
245 250 255  
Val Lys Asn Lys Asp Gly Leu Thr Pro Leu Gly Leu Cys Leu Tyr Leu  
260 265 270  
Gly Arg Glu Ile Arg Thr Tyr Ala Gly Asp Glu Ala Val Glu Arg Val  
275 280 285  
Ser Thr  
290

(2) INFORMATION FOR SEQ ID NO:506:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1257 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..1257  
(D) OTHER INFORMATION: / Ceres Seq. ID 1567168

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:506:

agattctttc ttctaaaccc attcgctctc tccgatcaac acaacatttg atctaacggt

|             |             |            |            |            |            |      |
|-------------|-------------|------------|------------|------------|------------|------|
| ttaattttct  | cgagaaacgg  | aagGaaaaca | aacagagcaa | tggcgctgat | gggacggtgc | 120  |
| ctgagctgaa  | attgagagtc  | gaagaagatt | cggataatgg | tgattatctg | aaattgagag | 180  |
| gaggatcaaa  | tgaagaagat  | gaaggatcat | cggcggaato | atcgagatgt | ccgataggat | 240  |
| cggttaacttc | tgtctggtttc | tgggtgaaat | tgatctcctt | ggtogtttgt | ttgggttcat | 300  |
| tggcctttgt  | tatcatcaaa  | tgggttgggc | cctttttgat | tgaaggagg  | ctgattccat | 360  |
| ttataaatgt  | gggtgagaaac | acattcagca | taccggttct | cggtctctca | ctattttgct | 420  |
| cagtggcatt  | gtttccaagc  | attcttcttc | cttcttcccc | ttccatgtgg | atggctggtc | 480  |
| ttacatttgg  | ttatggaaaa  | gggtttcttc | tgattttato | agctgcttcc | atcggttgta | 540  |
| ctcttctttt  | cttaattgga  | catctcttcc | tccacaagat | gcaagaatgg | ttgaagaaat | 600  |
| accctaaaaa  | agcagccata  | cttagagctg | ctggatgaag | aacctgggtt | catcagtttc | 660  |
| aagcagctac  | actaatccgt  | gtctctccat | tctcttacct | catttacaac | tactgcgctt | 720  |
| tagcgactgg  | agtttcattat | ggtccttata | tcttaggctc | tctgtttgga | atggttcctg | 780  |
| agatctttgt  | ctcaatttac  | acgggtataa | tgctaaggac | actagcagtt | gcactagaca | 840  |
| cgagacacac  | actttcgggt  | gtggagatag | tgtggaatgt | tcttggcttc | tgtgtaactg | 900  |
| cgagcgcgac  | tatagtcttg  | acaatctatg | cgaagaagaa | gctaagtcg  | atgcaatcag | 960  |
| aggacgtaga  | gacattacaa  | aatccaatac | tttattaact | cttttcacca | tgaccacaa  | 1020 |
| ataccatcat  | ctaacacgat  | cttgaaattg | ataatatata | atgttttttt | cttttttttg | 1080 |
| ttattcttat  | tcaattgaaa  | atgaatattt | atgtcttttt | ctctgtgata | tatgatattg | 1140 |
| atcaattgaa  | ttttgaaaa   | ttccaatgta | tatttattag | atcatctaa  | ctcttttctt | 1200 |
| ctcttgata   | taattccact  | tatgtatcat | ggaacaatgt | ctgtgtgggt | ttgtgttc   |      |

(2) INFORMATION FOR SEQ ID NO:507:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 177 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..177

(D) OTHER INFORMATION: / Ceres Seq. ID 1567169

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:507:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Trp | Met | Ala | Gly | Leu | Thr | Phe | Gly | Tyr | Gly | Lys | Gly | Phe | Leu | Leu |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ile | Leu | Ser | Ala | Ala | Ser | Ile | Gly | Val | Thr | Leu | Pro | Phe | Leu | Ile | Gly |
|     |     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |
| His | Leu | Phe | Leu | His | Lys | Met | Gln | Glu | Trp | Leu | Lys | Lys | Tyr | Pro | Lys |
|     |     |     | 35  |     |     |     |     |     | 40  |     |     |     |     | 45  |     |
| Lys | Ala | Ala | Ile | Leu | Arg | Ala | Ala | Gly | Glu | Gly | Thr | Trp | Phe | His | Gln |
|     |     |     | 50  |     |     |     |     |     | 55  |     |     |     |     | 60  |     |
| Phe | Gln | Ala | Val | Thr | Leu | Ile | Arg | Val | Ser | Pro | Phe | Pro | Tyr | Ile | Ile |
|     |     |     | 65  |     |     |     |     |     | 70  |     |     |     |     | 75  |     |
| Tyr | Asn | Tyr | Cys | Ala | Leu | Ala | Thr | Gly | Val | His | Tyr | Gly | Pro | Tyr | Ile |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Leu | Gly | Ser | Leu | Val | Gly | Met | Val | Pro | Glu | Ile | Phe | Val | Ser | Ile | Tyr |
|     |     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |
| Thr | Gly | Ile | Met | Leu | Arg | Thr | Leu | Ala | Val | Ala | Ser | Asp | Thr | Arg | His |
|     |     |     | 115 |     |     |     |     |     | 120 |     |     |     |     | 125 |     |
| Thr | Leu | Ser | Val | Val | Glu | Ile | Val | Val | Asn | Val | Leu | Gly | Phe | Cys | Val |
|     |     |     | 130 |     |     |     |     |     | 135 |     |     |     |     | 140 |     |
| Thr | Ala | Ser | Ala | Thr | Ile | Val | Cys | Thr | Ile | Tyr | Ala | Lys | Lys | Lys | Leu |
|     |     |     | 145 |     |     |     |     |     | 150 |     |     |     |     | 155 |     |
| Ser | Ala | Met | Gln | Ser | Glu | Asp | Val | Glu | Thr | Leu | Gln | Asn | Pro | Ile | Leu |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |

Tyr

(2) INFORMATION FOR SEQ ID NO:508:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 175 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

- (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:

(A) NAME/KEY: peptide  
(B) LOCATION: 1..175

(D) OTHER INFORMATION: / Ceres Seq. ID 1567170

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:508:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Gly | Leu | Thr | Phe | Gly | Tyr | Gly | Lys | Gly | Phe | Leu | Leu | Ile | Leu |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Ser | Ala | Ala | Ser | Ile | Gly | Val | Thr | Leu | Pro | Phe | Leu | Ile | Gly | His | Leu |
|     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |     |
| Phe | Leu | His | Lys | Met | Gln | Glu | Trp | Leu | Lys | Lys | Tyr | Pro | Lys | Lys | Ala |
|     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| Ala | Ile | Leu | Arg | Ala | Ala | Gly | Glu | Gly | Thr | Trp | Phe | His | Gln | Phe | Gln |
|     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |
| Ala | Val | Thr | Leu | Ile | Arg | Val | Ser | Pro | Phe | Pro | Tyr | Ile | Ile | Tyr | Asn |
|     | 65  |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Tyr | Cys | Ala | Leu | Ala | Thr | Gly | Val | His | Tyr | Gly | Pro | Tyr | Ile | Leu | Gly |
|     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Ser | Leu | Val | Gly | Met | Val | Pro | Glu | Ile | Phe | Val | Ser | Ile | Tyr | Thr | Gly |
|     | 100 |     |     |     |     |     | 105 |     |     |     |     |     | 110 |     |     |
| Ile | Met | Leu | Arg | Thr | Leu | Ala | Val | Ala | Ser | Asp | Thr | Arg | His | Thr | Leu |
|     | 115 |     |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Ser | Val | Val | Glu | Ile | Val | Val | Asn | Val | Leu | Gly | Phe | Cys | Val | Thr | Ala |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Ser | Ala | Thr | Ile | Val | Cys | Thr | Ile | Tyr | Ala | Lys | Lys | Lys | Leu | Ser | Ala |
|     | 145 |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |     |
| Met | Gln | Ser | Glu | Asp | Val | Glu | Thr | Leu | Gln | Asn | Pro | Ile | Leu | Tyr |     |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | 175 |     |

- (2) INFORMATION FOR SEQ ID NO:509:

- (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 139 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide

- (ix) FEATURE:

(A) NAME/KEY: peptide  
(B) LOCATION: 1..139

(D) OTHER INFORMATION: / Ceres Seq. ID 1567171

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:509:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Gln | Glu | Trp | Leu | Lys | Lys | Tyr | Pro | Lys | Lys | Ala | Ala | Ile | Leu | Arg |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Ala | Ala | Gly | Glu | Gly | Thr | Trp | Phe | His | Gln | Phe | Gln | Ala | Val | Thr | Leu |
|     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |     |
| Ile | Arg | Val | Ser | Pro | Phe | Pro | Tyr | Ile | Ile | Tyr | Asn | Tyr | Cys | Ala | Leu |
|     | 35  |     |     |     |     | 40  |     |     |     | 45  |     |     |     |     |     |
| Ala | Thr | Gly | Val | His | Tyr | Gly | Pro | Tyr | Ile | Leu | Gly | Ser | Leu | Val | Gly |
|     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |
| Met | Val | Pro | Glu | Ile | Phe | Val | Ser | Ile | Tyr | Thr | Gly | Ile | Met | Leu | Arg |
|     | 65  |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |     |
| Thr | Leu | Ala | Val | Ala | Ser | Asp | Thr | Arg | His | Thr | Leu | Ser | Val | Val | Glu |
|     |     | 85  |     |     |     | 90  |     |     |     |     |     | 95  |     |     |     |
| Ile | Val | Val | Asn | Val | Leu | Gly | Phe | Cys | Val | Thr | Ala | Ser | Ala | Thr | Ile |
|     | 100 |     |     |     |     | 105 |     |     |     |     |     | 110 |     |     |     |
| Val | Cys | Thr | Ile | Tyr | Ala | Lys | Lys | Lys | Leu | Ser | Ala | Met | Gln | Ser | Glu |
|     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |     |
| Asp | Val | Glu | Thr | Leu | Gln | Asn | Pro | Ile | Leu | Tyr |     |     |     |     |     |
|     | 130 |     |     |     |     | 135 |     |     |     |     |     |     |     |     |     |

- (2) INFORMATION FOR SEQ ID NO:510:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1592 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
(A) NAME/KEY: -  
(B) LOCATION: 1..1592  
(D) OTHER INFORMATION: / Ceres Seq. ID 1567172

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:510:

|             |             |            |            |             |             |      |
|-------------|-------------|------------|------------|-------------|-------------|------|
| gtagtctctc  | ttttataaac  | cacttctcga | aaactgaaac | ctttgtagag  | agaaccata   | 60   |
| gttcgataaa  | acattctttt  | tgcacctgag | acttgccaac | ttggttttac  | tcaaatgaag  | 120  |
| atcttctctt  | gttgatgggt  | ataagttcaa | tatgatgaaa | agtittggcta | gtgcggttgg  | 180  |
| agggaaagcg  | gcgaggcgat  | gtgatagctg | cgtaagagg  | cgggcacgtt  | ggtattgcgc  | 240  |
| agctgatgat  | gcctttcttt  | gccatgcttg | tgacgggttg | gtccactcgg  | caaaccctct  | 300  |
| tgctcgtaga  | cacgagagag  | ttcgcttgaa | atcggtcagc | gcgggaaaaa  | atcgccatgc  | 360  |
| ctcgccgctc  | caccaagcca  | cgtggcatca | gggattttac | cgtaaacgctc | ggaccacca   | 420  |
| tgagggcaag  | aagagccaca  | cgatggtttt | tcatgatctt | gtgccggaga  | tgagccagga  | 480  |
| ggatcaagcg  | gagagttacg  | aggtggaaga | gcagtcata  | tttgaggtgc  | cggtgatgaa  | 540  |
| ctcgatgggt  | gaggagcaat  | gctttaacca | atccctggag | aaacagaaat  | agtttccaat  | 600  |
| gatgccctta  | agttttcaaga | gtagtgaacg | agaagatgac | gacaacgctg  | agagtgtgtc  | 660  |
| gaatgggttt  | ttcccaaccg  | acatggaact | agctcagttc | acagctgacg  | tgagagctct  | 720  |
| actcgttgga  | ggggatcgag  | agtttcatc  | catagaagaa | ctagggttag  | gtgaagtgtt  | 780  |
| aaagatcgaa  | aaagaggagg  | tgaggagaag | ggaaggaggt | gtgacaagag  | aaagtcatga  | 840  |
| tcaagatgaa  | ggtgatgaga  | catccccatt | tgaataaagc | tttgactacg  | agtacacaca  | 900  |
| caagaccaca  | ttcgatgaag  | gagaagaaga | tgagaagaaa | gacgtgatga  | agaatgtgat  | 960  |
| ggagatggga  | gtgaatgaga  | tgagtgggtg | gattaaagaa | gagaagaagg  | agaagcctct  | 1020 |
| tatgcttaga  | ttggactatg  | aatcagtcac | ttccacttgg | ggaggccaa   | ggagcccatg  | 1080 |
| gaccgcocg   | gtgccatctg  | aaatagacct | cgacatggtt | tgtttcccaa  | cccatccatt  | 1140 |
| gggtgaaagt  | ggagcagagg  | ctcatcatca | caaccacttc | gcggcctcag  | ggttacacct  | 1200 |
| aggagatgct  | ggggatggag  | gaagagagcg | taggttttca | agataccogag | agaaaaaggag | 1260 |
| gacaaggttg  | ttctccaaga  | agataaggta | cgaggtacgt | aaattgaagg  | cagataaaag  | 1320 |
| gcctcgcatg  | aaaggaagggt | tcgtcaagag | atcttcaatt | ggtgttgctc  | actaaagaac  | 1380 |
| ttaatttaatt | atggatatta  | aattactttg | ctctcatctt | gctttttgtg  | tgctatagtt  | 1440 |
| ttggtgattg  | ttagctttct  | ttttctgcat | tcatagagaa | ttttgcacgt  | ttttgtgagc  | 1500 |
| tacgtatgta  | cataaatata  | tcacaaaaaa | atgtgacat  | cttgtaagca  | ctgatttata  | 1560 |

(2) INFORMATION FOR SEQ ID NO:511:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 407 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..407  
(D) OTHER INFORMATION: / Ceres Seq. ID 1567173

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:511:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Met | Lys | Ser | Leu | Ala | Ser | Ala | Val | Gly | Gly | Lys | Thr | Ala | Arg | Ala |
| 1   |     |     |     | 5   |     |     |     |     |     | 10  |     |     |     | 15  |     |
| Cys | Asp | Ser | Cys | Val | Lys | Arg | Arg | Ala | Arg | Thr | Tyr | Cys | Ala | Ala | Asp |
|     |     |     |     | 20  |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Asp | Ala | Phe | Leu | Cys | His | Ala | Cys | Asp | Gly | Ser | Val | His | Ser | Ala | Asn |
|     |     |     |     | 35  |     |     |     | 40  |     |     |     | 45  |     |     |     |
| Pro | Leu | Ala | Arg | Arg | His | Glu | Arg | Val | Arg | Leu | Lys | Ser | Ala | Ser | Ala |
|     |     |     |     | 50  |     |     | 55  |     |     |     | 60  |     |     |     |     |
| Gly | Lys | Tyr | Arg | His | Ala | Ser | Pro | Pro | His | Gln | Ala | Thr | Trp | His | Gln |
|     |     |     |     | 65  |     | 70  |     |     |     | 75  |     |     |     | 80  |     |
| Gly | Phe | Thr | Arg | Lys | Lys | Ala | Thr | Pro | Arg | Gly | Gly | Lys | Lys | Ser | His |
|     |     |     |     | 85  |     |     |     | 90  |     |     |     |     |     | 95  |     |

Thr Met Val Phe His Asp Leu Val Pro Glu Met Ser Thr Glu Asp Gln  
100 105 110  
Ala Glu Ser Tyr Glu Val Glu Glu Gln Leu Ile Phe Glu Val Pro Val  
115 120 125  
Met Asn Ser Met Val Glu Glu Gln Cys Phe Asn Gln Ser Leu Glu Lys  
130 135 140  
Gln Asn Glu Phe Pro Met Met Pro Leu Ser Phe Lys Ser Ser Asp Glu  
145 150 155 160  
Glu Asp Asp Asp Asn Ala Glu Ser Cys Leu Asn Gly Leu Phe Pro Thr  
165 170 175  
Asp Met Glu Leu Ala Gln Phe Thr Ala Asp Val Glu Thr Leu Leu Gly  
180 185 190  
Gly Gly Asp Arg Glu Phe His Ser Ile Glu Glu Leu Gly Leu Gly Glu  
195 200 205  
Met Leu Lys Ile Glu Lys Glu Glu Val Glu Glu Glu Glu Gly Val Val  
210 215 220  
Thr Arg Glu Val His Asp Gln Asp Glu Gly Asp Glu Thr Ser Pro Phe  
225 230 235 240  
Glu Ile Ser Phe Asp Tyr Glu Tyr Thr His Lys Thr Thr Phe Asp Glu  
245 250 255  
Gly Glu Glu Asp Glu Lys Glu Asp Val Met Lys Asn Val Met Glu Met  
260 265 270  
Gly Val Asn Glu Met Ser Gly Gly Ile Lys Glu Glu Lys Lys Glu Lys  
275 280 285  
Ala Leu Met Leu Arg Leu Asp Tyr Glu Ser Val Ile Ser Thr Trp Gly  
290 295 300  
Gly Gln Gly Ile Pro Trp Thr Ala Arg Val Pro Ser Glu Ile Asp Leu  
305 310 315 320  
Asp Met Val Cys Phe Pro Thr His Thr Met Gly Glu Ser Gly Ala Glu  
325 330 335  
Ala His His His Asn His Phe Arg Gly Leu Gly Leu His Leu Gly Asp  
340 345 350  
Ala Gly Asp Gly Gly Arg Glu Ala Arg Val Ser Arg Tyr Arg Glu Lys  
355 360 365  
Arg Arg Thr Arg Leu Phe Ser Lys Lys Ile Arg Tyr Glu Val Arg Lys  
370 375 380  
Leu Asn Ala Asp Lys Arg Pro Arg Met Lys Gly Arg Phe Val Lys Arg  
385 390 395 400  
Ser Ser Ile Gly Val Ala His  
405

(2) INFORMATION FOR SEQ ID NO:512:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 406 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..406

(D) OTHER INFORMATION: / Ceres Seq. ID 1567174

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:512:

Met Lys Ser Leu Ala Ser Ala Val Gly Gly Lys Thr Ala Arg Ala Cys  
1 5 10 15  
Asp Ser Cys Val Lys Arg Arg Ala Arg Trp Tyr Cys Ala Ala Asp Asp  
20 25 30  
Ala Phe Leu Cys His Ala Cys Asp Gly Ser Val His Ser Ala Asn Pro  
35 40 45  
Leu Ala Arg Arg His Glu Arg Val Arg Leu Lys Ser Ala Ser Ala Gly  
50 55 60  
Lys Tyr Arg His Ala Ser Pro His Gln Ala Thr Trp His Gln Gly

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Phe | Thr | Arg | Lys | Ala | Arg | Thr | Pro | Arg | Gly | Gly | Lys | Lys | Ser | His | Thr |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Met | Val | Phe | His | Asp | Leu | Val | Pro | Glu | Met | Ser | Thr | Glu | Asp | Gln | Ala |
|     |     |     |     | 100 |     |     |     |     | 105 |     |     |     | 110 |     |     |
| Glu | Ser | Tyr | Glu | Val | Glu | Glu | Gln | Leu | Ile | Phe | Glu | Val | Pro | Val | Met |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Asn | Ser | Met | Val | Glu | Glu | Gln | Cys | Phe | Asn | Gln | Ser | Leu | Glu | Lys | Gln |
|     |     | 130 |     |     |     |     | 135 |     |     |     | 140 |     |     |     |     |
| Asn | Glu | Phe | Pro | Met | Met | Pro | Leu | Ser | Phe | Lys | Ser | Ser | Asp | Glu | Glu |
|     |     | 145 |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |     |
| Asp | Asp | Asp | Asn | Ala | Glu | Ser | Cys | Leu | Asn | Gly | Leu | Phe | Pro | Thr | Asp |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Met | Glu | Leu | Ala | Gln | Phe | Thr | Ala | Asp | Val | Glu | Thr | Leu | Leu | Gly | Gly |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Gly | Asp | Arg | Glu | Phe | His | Ser | Ile | Glu | Glu | Leu | Gly | Leu | Gly | Glu | Met |
|     |     | 195 |     |     |     |     | 200 |     |     |     | 205 |     |     |     |     |
| Leu | Lys | Ile | Glu | Lys | Glu | Glu | Val | Glu | Glu | Glu | Gly | Val | Val | Thr |     |
|     |     | 210 |     |     |     |     | 215 |     |     |     | 220 |     |     |     |     |
| Arg | Glu | Val | His | Asp | Gln | Asp | Glu | Gly | Asp | Glu | Thr | Ser | Pro | Phe | Glu |
|     |     | 225 |     |     | 230 |     |     |     | 235 |     |     |     |     |     | 240 |
| Ile | Ser | Phe | Asp | Tyr | Glu | Tyr | Thr | His | Lys | Thr | Thr | Phe | Asp | Glu | Gly |
|     |     |     | 245 |     |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Glu | Glu | Asp | Glu | Lys | Glu | Asp | Val | Met | Lys | Asn | Val | Met | Glu | Met | Gly |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Val | Asn | Glu | Met | Ser | Gly | Gly | Ile | Lys | Glu | Glu | Lys | Lys | Glu | Lys | Ala |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Leu | Met | Leu | Arg | Leu | Asp | Tyr | Glu | Ser | Val | Ile | Ser | Thr | Trp | Gly | Gly |
|     |     | 290 |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Gln | Gly | Ile | Pro | Trp | Thr | Ala | Arg | Val | Pro | Ser | Glu | Ile | Asp | Leu | Asp |
|     |     | 305 |     |     | 310 |     |     |     | 315 |     |     |     |     | 320 |     |
| Met | Val | Cys | Phe | Pro | Thr | His | Thr | Met | Gly | Glu | Ser | Gly | Ala | Glu | Ala |
|     |     |     | 325 |     |     |     |     |     | 330 |     |     |     | 335 |     |     |
| His | His | His | Asn | His | Phe | Arg | Gly | Leu | Gly | Leu | His | Leu | Gly | Asp | Ala |
|     |     |     | 340 |     |     |     | 345 |     |     |     |     | 350 |     |     |     |
| Gly | Asp | Gly | Gly | Arg | Glu | Ala | Arg | Val | Ser | Arg | Tyr | Arg | Glu | Lys | Arg |
|     |     | 355 |     |     |     |     | 360 |     |     |     | 365 |     |     |     |     |
| Arg | Thr | Arg | Leu | Phe | Ser | Lys | Lys | Ile | Arg | Tyr | Glu | Val | Arg | Lys | Leu |
|     |     | 370 |     |     |     | 375 |     |     |     |     | 380 |     |     |     |     |
| Asn | Ala | Asp | Lys | Arg | Pro | Arg | Met | Lys | Gly | Arg | Phe | Val | Lys | Arg | Ser |
|     |     | 385 |     |     | 390 |     |     |     |     | 395 |     |     |     |     | 400 |
| Ser | Ile | Gly | Val | Ala | His |     |     |     |     |     |     |     |     |     |     |
|     |     |     |     | 405 |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:513:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 310 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..310

(D) OTHER INFORMATION: / Ceres Seq. ID 1567175

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:513:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Val | Phe | His | Asp | Leu | Val | Pro | Glu | Met | Ser | Thr | Glu | Asp | Gln | Ala |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Glu | Ser | Tyr | Glu | Val | Glu | Glu | Gln | Leu | Ile | Phe | Glu | Val | Pro | Val | Met |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Asn | Ser | Met | Val | Glu | Glu | Gln | Cys | Phe | Asn | Gln | Ser | Leu | Glu | Lys | Gln |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |

Asn Glu Phe Pro Met Met Pro Leu Ser Phe Lys Ser Ser Asp Glu Glu  
50 55 60  
Asp Asp Asp Asn Ala Glu Ser Cys Leu Asn Gly Leu Phe Pro Thr Asp  
65 70 75 80  
Met Glu Leu Ala Gln Phe Thr Ala Asp Val Glu Thr Leu Leu Gly Gly  
85 90 95  
Gly Asp Arg Glu Phe His Ser Ile Glu Leu Gly Leu Gly Glu Met  
100 105 110  
Leu Lys Ile Glu Lys Glu Glu Val Glu Glu Glu Gly Val Val Thr  
115 120 125  
Arg Glu Val His Asp Gln Asp Glu Gly Asp Glu Thr Ser Pro Phe Glu  
130 135 140  
Ile Ser Phe Asp Tyr Glu Tyr Thr His Lys Thr Thr Phe Asp Glu Gly  
145 150 155 160  
Glu Glu Asp Glu Lys Glu Asp Val Met Lys Asn Val Met Glu Met Gly  
165 170 175  
Val Asn Glu Met Ser Gly Gly Ile Lys Glu Lys Lys Glu Lys Ala  
180 185 190  
Leu Met Leu Arg Leu Asp Tyr Glu Ser Val Ile Ser Thr Trp Gly Gly  
195 200 205  
Gln Gly Ile Pro Trp Thr Ala Arg Val Pro Ser Glu Ile Asp Leu Asp  
210 215 220  
Met Val Cys Phe Pro Thr His Thr Met Gly Glu Ser Gly Ala Glu Ala  
225 230 235 240  
His His His Asn His Phe Arg Gly Leu Gly Leu His Leu Gly Asp Ala  
245 250 255  
Gly Asp Gly Gly Arg Glu Ala Arg Val Ser Arg Tyr Arg Glu Lys Arg  
260 265 270  
Arg Thr Arg Leu Phe Ser Lys Lys Ile Arg Tyr Glu Val Arg Lys Leu  
275 280 285  
Asn Ala Asp Lys Arg Pro Arg Met Lys Gly Arg Phe Val Lys Arg Ser  
290 295 300  
Ser Ile Gly Val Ala His  
305 310

(2) INFORMATION FOR SEQ ID NO:514:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1071 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1071

(D) OTHER INFORMATION: / Ceres Seq. ID 1567183

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:514:

|             |             |             |             |             |             |     |
|-------------|-------------|-------------|-------------|-------------|-------------|-----|
| attgtgttag  | tggtaatcaa  | atccgggtgaa | aatggagcgg  | agccgagtgta | ccagagaagc  | 60  |
| accgaccgga  | accaggatcc  | tgcttgcttc  | actctctgcg  | atggttgacg  | agtcaagtac  | 120 |
| gtttccgatt  | gatctccaca  | agactagaat  | gcagctccat  | ggttccgggt  | ccgcttctgg  | 180 |
| tcgcgcatcg  | attggcgctt  | tcggagtcgt  | atcggagatt  | gcgagaaaag  | aaggagtgtg  | 240 |
| tggtctctac  | aaaggctctat | ctccggcgat  | tatcacacac  | ctgttctaca  | cgctatcag   | 300 |
| aatcatttga  | tacgagaatt  | tgaaaggact  | catcgtcaga  | tctgaaacta  | acaatagcga  | 360 |
| gtctctcttc  | ctccgccaca  | aggctctcgt  | cggaggattt  | tctggtgtta  | tagctcaggt  | 420 |
| agtgctagtg  | ccagctgatt  | tggtcaaatg  | gagaatgcac  | gcagatgtga  | gattgggtgag | 480 |
| ccaaggcctg  | aaaccgaggt  | actcgggacc  | aatcgaggct  | tttaccaaaa  | tcctacaatc  | 540 |
| agaaggagta  | aaagggttat  | ggaaagggtg  | tcttccaaac  | atccagagag  | cattttagtg  | 600 |
| gaatatggga  | gaactagctt  | gctatgatca  | cgccaaaacac | tttgtcatcg  | ataagaagat  | 660 |
| tgctgaggat  | aaactttttg  | cgcacactct  | tgctcttata  | atgtccggtc  | ttgcttcgac  | 720 |
| aagtgttagt  | tgctccagctg | atgtggtgga  | gacgaggatg  | atgaaccagg  | gtgaaaatgc  | 780 |
| tggtgacaga  | aattcttaac  | actgtttggc  | gaagacgggt  | aagtttgaa   | gaataagagc  | 840 |
| tttgtgtgaaa | ggttctctcc  | cgacatgggc  | aaggcttgga  | ccgtggcagtg | tcgtgttttg  | 900 |

gggtctcctat gagaagttaa gactgctggc aggaatctct tccttctaga cctgagaacc 960  
tggaagaacga aatttgagat ttgtgttctt tagttcttac ttgttagttg ttacacattt 1020  
tgtaagaacc ttgagaagta gcatcagttt ctgattaacg cgagaagagt t

(2) INFORMATION FOR SEQ ID NO:515:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 305 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..305

(D) OTHER INFORMATION: / Ceres Seq. ID 1567184

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:515:

Met Glu Arg Ser Arg Val Thr Arg Glu Ala Pro Thr Gly Thr Arg Ile  
1 5 10 15  
Leu Leu Ala Ser Leu Ser Ala Met Val Ala Glu Ser Val Thr Phe Pro  
20 25 30  
Ile Asp Leu Thr Lys Thr Arg Met Gln Leu His Gly Ser Gly Ser Ala  
35 40 45  
Ser Gly Ala His Arg Ile Gly Ala Phe Gly Val Val Ser Glu Ile Ala  
50 55 60  
Arg Lys Glu Gly Val Ile Gly Leu Tyr Lys Gly Leu Ser Pro Ala Ile  
65 70 75 80  
Ile Arg His Leu Phe Tyr Thr Pro Ile Arg Ile Ile Gly Tyr Glu Asn  
85 90 95  
Leu Lys Gly Leu Ile Val Arg Ser Glu Thr Asn Asn Ser Glu Ser Leu  
100 105 110  
Pro Leu Ala Thr Lys Ala Leu Val Gly Gly Phe Ser Gly Val Ile Ala  
115 120 125  
Gln Val Val Ala Ser Pro Ala Asp Leu Val Lys Val Arg Met Gln Ala  
130 135 140  
Asp Gly Arg Leu Val Ser Gln Gly Leu Lys Pro Arg Tyr Ser Gly Pro  
145 150 155 160  
Ile Glu Ala Phe Thr Lys Ile Leu Gln Ser Glu Gly Val Lys Gly Leu  
165 170 175  
Trp Lys Gly Val Leu Pro Asn Ile Gln Arg Ala Phe Leu Val Asn Met  
180 185 190  
Gly Glu Leu Ala Cys Tyr Asp His Ala Lys His Phe Val Ile Asp Lys  
195 200 205  
Lys Ile Ala Glu Asp Asn Ile Phe Ala His Thr Leu Ala Ser Ile Met  
210 215 220  
Ser Gly Leu Ala Ser Thr Ser Leu Ser Cys Pro Ala Asp Val Val Lys  
225 230 235 240  
Thr Arg Met Met Asn Gln Gly Glu Asn Ala Val Tyr Arg Asn Ser Tyr  
245 250 255  
Asp Cys Leu Val Lys Thr Val Lys Phe Glu Gly Ile Arg Ala Leu Trp  
260 265 270  
Lys Gly Phe Phe Pro Thr Trp Ala Arg Leu Gly Pro Trp Gln Phe Val  
275 280 285  
Phe Trp Val Ser Tyr Glu Lys Phe Arg Leu Leu Ala Gly Ile Ser Ser  
290 295 300  
Phe  
305

(2) INFORMATION FOR SEQ ID NO:516:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 282 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear



(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..282

(D) OTHER INFORMATION: / Ceres Seq. ID 1567185

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:516:

Met Val Ala Glu Ser Val Thr Phe Pro Ile Asp Leu Thr Lys Thr Arg  
1 5 10 15  
Met Gln Leu His Gly Ser Gly Ser Ala Ser Gly Ala His Arg Ile Gly  
20 25 30  
Ala Phe Gly Val Val Ser Glu Ile Ala Arg Lys Glu Gly Val Ile Gly  
35 40 45  
Leu Tyr Lys Gly Leu Ser Pro Ala Ile Ile Arg His Leu Phe Tyr Thr  
50 55 60  
Pro Ile Arg Ile Ile Gly Tyr Glu Asn Leu Lys Gly Leu Ile Val Arg  
65 70 75 80  
Ser Glu Thr Asn Asn Ser Glu Ser Leu Pro Leu Ala Thr Lys Ala Leu  
85 90 95  
Val Gly Gly Phe Ser Gly Val Ile Ala Gln Val Val Ala Ser Pro Ala  
100 105 110  
Asp Leu Val Lys Val Arg Met Gln Ala Asp Gly Arg Leu Val Ser Gln  
115 120 125  
Gly Leu Lys Pro Arg Tyr Ser Gly Pro Ile Glu Ala Phe Thr Lys Ile  
130 135 140  
Leu Gln Ser Glu Gly Val Lys Gly Leu Trp Lys Gly Val Leu Pro Asn  
145 150 155 160  
Ile Gln Arg Ala Phe Leu Val Asn Met Gly Glu Leu Ala Cys Tyr Asp  
165 170 175  
His Ala Lys His Phe Val Ile Asp Lys Lys Ile Ala Glu Asp Asn Ile  
180 185 190  
Phe Ala His Thr Leu Ala Ser Ile Met Ser Gly Leu Ala Ser Thr Ser  
195 200 205  
Leu Ser Cys Pro Ala Asp Val Val Lys Thr Arg Met Met Asn Gln Gly  
210 215 220  
Glu Asn Ala Val Tyr Arg Asn Ser Tyr Asp Cys Leu Val Lys Thr Val  
225 230 235 240  
Lys Phe Glu Gly Ile Arg Ala Leu Trp Lys Gly Phe Phe Pro Thr Trp  
245 250 255  
Ala Arg Leu Gly Pro Trp Gln Phe Val Phe Trp Val Ser Tyr Glu Lys  
260 265 270  
Phe Arg Leu Leu Ala Gly Ile Ser Ser Phe  
275 280

(2) INFORMATION FOR SEQ ID NO:517:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 266 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..266

(D) OTHER INFORMATION: / Ceres Seq. ID 1567186

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:517:

Met Gln Leu His Gly Ser Gly Ser Ala Ser Gly Ala His Arg Ile Gly  
1 5 10 15  
Ala Phe Gly Val Val Ser Glu Ile Ala Arg Lys Glu Gly Val Ile Gly  
20 25 30  
Leu Tyr Lys Gly Leu Ser Pro Ala Ile Ile Arg His Leu Phe Tyr Thr  
35 40 45  
Pro Ile Arg Ile Ile Gly Tyr Glu Asn Leu Lys Gly Leu Ile Val Arg

|                                                                 |     |     |     |
|-----------------------------------------------------------------|-----|-----|-----|
| 50                                                              | 55  | 60  |     |
| Ser Glu Thr Asn Asn Ser Glu Ser Leu Pro Leu Ala Thr Lys Ala Leu |     |     |     |
| 65                                                              | 70  | 75  | 80  |
| Val Gly Gly Phe Ser Gly Val Ile Ala Gln Val Val Ala Ser Pro Ala |     |     |     |
| 85                                                              | 90  | 95  |     |
| Asp Leu Val Lys Val Arg Met Gln Ala Asp Gly Arg Leu Val Ser Gln |     |     |     |
| 100                                                             | 105 | 110 |     |
| Gly Leu Lys Pro Arg Tyr Ser Gly Pro Ile Glu Ala Phe Thr Lys Ile |     |     |     |
| 115                                                             | 120 | 125 |     |
| Leu Gln Ser Glu Gly Val Lys Gly Leu Trp Lys Gly Val Leu Pro Asn |     |     |     |
| 130                                                             | 135 | 140 |     |
| Ile Gln Arg Ala Phe Leu Val Asn Met Gly Glu Leu Ala Cys Tyr Asp |     |     |     |
| 145                                                             | 150 | 155 | 160 |
| His Ala Lys His Phe Val Ile Asp Lys Lys Ile Ala Glu Asp Asn Ile |     |     |     |
| 165                                                             | 170 | 175 |     |
| Phe Ala His Thr Leu Ala Ser Ile Met Ser Gly Leu Ala Ser Thr Ser |     |     |     |
| 180                                                             | 185 | 190 |     |
| Leu Ser Cys Pro Ala Asp Val Val Lys Thr Arg Met Met Asn Gln Gly |     |     |     |
| 195                                                             | 200 | 205 |     |
| Glu Asn Ala Val Tyr Arg Asn Ser Tyr Asp Cys Leu Val Lys Thr Val |     |     |     |
| 210                                                             | 215 | 220 |     |
| Lys Phe Glu Gly Ile Arg Ala Leu Trp Lys Gly Phe Phe Pro Thr Trp |     |     |     |
| 225                                                             | 230 | 235 | 240 |
| Ala Arg Leu Gly Pro Trp Gln Phe Val Phe Trp Val Ser Tyr Glu Lys |     |     |     |
| 245                                                             | 250 | 255 |     |
| Phe Arg Leu Leu Ala Gly Ile Ser Ser Phe                         |     |     |     |
| 260                                                             | 265 |     |     |

(2) INFORMATION FOR SEQ ID NO:518:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1266 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1266
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567209

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:518:

|            |             |             |             |             |             |      |
|------------|-------------|-------------|-------------|-------------|-------------|------|
| gcgtgtgcat | cggttttctca | gattcctgaa  | taatcattcc  | cttcggattc  | caaaatcccc  | 60   |
| aaacctcacc | cactcctcca  | tctcccggtat | tcggattccc  | agaatcatgc  | ccatggagaaa | 120  |
| cgacaatggc | ccacacgttg  | gcaacgtcgt  | cgtcaccgct  | gagcaagcga  | ccaagattaa  | 180  |
| cgagactgat | ggacggttgc  | cgagagaatcg | gcagaccggt  | gttgctctct  | acaccggaaag | 240  |
| tggtagcgag | agagagagagc | aagggggttgg | agagtcggca  | gttgctgtgg  | cggtgccgggt | 300  |
| ggaggagagc | ggatcgattt  | cggtggggaga | gctacctgct  | ccccgatctt  | ctctctgtag  | 360  |
| agttccgttt | actaatctaa  | gccaaattga  | tgccgatctt  | gctcttgctc  | gcacactcca  | 420  |
| agaacaggag | cgggcgctata | tgatgttgac  | catgaatagt  | gaaatcagtg  | actatggagag | 480  |
| ctgggaaact | ggaagctatg  | tatacagatga | ggatgagttt  | gatgaccocg  | agaatgagga  | 540  |
| tgaggatgat | gatgaagatg  | aatatgaaac  | agatgatgat  | cctcaggaag  | atgggcttga  | 600  |
| tgccaattgt | cacgcctaag  | aagatgatca  | aggaagatgac | gggAactctg  | acattgaaga  | 660  |
| agttgtctat | acagatgatg  | aggcctatgc  | tagagctctt  | caagaagctg  | aagaaaagga  | 720  |
| tatggctgct | agattgtctg  | ccttatctgg  | gttagoaaac  | cggtgtggtg  | aaagctcaga  | 780  |
| ggatgagagt | catacttctc  | aggatgccag  | ggatgagatg  | gatcctgatg  | agctttcata  | 840  |
| tgaggagttg | cttgcaacttg | gcgacattgt  | gggaaccgaa  | agtagaggtat | tgtctctcga  | 900  |
| tacaattgct | tctttgcctt  | caaaaagata  | taaagaagga  | gacaatcaga  | acggaaccaa  | 960  |
| tgagtcatgt | gttatatgtc  | gtttagacta  | tgaggatgac  | gaagacctga  | tactgtctcc  | 1020 |
| atgcaaacat | tcttaaccat  | cggagtgcac  | aaacaactgg  | ttgaagataa  | ataaggtttg  | 1080 |
| ccccgtatgc | agtgcagaag  | tttcaacctc  | gaacctctga  | caaaagctga  | gagggcaaaag | 1140 |
| aagaaagatt | cagaaagaat  | cataagctaa  | gaacctcaaa  | accttagctg  | ccgtgtttga  | 1200 |
| cactctttat | aaacaaaata  | acatcatcag  | atttccttgg  | atcctttaaa  | aaatctcaaa  | 1260 |
| gattgg     |             |             |             |             |             |      |

(2) INFORMATION FOR SEQ ID NO:519:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 375 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..375

(D) OTHER INFORMATION: / Ceres Seq. ID 1567210

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:519:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Cys | His | Arg | Phe | Leu | Arg | Phe | Leu | Asn | Asn | His | Ser | Leu | Pro | Ile |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     | 15  |     |     |
| Pro | Lys | Ser | Pro | Asn | Leu | Ile | His | Ser | Ser | Ile | Ser | Arg | Ile | Arg | Ile |
|     |     |     | 20  |     |     |     |     |     | 25  |     |     |     | 30  |     |     |
| Pro | Arg | Ile | Met | Pro | Met | Glu | Asn | Asp | Asn | Gly | Pro | His | Val | Gly | Asn |
|     |     |     | 35  |     |     |     |     |     | 40  |     |     |     | 45  |     |     |
| Val | Val | Val | Thr | Ala | Glu | Gln | Ala | Thr | Lys | Ile | Asn | Glu | Thr | Asp | Gly |
|     |     |     | 50  |     |     |     |     |     | 55  |     |     |     | 60  |     |     |
| Arg | Leu | Pro | Glu | Asn | Arg | Gln | Thr | Gly | Val | Val | Ser | Asp | Thr | Gly | Ser |
|     |     |     | 65  |     |     |     |     |     | 70  |     |     |     | 75  |     |     |
| Gly | Ser | Glu | Arg | Gly | Glu | Gln | Gly | Val | Gly | Glu | Ser | Ala | Val | Ala | Val |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     | 95  |     |     |
| Ala | Val | Pro | Val | Glu | Glu | Ser | Gly | Ser | Ile | Ser | Val | Gly | Glu | Leu | Pro |
|     |     |     | 100 |     |     |     |     |     | 105 |     |     |     | 110 |     |     |
| Ala | Pro | Arg | Ser | Ser | Ser | Ala | Arg | Val | Pro | Phe | Thr | Asn | Leu | Ser | Gln |
|     |     |     | 115 |     |     |     |     |     | 120 |     |     |     | 125 |     |     |
| Ile | Asp | Ala | Asp | Leu | Ala | Leu | Ala | Arg | Thr | Leu | Gln | Glu | Gln | Glu | Arg |
|     |     |     | 130 |     |     |     |     |     | 135 |     |     |     | 140 |     |     |
| Ala | Tyr | Met | Met | Leu | Thr | Met | Asn | Ser | Glu | Ile | Ser | Asp | Tyr | Gly | Ser |
|     |     |     | 145 |     |     |     |     |     | 150 |     |     |     | 155 |     |     |
| Trp | Glu | Thr | Gly | Ser | Tyr | Val | Tyr | Asp | Glu | Asp | Glu | Phe | Asp | Asp | Pro |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     | 175 |     |     |
| Glu | Asn | Glu | Asp | Glu | Asp | Asp | Asp | Glu | Asp | Glu | Tyr | Glu | Thr | Asp | Asp |
|     |     |     | 180 |     |     |     |     |     | 185 |     |     |     | 190 |     |     |
| Asp | Pro | Gln | Glu | Asp | Gly | Leu | Asp | Val | Asn | Val | His | Ala | Asn | Glu | Asp |
|     |     |     | 195 |     |     |     |     |     | 200 |     |     |     | 205 |     |     |
| Asp | Gln | Glu | Asp | Asp | Gly | Asn | Ser | Asp | Ile | Glu | Glu | Val | Ala | Tyr | Thr |
|     |     |     | 210 |     |     |     |     |     | 215 |     |     |     | 220 |     |     |
| Asp | Asp | Glu | Ala | Tyr | Ala | Arg | Ala | Leu | Gln | Glu | Ala | Glu | Glu | Arg | Asp |
|     |     |     | 225 |     |     |     |     |     | 230 |     |     |     | 235 |     |     |
| Met | Ala | Ala | Arg | Leu | Ser | Ala | Leu | Ser | Gly | Leu | Ala | Asn | Arg | Val | Val |
|     |     |     | 245 |     |     |     |     |     | 250 |     |     |     | 255 |     |     |
| Glu | Asp | Leu | Glu | Asp | Glu | Ser | His | Thr | Ser | Gln | Asp | Ala | Arg | Asp | Glu |
|     |     |     | 260 |     |     |     |     |     | 265 |     |     |     | 270 |     |     |
| Met | Asp | Pro | Asp | Glu | Leu | Ser | Tyr | Glu | Glu | Leu | Leu | Ala | Leu | Gly | Asp |
|     |     |     | 275 |     |     |     |     |     | 280 |     |     |     | 285 |     |     |
| Ile | Val | Gly | Thr | Glu | Ser | Arg | Gly | Leu | Ser | Ala | Asp | Thr | Ile | Ala | Ser |
|     |     |     | 290 |     |     |     |     |     | 295 |     |     |     | 300 |     |     |
| Leu | Pro | Ser | Lys | Arg | Tyr | Lys | Glu | Gly | Asp | Asn | Gln | Asn | Gly | Thr | Asn |
|     |     |     | 305 |     |     |     |     |     | 310 |     |     |     | 315 |     |     |
| Glu | Ser | Cys | Val | Ile | Cys | Arg | Leu | Asp | Tyr | Glu | Asp | Asp | Glu | Asp | Leu |
|     |     |     | 325 |     |     |     |     |     | 330 |     |     |     | 335 |     |     |
| Ile | Leu | Leu | Pro | Cys | Lys | His | Ser | Tyr | His | Ser | Glu | Cys | Ile | Asn | Asn |
|     |     |     | 340 |     |     |     |     |     | 345 |     |     |     | 350 |     |     |
| Trp | Leu | Lys | Ile | Asn | Lys | Val | Cys | Pro | Val | Cys | Ser | Ala | Glu | Val | Ser |
|     |     |     | 355 |     |     |     |     |     | 360 |     |     |     | 365 |     |     |
| Thr | Ser | Thr | Ser | Gly | Gln | Ser |     |     |     |     |     |     |     |     |     |
|     |     |     | 370 |     |     |     |     |     | 375 |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:520:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 340 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..340  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1567211  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:520:

Met Pro Met Glu Asn Asp Asn Gly Pro His Val Gly Asn Val Val Val  
1 5 10 15  
Thr Ala Glu Gln Ala Thr Lys Ile Asn Glu Thr Asp Gly Arg Leu Pro  
20 25 30  
Glu Asn Arg Gln Thr Gly Val Val Ser Asp Thr Gly Ser Gly Ser Glu  
35 40 45  
Arg Gly Glu Gln Gly Val Gly Glu Ser Ala Val Ala Val Ala Val Pro  
50 55 60  
Val Glu Glu Ser Gly Ser Ile Ser Val Gly Glu Leu Pro Ala Pro Arg  
65 70 75 80  
Ser Ser Ser Ala Arg Val Pro Phe Thr Asn Leu Ser Gln Ile Asp Ala  
85 90 95  
Asp Leu Ala Leu Ala Arg Thr Leu Gln Glu Gln Glu Arg Ala Tyr Met  
100 105 110  
Met Leu Thr Met Asn Ser Glu Ile Ser Asp Tyr Gly Ser Trp Glu Thr  
115 120 125  
Gly Ser Tyr Val Tyr Asp Glu Asp Glu Phe Asp Asp Pro Glu Asn Glu  
130 135 140  
Asp Glu Asp Asp Asp Glu Asp Glu Tyr Glu Thr Asp Asp Pro Gln  
145 150 155 160  
Glu Asp Gly Leu Asp Val Asn Val His Ala Asn Glu Asp Asp Gln Glu  
165 170 175  
Asp Asp Gly Asn Ser Asp Ile Glu Glu Val Ala Tyr Thr Asp Asp Glu  
180 185 190  
Ala Tyr Ala Arg Ala Leu Gln Glu Ala Glu Glu Arg Asp Met Ala Ala  
195 200 205  
Arg Leu Ser Ala Leu Ser Gly Leu Ala Asn Arg Val Val Glu Asp Leu  
210 215 220  
Glu Asp Glu Ser His Thr Ser Gln Asp Ala Arg Asp Glu Met Asp Pro  
225 230 235 240  
Asp Glu Leu Ser Tyr Glu Glu Leu Leu Ala Leu Gly Asp Ile Val Gly  
245 250 255  
Thr Glu Ser Arg Gly Leu Ser Ala Asp Thr Ile Ala Ser Leu Pro Ser  
260 265 270  
Lys Arg Tyr Lys Glu Gly Asp Asn Gln Asn Gly Thr Asn Glu Ser Cys  
275 280 285  
Val Ile Cys Arg Leu Asp Tyr Glu Asp Asp Glu Asp Leu Ile Leu Leu  
290 295 300  
Pro Cys Lys His Ser Tyr His Ser Glu Cys Ile Asn Asn Trp Leu Lys  
305 310 315 320  
Ile Asn Lys Val Cys Pro Val Cys Ser Ala Glu Val Ser Thr Ser Thr  
325 330 335  
Ser Gly Gln Ser  
340

- (2) INFORMATION FOR SEQ ID NO:521:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 338 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..338

(D) OTHER INFORMATION: / Ceres Seq. ID 1567212

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:521:

Met Glu Asn Asp Asn Gly Pro His Val Gly Asn Val Val Val Thr Ala  
1 5 10 15  
Glu Gln Ala Thr Lys Ile Asn Glu Thr Asp Gly Arg Leu Pro Glu Asn  
20 25 30  
Arg Gln Thr Gly Val Val Ser Asp Thr Gly Ser Gly Ser Glu Arg Gly  
35 40 45  
Glu Gln Gly Val Gly Glu Ser Ala Val Ala Val Ala Val Pro Val Glu  
50 55 60  
Glu Ser Gly Ser Ile Ser Val Gly Glu Leu Pro Ala Pro Arg Ser Ser  
65 70 75 80  
Ser Ala Arg Val Pro Phe Thr Asn Leu Ser Gln Ile Asp Ala Asp Leu  
85 90 95  
Ala Leu Ala Arg Thr Leu Gln Glu Gln Glu Arg Ala Tyr Met Met Leu  
100 105 110  
Thr Met Asn Ser Glu Ile Ser Asp Tyr Gly Ser Trp Glu Thr Gly Ser  
115 120 125  
Tyr Val Tyr Asp Glu Asp Glu Phe Asp Asp Pro Glu Asn Glu Asp Glu  
130 135 140  
Asp Asp Asp Glu Asp Glu Tyr Glu Thr Asp Asp Asp Pro Gln Glu Asp  
145 150 155 160  
Gly Leu Asp Val Asn Val His Ala Asn Glu Asp Asp Gln Glu Asp Asp  
165 170 175  
Gly Asn Ser Asp Ile Glu Glu Val Ala Tyr Thr Asp Asp Glu Ala Tyr  
180 185 190  
Ala Arg Ala Leu Gln Glu Ala Glu Glu Arg Asp Met Ala Ala Arg Leu  
195 200 205  
Ser Ala Leu Ser Gly Leu Ala Asn Arg Val Val Glu Asp Leu Glu Asp  
210 215 220  
Glu Ser His Thr Ser Gln Asp Ala Arg Asp Glu Met Asp Pro Asp Glu  
225 230 235 240  
Leu Ser Tyr Glu Glu Leu Leu Ala Leu Gly Asp Ile Val Gly Thr Glu  
245 250 255  
Ser Arg Gly Leu Ser Ala Asp Thr Ile Ala Ser Leu Pro Ser Lys Arg  
260 265 270  
Tyr Lys Glu Gly Asp Asn Gln Asn Gly Thr Asn Glu Ser Cys Val Ile  
275 280 285  
Cys Arg Leu Asp Tyr Glu Asp Asp Glu Asp Leu Ile Leu Leu Pro Cys  
290 295 300  
Lys His Ser Tyr His Ser Glu Cys Ile Asn Asn Trp Leu Lys Ile Asn  
305 310 315 320  
Lys Val Cys Pro Val Cys Ser Ala Glu Val Ser Thr Ser Thr Ser Gly  
325 330 335  
Gln Ser

(2) INFORMATION FOR SEQ ID NO:522:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1665 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1665

(D) OTHER INFORMATION: / Ceres Seq. ID 1567213

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:522:

|             |             |             |            |             |             |      |
|-------------|-------------|-------------|------------|-------------|-------------|------|
| gttaagagat  | cettctccct  | cttcgaagat  | gagcggtagc | gtgaaggata  | tcgtttcaaa  | 60   |
| ggcggaGctt  | gataacttgc  | gccagagcgg  | cgcaccagtc | gtgcttcact  | ctcgggcttc  | 120  |
| ttggtgtgat  | gcttcgaagc  | agatggatca  | agttttctct | catctcgtca  | ctgatttccc  | 180  |
| tcgtgctcac  | ttctttaggg  | ttgaagctga  | ggaacatcct | gagatatctg  | aggcttactc  | 240  |
| tggtgctgct  | gtgccttatt  | togtctctct  | caaggatggt | aaaactgtgg  | atacacttga  | 300  |
| gggtgcagat  | ccatcaagtt  | tagctaataa  | ggttggcaaa | gttgctggtt  | ctagtacttc  | 360  |
| tcgggaGcct  | gctgctcctg  | caagcttagg  | gttggtgctg | gggccaacga  | ttcttgaaac  | 420  |
| tgtaagagag  | aatgcgaaag  | cttctttaca  | agaccgagct | cagcctgtat  | ctaccgcgca  | 480  |
| tgctctcaag  | agccgttttg  | aaaagctcac  | taattctcac | cctgtcatgt  | tattcatgaa  | 540  |
| aggtattctt  | gaagagccta  | gggtgtgggtt | tagcaggaaa | gtagttgaca  | ttttgaaaga  | 600  |
| ggttaacgct  | gattttggaa  | gttttgacat  | actatcggt  | aacgaaagtc  | gagagggttt  | 660  |
| gaagaatttc  | tctaactggc  | caacgtttcc  | tcagctgtac | tgcaacggag  | agcctcttgg  | 720  |
| tggaagctat  | atcgcacatg  | cgtgcacga   | gagcggtgaa | ctaaaagatg  | ctttcaaaaga | 780  |
| tcctggggatc | acgacagttg  | gttcacaaaga | aagtcaggat | gaagctggaa  | aaggaggagg  | 840  |
| ggtagtttca  | ggaaacacag  | gcttaagtga  | gacctccga  | gctcggctcg  | aaggtctggt  | 900  |
| caattccaaa  | ccagttatgc  | tgttcatgaa  | aggaagacca | gaagaaccac  | agtgtggggt  | 960  |
| cagtgggaaa  | gtgggttgaaa | tcttcaacca  | agaaaaaatc | gagtttgga   | gtttcgatat  | 1020 |
| ccctcttagat | gacgaagttc  | gccaaaggct  | taaaagtgat | tcaaaactgtg | caagctatcc  | 1080 |
| tcagctttac  | gtgaaaggcg  | agcttatggg  | tggatcagac | attgtcttgg  | agatgcacaa  | 1140 |
| gagcggtagg  | gtcaaaaaag  | tctaccgaga  | aagggatcac | tggagaacag  | agtcttgaag  | 1200 |
| atagattgaa  | ggcactgatt  | aattcctcgg  | aagtaatgct | attcatgaaa  | ggttcaccag  | 1260 |
| atgaaccgaa  | atgcggattt  | agctccaaa   | ttgtgaaaag | attgagagga  | gaaaacgtga  | 1320 |
| gtttcggatc  | gtttgatatc  | ttgactgatg  | aagaagtaag | gcaagggatt  | aagaatttct  | 1380 |
| caaatcgccc  | aacttttctc  | cagctatact  | acaaaggtga | gttaatttga  | ggatgtgata  | 1440 |
| tcattatgga  | gctaaagtga  | agtggtgatc  | tcacagcaac | tctatccgat  | taagtaatat  | 1500 |
| atacaagctt  | ctgtctgctg  | gtttgccttg  | gtgagagaga | acatttcagt  | tatggttaata | 1560 |
| atagtcttta  | gggtgttaca  | acattgatat  | tggtgcttct | caagcttttg  | cttgttattt  | 1620 |
| ctattgctga  | gtctattaga  | ttcataacta  | ttttctctct | tttgt       |             |      |

(2) INFORMATION FOR SEQ ID NO:523:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 398 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..398

(D) OTHER INFORMATION: / Ceres Seq. ID 1567214

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:523:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Arg | Asp | Pro | Ser | Pro | Ser | Ser | Lys | Met | Ser | Gly | Thr | Val | Lys | Asp |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Ile | Val | Ser | Lys | Ala | Glu | Leu | Asp | Asn | Leu | Arg | Gln | Ser | Gly | Ala | Pro |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     |     | 30  |     |
| Val | Val | Leu | His | Phe | Trp | Ala | Ser | Trp | Cys | Asp | Ala | Ser | Lys | Gln | Met |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Asp | Gln | Val | Phe | Ser | His | Leu | Ala | Thr | Asp | Phe | Pro | Arg | Ala | His | Phe |
|     |     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |
| Phe | Arg | Val | Glu | Ala | Glu | Glu | His | Pro | Glu | Ile | Ser | Glu | Ala | Tyr | Ser |
|     |     |     | 65  |     |     |     | 70  |     |     | 75  |     |     |     | 80  |     |
| Val | Ala | Ala | Val | Pro | Tyr | Phe | Val | Phe | Phe | Lys | Asp | Gly | Lys | Thr | Val |
|     |     |     | 85  |     |     |     | 90  |     |     |     |     |     | 95  |     |     |
| Asp | Thr | Leu | Glu | Gly | Ala | Asp | Pro | Ser | Ser | Leu | Ala | Asn | Lys | Val | Gly |
|     |     |     | 100 |     |     |     | 105 |     |     |     |     |     | 110 |     |     |
| Lys | Val | Ala | Gly | Ser | Ser | Thr | Ser | Ala | Glu | Pro | Ala | Ala | Pro | Ala | Ser |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     |     | 125 |     |     |
| Leu | Gly | Leu | Ala | Ala | Gly | Pro | Thr | Ile | Leu | Glu | Thr | Val | Lys | Glu | Asn |
|     |     |     | 130 |     |     |     | 135 |     |     |     |     |     | 140 |     |     |
| Ala | Lys | Ala | Ser | Leu | Gln | Asp | Arg | Ala | Gln | Pro | Val | Ser | Thr | Ala | Asp |
|     |     |     | 145 |     |     |     | 150 |     |     |     | 155 |     |     |     | 160 |

Ala Leu Lys Ser Arg Leu Glu Lys Leu Thr Asn Ser His Pro Val Met  
165 170 175  
Leu Phe Met Lys Gly Ile Pro Glu Glu Pro Arg Cys Gly Phe Ser Arg  
180 185 190  
Lys Val Val Asp Ile Leu Lys Glu Val Asn Val Asp Phe Gly Ser Phe  
195 200 205  
Asp Ile Leu Ser Asp Asn Glu Val Arg Glu Gly Leu Lys Lys Phe Ser  
210 215 220  
Asn Trp Pro Thr Phe Pro Gln Leu Tyr Cys Asn Gly Glu Leu Leu Gly  
225 230 235 240  
Gly Ala Asp Ile Ala Ile Ala Met His Glu Ser Gly Glu Leu Lys Asp  
245 250 255  
Ala Phe Lys Asp Leu Gly Ile Thr Thr Val Gly Ser Lys Glu Ser Gln  
260 265 270  
Asp Glu Ala Gly Lys Gly Gly Gly Val Ser Ser Gly Asn Thr Gly Leu  
275 280 285  
Ser Glu Thr Leu Arg Ala Arg Leu Glu Gly Leu Val Asn Ser Lys Pro  
290 295 300  
Val Met Leu Phe Met Lys Gly Arg Pro Glu Glu Pro Lys Cys Gly Phe  
305 310 315 320  
Ser Gly Lys Val Val Glu Ile Leu Asn Gln Glu Lys Ile Glu Phe Gly  
325 330 335  
Ser Phe Asp Ile Leu Leu Asp Asp Glu Val Arg Gln Gly Leu Lys Val  
340 345 350  
Tyr Ser Asn Trp Ser Ser Tyr Pro Gln Leu Tyr Val Lys Gly Glu Leu  
355 360 365  
Met Gly Gly Ser Asp Ile Val Leu Glu Met Gln Lys Ser Gly Glu Leu  
370 375 380  
Lys Lys Val Tyr Arg Glu Arg Asp His Trp Arg Thr Glu Ser  
385 390 395

(2) INFORMATION FOR SEQ ID NO:524:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 389 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..389

(D) OTHER INFORMATION: / Ceres Seq. ID 1567215

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:524:

Met Ser Gly Thr Val Lys Asp Ile Val Ser Lys Ala Glu Leu Asp Asn  
1 5 10 15  
Leu Arg Gln Ser Gly Ala Pro Val Val Leu His Phe Trp Ala Ser Trp  
20 25 30  
Cys Asp Ala Ser Lys Gln Met Asp Gln Val Phe Ser His Leu Ala Thr  
35 40 45  
Asp Phe Pro Arg Ala His Phe Phe Arg Val Glu Ala Glu Glu His Pro  
50 55 60  
Glu Ile Ser Glu Ala Tyr Ser Val Ala Ala Val Pro Tyr Phe Val Phe  
65 70 75 80  
Phe Lys Asp Gly Lys Thr Val Asp Thr Leu Glu Gly Ala Asp Pro Ser  
85 90 95  
Ser Leu Ala Asn Lys Val Gly Lys Val Ala Gly Ser Ser Thr Ser Ala  
100 105 110  
Glu Pro Ala Ala Pro Ala Ser Leu Gly Leu Ala Ala Gly Pro Thr Ile  
115 120 125  
Leu Glu Thr Val Lys Glu Asn Ala Lys Ala Ser Leu Gln Asp Arg Ala  
130 135 140  
Gln Pro Val Ser Thr Ala Asp Ala Leu Lys Ser Arg Leu Glu Lys Leu

145 150 155 160  
Thr Asn Ser His Pro Val Met Leu Phe Met Lys Gly Ile Pro Glu Glu  
165 170 175  
Pro Arg Cys Gly Phe Ser Arg Lys Val Val Asp Ile Leu Lys Glu Val  
180 185 190  
Asn Val Asp Phe Gly Ser Phe Asp Ile Leu Ser Asp Asn Glu Val Arg  
195 200 205  
Glu Gly Leu Lys Lys Phe Ser Asn Trp Pro Thr Phe Pro Gln Leu Tyr  
210 215 220  
Cys Asn Gly Glu Leu Leu Gly Gly Ala Asp Ile Ala Ile Ala Met His  
225 230 235 240  
Glu Ser Gly Glu Leu Lys Asp Ala Phe Lys Asp Leu Gly Ile Thr Thr  
245 250 255  
Val Gly Ser Lys Glu Ser Gln Asp Glu Ala Gly Lys Gly Gly Val  
260 265 270  
Ser Ser Gly Asn Thr Gly Leu Ser Glu Thr Leu Arg Ala Arg Leu Glu  
275 280 285  
Gly Leu Val Asn Ser Lys Pro Val Met Leu Phe Met Lys Gly Arg Pro  
290 295 300  
Glu Glu Pro Lys Cys Gly Phe Ser Gly Lys Val Val Glu Ile Leu Asn  
305 310 315 320  
Gln Glu Lys Ile Glu Phe Gly Ser Phe Asp Ile Leu Leu Asp Asp Glu  
325 330 335  
Val Arg Gln Gly Leu Lys Val Tyr Ser Asn Trp Ser Ser Tyr Pro Gln  
340 345 350  
Leu Tyr Val Lys Gly Glu Leu Met Gly Gly Ser Asp Ile Val Leu Glu  
355 360 365  
Met Gln Lys Ser Gly Glu Leu Lys Lys Val Tyr Arg Glu Arg Asp His  
370 375 380  
Trp Arg Thr Glu Ser  
385

(2) INFORMATION FOR SEQ ID NO:525:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 351 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..351

(D) OTHER INFORMATION: / Ceres Seq. ID 1567216

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:525:

Met Asp Gln Val Phe Ser His Leu Ala Thr Asp Phe Pro Arg Ala His  
1 5 10 15  
Phe Phe Arg Val Glu Ala Glu Glu His Pro Glu Ile Ser Glu Ala Tyr  
20 25 30  
Ser Val Ala Ala Val Pro Tyr Phe Val Phe Phe Lys Asp Gly Lys Thr  
35 40 45  
Val Asp Thr Leu Glu Gly Ala Asp Pro Ser Ser Leu Ala Asn Lys Val  
50 55 60  
Gly Lys Val Ala Gly Ser Ser Thr Ser Ala Glu Pro Ala Ala Pro Ala  
65 70 75 80  
Ser Leu Gly Leu Ala Ala Gly Pro Thr Ile Leu Glu Thr Val Lys Glu  
85 90 95  
Asn Ala Lys Ala Ser Leu Gln Asp Arg Ala Gln Pro Val Ser Thr Ala  
100 105 110  
Asp Ala Leu Lys Ser Arg Leu Glu Lys Leu Thr Asn Ser His Pro Val  
115 120 125  
Met Leu Phe Met Lys Gly Ile Pro Glu Glu Pro Arg Cys Gly Phe Ser  
130 135 140



Arg Lys Val Val Asp Ile Leu Lys Glu Val Asn Val Asp Phe Gly Ser  
145 150 155 160  
Phe Asp Ile Leu Ser Asp Asn Glu Val Arg Glu Gly Leu Lys Lys Phe  
165 170 175  
Ser Asn Trp Pro Thr Phe Pro Gln Leu Tyr Cys Asn Gly Glu Leu Leu  
180 185 190  
Gly Gly Ala Asp Ile Ala Ile Ala Met His Glu Ser Gly Glu Leu Lys  
195 200 205  
Asp Ala Phe Lys Asp Leu Gly Ile Thr Thr Val Gly Ser Lys Glu Ser  
210 215 220  
Gln Asp Glu Ala Gly Lys Gly Gly Gly Val Ser Ser Gly Asn Thr Gly  
225 230 235 240  
Leu Ser Glu Thr Leu Arg Ala Arg Leu Glu Gly Leu Val Asn Ser Lys  
245 250 255  
Pro Val Met Leu Phe Met Lys Gly Arg Pro Glu Glu Pro Lys Cys Gly  
260 265 270  
Phe Ser Gly Lys Val Val Glu Ile Leu Asn Gln Glu Lys Ile Glu Phe  
275 280 285  
Gly Ser Phe Asp Ile Leu Leu Asp Asp Glu Val Arg Gln Gly Leu Lys  
290 295 300  
Val Tyr Ser Asn Trp Ser Ser Tyr Pro Gln Leu Tyr Val Lys Gly Glu  
305 310 315 320  
Leu Met Gly Gly Ser Asp Ile Val Leu Glu Met Gln Lys Ser Gly Glu  
325 330 335  
Leu Lys Lys Val Tyr Arg Glu Arg Asp His Trp Arg Thr Glu Ser  
340 345 350

(2) INFORMATION FOR SEQ ID NO:526:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 788 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..788

(D) OTHER INFORMATION: / Ceres Seq. ID 1567240

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:526:

|             |            |            |            |            |            |     |
|-------------|------------|------------|------------|------------|------------|-----|
| aaaaacggtag | aaaccttggt | ttaaacgctc | acggtcccta | tataaaccta | tgagctagcg | 60  |
| acgacaagta  | ttcagtataa | tcaatcagaa | aacaagtaga | aactttaaaa | cgagagagag | 120 |
| agaaagaaat  | ggcgacatcg | ggaacgtacg | tgacggaggt | tcggttgaaa | ggatcggcgg | 180 |
| agaaacacata | caagagctgg | aagagcgaga | accatgtctt | cgctgacgcc | attggccacc | 240 |
| acatccaaaa  | tgtcgttggt | cacgaaggcg | aacatgaact | tcacgggtct | atcaggagtt | 300 |
| gggactacac  | atatgatgga | aagaaggaga | tgttcaaaga | gaagagagag | atagatgatg | 360 |
| agaaataaac  | attgacgaaa | agaggactgg | atggtcacgt | gatggagcat | tcocaaagat | 420 |
| ttgatatacat | ctacgaattt | attcccaaat | ctgaggatag | ctgcgtctgc | aaaatcacta | 480 |
| tgatatggga  | gaagcgcaac | gatgactttc | ccgaaccaag | cggtcacatg | aaattcgtea | 540 |
| agcaaatggg  | tgttgacatt | gaagcgacag | tcaacaaaag | ttaacccaaa | ccatcacogt | 600 |
| catcacatct  | tcgatcgata | ttgtattatt | atggtgtctt | ttcgataaat | aatataataa | 660 |
| agggggtctt  | gtggagtttc | tattctctgt | aactgtttgg | ttttggaata | tgctgtgata | 720 |
| tgttgtCtat  | gctcatcata | tatcggtttc | gatataatga | gtattaataa | aagtagcttc | 780 |
| agtatatcc   |            |            |            |            |            |     |

(2) INFORMATION FOR SEQ ID NO:527:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 151 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..151

(D) OTHER INFORMATION: / Ceres Seq. ID 1567241

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:527:

Met Ala Thr Ser Gly Thr Tyr Val Thr Glu Val Pro Leu Lys Gly Ser  
1 5 10 15  
Ala Glu Lys His Tyr Lys Ser Trp Lys Ser Glu Asn His Val Phe Ala  
20 25 30  
Asp Ala Ile Gly His His Ile Gln Asn Val Val Val His Glu Gly Glu  
35 40 45  
His Asp Ser His Gly Ser Ile Arg Ser Trp Asp Tyr Thr Tyr Asp Gly  
50 55 60  
Lys Lys Glu Met Phe Lys Lys Arg Glu Ile Asp Asp Glu Asn Lys  
65 70 75 80  
Thr Leu Thr Lys Arg Gly Leu Asp Gly His Val Met Glu His Leu Lys  
85 90 95  
Val Phe Asp Ile Ile Tyr Glu Phe Ile Pro Lys Ser Glu Asp Ser Cys  
100 105 110  
Val Cys Lys Ile Thr Met Ile Trp Glu Lys Arg Asn Asp Asp Phe Pro  
115 120 125  
Glu Pro Ser Gly Tyr Met Lys Phe Val Lys Gln Met Val Val Asp Ile  
130 135 140  
Glu Gly His Val Asn Lys Ala  
145 150

(2) INFORMATION FOR SEQ ID NO:528:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 84 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..84

(D) OTHER INFORMATION: / Ceres Seq. ID 1567242

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:528:

Met Phe Lys Glu Lys Arg Glu Ile Asp Asp Glu Asn Lys Thr Leu Thr  
1 5 10 15  
Lys Arg Gly Leu Asp Gly His Val Met Glu His Leu Lys Val Phe Asp  
20 25 30  
Ile Ile Tyr Glu Phe Ile Pro Lys Ser Glu Asp Ser Cys Val Cys Lys  
35 40 45  
Ile Thr Met Ile Trp Glu Lys Arg Asn Asp Asp Phe Pro Glu Pro Ser  
50 55 60  
Gly Tyr Met Lys Phe Val Lys Gln Met Val Val Asp Ile Glu Gly His  
65 70 75 80  
Val Asn Lys Ala

(2) INFORMATION FOR SEQ ID NO:529:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1311 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1311

(D) OTHER INFORMATION: / Ceres Seq. ID 1567251

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:529:

aagttttcttt atcttttagt ttcccggtaa aaaatctctc tgctcatgtct atgtttcttcc 60  
acgtcggttc taattctcca agacagaatc tctaaacttc attttgctcc ttttccacac 120

```

aaaaattttTc tctccctcca aagaccacaa aaaaattttt tcttctcttc aacttcaagt 180
atctctctttt attcacacag atagcatcca aaacccaaaa tccataaaccc ttctctctgtt 240
aaaagattttc tctttttcaa cttcccacga aaaaaaaaaa aaaaacattc tgtttagaaaa 300
ccatgagaggg tctgcgggct tgttacagtg aacacgccat aaagtatcca gatacatatt 360
gttcaggcttc ttccaatcat tcttatatat ctccgacatt acctcttcca atccccgaca 420
cagtaaacac cacttataaa tcatatctcc cttcttcoga aaaaaccgct tctgtttcac 480
tcacctgggt ggataaatctc accgtctgtc tctcaaacgcc gccgaataca tactctgttt 540
cactcagaaa accctaaagg tcaagaaagt tgactttctc ctccggttca ctcaacggcg 600
agatccctatg ggaattatcg gaagagagta cgaatacaac ggacctgaac caataagaag 660
attcttctgt gtcgtctgtg taaattccga gattaccctc ggagtcggcg acgttgacca 720
cgagcgagac acgtcatcat cgtcgtctgt gcgagtctca aaaaacggga gattctcttg 780
aacttggttg ctcacgacga aagctcaatt ctccgacgtc ggaaggaaac acgagataca 840
gattcaatgc ggcggaggag gwggwggagg aggaggagag gaagggattt tatggaaagt 900
gaaaagctct gaaaagatg cggtttatgt tgataaagg aaagtgtttt cggtagaaga 960
ggttaagtgg aacttttaga ggaatcaaac catgtttttc gatggaatgc ttatagacat 1020
gatgtgggat ttacacgact ggttctacaa agaaacggtt tctgtctgtt cgactagttc 1080
atcgtctaaa acggcgctgt cgtcatcgct ttcttcaact tcatcgctca ctctccgtg 1140
tgctgtgttt atgttttaga ggaggagtgt tttgatagt agattatgga ttgatgaaga 1200
tgaacaagag agtaagatga agaagaatat tggttctaga gatgagaaac atctgttttc 1260
atttattcatt tgtgcctcta aaaagtgacc aaataaacia ataaacattt t

```

(2) INFORMATION FOR SEQ ID NO:530:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..117
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567252

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:530:

```

Met Arg Gly Leu Ala Ala Cys Tyr Ser Glu His Ala Ile Lys Val Ser
1 5 10 15
Asp Thr Tyr Cys Ser Gly Pro Ser Asn His Ser Tyr Ile Ser Pro Thr
20 25 30
Leu Pro Pro Ser Ile Pro Asp Thr Val Thr Thr Thr Tyr Lys Ser Tyr
35 40 45
Leu Pro Ser Ser Asp Lys Pro Val Ser Val Ser Leu Thr Trp Ser Asp
50 55 60
Asn Leu Thr Val Val Ile Ser Thr Pro Pro Lys Ser Tyr Ser Val Ser
65 70 75 80
Leu Arg Lys Pro Lys Gly Ser Arg Lys Leu Thr Ser Ser Ser Gly Ser
85 90 95
Leu Asn Ala Glu Ile Leu Trp Asp Leu Ser Glu Glu Ser Thr Lys Thr
100 105 110
Thr Asp Leu Asn Gln
115

```

(2) INFORMATION FOR SEQ ID NO:531:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 226 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..226
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567253

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:531:

```

Met Gly Ser Ile Gly Arg Glu Tyr Glu Asn Asn Gly Pro Glu Pro Ile

```

|                                                                 |     |     |     |
|-----------------------------------------------------------------|-----|-----|-----|
| 1                                                               | 5   | 10  | 15  |
| Arg Arg Phe Phe Val Val Val Val Val Asn Ser Glu Ile Thr Leu Gly |     |     |     |
| 20                                                              | 25  | 30  |     |
| Val Gly Asp Val Asp His Glu Arg Asp Thr Ser Ser Ser Ser Trp     |     |     |     |
| 35                                                              | 40  | 45  |     |
| Arg Val Ser Lys Thr Glu Arg Phe Ser Gly Thr Cys Trp Leu Thr Thr |     |     |     |
| 50                                                              | 55  | 60  |     |
| Lys Ala Gln Phe Ser Asp Val Gly Arg Lys His Glu Ile Gln Ile Gln |     |     |     |
| 65                                                              | 70  | 75  | 80  |
| Cys Gly Gly Gly Xaa Xaa Gly Gly Gly Glu Gly Tyr Leu Trp         |     |     |     |
| 85                                                              | 90  | 95  |     |
| Lys Val Lys Ser Pro Glu Thr Met Ser Val Tyr Val Asp Lys Arg Lys |     |     |     |
| 100                                                             | 105 | 110 |     |
| Val Phe Ser Val Lys Lys Leu Lys Trp Asn Phe Arg Gly Asn Gln Thr |     |     |     |
| 115                                                             | 120 | 125 |     |
| Met Phe Phe Asp Gly Met Leu Ile Asp Met Met Trp Asp Leu His Asp |     |     |     |
| 130                                                             | 135 | 140 |     |
| Trp Phe Tyr Lys Glu Thr Leu Ser Ser Val Ser Thr Ser Ser Ser Ser |     |     |     |
| 145                                                             | 150 | 155 | 160 |
| Lys Thr Ala Ser Ser Ser Ser Ser Ser Ser Thr Ser Ser Ser Thr Pro |     |     |     |
| 165                                                             | 170 | 175 |     |
| Pro Cys Ala Val Phe Met Phe Arg Arg Arg Ser Gly Phe Asp Ser Arg |     |     |     |
| 180                                                             | 185 | 190 |     |
| Leu Trp Ile Asp Glu Asp Glu Gln Glu Ser Lys Met Lys Lys Asn Ile |     |     |     |
| 195                                                             | 200 | 205 |     |
| Gly Ser Arg Asp Glu Lys His Ser Phe Ser Leu Ile Cys Ala Ser     |     |     |     |
| 210                                                             | 215 | 220 |     |
| Lys Lys                                                         |     |     |     |
| 225                                                             |     |     |     |

(2) INFORMATION FOR SEQ ID NO:532:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 123 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..123

(D) OTHER INFORMATION: / Ceres Seq. ID 1567254

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:532:

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| Met Ser Val Tyr Val Asp Lys Arg Lys Val Phe Ser Val Lys Lys Leu |     |
| 1                                                               | 5   |
| Lys Trp Asn Phe Arg Gly Asn Gln Thr Met Phe Phe Asp Gly Met Leu |     |
| 20                                                              | 25  |
| Ile Asp Met Met Trp Asp Leu His Asp Trp Phe Tyr Lys Glu Thr Leu |     |
| 35                                                              | 40  |
| Ser Ser Val Ser Thr Ser Ser Ser Ser Lys Thr Ala Ser Ser Ser Ser |     |
| 50                                                              | 55  |
| Ser Ser Ser Thr Ser Ser Ser Thr Pro Pro Cys Ala Val Phe Met Phe |     |
| 65                                                              | 70  |
| Arg Arg Arg Ser Gly Phe Asp Ser Arg Leu Trp Ile Asp Glu Asp Glu |     |
| 85                                                              | 90  |
| Gln Glu Ser Lys Met Lys Lys Asn Ile Gly Ser Arg Asp Glu Lys His |     |
| 100                                                             | 105 |
| Ser Phe Ser Leu Ile Ile Cys Ala Ser Lys Lys                     |     |
| 115                                                             | 120 |

(2) INFORMATION FOR SEQ ID NO:533:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1590 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(A) NAME/KEY: -  
(B) LOCATION: 1..1590  
(D) OTHER INFORMATION: / Ceres Seq. ID 1567261

|             |             |             |             |             |             |      |
|-------------|-------------|-------------|-------------|-------------|-------------|------|
| tctgcttgcga | tagctactaca | tttgattttca | tggtttcgttc | cagtcgcccca | aggtgtcaact | 60   |
| cgcacacgcgt | ggcaattacta | cgcgatctctc | ctcgcaccca  | ctctcgcttat | ctactaccag  | 120  |
| cgcctctcttc | tcggtgtgtgt | tgcctctaagt | ggattaggagg | tcttcggtgt  | caccacaaacc | 180  |
| ctaacgttgct | cgcgcgcgctt | ctccgctctt  | ggagatccaa  | tcacgctggt  | catcgctctt  | 240  |
| gcacctttctt | tcgtcgcggt  | tttctacaaa  | accggtctcg  | tgaacgttgt  | agcttaccag  | 300  |
| ttcgcttagac | tcttcggtag  | ctcctccctt  | ggctctcggt  | acagctctcgt | cttcagtga   | 360  |
| gcctcttttag | ctccggcgat  | tcctctcttc  | tcgcctcgtg  | ctcggtgaat  | cttctcccg   | 420  |
| ttgttgaaat  | ctctctctgt  | tgccttgggg  | agtaacggtg  | gggagtgaac  | agagcacgct  | 480  |
| cttgctcgtc  | gggtgatcgt  | tactctgttc  | cagactctctg | tgatctcttc  | ttctatgttc  | 540  |
| ttgcacggcta | ttgctgcgaa  | tcctttagtt  | gctaatttgc  | cggtttaaac  | gattaaagca  | 600  |
| acgattggat  | ggagctgatt  | ggctaaaagt  | gcgattgtac  | gaggaacttg  | tcctttgatt  | 660  |
| gtgtgttcgt  | ttctttttga  | ttctcatct   | ccctctacgg  | tgaagagcag  | tcctgatgct  | 720  |
| ctcaagctgt  | ctcagggaaa  | gtctgacaa   | attggacaata | tgtctaaaga  | cgaattgatt  | 780  |
| atcggtgcga  | ctttattctc  | caogtgttgt  | ctctggaatt  | tttgagacta  | gttggttgta  | 840  |
| gatgctgtga  | ctcgagcact  | ttctggatta  | tcagctcttc  | ttgtgacagg  | tgctgtgaca  | 900  |
| tgtaaaagagt | gcttatgtga  | gtcgctgcga  | tgggacacac  | tcaacctgct  | cgctgccttc  | 960  |
| attcgctggtg | ctggttatct  | taacaaatct  | gggtctcattg | agtgtgtcag  | cacagacccta | 1020 |
| tgcaagttgt  | tgggagattt  | ttgtttgtca  | tggcagctat  | cttttggaa   | ctctgcgttc  | 1080 |
| ttgtattttt  | acaactcacta | ctctcttgtc  | agtgaggctg  | cccaacttgg  | tgcttatgtt  | 1140 |
| cactgccttt  | ttatcgtggt  | caaccgcttc  | aggcaactca  | ctcttaactt  | cagccttggt  | 1200 |
| tcttgcgttc  | ctttccaacc  | tgatggggag  | attgacccat  | tatgggtatg  | gggtcgcgcc  | 1260 |
| tatctctcac  | ggagactaat  | acgtgcgcgt  | ggctaaaatg  | tgggctgtat  | gattctcatt  | 1320 |
| ttcaaatagt  | aaactattca  | ttctggtctg  | tctaggttgt  | tgctgttggg  | agttcacagg  | 1380 |
| cttgtgggtga | gcgacacact  | acacaaactt  | tccactcttt  | ttctcttaat  | atatataata  | 1440 |
| ttctcttgaaa | cggctttgag  | atttcagatt  | gagaagagtt  | gaatcacagg  | ttataagatt  | 1500 |
| tgcagcagatt | ttttctgcga  | tttttattct  | cactcacaca  | cattttgaag  | tgtaagcaat  | 1560 |
| ctctaaactgc | ctcaattttg  | tttgatttcc  |             |             |             |      |

(2) INFORMATION FOR SEQ ID NO:534:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 425 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

```
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
```

```
(A) NAME/KEY: peptide
(B) LOCATION: 1..425
(D) OTHER INFORMATION: / Ceres Seq. ID 1567262
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:534:
```

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Ala | Ser | Ile | Ala | Thr | Asp | Leu | Ile | Leu | Trp | Phe | Val | Pro | Val | Pro |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Glu | Gly | Val | Thr | Arg | Asn | Ala | Trp | Gln | Leu | Leu | Ala | Ile | Phe | Leu | Ala |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     | 30  |     |     |     |
| Thr | Ile | Val | Gly | Ile | Ile | Thr | Gln | Pro | Leu | Pro | Leu | Gly | Ala | Val | Ala |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Leu | Met | Gly | Leu | Gly | Ala | Ser | Val | Leu | Thr | Lys | Thr | Leu | Thr | Phe | Ala |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Ala | Ala | Phe | Ser | Ala | Phe | Gly | Asp | Pro | Ile | Pro | Trp | Leu | Ile | Ala | Leu |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Ala | Phe | Phe | Phe | Ala | Arg | Gly | Phe | Ile | Lys | Thr | Gly | Leu | Gly | Asn | Arg |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Val | Ala | Tyr | Gln | Phe | Val | Arg | Leu | Phe | Gly | Ser | Ser | Ser | Leu | Gly | Leu |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |

Gly Tyr Ser Leu Val Phe Ser Glu Ala Leu Leu Ala Pro Ala Ile Pro  
115 120 125  
Ser Val Ser Ala Arg Ala Gly Gly Ile Phe Leu Pro Leu Val Lys Ser  
130 135 140  
Leu Cys Val Ala Cys Gly Ser Asn Val Gly Asp Gly Thr Glu His Arg  
145 150 155 160  
Leu Gly Ser Trp Leu Met Leu Thr Cys Phe Gln Thr Ser Val Ile Ser  
165 170 175  
Ser Ser Met Phe Leu Thr Ala Met Ala Ala Asn Pro Leu Ser Ala Asn  
180 185 190  
Leu Ala Phe Asn Thr Ile Lys Gln Thr Ile Gly Trp Thr Asp Trp Ala  
195 200 205  
Lys Ala Ala Ile Val Pro Gly Leu Val Ser Leu Ile Val Val Pro Phe  
210 215 220  
Leu Leu Tyr Leu Ile Tyr Pro Pro Thr Val Lys Ser Ser Pro Asp Ala  
225 230 235 240  
Pro Lys Leu Ala Gln Glu Lys Leu Asp Lys Met Gly Pro Met Ser Lys  
245 250 255  
Asn Glu Leu Ile Met Ala Ala Thr Leu Phe Leu Thr Val Gly Leu Trp  
260 265 270  
Ile Phe Gly Ala Lys Leu Gly Val Asp Ala Val Thr Ala Ala Ile Leu  
275 280 285  
Gly Leu Ser Val Leu Leu Val Thr Gly Val Val Thr Trp Lys Glu Cys  
290 295 300  
Leu Ala Glu Ser Val Ala Trp Asp Thr Leu Thr Trp Phe Ala Ala Leu  
305 310 315 320  
Ile Ala Met Ala Gly Tyr Leu Asn Lys Tyr Gly Leu Ile Glu Trp Phe  
325 330 335  
Ser Gln Thr Val Val Lys Phe Val Gly Gly Leu Gly Leu Ser Trp Gln  
340 345 350  
Leu Ser Phe Gly Ile Leu Val Leu Leu Tyr Phe Tyr Thr His Tyr Phe  
355 360 365  
Phe Ala Ser Gly Ala Ala His Ile Gly Ala Tyr Val His Cys Leu Phe  
370 375 380  
Ile Gly Phe Asn Arg Ser Arg His Ser Thr Leu Leu Cys Ser Leu Gly  
385 390 395 400  
Ser Cys Val Pro Phe Gln Pro Asp Gly Arg Ile Asp Pro Leu Trp Tyr  
405 410 415  
Arg Val Cys Ala Tyr Leu Leu Arg Ser  
420 425

(2) INFORMATION FOR SEQ ID NO:535:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 376 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..376

(D) OTHER INFORMATION: / Ceres Seq. ID 1567263

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:535:

Met Gly Leu Gly Ala Ser Val Leu Thr Lys Thr Leu Thr Phe Ala Ala  
1 5 10 15  
Ala Phe Ser Ala Phe Gly Asp Pro Ile Pro Trp Leu Ile Ala Leu Ala  
20 25 30  
Phe Phe Phe Ala Arg Gly Phe Ile Lys Thr Gly Leu Gly Asn Arg Val  
35 40 45  
Ala Tyr Gln Phe Val Arg Leu Phe Gly Ser Ser Ser Leu Gly Leu Gly  
50 55 60  
Tyr Ser Leu Val Phe Ser Glu Ala Leu Leu Ala Pro Ala Ile Pro Ser

|                                                                 |                                                 |     |     |
|-----------------------------------------------------------------|-------------------------------------------------|-----|-----|
| 65                                                              | 70                                              | 75  | 80  |
| Val Ser Ala Arg                                                 | Ala Gly Gly Ile Phe Leu Pro Leu Val Lys Ser Leu |     |     |
|                                                                 | 85                                              | 90  | 95  |
| Cys Val Ala Cys                                                 | Gly Ser Asn Val Gly Asp Gly Thr Glu His Arg Leu |     |     |
|                                                                 | 100                                             | 105 | 110 |
| Gly Ser Trp Leu Met Leu Thr Cys Phe Gln Thr Ser Val Ile Ser Ser |                                                 |     |     |
|                                                                 | 115                                             | 120 | 125 |
| Ser Met Phe Leu Thr Ala Met Ala Ala Asn Pro Leu Ser Ala Asn Leu |                                                 |     |     |
|                                                                 | 130                                             | 135 | 140 |
| Ala Phe Asn Thr Ile Lys Gln Thr Ile Gly Trp Thr Asp Trp Ala Lys |                                                 |     |     |
|                                                                 | 145                                             | 150 | 155 |
| Ala Ala Ile Val Pro Gly Leu Val Ser Leu Ile Val Val Pro Phe Leu |                                                 |     |     |
|                                                                 | 165                                             | 170 | 175 |
| Leu Tyr Leu Ile Tyr Pro Pro Thr Val Lys Ser Ser Pro Asp Ala Pro |                                                 |     |     |
|                                                                 | 180                                             | 185 | 190 |
| Lys Leu Ala Gln Glu Lys Leu Asp Lys Met Gly Pro Met Ser Lys Asn |                                                 |     |     |
|                                                                 | 195                                             | 200 | 205 |
| Glu Leu Ile Met Ala Ala Thr Leu Phe Leu Thr Val Gly Leu Trp Ile |                                                 |     |     |
|                                                                 | 210                                             | 215 | 220 |
| Phe Gly Ala Lys Leu Gly Val Asp Ala Val Thr Ala Ala Ile Leu Gly |                                                 |     |     |
|                                                                 | 225                                             | 230 | 235 |
| Leu Ser Val Leu Leu Val Thr Gly Val Val Thr Trp Lys Glu Cys Leu |                                                 |     |     |
|                                                                 | 245                                             | 250 | 255 |
| Ala Glu Ser Val Ala Trp Asp Thr Leu Thr Trp Phe Ala Ala Leu Ile |                                                 |     |     |
|                                                                 | 260                                             | 265 | 270 |
| Ala Met Ala Gly Tyr Leu Asn Lys Tyr Gly Leu Ile Glu Trp Phe Ser |                                                 |     |     |
|                                                                 | 275                                             | 280 | 285 |
| Gln Thr Val Val Lys Phe Val Gly Gly Leu Gly Leu Ser Trp Gln Leu |                                                 |     |     |
|                                                                 | 290                                             | 295 | 300 |
| Ser Phe Gly Ile Leu Val Leu Leu Tyr Phe Tyr Thr His Tyr Phe Phe |                                                 |     |     |
|                                                                 | 305                                             | 310 | 315 |
| Ala Ser Gly Ala Ala His Ile Gly Ala Tyr Val His Cys Leu Phe Ile |                                                 |     |     |
|                                                                 | 325                                             | 330 | 335 |
| Gly Phe Asn Arg Ser Arg His Ser Thr Leu Leu Cys Ser Leu Gly Ser |                                                 |     |     |
|                                                                 | 340                                             | 345 | 350 |
| Cys Val Pro Phe Gln Pro Asp Gly Arg Ile Asp Pro Leu Trp Tyr Arg |                                                 |     |     |
|                                                                 | 355                                             | 360 | 365 |
| Val Cys Ala Tyr Leu Leu Arg Ser                                 |                                                 |     |     |
|                                                                 | 370                                             | 375 |     |

(2) INFORMATION FOR SEQ ID NO:536:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 260 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..260
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567264

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:536:

|                                                                 |    |    |    |
|-----------------------------------------------------------------|----|----|----|
| Met Leu Thr Cys Phe Gln Thr Ser Val Ile Ser Ser Ser Met Phe Leu |    |    |    |
| 1                                                               | 5  | 10 | 15 |
| Thr Ala Met Ala Ala Asn Pro Leu Ser Ala Asn Leu Ala Phe Asn Thr |    |    |    |
|                                                                 | 20 | 25 | 30 |
| Ile Lys Gln Thr Ile Gly Trp Thr Asp Trp Ala Lys Ala Ala Ile Val |    |    |    |
|                                                                 | 35 | 40 | 45 |
| Pro Gly Leu Val Ser Leu Ile Val Val Pro Phe Leu Leu Tyr Leu Ile |    |    |    |
|                                                                 | 50 | 55 | 60 |
| Tyr Pro Pro Thr Val Lys Ser Ser Pro Asp Ala Pro Lys Leu Ala Gln |    |    |    |
| 65                                                              | 70 | 75 | 80 |

Glu Lys Leu Asp Lys Met Gly Pro Met Ser Lys Asn Glu Leu Ile Met  
85 90 95  
Ala Ala Thr Leu Phe Leu Thr Val Gly Leu Trp Ile Phe Gly Ala Lys  
100 105 110  
Leu Gly Val Asp Ala Val Thr Ala Ala Ile Leu Gly Leu Ser Val Leu  
115 120 125  
Leu Val Thr Gly Val Val Thr Trp Lys Glu Cys Leu Ala Glu Ser Val  
130 135 140  
Ala Trp Asp Thr Leu Thr Trp Phe Ala Ala Leu Ile Ala Met Ala Gly  
145 150 155 160  
Tyr Leu Asn Lys Tyr Gly Leu Ile Glu Trp Phe Ser Gln Thr Val Val  
165 170 175  
Lys Phe Val Gly Gly Leu Gly Leu Ser Trp Gln Leu Ser Phe Gly Ile  
180 185 190  
Leu Val Leu Leu Tyr Phe Tyr Thr His Tyr Phe Phe Ala Ser Gly Ala  
195 200 205  
Ala His Ile Gly Ala Tyr Val His Cys Leu Phe Ile Gly Phe Asn Arg  
210 215 220  
Ser Arg His Ser Thr Leu Leu Cys Ser Leu Gly Ser Cys Val Pro Phe  
225 230 235 240  
Gln Pro Asp Gly Arg Ile Asp Pro Leu Trp Tyr Arg Val Cys Ala Tyr  
245 250 255  
Leu Leu Arg Ser  
260

(2) INFORMATION FOR SEQ ID NO:537:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1170 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1170
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567265

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:537:

|            |             |            |            |             |            |      |
|------------|-------------|------------|------------|-------------|------------|------|
| actgggtctt | cttcagcttc  | tgagttctct | cctctctctc | tatctctcaa  | gtgggctttg | 60   |
| ctttgtcgtt | tttgtctctc  | ctcgacgact | cacttttgca | gattctcata  | aattcttcaa | 120  |
| agctttgagt | cttttttcag  | attcgaagg  | cggttttata | tatgcttcaa  | atctcttacc | 180  |
| caaatcaggt | atggagactc  | tgcatccatt | ctctcacta  | cctatctctg  | accaccggtt | 240  |
| cgttttcaa  | gagatgggtg  | gctttcacag | ctcgagtgcg | ggtagctgga  | ctaaagaaga | 300  |
| gaacaagatg | ttcgacagag  | ctcttgcgat | atacgtgcga | gactcgcctg  | atcgtcggtt | 360  |
| taaaattgct | tccatgatcc  | ctggaaagac | tgtttttgat | gttatgaagc  | aataatgtaa | 420  |
| gcttgaagaa | gacgttttgc  | atattgaagc | aggacgtgtt | cccattcctg  | gttatcctgc | 480  |
| agctttctct | cccttggggg  | ttgacacgga | catgtgtcgt | aaacggccta  | gtggagctag | 540  |
| aggatctgat | caagatcgaa  | agaaaggagt | cccttgga   | gaggaagaac  | acaggagatt | 600  |
| cttgttaggc | ctactcaagt  | acggtaaagg | agattggaga | aacatatacg  | gaaacttcgt | 660  |
| gggtgcaaa  | acgccaacgc  | aagtgccgag | ccacgcccaa | aagtattacc  | agagacagct | 720  |
| ctccggagcc | aaggacaaac  | cgaggccaag | tatccatgac | atcacaccgc  | gcaatctctc | 780  |
| tcaatgccaa | tctcaacgtg  | tctttttccg | atcatagaga | tattctccct  | gatttagggt | 840  |
| ttatcgataa | ggatgatacg  | gaggaggagg | taattattat | gggtcagaat  | ctctcttcag | 900  |
| aaaatctgtt | ttctccatca  | ccaacttcat | tcgaagctgc | cattaaactc  | gccggagaaa | 960  |
| atgtcttcag | tgccggagct  | taaggcaaca | tagaatcccc | aaactcagcg  | ttcttaagaa | 1020 |
| ctctgagttt | gaaactgtta  | ttagagaaat | ataagcaaaa | ccaagtattat | tatatatgta | 1080 |
| tttgtgtggt | taaaaagtaag | aacttgtttt | tactctgtat | ttttgtgttt  | ctgtctacta | 1140 |
| aatacctggt | atgttaaaaa  | attctgtgct |            |             |            |      |

(2) INFORMATION FOR SEQ ID NO:538:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 271 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:



- (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..271  
(D) OTHER INFORMATION: / Ceres Seq. ID 1567266

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:538:

Leu Gly Leu Leu Gln Leu Leu Ser Leu Leu Ser Leu Tyr Leu Ser  
1 5 10 15  
Ser Gly Leu Cys Phe Ala Val Phe Val Phe Leu Arg Arg Leu Thr Phe  
20 25 30  
Ala Asp Ser His Lys Phe Phe Lys Ala Leu Ser Leu Phe Ser Asp Ser  
35 40 45  
Lys Val Gly Phe Ile Tyr Ala Ser Asn Leu Leu Pro Lys Ser Gly Met  
50 55 60  
Glu Thr Leu His Pro Phe Ser His Leu Pro Ile Ser Asp His Arg Phe  
65 70 75 80  
Val Val Gln Glu Met Val Ser Phe His Ser Ser Ser Ser Gly Ser Trp  
85 90 95  
Thr Lys Glu Glu Asn Lys Met Phe Glu Arg Ala Leu Ala Ile Tyr Ala  
100 105 110  
Glu Asp Ser Pro Asp Arg Trp Phe Lys Val Ala Ser Met Ile Pro Gly  
115 120 125  
Lys Thr Val Phe Asp Val Met Lys Gln Tyr Ser Lys Leu Glu Glu Asp  
130 135 140  
Val Phe Asp Ile Glu Ala Gly Arg Val Pro Ile Pro Gly Tyr Pro Ala  
145 150 155 160  
Ala Ser Ser Pro Leu Gly Phe Asp Thr Asp Met Cys Arg Lys Arg Pro  
165 170 175  
Ser Gly Ala Arg Gly Ser Asp Gln Asp Arg Lys Lys Gly Val Pro Trp  
180 185 190  
Thr Glu Glu Glu His Arg Arg Phe Leu Leu Gly Leu Leu Lys Tyr Gly  
195 200 205  
Lys Gly Asp Trp Arg Asn Ile Ser Arg Asn Phe Val Val Ser Lys Thr  
210 215 220  
Pro Thr Gln Val Ala Ser His Ala Gln Lys Tyr Tyr Gln Arg Gln Leu  
225 230 235 240  
Ser Gly Ala Lys Asp Lys Arg Arg Pro Ser Ile His Asp Ile Thr Thr  
245 250 255  
Gly Lys Ser Ser Gln Cys Gln Ser Gln Pro Phe Leu Phe Arg Ser  
260 265 270

(2) INFORMATION FOR SEQ ID NO:539:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 208 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..208  
(D) OTHER INFORMATION: / Ceres Seq. ID 1567267

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:539:

Met Glu Thr Leu His Pro Phe Ser His Leu Pro Ile Ser Asp His Arg  
1 5 10 15  
Phe Val Val Gln Glu Met Val Ser Phe His Ser Ser Ser Ser Gly Ser  
20 25 30  
Trp Thr Lys Glu Glu Asn Lys Met Phe Glu Arg Ala Leu Ala Ile Tyr  
35 40 45  
Ala Glu Asp Ser Pro Asp Arg Trp Phe Lys Val Ala Ser Met Ile Pro  
50 55 60

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gly | Lys | Thr | Val | Phe | Asp | Val | Met | Lys | Gln | Tyr | Ser | Lys | Leu | Glu | Glu |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Asp | Val | Phe | Asp | Ile | Glu | Ala | Gly | Arg | Val | Pro | Ile | Pro | Gly | Tyr | Pro |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Ala | Ala | Ser | Ser | Pro | Leu | Gly | Phe | Asp | Thr | Asp | Met | Cys | Arg | Lys | Arg |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Pro | Ser | Gly | Ala | Arg | Gly | Ser | Asp | Gln | Asp | Arg | Lys | Lys | Gly | Val | Pro |
|     |     | 115 |     |     |     |     | 120 |     |     |     | 125 |     |     |     |     |
| Trp | Thr | Glu | Glu | Glu | His | Arg | Arg | Phe | Leu | Leu | Gly | Leu | Leu | Lys | Tyr |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Gly | Lys | Gly | Asp | Trp | Arg | Asn | Ile | Ser | Arg | Asn | Phe | Val | Val | Ser | Lys |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |     |
| Thr | Pro | Thr | Gln | Val | Ala | Ser | His | Ala | Gln | Lys | Tyr | Tyr | Gln | Arg | Gln |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Leu | Ser | Gly | Ala | Lys | Asp | Lys | Arg | Arg | Pro | Ser | Ile | His | Asp | Ile | Thr |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Thr | Gly | Lys | Ser | Ser | Gln | Cys | Gln | Ser | Gln | Pro | Phe | Leu | Phe | Arg | Ser |
|     | 195 |     |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |

(2) INFORMATION FOR SEQ ID NO:540:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 187 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..187

(D) OTHER INFORMATION: / Ceres Seq. ID 1567268

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:540:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Val | Ser | Phe | His | Ser | Ser | Ser | Ser | Gly | Ser | Trp | Thr | Lys | Glu | Glu |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     | 15  |     |     |
| Asn | Lys | Met | Phe | Glu | Arg | Ala | Leu | Ala | Ile | Tyr | Ala | Glu | Asp | Ser | Pro |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     | 30  |     |     |     |
| Asp | Arg | Trp | Phe | Lys | Val | Ala | Ser | Met | Ile | Pro | Gly | Lys | Thr | Val | Phe |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Asp | Val | Met | Lys | Gln | Tyr | Ser | Lys | Leu | Glu | Glu | Asp | Val | Phe | Asp | Ile |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Glu | Ala | Gly | Arg | Val | Pro | Ile | Pro | Gly | Tyr | Pro | Ala | Ala | Ser | Ser | Pro |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     | 80  |     |     |
| Leu | Gly | Phe | Asp | Thr | Asp | Met | Cys | Arg | Lys | Arg | Pro | Ser | Gly | Ala | Arg |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     | 95  |     |     |
| Gly | Ser | Asp | Gln | Asp | Arg | Lys | Lys | Gly | Val | Pro | Trp | Thr | Glu | Glu | Glu |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| His | Arg | Arg | Phe | Leu | Leu | Gly | Leu | Leu | Lys | Tyr | Gly | Lys | Gly | Asp | Trp |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Arg | Asn | Ile | Ser | Arg | Asn | Phe | Val | Val | Ser | Lys | Thr | Pro | Thr | Gln | Val |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Ala | Ser | His | Ala | Gln | Lys | Tyr | Tyr | Gln | Arg | Gln | Leu | Ser | Gly | Ala | Lys |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |     |
| Asp | Lys | Arg | Arg | Pro | Ser | Ile | His | Asp | Ile | Thr | Thr | Gly | Lys | Ser | Ser |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Gln | Cys | Gln | Ser | Gln | Pro | Phe | Leu | Phe | Arg | Ser |     |     |     |     |     |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:541:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 480 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
    (A) NAME/KEY: -  
    (B) LOCATION: 1..480  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1567273  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:541:  
ctaaagattg caaatccgtg ttctatctct ctcaacaatt atttcccctg cttccaaagc 60  
tttgacaaca ttctatttca aaaacttttag ttttgagttt tttttttctt gtatactttc 120  
ccccaaaata tgagcgatcc caagtatgca tatccttacc cgccaccggg aaattaccoc 180  
caaggtccgc Caccgcgcgt ggGagtaccg ccacagtatt atcctccacc accgccaccg 240  
cctctctctc caccaccacc acgaaaagtt ggttttcttg aaggactatt agcagctctg 300  
tgttgtgtgt gcttgggtgga tgaatgttgc tgtgaccoga ccattatatg ctttgattaa 360  
gttttcagga aaaagtagt ctgttaattt cattatgctt atgagggtta tacaataatt 420  
gtttgatat catgtgacta ctactttctt ttctgtgcgc ttttaattagg ttttagtctt 480

(2) INFORMATION FOR SEQ ID NO:542:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 76 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..76  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1567274  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:542:  
Met Ser Asp Pro Lys Tyr Ala Tyr Pro Tyr Pro Ala Pro Gly Asn Tyr  
1 5 10 15  
Pro Gln Gly Pro Pro Pro Pro Val Gly Val Pro Pro Gln Tyr Tyr Pro  
20 25 30  
Pro Pro Pro Pro Pro Pro Pro Pro Pro Pro Arg Lys Val Gly  
35 40 45  
Phe Leu Glu Gly Leu Leu Ala Ala Leu Cys Cys Cys Cys Leu Val Asp  
50 55 60  
Glu Cys Cys Cys Asp Pro Thr Ile Ile Cys Phe Asp  
65 70 75

(2) INFORMATION FOR SEQ ID NO:543:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 48 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..48  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1567275  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:543:  
Met His Ile Leu Thr Arg His Arg Glu Ile Thr Arg Lys Val Arg His  
1 5 10 15  
Arg Arg Trp Glu Tyr Arg His Ser Ile Ile Leu His His Arg His Arg  
20 25 30  
Leu Leu Leu His His His His Glu Lys Leu Val Phe Leu Lys Asp Tyr  
35 40 45

(2) INFORMATION FOR SEQ ID NO:544:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 949 base pairs

(A) NAME/KEY: -  
(B) LOCATION: 1..949  
(D) OTHER INFORMATION: / Ceres Seq. ID 1567284

|            |             |             |             |            |            |     |
|------------|-------------|-------------|-------------|------------|------------|-----|
| atctctctgt | cgtaatttt   | tgtctctacc  | gttgaaatctg | aaaatgatcg | cgcgagatt  | 60  |
| gcgcgatatt | tcaactccgt  | ctggagcagc  | tctctccgcg  | gcgttagcct | ccttcaattc | 120 |
| ttctttatgc | cacaattctca | cctccggcac  | caccggagct  | tccgtcaagt | ctcgattcac | 180 |
| tctcgcgatg | tctctctaatt | cgttttggcat | cagagcgagg  | aaatcacaca | ttgatgtctg | 240 |
| gcgcgtcgat | attgtttcccg | ctcagaagct  | gtccaaaggt  | tgcaccagta | tcaacaagga | 300 |
| gcgcgaaaaa | gagattaaaga | aagctaaagt  | taaaatttct  | cgcagacaat | tcagaccatt | 360 |
| gagtagaaga | gtcagatgcct | tccagaaaga  | gcgcgcagaa  | gaagacacat | caaagataaa | 420 |
| aggaaacaaa | atttttatag  | cgattccgct  | ttttgttaac  | cgcgaaagac | aagctgtgtg | 480 |
| tctctctctc | cacactcgta  | agaatcgcta  | gcgcgatata  | cgaactctgt | acacggtgct | 540 |
| gcggtcgctc | cacgtcgata  | agaagtctag  | agaacagttt  | gagatgaggt | tcaagaaaac | 600 |
| ttttcttgtt | atcaaaagtc  | agagtcgaat  | gttgacgaag  | agactgtttt | ggtttaaaag | 660 |
| ttatctgatt | ctttgagctc  | aaatgaacta  | ccagttccat  | tgcgaacacc | ttgttgatat | 720 |
| gactcaagtg | ttaggacaaca | tcaattgctc  | gccaccacat  | gtctactgag | atggtcataa | 780 |
| acatcaattt | gttagaagttt | caagacccca  | cgcggtaact  | tgcataaatt | tgcagaccta | 840 |
| cgactccatg | aaaccagctt  | tgttccatcat | cagatcaagt  | agttattctt | ttgcttagta | 900 |
| taaacatcgt | tttttgaacg  | ttttttaaag  | atacataatg  | atgttcagtt |            |     |

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:545:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 1   | Leu | Ser | Arg | Arg | His | Phe | Phe | Val | Ser | Pro | Leu | Asn | Leu | Lys | Met | Ile |
| 1   | Ala | Gly | Val | Leu | Arg | Arg | Ser | Ser | Leu | Pro | Ser | Arg | Gln | Thr | Leu | Ser |
|     |     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ala | Ala | Leu | Ala | Ser | Phe | Asn | Ser | Cys | Ile | Ser | His | Asn | Leu | Thr | Pro |     |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| Ala | Thr | Thr | Gly | Ala | Ser | Val | Ser | Ser | Arg | Phe | Thr | Leu | Ala | Ser | Ser |     |
|     |     | 50  |     |     |     | 55  |     |     |     |     |     | 60  |     |     |     |     |
| Pro | Asn | Ser | Phe | Gly | Ile | Arg | Ala | Arg | Asn | Ile | His | Ile | Arg | Ser | Glu |     |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Pro | Ser | Met | Ile | Val | Pro | Ala | Gly | Ile | Ala | Ser | Gln | Gly | Tyr | Ala | Thr |     |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Val | Thr | Lys | Asp | Arg | Lys | Asn | Glu | Ile | Lys | Lys | Ala | Lys | Ile | Lys | Ile |     |
|     |     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Ser | Pro | Asp | Asn | Val | Arg | Pro | Leu | Ser | Arg | Lys | Glu | Ile | Ala | Leu | Gln |     |
|     |     |     |     | 115 |     |     |     | 120 |     |     |     | 125 |     |     |     |     |
| Lys | Glu | Pro | Ala | Glu | Glu | Ser | Thr | Ser | Lys | Ile | Lys | Gly | Thr | Lys | Ile |     |
|     |     |     |     | 130 |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Cys | Ile | Ala | Ile | Arg | Ser | Phe | Val | Asn | Pro | Glu | Lys | Gln | Ala | Trp | Cys |     |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |     |
| Leu | Pro | Pro | His | Thr | Arg | Lys | Val | Ala | Met | Pro | Asp | Thr | Arg | Thr | Leu |     |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |     |
| Tyr | Thr | Val | Leu | Arg | Ser | Pro | His | Val | Asp | Lys | Lys | Ser | Arg | Glu | Gln |     |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |     |

Phe Glu Met Arg Phe Lys Lys Arg Phe Leu Val Ile Lys Ala Gln Ser  
195 200 205  
His Glu Leu Ser Lys Lys Leu Phe Trp Leu Lys Arg Tyr Arg Ile Leu  
210 215 220  
Gly Ala Gln Tyr Glu Leu Gln Phe His Cys Lys Thr Arg Leu Asp Met  
225 230 235 240  
Thr Gln Val Leu Gly Asn Ile Asn Gly Ser Thr Thr Asn Ala Tyr  
245 250 255

(2) INFORMATION FOR SEQ ID NO:546:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 241 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..241

(D) OTHER INFORMATION: / Ceres Seq. ID 1567286

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:546:

Met Ile Ala Gly Val Leu Arg Arg Ser Ser Leu Pro Ser Arg Gln Thr  
1 5 10 15  
Leu Ser Ala Ala Leu Ala Ser Phe Asn Ser Cys Ile Ser His Asn Leu  
20 25 30  
Thr Pro Ala Thr Thr Gly Ala Ser Val Ser Ser Arg Phe Thr Leu Ala  
35 40 45  
Ser Ser Pro Asn Ser Phe Gly Ile Arg Ala Arg Asn Ile His Ile Arg  
50 55 60  
Ser Glu Pro Ser Met Ile Val Pro Ala Gly Ile Ala Ser Gln Gly Tyr  
65 70 75 80  
Ala Thr Val Thr Lys Asp Arg Lys Asn Glu Ile Lys Lys Ala Lys Ile  
85 90 95  
Lys Ile Ser Pro Asp Asn Val Arg Pro Leu Ser Arg Lys Glu Ile Ala  
100 105 110  
Leu Gln Lys Glu Pro Ala Glu Glu Ser Thr Ser Lys Ile Lys Gly Thr  
115 120 125  
Lys Ile Cys Ile Ala Ile Arg Ser Phe Val Asn Pro Glu Lys Gln Ala  
130 135 140  
Trp Cys Leu Pro Pro His Thr Arg Lys Val Ala Met Pro Asp Thr Arg  
145 150 155 160  
Thr Leu Tyr Thr Val Leu Arg Ser Pro His Val Asp Lys Lys Ser Arg  
165 170 175  
Glu Gln Phe Glu Met Arg Phe Lys Lys Arg Phe Leu Val Ile Lys Ala  
180 185 190  
Gln Ser His Glu Leu Ser Lys Lys Leu Phe Trp Leu Lys Arg Tyr Arg  
195 200 205  
Ile Leu Gly Ala Gln Tyr Glu Leu Gln Phe His Cys Lys Thr Arg Leu  
210 215 220  
Asp Met Thr Gln Val Leu Gly Asn Ile Asn Gly Ser Thr Thr Asn Ala  
225 230 235 240  
Tyr

(2) INFORMATION FOR SEQ ID NO:547:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 173 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

000001 1560000000

(B) LOCATION: 1..173

(D) OTHER INFORMATION: / Ceres Seq. ID 1567287

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:547:

```
Met Ile Val Pro Ala Gly Ile Ala Ser Gln Gly Tyr Ala Thr Val Thr
1 5 10 15
Lys Asp Arg Lys Asn Glu Ile Lys Lys Ala Lys Ile Lys Ile Ser Pro
20 25 30
Asp Asn Val Arg Pro Leu Ser Arg Lys Glu Ile Ala Leu Gln Lys Glu
35 40 45
Pro Ala Glu Glu Ser Thr Ser Lys Ile Lys Gly Thr Lys Ile Cys Ile
50 55 60
Ala Ile Arg Ser Phe Val Asn Pro Glu Lys Gln Ala Trp Cys Leu Pro
65 70 75 80
Pro His Thr Arg Lys Val Ala Met Pro Asp Thr Arg Thr Leu Tyr Thr
85 90 95
Val Leu Arg Ser Pro His Val Asp Lys Lys Ser Arg Glu Gln Phe Glu
100 105 110
Met Arg Phe Lys Lys Arg Phe Leu Val Ile Lys Ala Gln Ser His Glu
115 120 125
Leu Ser Lys Lys Leu Phe Trp Leu Lys Arg Tyr Arg Ile Leu Gly Ala
130 135 140
Gln Tyr Glu Leu Gln Phe His Cys Lys Thr Arg Leu Asp Met Thr Gln
145 150 155 160
Val Leu Gly Asn Ile Asn Gly Ser Thr Thr Asn Ala Tyr
165 170
```

(2) INFORMATION FOR SEQ ID NO:548:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1698 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1698

(D) OTHER INFORMATION: / Ceres Seq. ID 1567288

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:548:

```
cywagamacat cctaatacaaa aaatacaatc gtctctttcta tcatatttcto ttcttcttct 60
ccaagaaaac actgaagaag aaatgggggt ccttaaggcca accatggcgga ttctttttct 120
agcgatgtgtc gcggtttatc cagccgtgga catgtcaatc atctcctacg acgagaaaaca 180
tggcgctctcc accaccggtg gcggtagcga agccgaggtt atgagtatct acgagcatg 240
gttggtgaaa caccgcaagg ctccagagcca gaactctctt gttgagaaag atccagcgtt 300
cgagatcttt aaagacaatc ttctgtttctg cgatgaacat aacgagaaga atcttagtta 360
tagattgggt ttgactcgtt ttgcggatct tactaacgat gagtatagat ccaagtatct 420
tggagctaaag atggagaaga aaggtgagag aaggactagc ctacggtaag aggtcgtgt 480
cggtgatgag ctaccggagt ctattgactg gaggaagaaa ggagccgtgg ctgaggtcaa 540
agatcagggt ggttgcgga gttgttgggc gttttcaacc attggagcag tggagggaat 600
aaaccagcat gtaaccggag acctaaataac ctgtgtcgaa caagagtgtg tcgattgtga 660
cacttcaatc aacgaaggtt gtaacggagg tcttatggac tatgcttttg agttcattat 720
caagaatggt ggaatcgata cagacaaaaga ttatccttac aagggtgttg atggaacttg 780
tgaccagatc aggaaaaacg ctaaaagtgt cactatcgat tcatatgagg atgttccaac 840
ttaccgcgag gaatcggtga aAgaagcag ttgctcatca accattaAg catgccatt 900
gasgctggtg gtctgtcgct ccagctctat gattcgggta tattttatgg aagtgttgga 960
acacaacgag accaccgagt ttgctgggtt ggatacgaaa ctgagaacgg caaagattac 1020
tggattgtga gaaactcatg gggtaaaaagc tggggagaga gtggatacct aaggatggcg 1080
cgtaaatcgtt cgtcttcatc aggaaaaatgt ggaatcgcca ttgaaccttc ataccogata 1140
aagaattggc aaaaaccggc aaaccoggga ccttccactc catctcccat caagctccca 1200
accctaagtt acagtttact cacttgtcct gagagcaaca cttgtgtgtg tctgttttag 1260
tatgccaagt atgtctttgc ttggggatgt tgcccactag aagcagccac ttctgtgtgt 1320
gacaaatata gtgtgtgccc tcacgagtac ccggtttgtg accttgatca aggaacctgt 1380
ttattgagca agaacagctc atttagtgtt aaggccttaa agcgtaaac ccgaacggcca 1440
```

2025 RELEASE UNDER E.O. 14176

|                                                                     |      |
|---------------------------------------------------------------------|------|
| ttctgtgtcac aaggcagaaaa gaacattgcc taaacattgc ttcttcaaga ggactctggc | 1500 |
| tcattgagaga agagatctct ctgaagggat ttatcagatg ctttttaagt ttgtgtttta  | 1560 |
| tgccataact agatacataa aaaatgcagc tgttgggttt cgtgtatata aaaaaaggac   | 1620 |
| cctatgtttt attcagtttc atagtgggtt ttcattgata cagtacattt attgttaatt   | 1680 |
| caagaaaatt gaattttt                                                 |      |

(2) INFORMATION FOR SEQ ID NO:549:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 295 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..295
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567289

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:549:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Xaa | Xaa | His | Pro | Asn | Gln | Lys | Ile | Gln | Ser | Ser | Ser | Ser | Ser | Phe | Ser |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Leu | Leu | Leu | Leu | Gln | Glu | Asn | Thr | Glu | Glu | Met | Gly | Phe | Leu | Lys |     |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     | 30  |     |     |     |
| Pro | Thr | Met | Ala | Ile | Leu | Phe | Leu | Ala | Met | Val | Ala | Val | Ser | Ser | Ala |
|     |     | 35  |     |     |     |     | 40  |     |     |     | 45  |     |     |     |     |
| Val | Asp | Met | Ser | Ile | Ile | Ser | Tyr | Asp | Glu | Lys | His | Gly | Val | Ser | Thr |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Thr | Gly | Gly | Arg | Ser | Glu | Ala | Glu | Val | Met | Ser | Ile | Tyr | Glu | Ala | Trp |
|     | 65  |     |     |     | 70  |     |     |     | 75  |     |     |     | 80  |     |     |
| Leu | Val | Lys | His | Gly | Lys | Ala | Gln | Ser | Gln | Asn | Ser | Leu | Val | Glu | Lys |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Asp | Arg | Arg | Phe | Glu | Ile | Phe | Lys | Asp | Asn | Leu | Arg | Phe | Val | Asp | Glu |
|     |     |     | 100 |     |     |     | 105 |     |     |     |     | 110 |     |     |     |
| His | Asn | Glu | Lys | Asn | Leu | Ser | Tyr | Arg | Leu | Gly | Leu | Thr | Arg | Phe | Ala |
|     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |     |
| Asp | Leu | Thr | Asn | Asp | Glu | Tyr | Arg | Ser | Lys | Tyr | Leu | Gly | Ala | Lys | Met |
|     | 130 |     |     |     | 135 |     |     |     |     |     | 140 |     |     |     |     |
| Glu | Lys | Lys | Gly | Glu | Arg | Arg | Thr | Ser | Leu | Arg | Tyr | Glu | Ala | Arg | Val |
|     | 145 |     |     |     | 150 |     |     |     | 155 |     |     |     |     | 160 |     |
| Gly | Asp | Glu | Leu | Pro | Glu | Ser | Ile | Asp | Trp | Arg | Lys | Lys | Gly | Ala | Val |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |     |
| Ala | Glu | Val | Lys | Asp | Gln | Gly | Gly | Cys | Gly | Ser | Cys | Trp | Ala | Phe | Ser |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Thr | Ile | Gly | Ala | Val | Glu | Gly | Ile | Asn | Gln | Ile | Val | Thr | Gly | Asp | Leu |
|     | 195 |     |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Ile | Thr | Leu | Ser | Glu | Gln | Glu | Leu | Val | Asp | Cys | Asp | Thr | Ser | Tyr | Asn |
|     | 210 |     |     |     | 215 |     |     |     |     |     | 220 |     |     |     |     |
| Glu | Gly | Cys | Asn | Gly | Gly | Leu | Met | Asp | Tyr | Ala | Phe | Glu | Phe | Ile | Ile |
|     | 225 |     |     |     | 230 |     |     |     |     | 235 |     |     |     | 240 |     |
| Lys | Asn | Gly | Gly | Ile | Asp | Thr | Asp | Lys | Asp | Tyr | Pro | Tyr | Lys | Gly | Val |
|     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |     |
| Asp | Gly | Thr | Cys | Asp | Gln | Ile | Arg | Lys | Asn | Ala | Lys | Val | Val | Thr | Ile |
|     |     |     | 260 |     |     |     | 265 |     |     |     |     | 270 |     |     |     |
| Asp | Ser | Tyr | Glu | Asp | Val | Pro | Thr | Tyr | Ser | Glu | Glu | Ser | Leu | Lys | Glu |
|     | 275 |     |     |     |     | 280 |     |     |     |     |     | 285 |     |     |     |
| Ser | Ser | Cys | Ser | Ser | Thr | His |     |     |     |     |     |     |     |     |     |
|     | 290 |     |     |     | 295 |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:550:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 268 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..268

(D) OTHER INFORMATION: / Ceres Seq. ID 1567290

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:550:

```
Met Gly Phe Leu Lys Pro Thr Met Ala Ile Leu Phe Leu Ala Met Val
1 5 10 15
Ala Val Ser Ser Ala Val Asp Met Ser Ile Ile Ser Tyr Asp Glu Lys
20 25 30
His Gly Val Ser Thr Thr Gly Gly Arg Ser Glu Ala Glu Val Met Ser
35 40 45
Ile Tyr Glu Ala Trp Leu Val Lys His Gly Lys Ala Gln Ser Gln Asn
50 55 60
Ser Leu Val Glu Lys Asp Arg Arg Phe Glu Ile Phe Lys Asp Asn Leu
65 70 75 80
Arg Phe Val Asp Glu His Asn Glu Lys Asn Leu Ser Tyr Arg Leu Gly
85 90 95
Leu Thr Arg Phe Ala Asp Leu Thr Asn Asp Glu Tyr Arg Ser Lys Tyr
100 105 110
Leu Gly Ala Lys Met Glu Lys Lys Gly Glu Arg Arg Thr Ser Leu Arg
115 120 125
Tyr Glu Ala Arg Val Gly Asp Glu Leu Pro Glu Ser Ile Asp Trp Arg
130 135 140
Lys Lys Gly Ala Val Ala Glu Val Lys Asp Gln Gly Gly Cys Gly Ser
145 150 155 160
Cys Trp Ala Phe Ser Thr Ile Gly Ala Val Glu Gly Ile Asn Gln Ile
165 170 175
Val Thr Gly Asp Leu Ile Thr Leu Ser Glu Gln Glu Leu Val Asp Cys
180 185 190
Asp Thr Ser Tyr Asn Glu Gly Cys Asn Gly Gly Leu Met Asp Tyr Ala
195 200 205
Phe Glu Phe Ile Ile Lys Asn Gly Gly Ile Asp Thr Asp Lys Asp Tyr
210 215 220
Pro Tyr Lys Gly Val Asp Gly Thr Cys Asp Gln Ile Arg Lys Asn Ala
225 230 235 240
Lys Val Val Thr Ile Asp Ser Tyr Glu Asp Val Pro Thr Tyr Ser Glu
245 250 255
Glu Ser Leu Lys Glu Ser Ser Cys Ser Ser Thr His
260 265
```

(2) INFORMATION FOR SEQ ID NO:551:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 261 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..261

(D) OTHER INFORMATION: / Ceres Seq. ID 1567291

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:551:

```
Met Ala Ile Leu Phe Leu Ala Met Val Ala Val Ser Ser Ala Val Asp
1 5 10 15
Met Ser Ile Ile Ser Tyr Asp Glu Lys His Gly Val Ser Thr Thr Gly
20 25 30
Gly Arg Ser Glu Ala Glu Val Met Ser Ile Tyr Glu Ala Trp Leu Val
35 40 45
Lys His Gly Lys Ala Gln Ser Gln Asn Ser Leu Val Glu Lys Asp Arg
50 55 60
Arg Phe Glu Ile Phe Lys Asp Asn Leu Arg Phe Val Asp Glu His Asn
```



|                                                                 |                             |                             |     |    |     |    |
|-----------------------------------------------------------------|-----------------------------|-----------------------------|-----|----|-----|----|
| 65                                                              |                             | 70                          |     | 75 |     | 80 |
| Glu Lys Asn Leu Ser                                             | Tyr Arg Leu Gly             | Leu Thr Arg Phe Ala Asp Leu |     |    |     |    |
|                                                                 | 85                          |                             | 90  |    | 95  |    |
| Thr Asn Asp Glu Tyr Arg Ser Lys Tyr                             | Leu Gly Ala Lys Met Glu Lys |                             |     |    |     |    |
|                                                                 | 100                         |                             | 105 |    | 110 |    |
| Lys Gly Glu Arg Arg Thr Ser Leu Arg Tyr Glu Ala Arg Val Gly Asp |                             |                             |     |    |     |    |
|                                                                 | 115                         |                             | 120 |    | 125 |    |
| Glu Leu Pro Glu Ser Ile Asp Trp Arg Lys Lys Gly Ala Val Ala Glu |                             |                             |     |    |     |    |
|                                                                 | 130                         |                             | 135 |    | 140 |    |
| Val Lys Asp Gln Gly Gly Cys Gly Ser Cys Trp Ala Phe Ser Thr Ile |                             |                             |     |    |     |    |
|                                                                 | 145                         |                             | 150 |    | 155 |    |
| Gly Ala Val Glu Gly Ile Asn Gln Ile Val Thr Gly Asp Leu Ile Thr |                             |                             |     |    |     |    |
|                                                                 | 165                         |                             | 170 |    | 175 |    |
| Leu Ser Glu Gln Glu Leu Val Asp Cys Asp Thr Ser Tyr Asn Glu Gly |                             |                             |     |    |     |    |
|                                                                 | 180                         |                             | 185 |    | 190 |    |
| Cys Asn Gly Gly Leu Met Asp Tyr Ala Phe Glu Phe Ile Ile Lys Asn |                             |                             |     |    |     |    |
|                                                                 | 195                         |                             | 200 |    | 205 |    |
| Gly Gly Ile Asp Thr Asp Lys Asp Tyr Pro Tyr Lys Gly Val Asp Gly |                             |                             |     |    |     |    |
|                                                                 | 210                         |                             | 215 |    | 220 |    |
| Thr Cys Asp Gln Ile Arg Lys Asn Ala Lys Val Val Thr Ile Asp Ser |                             |                             |     |    |     |    |
|                                                                 | 225                         |                             | 230 |    | 235 |    |
| Tyr Glu Asp Val Pro Thr Tyr Ser Glu Glu Ser Leu Lys Glu Ser Ser |                             |                             |     |    |     |    |
|                                                                 | 245                         |                             | 250 |    | 255 |    |
| Cys Ser Ser Thr His                                             |                             |                             |     |    |     |    |
|                                                                 | 260                         |                             |     |    |     |    |

(2) INFORMATION FOR SEQ ID NO:552:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1326 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1326
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567305

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:552:

|             |             |             |             |            |             |      |
|-------------|-------------|-------------|-------------|------------|-------------|------|
| aactctcatc  | ttctttttct  | ttctttttct  | ctctttttct  | attgcttggt | gattgatgat  | 60   |
| cttgaagcaa  | ggatcatgag  | gttccttcac  | agatttctgt  | tggaggatat | gcccaaaagaa | 120  |
| accttttctg  | actctctctg  | taaaaaataa  | tgcataccaag | agttgaaaaa | ctcaggatcac | 180  |
| tgctcatctg  | attgtcttga  | cgagtgctct  | tccatctgcg  | agatcgctcg | aattcaggtt  | 240  |
| ctttccaccac | ctgcagagat  | ccaccacgac  | gacaacttaa  | agaggatctt | gatcatctct  | 300  |
| gcttcatctc  | tcatacaaac  | ctgtgtttct  | cttactttac  | ttgttctctg | cttcaagttt  | 360  |
| tactatagga  | ggagaagatc  | aataacaaca  | tcaagaagat  | ggagtaggga | agaagctagg  | 420  |
| aattgggatt  | ttgatggacc  | agcaccctgt  | attgttgatc  | atccgatttg | gcatacaga   | 480  |
| accatagggt  | tgaattccaac | ggttataagt  | tccatacaag  | tttgtcagta | tagtaaaaaa  | 540  |
| gatgggtgtg  | tggaaaggaac | tgattgtctc  | gtttgtttaa  | gcgaatttca | agaagaagag  | 600  |
| acgcttagat  | tgttaccaaa  | gtgtaaacat  | gcttttcatc  | ttatttgat  | tgatacttgg  | 660  |
| cttagatcac  | acaccaattg  | tcctgttagt  | cggtgtccta  | tcgttgaggc | caacacaatg  | 720  |
| attgatgatc  | atagtgaagg  | gctagaggag  | ataagtgtag  | tgattccaga | agaaaatgga  | 780  |
| gatgataccg  | atgaagaaat  | cgagggaagaa | agagatggct  | ttgttagtaa | tattagttaga | 840  |
| gatcatgggt  | agtcacaaca  | acagcagagt  | agacgatcac  | tgctgttgga | tcgtttatog  | 900  |
| ggttttaagg  | taagtgaagt  | tggtgtgggt  | agagaaaagg  | agaagttgaa | gagaggcaat  | 960  |
| aattatggt   | ctgggagctg  | aagttttatt  | aagagatcta  | tcctttacag | tgaaaagttag | 1020 |
| tactagctag  | cttcagtgct  | aataataaaa  | acaagaagtc  | cataaaagta | gtaagtttct  | 1080 |
| tgaagaagaa  | aatcaaatca  | aacccaacaa  | catatagggt  | gtattcatat | gtatgaaggt  | 1140 |
| gataataagt  | tacgattatc  | aaagctatgc  | actcttgtaa  | agtttaaaag | gagttttgac  | 1200 |
| aaactctact  | actctgtcta  | gataactctg  | atttgtggat  | taagtataaa | tatacaccaa  | 1260 |
| actTcgtttt  | gtatgttaac  | tattttattg  | tcctcaagaa  | ataccatctg | gatttttaatt | 1320 |
| attttt      |             |             |             |            |             |      |

(2) INFORMATION FOR SEQ ID NO:553:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 339 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..339  
(D) OTHER INFORMATION: / Ceres Seq. ID 1567306  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:553:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asn | Ser | His | Leu | Leu | Phe | Ser | Phe | Phe | Phe | Leu | Phe | Leu | His | Cys | Leu |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Leu | Ile | Asp | Asp | Leu | Glu | Ala | Arg | Ile | Met | Arg | Phe | Leu | His | Arg | Phe |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Leu | Leu | Glu | Asp | Met | Pro | Lys | Glu | Thr | Phe | Ser | Asp | Ser | Leu | Cys | Lys |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Asn | Asn | Cys | Ile | Gln | Glu | Leu | Lys | Thr | Leu | Gly | Tyr | Cys | Ser | Ser | Tyr |
|     |     |     | 50  |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Cys | Leu | Asp | Glu | Cys | Pro | Ser | Ile | Cys | Glu | Ile | Val | Val | Ile | Ser | Gly |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Leu | Ser | Pro | Pro | Ala | Glu | Ile | His | His | Asp | Asp | Asn | Leu | Lys | Arg | Ile |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     | 95  |     |     |
| Leu | Ile | Ile | Ser | Ala | Ser | Ser | Ile | Ile | Thr | Thr | Leu | Phe | Leu | Leu | Thr |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Leu | Leu | Val | Leu | Cys | Phe | Lys | Phe | Tyr | Arg | Arg | Arg | Arg | Ser | Ile |     |
|     |     |     | 115 |     |     |     | 120 |     |     |     | 125 |     |     |     |     |
| Thr | Thr | Ser | Arg | Arg | Trp | Ser | Met | Glu | Glu | Ala | Arg | Asn | Trp | Asp | Phe |
|     |     |     | 130 |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Asp | Gly | Pro | Ala | Pro | Val | Ile | Val | Asp | His | Pro | Ile | Trp | His | Ile | Arg |
| 145 |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |     |
| Thr | Ile | Gly | Leu | Asn | Pro | Thr | Val | Ile | Ser | Ser | Ile | Lys | Val | Cys | Gln |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |     |
| Tyr | Ser | Lys | Lys | Asp | Gly | Val | Val | Glu | Gly | Thr | Asp | Cys | Ser | Val | Cys |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     | 190 |     |     |     |
| Leu | Ser | Glu | Phe | Glu | Glu | Glu | Thr | Leu | Arg | Leu | Leu | Pro | Lys | Cys |     |
|     |     |     | 195 |     |     | 200 |     |     |     |     | 205 |     |     |     |     |
| Lys | His | Ala | Phe | His | Leu | Tyr | Cys | Ile | Asp | Thr | Trp | Leu | Arg | Ser | His |
|     |     |     | 210 |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Thr | Asn | Cys | Pro | Leu | Ser | Arg | Ala | Pro | Ile | Val | Glu | Ala | Asn | Thr | Met |
| 225 |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |     |
| Ile | Asp | Asp | His | Ser | Glu | Gly | Leu | Glu | Glu | Ile | Ser | Val | Met | Ile | Pro |
|     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |     |
| Glu | Glu | Asn | Gly | Asp | Asp | Thr | Asp | Glu | Glu | Ile | Glu | Glu | Glu | Arg | Asp |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Gly | Phe | Val | Ser | Asn | Ile | Ser | Arg | Asp | His | Gly | Glu | Ser | Gln | Gln | Gln |
|     |     |     | 275 |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Arg | Val | Arg | Arg | Ser | Val | Ser | Leu | Asp | Ser | Leu | Ser | Gly | Leu | Arg | Val |
|     |     |     | 290 |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Ser | Glu | Val | Val | Val | Gly | Arg | Glu | Lys | Glu | Lys | Leu | Lys | Arg | Gly | Asn |
| 305 |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |     |
| Asn | Ile | Gly | Ser | Gly | Arg | Ser | Ser | Leu | Leu | Lys | Arg | Ser | Ile | Ser | Tyr |
|     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |     |     |

Ser Gly Lys

(2) INFORMATION FOR SEQ ID NO:554:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 314 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..314

(D) OTHER INFORMATION: / Ceres Seq. ID 1567307

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:554:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Arg | Phe | Leu | His | Arg | Phe | Leu | Leu | Glu | Asp | Met | Pro | Lys | Glu | Thr |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Phe | Ser | Asp | Ser | Leu | Cys | Lys | Asn | Asn | Cys | Ile | Gln | Glu | Leu | Lys | Thr |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Leu | Gly | Tyr | Cys | Ser | Ser | Tyr | Cys | Leu | Asp | Glu | Cys | Pro | Ser | Ile | Cys |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Glu | Ile | Val | Val | Ile | Ser | Gly | Leu | Ser | Pro | Pro | Ala | Glu | Ile | His | His |
|     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Asp | Asp | Asn | Leu | Lys | Arg | Ile | Leu | Ile | Ile | Ser | Ala | Ser | Ser | Ile | Ile |
|     |     | 65  |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Thr | Thr | Leu | Phe | Leu | Leu | Thr | Leu | Leu | Val | Leu | Cys | Phe | Lys | Phe | Tyr |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     | 95  |     |     |
| Tyr | Arg | Arg | Arg | Arg | Ser | Ile | Thr | Thr | Ser | Arg | Arg | Trp | Ser | Met | Glu |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Glu | Ala | Arg | Asn | Trp | Asp | Phe | Asp | Gly | Pro | Ala | Pro | Val | Ile | Val | Asp |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| His | Pro | Ile | Trp | His | Ile | Arg | Thr | Ile | Gly | Leu | Asn | Pro | Thr | Val | Ile |
|     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Ser | Ser | Ile | Lys | Val | Cys | Gln | Tyr | Ser | Lys | Lys | Asp | Gly | Val | Val | Glu |
|     |     | 145 |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |     |
| Gly | Thr | Asp | Cys | Ser | Val | Cys | Leu | Ser | Glu | Phe | Glu | Glu | Glu | Glu | Thr |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     | 175 |     |     |
| Leu | Arg | Leu | Leu | Pro | Lys | Cys | Lys | His | Ala | Phe | His | Leu | Tyr | Cys | Ile |
|     |     | 180 |     |     |     |     | 185 |     |     |     |     |     | 190 |     |     |
| Asp | Thr | Trp | Leu | Arg | Ser | His | Thr | Asn | Cys | Pro | Leu | Ser | Arg | Ala | Pro |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Ile | Val | Glu | Ala | Asn | Thr | Met | Ile | Asp | Asp | His | Ser | Glu | Gly | Leu | Glu |
|     |     | 210 |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Glu | Ile | Ser | Val | Met | Ile | Pro | Glu | Glu | Asn | Gly | Asp | Asp | Thr | Asp | Glu |
|     |     | 225 |     |     | 230 |     |     |     |     | 235 |     |     |     | 240 |     |
| Glu | Ile | Glu | Glu | Glu | Arg | Asp | Gly | Phe | Val | Ser | Asn | Ile | Ser | Arg | Asp |
|     |     |     | 245 |     |     |     |     |     | 250 |     |     |     |     | 255 |     |
| His | Gly | Glu | Ser | Gln | Gln | Arg | Val | Arg | Arg | Ser | Val | Ser | Leu | Asp |     |
|     |     | 260 |     |     |     | 265 |     |     |     |     | 270 |     |     |     |     |
| Ser | Leu | Ser | Gly | Leu | Arg | Val | Ser | Glu | Val | Val | Val | Gly | Arg | Glu | Lys |
|     |     | 275 |     |     |     | 280 |     |     |     |     | 285 |     |     |     |     |
| Glu | Lys | Leu | Lys | Arg | Gly | Asn | Asn | Ile | Gly | Ser | Gly | Arg | Ser | Ser | Leu |
|     |     | 290 |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Leu | Lys | Arg | Ser | Ile | Ser | Tyr | Ser | Gly | Lys |     |     |     |     |     |     |
|     |     | 305 |     |     | 310 |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:555:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 303 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..303

(D) OTHER INFORMATION: / Ceres Seq. ID 1567308

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:555:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Pro | Lys | Glu | Thr | Phe | Ser | Asp | Ser | Leu | Cys | Lys | Asn | Asn | Cys | Ile |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Gln | Glu | Leu | Lys | Thr | Leu | Gly | Tyr | Cys | Ser | Ser | Tyr | Cys | Leu | Asp | Glu |

$$\frac{d}{dx} \left( x^{\frac{m+1}{n}} \right) = \frac{m+1}{n} x^{\frac{m+1}{n}-1}$$

|             |            |            |            |             |             |     |
|-------------|------------|------------|------------|-------------|-------------|-----|
| aaaagaagatc | aaacatacga | tagcttggac | tctttttggc | gtcatgatgc  | tctctcaatc  | 60  |
| tctcatctta  | gctttctctc | tctctctctt | tgctggatca | ttgtttttatc | tcacataatgg | 120 |
| attccaattt  | tcattactcg | atagatctta | acgaagatca | aaacccatcac | gaccaacccct | 180 |
| ttttctatcc  | tcttgagctc | tcttctctgc | ttcatcatca | tcatcattcat | catcatcatc  | 240 |
| aagtcctctc  | taattcttca | tcttcttctt | cgctccattc | atcgctctctc | tcttaacctc  | 300 |
| ctttcttgat  | caactctcaa | gaagatcaac | atgttgctca | gacacacatc  | gatcactcgtg | 360 |
| atcatcttca  | ttttctctca | cccctcaagg | ccaagatggt | tgtggctaac  | tgtgggatcat | 420 |
| catcatgcga  | tcacatggtg | ccaaggatgc | agacaagatg | gaactaacgc  | ataaagaaaa  | 480 |
| aagatcacga  | agaccaacc  | catctctctc | atcaaaaacc | gacaaaacc   | gttcagactc  | 540 |
| gcacagaagt  | gttgatgtcc | ccaaagatgc | ggttgatcaa | gaaaaaacatc | accacaata   | 600 |
| aacagctcac  | tgatcagact | aataataata | atcataaaga | aagtgtcatc  | tacctgttga  | 660 |
| atcataagac  | taattctgac | gaggatcaca | atgaagatct | taatttcaag  | agctctctga  | 720 |
| ccaggaaagac | cacggccgcg | atcccgcaga | atcgctacaa | tacataatcac | gagacagcgtt | 780 |
| atagtaatac  | caatgcgtgc | attagcctgc | tgtcggatgt | taaacacac   | aagactcctc  | 840 |

|            |             |             |            |            |             |      |
|------------|-------------|-------------|------------|------------|-------------|------|
| tttggcgaag | tggacctcga  | ggtcccaagt  | ctctttgtaa | cgcgatgtgt | atacggcaaa  | 900  |
| gaaaggcaag | gogagccgct  | atggccgcgg  | ccgctgcagc | cggcgaccaa | gaggtggcgg  | 960  |
| tagcgcoccc | agtgcaacaa  | ttaccgcgtg  | aaaagaagtt | gcaaaataaa | aaaaaagaga  | 1020 |
| tcaaacggag | gggaaaaata  | caatcactct  | cctccaatgt | tggcccaagg | caaaaagtgc  | 1080 |
| aagatcaaa  | aggaagagga  | gaaggMaatg  | gaagcggaaa | cgggtgcggg | agattcagag  | 1140 |
| atcagcaaat | ctacaacttc  | ttctaattct  | tcgatttcgt | caaaacaatt | ttgcttcgat  | 1200 |
| gatttgacaa | taattgttgag | caaaaagctca | gcttatcaac | aagtgttccc | acaagatgag  | 1260 |
| aaggaggctg | ctgttttgcg  | catggctctg  | tcgtatggaa | tggttcacgg | ttgatcagat  | 1320 |
| catcacata  | tcttcattac  | aaaaagggtt  | attttaata  | taatatatag | attatagtaa  | 1380 |
| tcataataat | gattgattgt  | taaatcttgg  | agtgattagt | ttagtttttg | cagttggctc  | 1440 |
| aaatatcaga | gtcaaaacat  | tttataataa  | gagtggttga | gagtttaata | tgataaattaa | 1500 |
| tagctctata | taagttttgg  | gagattttgg  | ttttagtttt | gtgtgttttt | tgttttccga  | 1560 |
| tggaaacga  | attagtcacc  | cgataatgtg  | ggtaattctt | gttcatttac | aagttttata  | 1620 |
| tgactgtatt | gtgtaacgag  | gttgagagaa  | taataataac | aattaagggt |             |      |

(2) INFORMATION FOR SEQ ID NO:557:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 349 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..349
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567310

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:557:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Asp | Ser | Asn | Phe | His | Tyr | Ser | Ile | Asp | Leu | Asn | Glu | Asp | Gln | Asn |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| His | His | Glu | Gln | Pro | Phe | Phe | Tyr | Pro | Leu | Gly | Ser | Ser | Ser | Ser | Leu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     |     | 30  |     |
| His | His | His | His | His | His | His | His | Gln | Val | Pro | Ser | Asn | Ser | Ser |     |
|     |     |     | 35  |     |     |     | 40  |     |     |     | 45  |     |     |     |     |
| Ser | Ser | Ser | Ser | Ser | Ile | Ser | Ser | Leu | Ser | Ser | Tyr | Leu | Pro | Phe | Leu |
|     |     |     | 50  |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ile | Asn | Ser | Gln | Glu | Asp | Gln | His | Val | Ala | Tyr | Asn | Asn | Thr | Tyr | His |
|     |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Ala | Asp | His | Leu | His | Leu | Ser | Gln | Pro | Leu | Lys | Ala | Lys | Met | Phe | Val |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Ala | Asn | Gly | Gly | Ser | Ser | Cys | Asp | His | Met | Val | Pro | Lys | Lys | Glu |     |
|     |     |     | 100 |     |     |     | 105 |     |     |     |     | 110 |     |     |     |
| Thr | Arg | Leu | Lys | Leu | Thr | Ile | Arg | Lys | Lys | Asp | His | Glu | Asp | Gln | Pro |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| His | Pro | Leu | His | Gln | Asn | Pro | Thr | Lys | Pro | Asp | Ser | Asp | Ser | Asp | Lys |
|     |     |     | 130 |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Trp | Leu | Met | Ser | Pro | Lys | Met | Arg | Leu | Ile | Lys | Lys | Thr | Ile | Thr | Asn |
|     |     |     | 145 |     |     | 150 |     |     |     | 155 |     |     |     |     | 160 |
| Asn | Lys | Gln | Leu | Thr | Asp | Gln | Thr | Asn | Asn | Asn | Asn | His | Lys | Glu | Ser |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Asp | His | Tyr | Pro | Leu | Asn | His | Lys | Thr | Asn | Phe | Asp | Glu | Asp | His | His |
|     |     |     | 180 |     |     |     | 185 |     |     |     |     | 190 |     |     |     |
| Glu | Asp | Leu | Asn | Phe | Lys | Asn | Val | Leu | Thr | Arg | Lys | Thr | Thr | Ala | Ala |
|     |     |     | 195 |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Thr | Thr | Glu | Asn | Arg | Tyr | Asn | Thr | Ile | Asn | Glu | Asn | Gly | Tyr | Ser | Asn |
|     |     |     | 210 |     |     | 215 |     |     |     |     |     | 220 |     |     |     |
| Asn | Asn | Gly | Val | Ile | Arg | Val | Cys | Ser | Asp | Cys | Asn | Thr | Thr | Lys | Thr |
|     |     |     | 225 |     |     | 230 |     |     |     | 235 |     |     |     |     | 240 |
| Pro | Leu | Trp | Arg | Ser | Gly | Pro | Arg | Gly | Pro | Lys | Ser | Leu | Cys | Asn | Ala |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Cys | Gly | Ile | Arg | Gln | Arg | Lys | Ala | Arg | Arg | Ala | Ala | Met | Ala | Ala | Ala |
|     |     |     | 260 |     |     |     | 265 |     |     |     |     | 270 |     |     |     |
| Ala | Ala | Ala | Gly | Asp | Gln | Glu | Val | Ala | Val | Ala | Pro | Arg | Val | Gln | Gln |

(2) INFORMATION FOR SEQ ID NO:558:

(A) LENGTH: 256 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..256

(D) OTHER INFORMATION: / Ceres Seq. ID 1567311

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:558:

(2) INFORMATION FOR SEQ ID NO:559:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 243 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..243  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1567312  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:559:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Val | Pro | Lys | Lys | Glu | Thr | Arg | Leu | Lys | Leu | Thr | Ile | Arg | Lys | Lys |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Asp | His | Glu | Asp | Gln | Pro | His | Pro | Leu | His | Gln | Asn | Pro | Thr | Lys | Pro |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     | 30  |     |     |     |
| Asp | Ser | Asp | Ser | Asp | Lys | Trp | Leu | Met | Ser | Pro | Lys | Met | Arg | Leu | Ile |
|     |     | 35  |     |     |     |     | 40  |     |     |     | 45  |     |     |     |     |
| Lys | Lys | Thr | Ile | Thr | Asn | Asn | Lys | Gln | Leu | Thr | Asp | Gln | Thr | Asn | Asn |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Asn | Asn | His | Lys | Glu | Ser | Asp | His | Tyr | Pro | Leu | Asn | His | Lys | Thr | Asn |
|     | 65  |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |     |
| Phe | Asp | Glu | Asp | His | His | Glu | Asp | Leu | Asn | Phe | Lys | Asn | Val | Leu | Thr |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Arg | Lys | Thr | Thr | Ala | Ala | Thr | Thr | Glu | Asn | Arg | Tyr | Asn | Thr | Ile | Asn |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Glu | Asn | Gly | Tyr | Ser | Asn | Asn | Asn | Gly | Val | Ile | Arg | Val | Cys | Ser | Asp |
|     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |     |
| Cys | Asn | Thr | Thr | Lys | Thr | Pro | Leu | Trp | Arg | Ser | Gly | Pro | Arg | Gly | Pro |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Lys | Ser | Leu | Cys | Asn | Ala | Cys | Gly | Ile | Arg | Gln | Arg | Lys | Ala | Arg | Arg |
|     | 145 |     |     | 150 |     |     |     | 155 |     |     |     |     |     | 160 |     |
| Ala | Ala | Met | Ala | Ala | Ala | Ala | Ala | Gly | Asp | Gln | Glu | Val | Ala | Val |     |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |     |
| Ala | Pro | Arg | Val | Gln | Gln | Leu | Pro | Leu | Lys | Lys | Lys | Leu | Gln | Asn | Lys |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Lys | Lys | Glu | Ile | Lys | Arg | Arg | Gly | Lys | Ile | Gln | Ser | Leu | Ser | Ser | Asn |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Gly | Gly | Gln | Gly | Gln | Lys | Val | Gln | Asp | Gln | Arg | Gly | Arg | Gly | Glu | Xaa |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Asn | Gly | Ser | Gly | Asn | Gly | Cys | Arg | Arg | Phe | Arg | Asp | Gln | Gln | Ile | Tyr |
|     | 225 |     |     |     | 230 |     |     |     | 235 |     |     |     |     | 240 |     |
| Asn | Phe | Phe |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:560:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 1018 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (ix) FEATURE:  
    (A) NAME/KEY: -  
    (B) LOCATION: 1..1018  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1567317

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:560:

|             |             |             |             |             |             |     |
|-------------|-------------|-------------|-------------|-------------|-------------|-----|
| accttttacaa | ctaaactcata | agtaaaacac  | agacagtttt  | tagatggcata | agatatattc  | 60  |
| cccttctttt  | cccggtactc  | tctgtctttg  | cattttttact | ctcttgacgc  | taatgttcat  | 120 |
| tcgggttttc  | gctcgaccgc  | cgacattcgt  | cgaggatttc  | aaagccgcct  | ggctgggaatc | 180 |
| tcacatcgt   | caaatggaag  | acggaaaagc  | tatccagctc  | gtccttgatc  | agagcaactgg | 240 |
| atgtgggatt  | gcttccaaaa  | gaaaatatct  | attcggaaga  | gtgagcatga  | ggatcaaaat  | 300 |
| cattcccgga  | gactctgcgc  | gtacgGtcac  | cgcttttctac | atgaactccg  | atacggccac  | 360 |
| ggtgagagac  | gagctagatt  | ttgagttctt  | gggaaaacaga | agtggtcaac  | cttactcaagt | 420 |
| gaaacacaac  | atatttgtct  | atggcacaag  | agatagagaa  | caaagagtta  | atcttttggt  | 480 |
| cgacccatct  | atggattacc  | acactttacac | tatcttatgg  | tcacacaaac  | acattgtttt  | 540 |
| ttacgtagac  | gatgtgccaa  | taagagaata  | caaaaacac   | gaagccaaga  | acatagctta  | 600 |
| cccaacatca  | caacctatgg  | gagtatactc  | aacattatgg  | gaagcagatg  | actggggcaac | 660 |

acgtgggtgga ttagagaaaa ttgattggag caaagctcca ttttatgctt attacaagaa 720  
tttcgacatc gaaggttgctc ctgttctctg accaaccttt tTgtccatcg aaccttcata 780  
atttggtggga aggtttatgcc tatcagtctc ttaacgccgt tgaagctoga cggtaccggg 840  
gggtagtagt aaaccatattg gtttatgatt attgtactga ccggtctagg ttctctgtcc 900  
caccaccgga gtgtcgtgct tgaataat tgcatacgt cgttgcagt atcatgttc 960  
gtctgtacg agatattata tataaattg gggaaaatgt ggattgtatt gtcctctt

(2) INFORMATION FOR SEQ ID NO:561:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 245 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..245

(D) OTHER INFORMATION: / Ceres Seq. ID 1567318

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:561:

Met Ala Lys Ile Tyr Ser Pro Ser Phe Pro Gly Thr Leu Cys Leu Cys  
1 5 10 15  
Ile Phe Thr Leu Leu Thr Leu Met Phe Ile Arg Val Ser Ala Arg Pro  
20 25 30  
Ala Thr Phe Val Glu Asp Phe Lys Ala Ala Trp Ser Glu Ser His Ile  
35 40 45  
Arg Gln Met Glu Asp Gly Lys Ala Ile Gln Leu Val Leu Asp Gln Ser  
50 55 60  
Thr Gly Cys Gly Phe Ala Ser Lys Arg Lys Tyr Leu Phe Gly Arg Val  
65 70 75 80  
Ser Met Arg Ile Lys Leu Ile Pro Gly Asp Ser Ala Gly Thr Val Thr  
85 90 95  
Ala Phe Tyr Met Asn Ser Asp Thr Ala Thr Val Arg Asp Glu Leu Asp  
100 105 110  
Phe Glu Phe Leu Gly Asn Arg Ser Gly Gln Pro Tyr Ser Val Gln Thr  
115 120 125  
Asn Ile Phe Ala His Gly Lys Gly Asp Arg Glu Gln Arg Val Asn Leu  
130 135 140  
Trp Phe Asp Pro Ser Met Asp Tyr His Thr Tyr Thr Ile Leu Trp Ser  
145 150 155 160  
His Lys His Ile Val Phe Tyr Val Asp Asp Val Pro Ile Arg Glu Tyr  
165 170 175  
Lys Asn Asn Glu Ala Lys Asn Ile Ala Tyr Pro Thr Ser Gln Pro Met  
180 185 190  
Gly Val Tyr Ser Thr Leu Trp Glu Ala Asp Asp Trp Ala Thr Arg Gly  
195 200 205  
Gly Leu Glu Lys Ile Asp Trp Ser Lys Ala Pro Phe Tyr Ala Tyr Tyr  
210 215 220  
Lys Asp Phe Asp Ile Glu Gly Cys Pro Val Pro Gly Pro Thr Phe Leu  
225 230 235 240  
Ser Ile Glu Pro Ser  
245

(2) INFORMATION FOR SEQ ID NO:562:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 222 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..222

(D) OTHER INFORMATION: / Ceres Seq. ID 1567319



(xi) SEQUENCE DESCRIPTION: SEQ ID NO:562:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Phe | Ile | Arg | Val | Ser | Ala | Arg | Pro | Ala | Thr | Phe | Val | Glu | Asp | Phe |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Lys | Ala | Ala | Trp | Ser | Glu | Ser | His | Ile | Arg | Gln | Met | Glu | Asp | Gly | Lys |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ala | Ile | Gln | Leu | Val | Leu | Asp | Gln | Ser | Thr | Gly | Cys | Gly | Phe | Ala | Ser |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Lys | Arg | Lys | Tyr | Leu | Phe | Gly | Arg | Val | Ser | Met | Arg | Ile | Lys | Leu | Ile |
|     |     |     | 50  |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Pro | Gly | Asp | Ser | Ala | Gly | Thr | Val | Thr | Ala | Phe | Tyr | Met | Asn | Ser | Asp |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Thr | Ala | Thr | Val | Arg | Asp | Glu | Leu | Asp | Phe | Glu | Phe | Leu | Gly | Asn | Arg |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Ser | Gly | Gln | Pro | Tyr | Ser | Val | Gln | Thr | Asn | Ile | Phe | Ala | His | Gly | Lys |
|     |     |     | 100 |     |     |     | 105 |     |     |     |     |     | 110 |     |     |
| Gly | Asp | Arg | Glu | Gln | Arg | Val | Asn | Leu | Trp | Phe | Asp | Pro | Ser | Met | Asp |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Tyr | His | Thr | Tyr | Thr | Ile | Leu | Trp | Ser | His | Lys | His | Ile | Val | Phe | Tyr |
|     |     |     | 130 |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Val | Asp | Asp | Val | Pro | Ile | Arg | Glu | Tyr | Lys | Asn | Asn | Glu | Ala | Lys | Asn |
| 145 |     |     |     |     | 150 |     |     |     | 155 |     |     |     |     | 160 |     |
| Ile | Ala | Tyr | Pro | Thr | Ser | Gln | Pro | Met | Gly | Val | Tyr | Ser | Thr | Leu | Trp |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Glu | Ala | Asp | Asp | Trp | Ala | Thr | Arg | Gly | Gly | Leu | Glu | Lys | Ile | Asp | Trp |
|     |     |     |     | 180 |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Ser | Lys | Ala | Pro | Phe | Tyr | Ala | Tyr | Tyr | Lys | Asp | Phe | Asp | Ile | Glu | Gly |
|     |     |     | 195 |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Cys | Pro | Val | Pro | Gly | Pro | Thr | Phe | Leu | Ser | Ile | Glu | Pro | Ser |     |     |
| 210 |     |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:563:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 195 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..195

(D) OTHER INFORMATION: / Ceres Seq. ID 1567320

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:563:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Glu | Asp | Gly | Lys | Ala | Ile | Gln | Leu | Val | Leu | Asp | Gln | Ser | Thr | Gly |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Cys | Gly | Phe | Ala | Ser | Lys | Arg | Lys | Tyr | Leu | Phe | Gly | Arg | Val | Ser | Met |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Arg | Ile | Lys | Leu | Ile | Pro | Gly | Asp | Ser | Ala | Gly | Thr | Val | Thr | Ala | Phe |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Tyr | Met | Asn | Ser | Asp | Thr | Ala | Thr | Val | Arg | Asp | Glu | Leu | Asp | Phe | Glu |
|     |     |     | 50  |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Phe | Leu | Gly | Asn | Arg | Ser | Gly | Gln | Pro | Tyr | Ser | Val | Gln | Thr | Asn | Ile |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Phe | Ala | His | Gly | Lys | Gly | Asp | Arg | Glu | Gln | Arg | Val | Asn | Leu | Trp | Phe |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Asp | Pro | Ser | Met | Asp | Tyr | His | Thr | Tyr | Thr | Ile | Leu | Trp | Ser | His | Lys |
|     |     |     | 100 |     |     |     | 105 |     |     |     |     |     | 110 |     |     |
| His | Ile | Val | Phe | Tyr | Val | Asp | Asp | Val | Pro | Ile | Arg | Glu | Tyr | Lys | Asn |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Asn | Glu | Ala | Lys | Asn | Ile | Ala | Tyr | Pro | Thr | Ser | Gln | Pro | Met | Gly | Val |
|     |     |     | 130 |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Tyr | Ser | Thr | Leu | Trp | Glu | Ala | Asp | Asp | Trp | Ala | Thr | Arg | Gly | Gly | Leu |
| 145 |     |     |     |     | 150 |     |     |     | 155 |     |     |     |     | 160 |     |

Glu Lys Ile Asp Trp Ser Lys Ala Pro Phe Tyr Ala Tyr Tyr Lys Asp  
165 170 175  
Phe Asp Ile Glu Gly Cys Pro Val Pro Gly Pro Thr Phe Leu Ser Ile  
180 185 190  
Glu Pro Ser  
195

(2) INFORMATION FOR SEQ ID NO:564:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 280 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..280
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567325

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:564:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| agaaagcgag agcgaNtgat tcagaagatt ctgagaatga agaggatgag gatgaagaag  | 60  |
| tagtagtaga agaagaagag gaggaagaag acgaggagag tagtgaagat gccggagagag | 120 |
| gaagtcaaaa cgaaggagaa ctaaaaactg aggatggtgg tgaaggagaa agcgaataat  | 180 |
| tgtaagatcg ttggtgtgtt gtaatgtagc ctagtctcac tatgtactgt ttagagagtgg | 240 |
| tgatatatttg taccttttta atgtgtcaat catatttatg                       |     |

(2) INFORMATION FOR SEQ ID NO:565:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..58
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567326

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:565:

|                                                                 |  |
|-----------------------------------------------------------------|--|
| Lys Ala Arg Ala Xaa Asp Ser Glu Asp Ser Glu Asn Glu Glu Asp Glu |  |
| 1 5 10 15                                                       |  |
| Asp Glu Glu Val Val Val Glu Glu Glu Glu Glu Glu Asp Glu Gly     |  |
| 20 25 30                                                        |  |
| Gly Ser Glu Asp Gly Gly Glu Gly Ser Gln Asn Glu Gly Glu Leu Lys |  |
| 35 40 45                                                        |  |
| Thr Glu Asp Gly Gly Glu Glu Ser Glu                             |  |
| 50 55                                                           |  |

(2) INFORMATION FOR SEQ ID NO:566:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1127 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1127
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567331

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:566:

|                                                                     |     |
|---------------------------------------------------------------------|-----|
| ctgccaaaca tatacatcaa agcttgactc tctttttctc tcccatggaa tcgacaaaaga  | 60  |
| agcaagtctc gctggagacta cttccatggt tagttgtcca caccgatgga accgtagaga  | 120 |
| gactagcggg aaccgaggtt tgtctctccg gtttgatccc aataaccggg gttttctcta   | 180 |
| aagatatcat tatcgaaaccg aaaaaccggtt tatctgcccg aatctatoga cctttctcga | 240 |
| ttcaaccggg tcagaagatt cctctcatgc tctattttca tggcggtgca tttctcatct   | 300 |
| cctccacttc cttccctctt taccacacca gtcttaacaa aattgtcaat caggctaacg   | 360 |

|             |             |             |             |             |            |      |
|-------------|-------------|-------------|-------------|-------------|------------|------|
| tcatagccgt  | ctctgtcaat  | tacagactag  | caccagaaca  | tcacttctct  | acagcgtaag | 420  |
| aagactcatg  | gactgcgcta  | aatactatcc  | aagccataaa  | cgagccgtgg  | atcaacgact | 480  |
| acgccgactt  | ggacagtata  | ttctagtgg   | gagatagcgc  | cggagctaata | atctcgacc  | 540  |
| acctgcatt   | togagccaaa  | caatctgacc  | Aaaacccgtga | aaataaaagg  | cattggaatg | 600  |
| atccaccact  | atttttggg   | aaacacaacct | atcggagcag  | agatcaaaga  | cgaagcgatg | 660  |
| aaacaaatgg  | tggaaggatg  | gtgggaattt  | gtgtgccctt  | ccaagaaagg  | atctgatgac | 720  |
| ccgtggatta  | atccgttttg  | ggacgggtca  | ccggatcttg  | gagggttagg  | gtgtgagaga | 780  |
| gtgatgatta  | ctgtggcgga  | gaaagatata  | ttgaatgaga  | gagggaaagt  | gtattttgaa | 840  |
| agatttggtga | agagtgagtg  | gaaaggaaaag | gttgagatta  | tggagacgaa  | agagaaagat | 900  |
| catgtttttc  | atatattttga | gcccgattgt  | gatgaagcta  | tggagatggt  | acgatgcttg | 960  |
| gctctcttta  | taaaccaagt  | tgaagcttga  | tattatttgt  | tttgccataa  | tttgatggct | 1020 |
| tttttaagt   | ttgtataaatt | tttcatgttt  | tgtaaattgt  | gtgttatttg  | tcttttcttt | 1080 |
| taaattgtg   | tattacattt  | atatgtggtt  | aaatttgtgt  | tttttcc     |            |      |

(2) INFORMATION FOR SEQ ID NO:567:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 237 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..237

- (D) OTHER INFORMATION: / Ceres Seq. ID 1567332

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:567:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Ala | Lys | His | Ile | His | Gln | Ser | Leu | Thr | Leu | Phe | Phe | Ser | Pro | Met | Glu |  |
| 1   |     | 5   |     |     |     |     |     | 10  |     |     |     |     |     | 15  |     |  |
| Ser | Thr | Lys | Lys | Gln | Val | Ser | Leu | Glu | Leu | Leu | Pro | Trp | Leu | Val | Val |  |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| His | Thr | Asp | Gly | Thr | Val | Glu | Arg | Leu | Ala | Gly | Thr | Glu | Val | Cys | Pro |  |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Pro | Gly | Leu | Asp | Pro | Ile | Thr | Gly | Val | Phe | Ser | Lys | Asp | Ile | Ile | Ile |  |
|     |     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |  |
| Glu | Pro | Lys | Thr | Gly | Leu | Ser | Ala | Arg | Ile | Tyr | Arg | Pro | Phe | Ser | Ile |  |
|     |     | 65  |     |     |     |     | 70  |     |     | 75  |     |     |     |     | 80  |  |
| Gln | Pro | Gly | Gln | Lys | Ile | Pro | Leu | Met | Leu | Tyr | Phe | His | Gly | Gly | Ala |  |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     |     | 95  |  |
| Phe | Leu | Ile | Ser | Ser | Thr | Ser | Phe | Pro | Ser | Tyr | His | Thr | Ser | Leu | Asn |  |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |
| Lys | Ile | Val | Asn | Gln | Ala | Asn | Val | Ile | Ala | Val | Ser | Val | Asn | Tyr | Arg |  |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     |     | 125 |     |     |  |
| Leu | Ala | Pro | Glu | His | Pro | Leu | Pro | Thr | Ala | Tyr | Glu | Asp | Ser | Trp | Thr |  |
|     |     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |  |
| Ala | Leu | Asn | Thr | Ile | Gln | Ala | Ile | Asn | Glu | Pro | Trp | Ile | Asn | Asp | Tyr |  |
|     |     |     | 145 |     |     |     | 150 |     |     |     | 155 |     |     |     | 160 |  |
| Ala | Asp | Leu | Asp | Ser | Ile | Phe | Leu | Val | Gly | Asp | Ser | Ala | Gly | Ala | Asn |  |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     |     | 175 |  |
| Ile | Ser | His | His | Leu | Ala | Phe | Arg | Ala | Lys | Gln | Ser | Asp | Gln | Asn | Arg |  |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |  |
| Glu | Asn | Lys | Arg | His | Trp | Asn | Asp | Pro | Pro | Ile | Phe | Leu | Gly | Asn | Thr |  |
|     |     |     | 195 |     |     |     | 200 |     |     |     |     | 205 |     |     |     |  |
| Thr | Tyr | Arg | Ser | Arg | Asp | Gln | Arg | Arg | Ser | Asp | Glu | Thr | Asn | Gly | Gly |  |
|     |     |     | 210 |     |     |     | 215 |     |     |     |     | 220 |     |     |     |  |
| Arg | Met | Val | Gly | Ile | Cys | Val | Pro | Leu | Gln | Glu | Arg | Ile |     |     |     |  |
|     |     |     | 225 |     |     |     | 230 |     |     |     | 235 |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:568:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 223 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..223

(D) OTHER INFORMATION: / Ceres Seq. ID 1567333

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:568:

```
Met Glu Ser Thr Lys Lys Gln Val Ser Leu Glu Leu Leu Pro Trp Leu
1 5 10 15
Val Val His Thr Asp Gly Thr Val Glu Arg Leu Ala Gly Thr Glu Val
 20 25 30
Cys Pro Pro Gly Leu Asp Pro Ile Thr Gly Val Phe Ser Lys Asp Ile
 35 40 45
Ile Ile Glu Pro Lys Thr Gly Leu Ser Ala Arg Ile Tyr Arg Pro Phe
50 55 60
Ser Ile Gln Pro Gly Gln Lys Ile Pro Leu Met Leu Tyr Phe His Gly
65 70 75 80
Gly Ala Phe Leu Ile Ser Ser Thr Ser Phe Pro Ser Tyr His Thr Ser
 85 90 95
Leu Asn Lys Ile Val Asn Gln Ala Asn Val Ile Ala Val Ser Val Asn
 100 105 110
Tyr Arg Leu Ala Pro Glu His Pro Leu Pro Thr Ala Tyr Glu Asp Ser
 115 120 125
Trp Thr Ala Leu Asn Thr Ile Gln Ala Ile Asn Glu Pro Trp Ile Asn
130 135 140
Asp Tyr Ala Asp Leu Asp Ser Ile Phe Leu Val Gly Asp Ser Ala Gly
145 150 155 160
Ala Asn Ile Ser His His Leu Ala Phe Arg Ala Lys Gln Ser Asp Gln
 165 170 175
Asn Arg Glu Asn Lys Arg His Trp Asn Asp Pro Pro Ile Phe Leu Gly
 180 185 190
Asn Thr Thr Tyr Arg Ser Arg Asp Gln Arg Arg Ser Asp Glu Thr Asn
195 200 205
Gly Gly Arg Met Val Gly Ile Cys Val Pro Leu Gln Glu Arg Ile
210 215 220
```

(2) INFORMATION FOR SEQ ID NO:569:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 149 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..149

(D) OTHER INFORMATION: / Ceres Seq. ID 1567334

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:569:

```
Met Leu Tyr Phe His Gly Gly Ala Phe Leu Ile Ser Ser Thr Ser Phe
1 5 10 15
Pro Ser Tyr His Thr Ser Leu Asn Lys Ile Val Asn Gln Ala Asn Val
 20 25 30
Ile Ala Val Ser Val Asn Tyr Arg Leu Ala Pro Glu His Pro Leu Pro
 35 40 45
Thr Ala Tyr Glu Asp Ser Trp Thr Ala Leu Asn Thr Ile Gln Ala Ile
50 55 60
Asn Glu Pro Trp Ile Asn Asp Tyr Ala Asp Leu Asp Ser Ile Phe Leu
65 70 75 80
Val Gly Asp Ser Ala Gly Ala Asn Ile Ser His His Leu Ala Phe Arg
 85 90 95
Ala Lys Gln Ser Asp Gln Asn Arg Glu Asn Lys Arg His Trp Asn Asp
100 105 110
Pro Pro Ile Phe Leu Gly Asn Thr Thr Tyr Arg Ser Arg Asp Gln Arg
```

115 120 125  
Arg Ser Asp Glu Thr Asn Gly Gly Arg Met Val Gly Ile Cys Val Pro  
130 135 140  
Leu Gln Glu Arg Ile  
145

(2) INFORMATION FOR SEQ ID NO:570:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1877 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1877
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567335

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:570:

|             |             |             |             |            |             |      |
|-------------|-------------|-------------|-------------|------------|-------------|------|
| aaacacaaac  | aMcaattaag  | ctaaaaaaa   | aaccaaaggga | tgtctcagaa | actcatgttc  | 60   |
| ttgttcaccc  | ttgcctgcct  | ctcctcggtta | ccatctcctt  | ttatctccgc | ccaaataccg  | 120  |
| gccattggaa  | atgccacttc  | accgtcaaat  | atatgtagat  | tgccgccgga | tcacatcttat | 180  |
| gtgatgcgg   | ttcttccaaa  | ccagcccgga  | gatataatt   | ctcaccgacg | tttgtctcta  | 240  |
| cgaagatccc  | tctccagccc  | gccggttcat  | ttcgtatgat  | gacgctgaac | ttgaccggaa  | 300  |
| aggcaaaagt  | ctcgtctaaat | ccacagtagg  | ggctctcgaa  | gactgcaaat | tcctagccag  | 360  |
| cctgactatg  | gactacctcc  | ttagtactgc  | acagacggct  | gattccaaca | aaacactgtc  | 420  |
| gttatctagg  | gccgaggatg  | ttcatcatt   | ttctgagtgt  | gccatcaaca | atgagcaaac  | 480  |
| ttgtcttgaa  | ggactttaaat | cgaaacggct  | ctttccgggt  | atcttttcaa | 540         |      |
| cgatacaaaa  | ctctatgggg  | ttgtctctgc  | ctttttctcc  | aaaggttggg | tgccaaagaa  | 600  |
| gcacaaagtc  | agaccgattt  | ggcaaccaca  | agccagggtc  | aaaaagtgtt | tttgtttccg  | 660  |
| taacggtaaa  | ttaccgttaa  | agatgacgga  | aagggcacgt  | gccgtttaca | acaccgtagc  | 720  |
| tagaagaaag  | ttcttccaat  | cggatgcaga  | cgccgttcag  | gtgagcgaca | ttgtgacggt  | 780  |
| gatccagaac  | gggacgggaa  | acttcacgac  | cataaaagcc  | gccattgcag | ctgcaccaaaa | 840  |
| taaaaactgac | ggtagtagcg  | gttacttctt  | gatctacgta  | acggccggat | gtgacgagaa  | 900  |
| atacgtggaa  | gttcccaaga  | acaagagata  | tgtgatgatg  | atcgggtgac | gcatcaacca  | 960  |
| gaccgttatc  | accggaaaca  | ggagtgtcgt  | tgatggatgg  | acaactttca | attcagccac  | 1020 |
| attttattcta | tcagggtccca | actttattgg  | tgtaaacata  | acaatccgca | atacggcgac  | 1080 |
| accaaccaaaa | ggccaagctt  | tgccattgag  | gagtggtggg  | gaactgtctg | ttttctacag  | 1140 |
| ttgtagtgtt  | gaagcctatc  | aagacacggt  | atacacacat  | ttcttcagac | agttttatcg  | 1200 |
| tgaattgtgat | gtctatggta  | ctgtttgatt  | tatatattgt  | aacgctgcag | ttgtattaca  | 1260 |
| aaactgtaat  | ttgtatccac  | gtcaaccctcg | caaaagttcaa | tcgaacggag | ttacgggtcca | 1320 |
| aggtcgtact  | gatccgaacc  | aaaacactgg  | gacggcaatt  | catggttgta | ctataagacc  | 1380 |
| ggcagatgat  | ttggctacga  | gcaactatac  | agtgaaagct  | tatcttggtc | gacctgagaa  | 1440 |
| ggaattattct | agaacccgtg  | tcattgcaaa  | ttacatagac  | gggtttctag | aacccagtggt | 1500 |
| ttggaatgca  | tggtctggtg  | attttgcatt  | gagcacactt  | tactacggcg | aatataataa  | 1560 |
| taaccggaact | ggtttctgaa  | cgacaaaacc  | agtcacttgg  | cctggtttac | acgtcatcaa  | 1620 |
| cgcaactgat  | gcttccaatt  | tcacgggtc   | caatttctct  | gttggtgaa  | gttggtatgg  | 1680 |
| acaaaaccgga | gtgccttttg  | gtgggtgact  | gatcgcataa  | tcaaccaacc | ttatactata  | 1740 |
| tatgatattgt | taattagtta  | aattatttaa  | tcattcatgt  | gttggttttt | taatcaaaa   | 1800 |
| attatttaagt | ggtgcctgat  | tcgaatacgt  | ttgaataaac  | tttaacttac | tattgtacaa  | 1860 |
| ccgaatggtt  | ttctctcg    |             |             |            |             |      |

(2) INFORMATION FOR SEQ ID NO:571:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 529 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..529
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567336

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:571:

Met Pro Leu His Arg Gln Ile Tyr Val Asp Ser Arg Arg Ile His Leu  
1 5 10 15  
Ile Val Asp Arg Phe Phe Gln Thr Ser Pro Glu Ile Tyr Ile Pro Thr  
20 25 30  
Asp Val Cys Leu Tyr Glu Asp Pro Ser Pro Ala Arg Arg Phe Ile Ser  
35 40 45  
Met Ile Asp Ala Glu Leu Asp Arg Lys Gly Lys Val Ala Ala Lys Ser  
50 55 60  
Thr Val Gly Ala Leu Glu Asp Cys Lys Phe Leu Ala Ser Leu Thr Met  
65 70 75 80  
Asp Tyr Leu Leu Ser Ser Ser Gln Thr Ala Asp Ser Thr Lys Thr Leu  
85 90 95  
Ser Leu Ser Arg Ala Glu Asp Val His Thr Phe Leu Ser Ala Ala Ile  
100 105 110  
Thr Asn Glu Gln Thr Cys Leu Glu Gly Leu Lys Ser Thr Ala Ser Glu  
115 120 125  
Asn Gly Leu Ser Gly Asp Leu Phe Asn Asp Thr Lys Leu Tyr Gly Val  
130 135 140  
Ser Leu Ala Leu Phe Ser Lys Gly Trp Val Pro Arg Arg Gln Arg Ser  
145 150 155 160  
Arg Pro Ile Trp Gln Pro Gln Ala Arg Phe Lys Lys Phe Phe Gly Phe  
165 170 175  
Arg Asn Gly Lys Leu Pro Leu Lys Met Thr Glu Arg Ala Arg Ala Val  
180 185 190  
Tyr Asn Thr Val Thr Arg Arg Lys Leu Leu Gln Ser Asp Ala Asp Ala  
195 200 205  
Val Gln Val Ser Asp Ile Val Thr Val Ile Gln Asn Gly Thr Gly Asn  
210 215 220  
Phe Thr Thr Ile Asn Ala Ala Ile Ala Ala Ala Pro Asn Lys Thr Asp  
225 230 235 240  
Gly Ser Asn Gly Tyr Phe Leu Ile Tyr Val Thr Ala Gly Leu Tyr Glu  
245 250 255  
Glu Tyr Val Glu Val Pro Lys Asn Lys Arg Tyr Val Met Met Ile Gly  
260 265 270  
Asp Gly Ile Asn Gln Thr Val Ile Thr Gly Asn Arg Ser Val Val Asp  
275 280 285  
Gly Trp Thr Thr Phe Asn Ser Ala Thr Phe Ile Leu Ser Gly Pro Asn  
290 295 300  
Phe Ile Gly Val Asn Ile Thr Ile Arg Asn Thr Ala Gly Pro Thr Lys  
305 310 315 320  
Gly Gln Ala Val Ala Leu Arg Ser Gly Gly Asp Leu Ser Val Phe Tyr  
325 330 335  
Ser Cys Ser Phe Glu Ala Tyr Gln Asp Thr Leu Tyr Thr His Ser Leu  
340 345 350  
Arg Gln Phe Tyr Arg Glu Cys Asp Val Tyr Gly Thr Val Asp Phe Ile  
355 360 365  
Phe Gly Asn Ala Ala Val Val Leu Gln Asn Cys Asn Leu Tyr Pro Arg  
370 375 380  
Gln Pro Arg Lys Gly Gln Ser Asn Glu Val Thr Ala Gln Gly Arg Thr  
385 390 395 400  
Asp Pro Asn Gln Asn Thr Gly Thr Ala Ile His Gly Cys Thr Ile Arg  
405 410 415  
Pro Ala Asp Asp Leu Ala Thr Ser Asn Tyr Thr Val Lys Thr Tyr Leu  
420 425 430  
Gly Arg Pro Trp Lys Glu Tyr Ser Arg Thr Val Val Met Gln Thr Tyr  
435 440 445  
Ile Asp Gly Phe Leu Glu Pro Ser Gly Trp Asn Ala Trp Ser Gly Asp  
450 455 460  
Phe Ala Leu Ser Thr Leu Tyr Tyr Ala Glu Tyr Asn Asn Thr Gly Pro  
465 470 475 480  
Gly Ser Asp Thr Thr Asn Arg Val Thr Trp Pro Gly Tyr His Val Ile

(2) INFORMATION FOR SEQ ID NO:572:

(A) LENGTH: 481 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: lin

MOLECULE TYPE: peptide

(ix) FEATURE:

## (1X) FEATURE. (A) NAM

(A) NAME/KEY: peptide  
(B) LOCATION: 1 481

(D) OTHER INFORMATION

SEQUENCE DESCRIPTION: SEQ ID NO:572:

(X1) SEQUENCE DESCRIPTION: SEQ ID NO:372:  
 Ile Asp Ala Gly Leu Asp Arg Lys Gly Lys V

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 1   | Met | Ile | Asp | Ala | Glu | Leu | Asp | Arg | Lys | Gly | Lys | Val | Ala | Ala | Lys | Ser |
| 10  | Thr | Val | Gly | Ala | Leu | Glu | Asp | Cys | Lys | Phe | Leu | Ala | Ser | Leu | Thr | Met |
| 20  | Asp | Tyr | Leu | Leu | Ser | Ser | Ser | Gln | Thr | Ala | Asp | Ser | Thr | Lys | Lys | Leu |
| 30  | Ser | Leu | Ser | Arg | Ala | Glu | Asp | Val | His | Thr | Phe | Leu | Ser | Ala | Ala | Ile |
| 40  | Thr | Asn | Glu | Gln | Thr | Cys | Leu | Glu | Gly | Leu | Lys | Ser | Thr | Ala | Ser | Glu |
| 50  | Asn | Gly | Leu | Ser | Gly | Asp | Leu | Phe | Asn | Asp | Thr | Lys | Leu | Tyr | Gly | Val |
| 60  | Ser | Leu | Ala | Leu | Phe | Ser | Lys | Gly | Trp | Val | Pro | Arg | Arg | Gln | Arg | Ser |
| 70  | Arg | Pro | Ile | Trp | Gln | Pro | Gln | Ala | Arg | Phe | Lys | Lys | Phe | Phe | Gly | Phe |
| 80  | Arg | Asn | Gly | Lys | Leu | Pro | Leu | Lys | Met | Thr | Glu | Arg | Ala | Arg | Ala | Val |
| 90  | Tyr | Asn | Thr | Val | Thr | Arg | Arg | Lys | Leu | Leu | Gln | Ser | Asp | Ala | Asp | Ala |
| 100 | Val | Gln | Val | Ser | Asp | Ile | Val | Thr | Val | Ile | Gln | Asn | Gly | Lys | Gly | Asn |
| 110 | Phe | Thr | Thr | Ile | Asn | Ala | Ala | Ile | Ala | Ala | Ala | Pro | Asn | Lys | Thr | Asp |
| 120 | Gly | Ser | Asn | Gly | Tyr | Phe | Leu | Ile | Tyr | Val | Thr | Ala | Gly | Leu | Tyr | Glu |
| 130 | Glu | Tyr | Val | Glu | Val | Pro | Lys | Asn | Lys | Arg | Tyr | Val | Met | Met | Ile | Gly |
| 140 | Asp | Gly | Ile | Asn | Gln | Thr | Val | Ile | Thr | Gly | Asn | Arg | Ser | Val | Val | Asp |
| 150 | Gly | Trp | Thr | Thr | Phe | Asn | Ser | Ala | Thr | Phe | Ile | Leu | Ser | Gly | Pro | Asn |
| 160 | Phe | Ile | Gly | Val | Asn | Ile | Thr | Ile | Arg | Asn | Thr | Ala | Gly | Pro | Thr | Lys |
| 170 | Gly | Gln | Ala | Val | Ala | Leu | Arg | Ser | Gly | Gly | Asp | Leu | Ser | Val | Phe | Tyr |
| 180 | Ser | Cys | Ser | Phe | Glu | Ala | Tyr | Gln | Asp | Thr | Leu | Tyr | Thr | His | Ser | Leu |
| 190 | Arg | Gln | Phe | Tyr | Arg | Glu | Cys | Asp | Val | Tyr | Gly | Thr | Val | Asp | Phe | Ile |
| 200 | Phe | Gly | Asn | Ala | Val | Val | Leu | Gln | Asn | Cys | Asn | Leu | Tyr | Pro | Arg | Arg |

Gln Pro Arg Lys Gly Gln Ser Asn Glu Val Thr Ala Gln Gly Arg Thr  
340 345 350  
Asp Pro Asn Gln Asn Thr Gly Thr Ala Ile His Gly Cys Thr Ile Arg  
355 360 365  
Pro Ala Asp Asp Leu Ala Thr Ser Asn Tyr Thr Val Lys Thr Tyr Leu  
370 375 380  
Gly Arg Pro Trp Lys Glu Tyr Ser Arg Thr Val Val Met Gln Thr Tyr  
385 390 395 400  
Ile Asp Gly Phe Leu Glu Pro Ser Gly Trp Asn Ala Trp Ser Gly Asp  
405 410 415  
Phe Ala Leu Ser Thr Leu Tyr Tyr Ala Glu Tyr Asn Asn Thr Gly Pro  
420 425 430  
Gly Ser Asp Thr Thr Asn Arg Val Thr Trp Pro Gly Tyr His Val Ile  
435 440 445  
Asn Ala Thr Asp Ala Ser Asn Phe Thr Val Thr Asn Phe Leu Val Gly  
450 455 460  
Glu Gly Trp Ile Gly Gln Thr Gly Val Pro Phe Val Gly Gly Leu Ile  
465 470 475 480  
Ala

(2) INFORMATION FOR SEQ ID NO:573:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 450 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..450

(D) OTHER INFORMATION: / Ceres Seq. ID 1567338

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:573:

Met Asp Tyr Leu Leu Ser Ser Ser Gln Thr Ala Asp Ser Thr Lys Thr  
1 5 10 15  
Leu Ser Leu Ser Arg Ala Glu Asp Val His Thr Phe Leu Ser Ala Ala  
20 25 30  
Ile Thr Asn Glu Gln Thr Cys Leu Glu Gly Leu Lys Ser Thr Ala Ser  
35 40 45  
Glu Asn Gly Leu Ser Gly Asp Leu Phe Asn Asp Thr Lys Leu Tyr Gly  
50 55 60  
Val Ser Leu Ala Leu Phe Ser Lys Gly Trp Val Pro Arg Arg Gln Arg  
65 70 75 80  
Ser Arg Pro Ile Trp Gln Pro Gln Ala Arg Phe Lys Lys Phe Phe Gly  
85 90 95  
Phe Arg Asn Gly Lys Leu Pro Leu Lys Met Thr Glu Arg Ala Arg Ala  
100 105 110  
Val Tyr Asn Thr Val Thr Arg Arg Lys Leu Leu Gln Ser Asp Ala Asp  
115 120 125  
Ala Val Gln Val Ser Asp Ile Val Thr Val Ile Gln Asn Gly Thr Gly  
130 135 140  
Asn Phe Thr Thr Ile Asn Ala Ala Ile Ala Ala Ala Pro Asn Lys Thr  
145 150 155 160  
Asp Gly Ser Asn Gly Tyr Phe Leu Ile Tyr Val Thr Ala Gly Leu Tyr  
165 170 175  
Glu Glu Tyr Val Glu Val Pro Lys Asn Lys Arg Tyr Val Met Met Ile  
180 185 190  
Gly Asp Gly Ile Asn Gln Thr Val Ile Thr Gly Asn Arg Ser Val Val  
195 200 205  
Asp Gly Trp Thr Thr Phe Asn Ser Ala Thr Phe Ile Leu Ser Gly Pro  
210 215 220  
Asn Phe Ile Gly Val Asn Ile Thr Ile Arg Asn Thr Ala Gly Pro Thr



225 230 235 240  
Lys Gly Gln Ala Val Ala Leu Arg Ser Gly Gly Asp Leu Ser Val Phe  
245 250 255  
Tyr Ser Cys Ser Phe Glu Ala Tyr Gln Asp Thr Leu Tyr Thr His Ser  
260 265 270  
Leu Arg Gln Phe Tyr Arg Glu Cys Asp Val Tyr Gly Thr Val Asp Phe  
275 280 285  
Ile Phe Gly Asn Ala Ala Val Val Leu Gln Asn Cys Asn Leu Tyr Pro  
290 295 300  
Arg Gln Pro Arg Lys Gly Gln Ser Asn Glu Val Thr Ala Gln Gly Arg  
305 310 315 320  
Thr Asp Pro Asn Gln Asn Thr Gly Thr Ala Ile His Gly Cys Thr Ile  
325 330 335  
Arg Pro Ala Asp Asp Leu Ala Thr Ser Asn Tyr Thr Val Lys Thr Tyr  
340 345 350  
Leu Gly Arg Pro Trp Lys Glu Tyr Ser Arg Thr Val Met Gln Thr  
355 360 365  
Tyr Ile Asp Gly Phe Leu Glu Pro Ser Gly Trp Asn Ala Trp Ser Gly  
370 375 380  
Asp Phe Ala Leu Ser Thr Leu Tyr Tyr Ala Glu Tyr Asn Asn Thr Gly  
385 390 395 400  
Pro Gly Ser Asp Thr Thr Asn Arg Val Thr Trp Pro Gly Tyr His Val  
405 410 415  
Ile Asn Ala Thr Asp Ala Ser Asn Phe Thr Val Thr Asn Phe Leu Val  
420 425 430  
Gly Glu Gly Trp Ile Gly Gln Thr Gly Val Pro Phe Val Gly Gly Leu  
435 440 445  
Ile Ala  
450

(2) INFORMATION FOR SEQ ID NO:574:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1212 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1212
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567343

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:574:

|             |            |             |            |             |             |      |
|-------------|------------|-------------|------------|-------------|-------------|------|
| aaaatctctc  | ttttcaagcc | aaatgaaagt  | ttaaaccctt | tgaattgttt  | attgaaagt   | 60   |
| tacatttttc  | tggtgaatcc | aactatgttt  | agattgagaa | gtctctttgc  | gctgaagagt  | 120  |
| tcttgatttg  | tagaattgtc | atcacaaaac  | gtcacagaag | caattcgctt  | cgctccattt  | 180  |
| cattcgacaa  | gtgtttctgc | tgaaaaatcg  | aggagtagat | ttggttctgc  | tagagattcc  | 240  |
| gaaGgcgaac  | gatcttcaac | gaactcctcc  | ataagattta | catgtaccgt  | aaaggagaaag | 300  |
| ggctgtaccca | gtgctaagaa | gactgtggat  | aaactccttt | tccacagggg  | aattaatgat  | 360  |
| ccgcttcagca | atgagtgcca | tttcggggcca | agtcgcgtta | tccgggatag  | gcataatgaag | 420  |
| aaaaaatctc  | cgctctgcag | gggaaagaag  | cctcgagata | agaaaaacaa  | acgatggcac  | 480  |
| agagaaggta  | atccggacga | tgatttttgc  | actgatgcta | ataatacat   | cgagaacaaa  | 540  |
| tggagagaac  | gctggacagc | tcaatctcag  | aaggcttcac | attcgaaga   | ctcgacacgc  | 600  |
| ggattgaaat  | ggagagaagg | ctggagctgg  | accaactaat | ctcagaggag  | caaaaagttgg | 660  |
| ataaagaagt  | ctttttagat | acctttgaac  | gttgagttaa | ggctctgagag | gaTgtttcta  | 720  |
| ggattgcctc  | ttgaaggtcc | catcaagggt  | gatgatgtta | agaatgcctt  | ccgatctctt  | 780  |
| gcgttgaagt  | ggcatccaga | taagcaccag  | gggcctttct | aggtggcagc  | gcaagagaaa  | 840  |
| ttcaaacctc  | gtgtttgatc | atacaagtcc  | ctctgtttct | cactcgcttg  | acgtttacaca | 900  |
| taggcattga  | tgcaccattt | gcatttagt   | tgataaggct | gctttctgaa  | cgttttccag  | 960  |
| agatacaccc  | gttttttagt | gatgggtttg  | atttggttca | tgagaatcca  | ccagctacaa  | 1020 |
| gattgcacac  | ggcacaccaa | tgtgtctctc  | gtttttttcc | aacatttgat  | acaaaaaaaca | 1080 |
| tgtatgtgaa  | agatttatgc | tagtgcacaa  | cttttagctg | actgctttct  | ttttttaaacc | 1140 |
| acactgatgt  | gaaagacaat | aacttgagaa  | tacatcgctg | atacaaaaaa  | ctattaaagc  | 1200 |

2025 RELEASE UNDER E.O. 14176

aattttatttt gt

(2) INFORMATION FOR SEQ ID NO:575:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 296 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..296

(D) OTHER INFORMATION: / Ceres Seq. ID 1567344

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:575:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Lys | Ile | Ser | Leu | Phe | Thr | Pro | Asn | Glu | Ser | Leu | Lys | Pro | Leu | Asn | Cys |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Leu | Leu | Lys | Val | Tyr | Ile | Phe | Leu | Leu | Asn | Pro | Thr | Met | Phe | Arg | Leu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Arg | Ser | Leu | Leu | Ser | Leu | Lys | Ser | Ser | Ser | Ile | Val | Glu | Leu | Ser | Ser |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Gln | Asn | Val | Thr | Glu | Ala | Ile | Arg | Phe | Ala | Pro | Phe | His | Ser | Thr | Ser |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Val | Leu | Ser | Glu | Lys | Ser | Arg | Ser | Arg | Phe | Gly | Ser | Ala | Arg | Asp | Ser |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Glu | Gly | Glu | Arg | Ser | Ser | Lys | Asn | Ser | Ser | Ile | Arg | Phe | Thr | Cys | Thr |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     | 95  |     |     |
| Val | Lys | Glu | Lys | Gly | Arg | Thr | Ser | Ala | Lys | Lys | Thr | Val | Asp | Lys | Leu |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Leu | Phe | His | Arg | Gly | Ile | Asn | Asp | Pro | Leu | Gln | Asn | Glu | Trp | His | Phe |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Gly | Pro | Ser | Pro | Leu | Ile | Arg | Asp | Arg | His | Met | Lys | Lys | Lys | Ser | Pro |
|     | 130 |     |     |     |     | 135 |     |     |     | 140 |     |     |     |     |     |
| Pro | Gly | Arg | Gly | Lys | Lys | Pro | Arg | Asp | Lys | Lys | Thr | Lys | Arg | Trp | His |
| 145 |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |     |
| Arg | Glu | Gly | Asn | Pro | Asp | Asp | Asp | Phe | Gly | Thr | Asp | Ala | Asn | Asn | Thr |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |     |
| Phe | Glu | Asn | Lys | Trp | Arg | Glu | Arg | Trp | Thr | Ala | Gln | Ser | Gln | Lys | Ala |
|     |     |     | 180 |     |     |     | 185 |     |     |     |     |     | 190 |     |     |
| Ser | Tyr | Ser | Lys | Asp | Ser | Thr | Ala | Gly | Phe | Glu | Trp | Arg | Glu | Gly | Trp |
|     | 195 |     |     |     |     | 200 |     |     |     |     |     | 205 |     |     |     |
| Ser | Trp | Thr | Thr | Gln | Ser | Gln | Arg | Ser | Lys | Ser | Trp | Asn | Lys | Glu | Ser |
|     | 210 |     |     |     |     | 215 |     |     |     |     |     | 220 |     |     |     |
| Phe | Asp | Glu | Pro | Leu | Asn | Val | Glu | Phe | Arg | Ser | Glu | Arg | Ile | Val | Leu |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     | 240 |     |
| Gly | Leu | Pro | Leu | Glu | Gly | Pro | Ile | Lys | Val | Asp | Asp | Val | Lys | Asn | Ala |
|     |     |     | 245 |     |     |     |     |     | 250 |     |     |     | 255 |     |     |
| Phe | Arg | Ser | Ser | Ala | Leu | Lys | Trp | His | Pro | Asp | Lys | His | Gln | Gly | Pro |
|     |     |     | 260 |     |     |     | 265 |     |     |     |     |     | 270 |     |     |
| Ser | Gln | Val | Ala | Ala | Gln | Glu | Lys | Phe | Lys | Leu | Cys | Val | Asp | Ala | Tyr |
|     |     |     | 275 |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Lys | Ser | Leu | Cys | Ser | Ala | Leu | Ala |     |     |     |     |     |     |     |     |
|     | 290 |     |     |     |     | 295 |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:576:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 268 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..268

(D) OTHER INFORMATION: / Ceres Seq. ID 1567345

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:576:

Met Phe Arg Leu Arg Ser Leu Leu Ser Leu Lys Ser Ser Ser Ile Val  
1 5 10 15  
Glu Leu Ser Ser Gln Asn Val Thr Glu Ala Ile Arg Phe Ala Pro Phe  
20 25 30  
His Ser Thr Ser Val Leu Ser Glu Lys Ser Arg Ser Arg Phe Gly Ser  
35 40 45  
Ala Arg Asp Ser Glu Gly Glu Arg Ser Ser Lys Asn Ser Ser Ile Arg  
50 55 60  
Phe Thr Cys Thr Val Lys Glu Lys Gly Arg Thr Ser Ala Lys Lys Thr  
65 70 75 80  
Val Asp Lys Leu Leu Phe His Arg Gly Ile Asn Asp Pro Leu Gln Asn  
85 90 95  
Glu Trp His Phe Gly Pro Ser Pro Leu Ile Arg Asp Arg His Met Lys  
100 105 110  
Lys Lys Ser Pro Pro Gly Arg Gly Lys Lys Pro Arg Asp Lys Lys Thr  
115 120 125  
Lys Arg Trp His Arg Glu Gly Asn Pro Asp Asp Asp Phe Gly Thr Asp  
130 135 140  
Ala Asn Asn Thr Phe Glu Asn Lys Trp Arg Glu Arg Trp Thr Ala Gln  
145 150 155 160  
Ser Gln Lys Ala Ser Tyr Ser Lys Asp Ser Thr Ala Gly Phe Glu Trp  
165 170 175  
Arg Glu Gly Trp Ser Trp Thr Thr Gln Ser Gln Arg Ser Lys Ser Trp  
180 185 190  
Asn Lys Glu Ser Phe Asp Glu Pro Leu Asn Val Glu Phe Arg Ser Glu  
195 200 205  
Arg Ile Val Leu Gly Leu Pro Leu Glu Gly Pro Ile Lys Val Asp Asp  
210 215 220  
Val Lys Asn Ala Phe Arg Ser Ser Ala Leu Lys Trp His Pro Asp Lys  
225 230 235 240  
His Gln Gly Pro Ser Gln Val Ala Ala Gln Glu Lys Phe Lys Leu Cys  
245 250 255  
Val Asp Ala Tyr Lys Ser Leu Cys Ser Ala Leu Ala  
260 265

(2) INFORMATION FOR SEQ ID NO:577:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 158 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..158

(D) OTHER INFORMATION: / Ceres Seq. ID 1567346

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:577:

Met Lys Lys Lys Ser Pro Pro Gly Arg Gly Lys Lys Pro Arg Asp Lys  
1 5 10 15  
Lys Thr Lys Arg Trp His Arg Glu Gly Asn Pro Asp Asp Asp Phe Gly  
20 25 30  
Thr Asp Ala Asn Asn Thr Phe Glu Asn Lys Trp Arg Glu Arg Trp Thr  
35 40 45  
Ala Gln Ser Gln Lys Ala Ser Tyr Ser Lys Asp Ser Thr Ala Gly Phe  
50 55 60  
Glu Trp Arg Glu Gly Trp Ser Trp Thr Thr Gln Ser Gln Arg Ser Lys  
65 70 75 80  
Ser Trp Asn Lys Glu Ser Phe Asp Glu Pro Leu Asn Val Glu Phe Arg  
85 90 95  
Ser Glu Arg Ile Val Leu Gly Leu Pro Leu Glu Gly Pro Ile Lys Val

100 105 110  
Asp Asp Val Lys Asn Ala Phe Arg Ser Ser Ala Leu Lys Trp His Pro  
115 120 125  
Asp Lys His Gln Gly Pro Ser Gln Val Ala Ala Gln Glu Lys Phe Lys  
130 135 140  
Leu Cys Val Asp Ala Tyr Lys Ser Leu Cys Ser Ala Leu Ala  
145 150 155

(2) INFORMATION FOR SEQ ID NO:578:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1077 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1077
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567347

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:578:

|            |             |            |             |             |             |      |
|------------|-------------|------------|-------------|-------------|-------------|------|
| actcacacat | ccacaaaag   | agagttagag | attccaagga  | ggagagtgcg  | tgagCgtgac  | 60   |
| aatggaaact | gacaaaagat  | ggtctctcgc | cgggaaaaca  | gctctggtaa  | ccggcgggac  | 120  |
| tcgtggaatc | ggagagcgag  | ttgtagagga | actagcaaaa  | tttttgcaaa  | agttcatact  | 180  |
| tgttcaagga | accagggaaga | gctaaatgca | tgcttgaatg  | attggaaaagc | gaatgggttta | 240  |
| gtcgtgtctg | gttcggtttg  | tgatgcttcg | gttagggatc  | agagggagaa  | gttgattcac  | 300  |
| gaagctctct | ctgccttcag  | tggaagctgc | aacatcctta  | taaaccaatgt | tggaactaat  | 360  |
| gtcaggaaac | caacagttga  | atactcaagc | gaggaatatg  | ccaaaatcat  | gtcgaccaac  | 420  |
| ttagaatccg | ctttccattt  | attccaaatt | gctcctcctc  | ttctaaaagc  | atctgtggttc | 480  |
| ggaagcattg | tggtcatctc  | ctctgtagct | ggcctgggtc  | atcttagcac  | tggtactatc  | 540  |
| tatgtgtcaa | ctaaaggagc  | acttaatcag | cttaacaagaa | atctagcttg  | cgagtgggca  | 600  |
| agcgacaaca | tcagaaccaa  | ttgcgtggcg | ccatgggtaca | caagacctc   | acttgtggaa  | 660  |
| acgctacttg | agaagaagaa  | atttgtggag | gctgtagttt  | caaggaccoc  | acttggggcg  | 720  |
| gttgagaaac | caagaggaag  | ctcatcgttg | gttgcccttc  | tctgccttc   | cgcactcatc  | 780  |
| tatattaccg | gacaggtcat  | atccgtcgat | ggaggattca  | ctgtcaacgg  | tttagtcat   | 840  |
| gctatgaagc | cttaaatctc  | aatcgcaaca | ttactaataa  | agcaagaatc  | ctcgtgatgt  | 900  |
| gttggtcttg | tttgtctctg  | tttagttttt | gtgacttctt  | taaacatata  | gtaatatcaa  | 960  |
| aacgtttgaa | tttctaattg  | agccgttaaa | taaatcaagg  | cacagtgttg  | caccagttta  | 1020 |
| gttagaccta | caacattttg  | catgtattta | ggtatatgga  | tgagagtatt  | ttgatcg     |      |

(2) INFORMATION FOR SEQ ID NO:579:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 258 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..258
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567348

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:579:

|                                                                 |  |
|-----------------------------------------------------------------|--|
| Met Val Ser Arg Arg Glu Asn Ser Ser Gly Asn Arg Arg Asp Ser Trp |  |
| 1 5 10 15                                                       |  |
| Asn Arg Glu Ser Ser Cys Arg Gly Thr Ser Lys Ile Phe Ala Lys Val |  |
| 20 25 30                                                        |  |
| His Thr Cys Ser Arg Asn Gln Glu Glu Leu Asn Ala Cys Leu Asn Asp |  |
| 35 40 45                                                        |  |
| Trp Lys Ala Asn Gly Leu Val Val Ser Gly Ser Val Cys Asp Ala Ser |  |
| 50 55 60                                                        |  |
| Val Arg Asp Gln Arg Glu Lys Leu Ile Gln Glu Ala Ser Ser Ala Phe |  |
| 65 70 75 80                                                     |  |
| Ser Gly Lys Leu Asn Ile Leu Ile Asn Asn Val Gly Thr Asn Val Arg |  |
| 85 90 95                                                        |  |

Lys Pro Thr Val Glu Tyr Ser Ser Glu Glu Tyr Ala Lys Ile Met Ser  
100 105 110  
Thr Asn Leu Glu Ser Ala Phe His Leu Ser Gln Ile Ala His Pro Leu  
115 120 125  
Leu Lys Ala Ser Gly Val Gly Ser Ile Val Phe Ile Ser Ser Val Ala  
130 135 140  
Gly Leu Val His Leu Ser Ser Gly Ser Ile Tyr Gly Ala Thr Lys Gly  
145 150 155 160  
Ala Leu Asn Gln Leu Thr Arg Asn Leu Ala Cys Glu Trp Ala Ser Asp  
165 170 175  
Asn Ile Arg Thr Asn Cys Val Ala Pro Trp Tyr Ile Lys Thr Ser Leu  
180 185 190  
Val Glu Thr Leu Leu Glu Lys Lys Glu Phe Val Glu Ala Val Val Ser  
195 200 205  
Arg Thr Pro Leu Gly Arg Val Gly Glu Pro Glu Glu Val Ser Ser Leu  
210 215 220  
Val Ala Phe Leu Cys Leu Pro Ala Ser Ser Tyr Ile Thr Gly Gln Val  
225 230 235 240  
Ile Ser Val Asp Gly Gly Phe Thr Val Asn Gly Phe Ser Tyr Ala Met  
245 250 255  
Lys Pro

(2) INFORMATION FOR SEQ ID NO:580:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 148 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..148
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567349

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:580:

Met Ser Thr Asn Leu Glu Ser Ala Phe His Leu Ser Gln Ile Ala His  
1 5 10 15  
Pro Leu Leu Lys Ala Ser Gly Val Gly Ser Ile Val Phe Ile Ser Ser  
20 25 30  
Val Ala Gly Leu Val His Leu Ser Ser Gly Ser Ile Tyr Gly Ala Thr  
35 40 45  
Lys Gly Ala Leu Asn Gln Leu Thr Arg Asn Leu Ala Cys Glu Trp Ala  
50 55 60  
Ser Asp Asn Ile Arg Thr Asn Cys Val Ala Pro Trp Tyr Ile Lys Thr  
65 70 75 80  
Ser Leu Val Glu Thr Leu Leu Glu Lys Lys Glu Phe Val Glu Ala Val  
85 90 95  
Val Ser Arg Thr Pro Leu Gly Arg Val Gly Glu Pro Glu Glu Val Ser  
100 105 110  
Ser Leu Val Ala Phe Leu Cys Leu Pro Ala Ser Ser Tyr Ile Thr Gly  
115 120 125  
Gln Val Ile Ser Val Asp Gly Gly Phe Thr Val Asn Gly Phe Ser Tyr  
130 135 140  
Ala Met Lys Pro  
145

(2) INFORMATION FOR SEQ ID NO:581:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1438 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Ile | Thr | 5   | Ala | Thr | Gln | Asn | Asp | Gly | 10  | Val | Ser | Leu | Asn | Ala | Asn | 15  |
| Lys | Ile | Ser | Thr | 20  | Asp | Leu | Val | Glu | Thr | Asp | 25  | Val | Glu | Ile | Ile | Thr | Ser | 30  |
| Gly | Arg | Arg | Ser | 35  | Ile | Pro | Ala | His | Ser | Gly | 40  | Ile | Leu | Ala | Ser | Val | Ser | 45  |
| Pro | Val | Leu | Thr | 50  | Asn | Ile | Ile | Glu | Lys | Pro | 55  | Arg | Gly | Ile | His | Gly | Gly | 60  |
| Ser | Ser | Lys | Lys | 70  | Val | Ile | Lys | Ile | Leu | Gly | 75  | Val | Pro | Cys | Asp | Ala | Val | 80  |
| Ser | Val | Phe | Val | 85  | Arg | Phe | Leu | Tyr | Ser | Pro | 90  | Ser | Val | Thr | Glu | Asn | Glu | 95  |
| Met | Glu | Lys | Thr | 100 | Gly | Ile | His | Leu | Leu | Ala | 105 | Leu | Ser | His | Val | Tyr | Met | 110 |
| Val | Thr | Gln | Leu | 115 | Lys | Gln | Arg | Cys | Thr | Lys | 120 | Gly | Val | Gly | Glu | Arg | Val | 125 |
| Thr | Ala | Glu | Asn | 130 | Val | Val | Asp | Ile | Leu | Gln | 135 | Leu | Ala | Arg | Leu | Cys | Asp | 140 |
| Ala | Pro | Asp | Leu | 145 | Cys | Leu | Lys | Cys | Met | Arg | 150 | Phe | Ile | His | Tyr | Lys | Phe | 155 |

Lys Thr Val Glu Gln Thr Glu Gly Trp Lys Phe Leu Gln Glu His Asp  
165 170 175  
Pro Phe Leu Glu Leu Asp Ile Leu Gln Phe Ile Asp Asp Ala Glu Ser  
180 185 190  
Arg Lys Lys Arg Arg Arg Arg His Arg Arg Glu Gln Asn Leu Tyr Leu  
195 200 205  
Gln Leu Ser Glu Ala Met Glu Cys Ile Glu His Ile Cys Thr Glu Gly  
210 215 220  
Cys Thr Leu Val Gly Pro Ser Ser Asn Leu Asp Asn Lys Ser Thr Cys  
225 230 235 240  
Gln Ala Lys Pro Gly Pro Cys Ser Ala Phe Ser Thr Cys  
245 250

(2) INFORMATION FOR SEQ ID NO:583:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 157 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..157
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567373

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:583:

Met Glu Lys Tyr Gly Ile His Leu Leu Ala Leu Ser His Val Tyr Met  
1 5 10 15  
Val Thr Gln Leu Lys Gln Arg Cys Thr Lys Gly Val Gly Glu Arg Val  
20 25 30  
Thr Ala Glu Asn Val Val Asp Ile Leu Gln Leu Ala Arg Leu Cys Asp  
35 40 45  
Ala Pro Asp Leu Cys Leu Lys Cys Met Arg Phe Ile His Tyr Lys Phe  
50 55 60  
Lys Thr Val Glu Gln Thr Glu Gly Trp Lys Phe Leu Gln Glu His Asp  
65 70 75 80  
Pro Phe Leu Glu Leu Asp Ile Leu Gln Phe Ile Asp Asp Ala Glu Ser  
85 90 95  
Arg Lys Lys Arg Arg Arg Arg His Arg Arg Glu Gln Asn Leu Tyr Leu  
100 105 110  
Gln Leu Ser Glu Ala Met Glu Cys Ile Glu His Ile Cys Thr Glu Gly  
115 120 125  
Cys Thr Leu Val Gly Pro Ser Ser Asn Leu Asp Asn Lys Ser Thr Cys  
130 135 140  
Gln Ala Lys Pro Gly Pro Cys Ser Ala Phe Ser Thr Cys  
145 150 155

(2) INFORMATION FOR SEQ ID NO:584:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 142 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..142
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567374

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:584:

Met Val Thr Gln Leu Lys Gln Arg Cys Thr Lys Gly Val Gly Glu Arg  
1 5 10 15  
Val Thr Ala Glu Asn Val Val Asp Ile Leu Gln Leu Ala Arg Leu Cys  
20 25 30  
Asp Ala Pro Asp Leu Cys Leu Lys Cys Met Arg Phe Ile His Tyr Lys

(D) OTHER INFORMATION: / Ceres Seq. ID 1567384



(xi) SEQUENCE DESCRIPTION: SEQ ID NO:586:

Met Ala Arg Lys Lys His Arg Lys Leu Phe Pro Thr Leu Ala Ser Glu  
1 5 10 15  
Thr Asn Lys Thr Leu Asp Cys Ser Asn Gly Val Cys Asp Pro Ile Cys  
20 25 30  
Pro Tyr Asn Cys Tyr Pro Glu Pro Asp Tyr Tyr Thr Ile Ser Pro Gln  
35 40 45  
Leu Pro Pro Trp Ser Ser Ser Pro Gln Pro Ser Pro Cys Pro Ser Pro  
50 55 60  
Ser Ile Ser Ala Val Tyr Leu Pro Ser Gln Asp Ser Ser Ser Ser Leu  
65 70 75 80  
Asp Ala Ile Ser Ile Thr Ile Thr Gly Ala Val Leu Ala Ile Leu  
85 90 95  
Leu Thr Gly Phe Phe Leu Val Ala Lys Phe Phe Ser Asp Ser Val Asn  
100 105 110  
Arg Val Asn Gln Gly Thr Tyr Gln Ser Asp Asn Glu Asp Asn Asp Thr  
115 120 125  
Val Met Glu Glu Glu Phe Gln Asp Arg Glu Gln Val Asp His Pro Ile  
130 135 140  
Trp Leu Ile Arg Thr Thr Gly Leu Gln Gln Ser Ile Ile Asn Ser Ile  
145 150 155 160  
Thr Ile Cys Asn Tyr Xaa Arg Gly Asp Gly Leu Ile Glu Arg Thr Asp  
165 170 175  
Cys Pro Val Cys Leu Asn Glu Phe Glu Glu Asp Glu Ser Leu Arg Leu  
180 185 190  
Leu Pro Lys Cys Asn His Ala Phe His Ile Ser Cys Ile Asp Thr Trp  
195 200 205  
Leu Ser Ser His Thr Asn Cys Pro Leu Cys Arg Ala Gly Ile Ala Met  
210 215 220  
Ile Ser Val Thr Thr Pro Arg Tyr Ser Gly Pro Val Glu Val Thr Pro  
225 230 235 240  
Gly Gly Ser Gly Ser His Leu Glu Asn Asp Gly Val Asp Glu Glu Asp  
245 250 255  
His Gly Glu Ile Glu Asn Arg Val Asp Ser Asp Phe Lys Glu Ser Asp  
260 265 270  
Asp Ser Asp Ile Arg Ile Glu Ile Tyr Arg Phe Asp Ser Asp Gly Asp  
275 280 285  
Gly Ser Glu Thr Glu Thr Lys Glu Arg Val Arg Val Leu Lys Glu Cys  
290 295 300  
Met Asp Pro Asn Gly Gly Asp Ser Val Asn Ser Leu Ser His Thr Lys  
305 310 315 320  
Thr His Val Glu Ser Val Asp Phe Pro Gly Lys Ser Cys Glu Asn Gln  
325 330 335  
Ser Glu Glu Phe Thr Arg His Asn Gly Glu Asp Glu Ala Ser Cys Ser  
340 345 350  
Glu Glu Asn Gly Gly Gly Ser Asn Gln Leu Arg Arg Ser Cys Asp Ser  
355 360 365  
Gly Glu Leu Asn Gly Glu Thr Thr Gly Asp Glu Gly Lys Ser Gln Ser  
370 375 380  
Asp Ile Ser Ser Ser Thr Leu Lys Thr Asn Gly Ser Ser Ser Ser Val  
385 390 395 400  
Ser Cys Phe Asn Lys Asn Lys Ser Ser Val Phe Pro Leu  
405 410

(2) INFORMATION FOR SEQ ID NO:587:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 284 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide  
(B) LOCATION: 1..284  
(D) OTHER INFORMATION: / Ceres Seq. ID 1567385  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:587:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Glu | Glu | Glu | Phe | Gln | Asp | Arg | Glu | Gln | Val | Asp | His | Pro | Ile | Trp |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Leu | Ile | Arg | Thr | Thr | Gly | Leu | Gln | Gln | Ser | Ile | Ile | Asn | Ser | Ile | Thr |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ile | Cys | Asn | Tyr | Xaa | Arg | Gly | Asp | Gly | Leu | Ile | Glu | Arg | Thr | Asp | Cys |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Pro | Val | Cys | Leu | Asn | Glu | Phe | Glu | Glu | Asp | Glu | Ser | Leu | Arg | Leu | Leu |
|     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Pro | Lys | Cys | Asn | His | Ala | Phe | His | Ile | Ser | Cys | Ile | Asp | Thr | Trp | Leu |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Ser | Ser | His | Thr | Asn | Cys | Pro | Leu | Cys | Arg | Ala | Gly | Ile | Ala | Met | Ile |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Ser | Val | Thr | Thr | Pro | Arg | Tyr | Ser | Gly | Pro | Val | Glu | Val | Thr | Pro | Gly |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Gly | Ser | Gly | Ser | His | Leu | Glu | Asn | Asp | Gly | Val | Asp | Glu | Glu | Asp | His |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Gly | Glu | Ile | Glu | Asn | Arg | Val | Asp | Ser | Asp | Phe | Lys | Glu | Ser | Asp | Asp |
|     |     | 130 |     |     | 135 |     |     |     |     |     | 140 |     |     |     |     |
| Ser | Asp | Ile | Arg | Ile | Glu | Ile | Tyr | Arg | Phe | Asp | Ser | Asp | Gly | Asp | Gly |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |     |
| Ser | Glu | Thr | Glu | Thr | Lys | Glu | Arg | Val | Arg | Val | Leu | Lys | Glu | Cys | Met |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | 175 |     |
| Asp | Pro | Asn | Gly | Gly | Asp | Ser | Val | Asn | Ser | Leu | Ser | His | Thr | Lys | Thr |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| His | Val | Glu | Ser | Val | Asp | Phe | Pro | Gly | Lys | Ser | Cys | Glu | Asn | Gln | Ser |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Glu | Glu | Phe | Thr | Arg | His | Asn | Gly | Glu | Asp | Glu | Ala | Ser | Cys | Ser | Glu |
|     |     | 210 |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Glu | Asn | Gly | Gly | Gly | Ser | Asn | Gln | Leu | Arg | Arg | Ser | Cys | Asp | Ser | Gly |
| 225 |     |     |     |     | 230 |     |     |     |     |     | 235 |     |     | 240 |     |
| Glu | Leu | Asn | Gly | Glu | Thr | Thr | Gly | Asp | Glu | Gly | Lys | Ser | Gln | Ser | Asp |
|     |     |     | 245 |     |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Ile | Ser | Ser | Ser | Thr | Leu | Lys | Thr | Asn | Gly | Ser | Ser | Ser | Ser | Val | Ser |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     |     | 270 |     |
| Cys | Phe | Asn | Lys | Asn | Lys | Ser | Ser | Val | Phe | Pro | Leu |     |     |     |     |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:588:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2184 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..2184

(D) OTHER INFORMATION: / Ceres Seq. ID 1567390

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:588:

|            |             |             |            |             |             |     |
|------------|-------------|-------------|------------|-------------|-------------|-----|
| accagccccc | taaataaac   | accgggctct  | gtttcaataa | aaaaaatccc  | ctccctctca  | 60  |
| tatttacctc | ccgaataaaa  | ccggaggagg  | agaaaaaaca | taaaaagcaa  | aaaaaaaggt  | 120 |
| aaaatcaaaa | agggaaaaaa  | tatatataca  | caaaaaaaa  | aagtttagaa  | aaatggcagt  | 180 |
| aggaaaggtt | gtggatcttg  | tgggcatcact | cctctagtgt | gtgggtgttg  | ccataggagt  | 240 |
| tatcacgttc | gttaataaag  | gaggcggcgc  | caatggcgac | agtaaatggtc | ccataaacctc | 300 |
| tcatcagaaa | cggggtccga  | caatttgcca  | gtcaaccaca | gaccaaggtt  | cgtagcgccga | 360 |
| aacactcgac | ccagtcacaaa | gtgatgatcc  | aagcaagctt | gtcaaaagctt | tcctgatggc  | 420 |
| tactaaagac | gcgatccaaa  | aatcctcaaa  | cttcacggct | tcgacccga   | Gaggtatggg  | 480 |
| tactaacatg | aacgcgacca  | gcaagccgt   | tcttgattac | tgcaagagag  | tattgatgta  | 540 |

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cgctcttgag gatcttgaga ccattgttga agagatgggt gaggatcttc agcagagtgg 600
aactaagctt gaccagctca aacaatgggt aactggagtt ttcaactacc aaaccgagtt 660
tctttgacgc atcgaggagc ttgactataa gaagatcatg ggtgaaggaa tctctaatc 720
caaggtttttg accagtaacg ctatcgatac ctccattccg gttgttaccg cgatggccca 780
aatgggtgtc aaaagtgcagc atatgaagaa cataaccatg ggagccggag ccggtggagc 840
tgcaogtcgc cttcttgaag acaacgactc taagggactc cccaaatggt tttctggtaa 900
agacaggaag cttatggcta aggcgggacg tggcgctcca gctggcggtg atgatggtat 960
cggtgaagcg ggtggtggtg gcggtgaagt caaggcgact catgtagtgg ctaagtagtg 1020
aagtgagcac ttttaagacca tttctgagcg ggttatggct tgcccggata aaaacctgtg 1080
aaggtgcatt atccatatac aggtcggtat ctacaatgaa ccactaagaa tccctaagaa 1140
gaagaacaac attttcatgt tcggtgatgg tgctacacaa accatcattt cctttgacag 1200
aagtgtaaaa cttagccacg gaaccactac ttcaactcagt ggacacogtc aggtcgaaic 1260
tgaggggatt atggcgaaat ggattgggtt taagaacact gctggtccat tgggacacca 1320
agcggtcgca ctcogtggta acggagacgg tcgcggtcata ttcaactgta gattcgacgg 1380
ttaccaagac acactctacg tcaacaacgg acgtcaattc tacaggaaca ttgtttatc 1440
cggtcacagt gatttcatct tcggaaaaatc cgcaactgtg atccaaaact ctctcatct 1500
cgctcgaaag ggaagcccg gacaatccaa ctacgttacg gctgacgcta atgaaaaggg 1560
tgacgagcat aagatcggtt tctgtctcca taactgccg atcataccgg acaaggagct 1620
cgaagctgac aagctaacca tcaaatcgta cctagggaag ccgtggaaga agtttgccac 1680
gactgtgatt attggaactg agattgggtg tttgattaaa ccagaaggat ggaccgaagt 1740
gcaaggagaa caaaaccaca agactgctaa atacattgag ttcaataacc gtggaccggg 1800
agctgcacat actcagagcg ctcttggttg taaggtggct aagctctcgg ctgaggttga 1860
aacttaccac gtggctaact gggttggtcc agctaactgg atccaagaag ccaacogtgc 1920
cgtccaacta ggtattgaag aggacaacac aaaaagttta agaataaaac agtatgtgat 1980
aatgtaagg taacgatacg acgtcgtctc tggggatcag aactcttttt tggatactat 2040
atacaagat aggttctag acgtgttgag atgatgttg tataagattg ctttctgtca 2100
cgtgcaaaag agggaaaaaa attgttttgt tatttttttt gtagtacaaa taattaatt 2160
ttttttatca catgttgat cctt

```

(2) INFORMATION FOR SEQ ID NO:589:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 588 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..588

(D) OTHER INFORMATION: / Ceres Seq. ID 1567391

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:589:

```

Met Ala Val Gly Lys Val Val Val Ser Val Ala Ser Leu Leu Leu Val
1 5 10 15
Val Gly Val Ala Ile Gly Val Ile Thr Phe Val Asn Lys Gly Gly Gly
20 25 30
Ala Asn Gly Asp Ser Asn Gly Pro Ile Asn Ser His Gln Lys Ala Val
35 40 45
Gln Thr Ile Cys Gln Ser Thr Thr Asp Gln Gly Ser Cys Ala Lys Thr
50 55 60
Leu Asp Pro Val Lys Ser Asp Asp Pro Ser Lys Leu Val Lys Ala Phe
65 70 75 80
Leu Met Ala Thr Lys Asp Ala Ile Thr Lys Ser Ser Asn Phe Thr Ala
85 90 95
Ser Thr Glu Gly Gly Met Gly Thr Asn Met Asn Ala Thr Ser Lys Ala
100 105 110
Val Leu Asp Tyr Cys Lys Arg Val Leu Met Tyr Ala Leu Glu Asp Leu
115 120 125
Glu Thr Ile Val Glu Glu Met Gly Glu Asp Leu Gln Gln Ser Gly Thr
130 135 140
Lys Leu Asp Gln Leu Lys Gln Trp Leu Thr Gly Val Phe Asn Tyr Gln
145 150 155 160
Thr Asp Cys Leu Asp Asp Ile Glu Glu Val Glu Leu Lys Lys Ile Met

```

(2) INFORMATION FOR SEQ ID NO:590:  
 (i) SEQUENCE CHARACTERISTICS:  
     (A) LENGTH: 507 amino acids  
     (B) TYPE: amino acid  
     (C) STRANDEDNESS:  
     (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: peptide  
 (ix) FEATURE:

(B) LOCATION: 1..507

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:590:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Thr | Lys | Asp | Ala | Ile | Thr | Lys | Ser | Ser | Asn | Phe | Thr | Ala | Ser |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Thr | Glu | Gly | Gly | Met | Gly | Thr | Asn | Met | Asn | Ala | Thr | Ser | Lys | Ala | Val |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Leu | Asp | Tyr | Cys | Lys | Arg | Val | Leu | Met | Tyr | Ala | Leu | Glu | Asp | Leu | Glu |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Thr | Ile | Val | Glu | Glu | Met | Gly | Glu | Asp | Leu | Gln | Gln | Ser | Gly | Thr | Lys |
|     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Leu | Asp | Gln | Leu | Lys | Gln | Trp | Leu | Thr | Gly | Val | Phe | Asn | Tyr | Gln | Thr |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Asp | Cys | Leu | Asp | Asp | Ile | Glu | Glu | Val | Glu | Leu | Lys | Lys | Ile | Met | Gly |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Glu | Gly | Ile | Ser | Ser | Asn | Ser | Lys | Val | Leu | Thr | Ser | Asn | Ala | Ile | Asp |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     |     | 110 |     |
| Phe | His | Ser | Val | Val | Thr | Ala | Met | Ala | Gln | Met | Gly | Val | Lys | Val | Asp |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Asp | Met | Lys | Asn | Ile | Thr | Met | Gly | Ala | Gly | Ala | Gly | Gly | Ala | Ala | Arg |
|     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Arg | Leu | Leu | Glu | Asp | Asn | Asp | Ser | Lys | Gly | Leu | Pro | Lys | Trp | Phe | Ser |
|     |     | 145 |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |     |
| Gly | Lys | Asp | Arg | Lys | Leu | Met | Ala | Lys | Ala | Gly | Arg | Gly | Ala | Pro | Ala |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Gly | Gly | Asp | Asp | Gly | Ile | Gly | Glu | Gly | Gly | Gly | Gly | Gly | Gly | Lys | Ile |
|     |     | 180 |     |     |     |     |     | 185 |     |     |     |     |     | 190 |     |
| Lys | Ala | Thr | His | Val | Val | Ala | Lys | Asp | Gly | Ser | Gly | Gln | Phe | Lys | Thr |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Ile | Ser | Glu | Ala | Val | Met | Ala | Cys | Pro | Asp | Lys | Asn | Pro | Gly | Arg | Cys |
|     |     | 210 |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Ile | Ile | His | Ile | Lys | Ala | Gly | Ile | Tyr | Asn | Glu | Gln | Val | Arg | Ile | Pro |
| 225 |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |     |
| Lys | Lys | Lys | Asn | Asn | Ile | Phe | Met | Phe | Gly | Asp | Gly | Ala | Thr | Gln | Thr |
|     |     |     | 245 |     |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Ile | Ile | Thr | Phe | Asp | Arg | Ser | Val | Lys | Leu | Ser | Pro | Gly | Thr | Thr | Thr |
|     |     | 260 |     |     |     |     |     | 265 |     |     |     |     |     | 270 |     |
| Ser | Leu | Ser | Gly | Thr | Val | Gln | Val | Glu | Ser | Glu | Gly | Phe | Met | Ala | Lys |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Trp | Ile | Gly | Phe | Lys | Asn | Thr | Ala | Gly | Pro | Leu | Gly | His | Gln | Ala | Val |
|     |     | 290 |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Ala | Leu | Arg | Val | Asn | Gly | Asp | Arg | Ala | Val | Ile | Phe | Asn | Cys | Arg | Phe |
| 305 |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |     |
| Asp | Gly | Tyr | Gln | Asp | Thr | Leu | Tyr | Val | Asn | Asn | Gly | Arg | Gln | Phe | Tyr |
|     |     |     | 325 |     |     |     |     | 330 |     |     |     |     |     | 335 |     |
| Arg | Asn | Ile | Val | Val | Ser | Gly | Thr | Val | Asp | Phe | Ile | Phe | Gly | Lys | Ser |
|     |     | 340 |     |     |     |     |     | 345 |     |     |     | 350 |     |     |     |
| Ala | Thr | Val | Ile | Gln | Asn | Ser |     |     |     |     |     |     |     |     |     |

|                                                                 |     |     |     |
|-----------------------------------------------------------------|-----|-----|-----|
| 450                                                             | 455 | 460 |     |
| Thr Thr Gln Arg Pro Pro Trp Val Lys Val Ala Lys Ser Ala Ala Glu |     |     |     |
| 465                                                             | 470 | 475 | 480 |
| Val Glu Thr Tyr Thr Val Ala Asn Trp Val Gly Pro Ala Asn Trp Ile |     |     |     |
|                                                                 | 485 | 490 | 495 |
| Gln Glu Ala Asn Val Pro Val Gln Leu Gly Leu                     |     |     |     |
|                                                                 | 500 | 505 |     |

(2) INFORMATION FOR SEQ ID NO:591:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 487 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..487
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567393

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:591:

|                                                                 |             |
|-----------------------------------------------------------------|-------------|
| Met Gly Thr Asn Met Asn Ala Thr Ser Lys Ala Val Leu Asp Tyr Cys |             |
| 1                                                               | 5 10 15     |
| Lys Arg Val Leu Met Tyr Ala Leu Glu Asp Leu Glu Thr Ile Val Glu |             |
|                                                                 | 20 25 30    |
| Glu Met Gly Glu Asp Leu Gln Gln Ser Gly Thr Lys Leu Asp Gln Leu |             |
|                                                                 | 35 40 45    |
| Lys Gln Trp Leu Thr Gly Val Phe Asn Tyr Gln Thr Asp Cys Leu Asp |             |
|                                                                 | 50 55 60    |
| Asp Ile Glu Glu Val Glu Leu Lys Lys Ile Met Gly Glu Gly Ile Ser |             |
| 65                                                              | 70 75 80    |
| Asn Ser Lys Val Leu Thr Ser Asn Ala Ile Asp Ile Phe His Ser Val |             |
|                                                                 | 85 90 95    |
| Val Thr Ala Met Ala Gln Met Gly Val Lys Val Asp Asp Met Lys Asn |             |
|                                                                 | 100 105 110 |
| Ile Thr Met Gly Ala Gly Ala Gly Gly Ala Ala Arg Arg Leu Leu Glu |             |
|                                                                 | 115 120 125 |
| Asp Asn Asp Ser Lys Gly Leu Pro Lys Trp Phe Ser Gly Lys Asp Arg |             |
|                                                                 | 130 135 140 |
| Lys Leu Met Ala Lys Ala Gly Arg Gly Ala Pro Ala Gly Gly Asp Asp |             |
| 145                                                             | 150 155 160 |
| Gly Ile Gly Glu Gly Gly Gly Gly Gly Lys Ile Lys Ala Thr His     |             |
|                                                                 | 165 170 175 |
| Val Val Ala Lys Asp Gly Ser Gly Gln Phe Lys Thr Ile Ser Glu Ala |             |
|                                                                 | 180 185 190 |
| Val Met Ala Cys Pro Asp Lys Asn Pro Gly Arg Cys Ile Ile His Ile |             |
|                                                                 | 195 200 205 |
| Lys Ala Gly Ile Tyr Asn Glu Gln Val Arg Ile Pro Lys Lys Lys Asn |             |
|                                                                 | 210 215 220 |
| Asn Ile Phe Met Phe Gly Asp Gly Ala Thr Gln Thr Ile Ile Thr Phe |             |
| 225                                                             | 230 235 240 |
| Asp Arg Ser Val Lys Leu Ser Pro Gly Thr Thr Thr Ser Leu Ser Gly |             |
|                                                                 | 245 250 255 |
| Thr Val Gln Val Glu Ser Glu Gly Phe Met Ala Lys Trp Ile Gly Phe |             |
|                                                                 | 260 265 270 |
| Lys Asn Thr Ala Gly Pro Leu Gly His Gln Ala Val Ala Leu Arg Val |             |
|                                                                 | 275 280 285 |
| Asn Gly Asp Arg Ala Val Ile Phe Asn Cys Arg Phe Asp Gly Tyr Gln |             |
| 290                                                             | 295 300     |
| Asp Thr Leu Tyr Val Asn Asn Gly Arg Gln Phe Tyr Arg Asn Ile Val |             |
| 305                                                             | 310 315 320 |
| Val Ser Gly Thr Val Asp Phe Ile Phe Gly Lys Ser Ala Thr Val Ile |             |
|                                                                 | 325 330 335 |

U.S. PAT. & TM. OFF.

(B) LOCATION: 1..206

(D) OTHER INFORMATION: / Ceres Seq. ID 1567395

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:593:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Tyr | Asn | Lys | Pro | Ser | Gly | Ala | Leu | His | Phe | Thr | Ala | Ser | Asn | Asn | Asp |  |
| 1   |     | 5   |     |     |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Cys | Gly | Val | Arg | Asp | Phe | Asp | Met | Glu | Arg | Tyr | Gln | Leu | Val | Lys | His |  |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Phe | Arg | Phe | Pro | Trp | Pro | Val | Asn | His | Ala | Ser | Leu | Ser | Pro | Asp | Gly |  |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Lys | Leu | Leu | Ala | Ile | Val | Gly | Asp | Asn | Pro | Glu | Gly | Leu | Ile | Val | Asp |  |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |  |
| Pro | Asn | Thr | Gly | Lys | Thr | Leu | Glu | Thr | Leu | Ser | Gly | His | Leu | Asp | Phe |  |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |  |
| Ser | Phe | Ala | Ser | Ala | Trp | His | Pro | Asp | Gly | Val | Thr | Phe | Ser | Thr | Gly |  |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |  |
| Asn | Gln | Asp | Lys | Thr | Cys | Arg | Val | Trp | Asp | Ile | Arg | Asn | Leu | Ser | Gln |  |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |
| Ser | Val | Thr | Val | Leu | Lys | Gly | Asn | Leu | Gly | Ala | Ile | Arg | Ser | Ile | Arg |  |
|     | 115 |     |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |  |
| Tyr | Thr | Ser | Asp | Gly | Lys | Tyr | Met | Ala | Glu | Pro | Ala | Asp | Phe |     |     |  |
|     | 130 |     |     |     |     | 135 |     |     | 140 |     |     |     |     |     |     |  |
| Val | His | Val | Tyr | Asp | Val | Ser | Asn | Gly | Tyr | Glu | Thr | Glu | Gln | Glu | Ile |  |
| 145 |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |     |  |
| Asp | Phe | Phe | Gly | Glu | Ile | Ser | Gly | Ile | Ser | Phe | Ser | Pro | Asp | Thr | Glu |  |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | 175 |     |  |
| Ala | Leu | Phe | Ile | Gly | Val | Trp | Asp | Arg | Thr | Tyr | Gly | Ser | Leu | Leu | Glu |  |
|     |     | 180 |     |     |     |     | 185 |     |     |     |     |     | 190 |     |     |  |
| Phe | Gly | Arg | Arg | Arg | Asn | Tyr | Ser | Tyr | Leu | Asp | Ser | Tyr | Leu |     |     |  |
|     | 195 |     |     |     |     | 200 |     |     |     |     |     | 205 |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:594:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 183 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..183

(D) OTHER INFORMATION: / Ceres Seq. ID 1567396

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:594:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Glu | Arg | Tyr | Gln | Leu | Val | Lys | His | Phe | Arg | Phe | Pro | Trp | Pro | Val |  |
| 1   |     | 5   |     |     |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Asn | His | Ala | Ser | Leu | Ser | Pro | Asp | Gly | Lys | Leu | Leu | Ala | Ile | Val | Gly |  |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Asp | Asn | Pro | Glu | Gly | Leu | Ile | Val | Asp | Pro | Asn | Thr | Gly | Lys | Thr | Leu |  |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Glu | Thr | Leu | Ser | Gly | His | Leu | Asp | Phe | Ser | Phe | Ala | Ser | Ala | Trp | His |  |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |  |
| Pro | Asp | Gly | Val | Thr | Phe | Ser | Thr | Gly | Asn | Gln | Asp | Lys | Thr | Cys | Arg |  |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |  |
| Val | Trp | Asp | Ile | Arg | Asn | Leu | Ser | Gln | Ser | Val | Thr | Val | Leu | Lys | Gly |  |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |  |
| Asn | Leu | Gly | Ala | Ile | Arg | Ser | Ile | Arg | Tyr | Thr | Ser | Asp | Gly | Lys | Tyr |  |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |
| Met | Ala | Met | Ala | Glu | Pro | Ala | Asp | Phe | Val | His | Val | Tyr | Asp | Val | Ser |  |
|     | 115 |     |     |     |     |     | 120 |     |     |     |     |     | 125 |     |     |  |
| Asn | Gly | Tyr | Glu | Thr | Glu | Gln | Glu | Ile | Asp | Phe | Phe | Gly | Glu | Ile | Ser |  |
|     | 130 |     |     |     |     | 135 |     |     |     |     |     | 140 |     |     |     |  |
| Gly | Ile | Ser | Phe | Ser | Pro | Asp | Thr | Glu | Ala | Leu | Phe | Ile | Gly | Val | Trp |  |
| 145 |     |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |     |     |  |
| Asp | Arg | Thr | Tyr | Gly | Ser | Leu | Leu | Glu | Phe | Gly | Arg | Arg | Arg | Asn | Tyr |  |



|             |             |             |             |            |            |      |
|-------------|-------------|-------------|-------------|------------|------------|------|
| aaccactcat  | ctcaatttct  | cccaacggtc  | agattctctc  | cgtctctatc | tctttccgga | 60   |
| gaaaattcgg  | gacacgcagt  | cacgcgcgtc  | tatcttttat  | cgtctctatc | tctttcgacc | 120  |
| ctattcagcg  | gattctctgt  | ctgttttaag  | agttcgtcga  | tgaagatttg | gaagaaaaat | 180  |
| ccacacggct  | ttaactgcac  | cgccgcgcgtc | ctcaaaagct  | aaccacgcag | gaaaatgagt | 240  |
| tgtcgtcgga  | gactttatct  | ggggaggagaa | acagttctcg  | ggaagtctcg | tctttgggat | 300  |
| tcgcgagaga  | ataaaatcct  | aagcttctccc | ggaaactcga  | aaaatctaa  | attcatcaag | 360  |
| agtcagtgaa  | tcgatggcca  | gattgttggt  | gcaaatcttg  | caagtcctag | actaagaacg | 420  |
| aagatgggaa  | tcttcacgct  | gtgtctaaag  | attctacttc  | tcgagaacaa | gagtactctg | 480  |
| tccaagaaac  | ctgcagaagt  | gtaataattc  | tacacgggtt  | tatggggtca | tcaacttttt | 540  |
| tgacdaaaac  | tgtatttgaa  | cacattcaaa  | aaagatgatta | taggctcttc | gcgactcgat | 600  |
| ttttggggatt | cgggggagagt | actaagccaa  | gggatagctc  | ctatacatct | aaagatcatg | 660  |
| tggatcacat  | agagagatct  | gtcataaagc  | acataccaat  | agattctctt | catgtgggtg | 720  |
| caactccaat  | gggttgctta  | attgctctgt  | ctttgggtcgc | taaacattct | aacattctga | 780  |
| aatccgttae  | tctttgttca  | cgcgcctatt  | ttctctctac  | gtgagatgcc | tcggtctgtg | 840  |
| accgaatcgc  | tagaaaacgg  | ttgtggccac  | cgccttcggt  | tgggaacagc | gtgatgcttc | 900  |
| ggatgaacca  | tatttggtga  | tcgctatgtt  | ctataactct  | caagcatcat | agaatatggg | 960  |
| agtgctcaat  | caagctatgt  | ataggtaaaa  | ggggagatcca | tgtgaagact | aaggacataa | 1020 |
| caaggcgaac  | acatcactct  | catggccata  | gtatgcacaa  | tgtataatg  | tgtagctcca | 1080 |

|                                                                    |      |
|--------------------------------------------------------------------|------|
| aagtcgctga tgaacatctt gaaaccctaa taaagtcctgg cgttaagatt cacttgatgc | 1140 |
| aaggcgactg tgaccacaatc gttccttcac attgctctgg caacatgaag aggacttttc | 1200 |
| cgccggtgga agttgatata attactgggtg ctgatcatga tagtatgata agcggaagag | 1260 |
| gagaagagtt tgctgagaaa ttggagagca tttgggtttc atttaaagag tctggttagt  | 1320 |
| tttttcaaac tttataggtg ggaggcactg tagtcgatgt cgactgacta caagtttgag  | 1380 |
| tccgattgta agatcaagtc tattgttaat gagccatcta atggagcgcct atatggagtc | 1440 |
| caattatcg                                                          |      |

(2) INFORMATION FOR SEQ ID NO:597:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 423 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..423

(D) OTHER INFORMATION: / Ceres Seq. ID 1567406

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:597:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ser | Phe | Pro | Arg | Lys | Phe | Gly | Thr | Ala | Ile | His | Ala | Ala | Leu | Ser |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Phe | Ile | Val | Phe | Phe | Phe | Asp | Leu | Ile | Asp | Ala | Ile | Leu | Cys | Val |     |
|     |     |     | 20  |     |     |     | 25  |     |     |     |     | 30  |     |     |     |
| Val | Tyr | Glu | Phe | Val | Asp | Glu | Ile | Leu | Glu | Glu | Asn | Ser | Thr | Gly | Cys |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Tyr | Cys | Thr | Ala | Ala | Ala | Pro | Gln | Ser | Leu | Thr | Thr | Asp | Glu | Asn | Glu |
|     |     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |
| Leu | Ser | Ser | Glu | Thr | Leu | Phe | Gly | Arg | Arg | Asn | Ser | Phe | Arg | Glu | Met |
|     |     |     | 65  |     |     | 70  |     |     |     | 75  |     |     |     | 80  |     |
| Trp | Phe | Leu | Gly | Phe | Ala | Arg | Glu | Phe | Lys | Ser | Lys | Leu | Ser | Arg | Lys |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Leu | Arg | Lys | Ser | Lys | Ile | His | Gln | Glu | Ser | Val | Asn | Arg | Trp | Ser | Asp |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Cys | Gly | Cys | Lys | Ser | Cys | Lys | Ser | Trp | Thr | Lys | Asn | Glu | Asp | Gly | Asn |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Leu | His | Val | Val | Val | Lys | Asp | Ser | Thr | Ser | Arg | Glu | Thr | Glu | Tyr | Ser |
|     |     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |
| Val | Gln | Glu | Pro | Ser | Glu | Asn | Val | Ile | Phe | Ile | His | Gly | Phe | Met | Gly |
|     |     |     | 145 |     |     | 150 |     |     |     | 155 |     |     |     | 160 |     |
| Ser | Ser | His | Phe | Trp | Thr | Glu | Thr | Val | Phe | Glu | His | Ile | Gln | Lys | Asp |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Asp | Tyr | Arg | Leu | Leu | Ala | Ile | Asp | Leu | Leu | Gly | Phe | Gly | Glu | Ser | Pro |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Lys | Pro | Arg | Asp | Ser | Leu | Tyr | Thr | Leu | Lys | Asp | His | Val | Asp | Thr | Ile |
|     |     |     | 195 |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Glu | Arg | Ser | Val | Ile | Lys | Pro | Tyr | Gln | Leu | Asp | Ser | Phe | His | Val | Val |
|     |     |     | 210 |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Ala | His | Ser | Met | Gly | Cys | Leu | Ile | Ala | Leu | Ala | Leu | Ala | Ala | Lys | His |
|     |     |     | 225 |     |     | 230 |     |     |     | 235 |     |     |     | 240 |     |
| Ser | Asn | Ile | Val | Lys | Ser | Val | Thr | Leu | Val | Ala | Pro | Pro | Tyr | Phe | Pro |
|     |     |     | 245 |     |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Ser | Ser | Val | Asp | Gly | Ser | Val | Leu | Asn | Arg | Ile | Ala | Arg | Lys | Arg | Leu |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Trp | Pro | Pro | Leu | Ala | Phe | Gly | Thr | Ala | Val | Met | Ser | Trp | Tyr | Glu | His |
|     |     |     | 275 |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Ile | Gly | Arg | Cys | Val | Cys | Phe | Ile | Ile | Cys | Lys | His | His | Lys | Ile | Trp |
|     |     |     | 290 |     |     |     | 295 |     |     |     |     | 300 |     |     |     |
| Glu | Trp | Leu | Ile | Lys | Leu | Cys | Ile | Gly | Lys | Arg | Glu | Ile | His | Trp | Lys |
|     |     |     | 305 |     |     | 310 |     |     |     | 315 |     |     |     | 320 |     |
| Ile | Lys | Asp | Ile | Thr | Arg | His | Thr | His | His | Ser | Ala | Trp | His | Ser | Met |
|     |     |     | 325 |     |     |     |     | 330 |     |     |     |     |     | 335 |     |

His Asn Val Ile Cys Gly Gly Ser Lys Val Ala Asp Glu His Leu Glu  
340 345 350  
Thr Leu Ile Lys Ser Gly Val Lys Ile His Leu Met Gln Gly Asp Cys  
355 360 365  
Asp Gln Ile Val Pro Ser His Cys Ser Gly Asn Met Lys Arg Thr Phe  
370 375 380  
Pro Ala Val Glu Val Asp Ile Ile Thr Gly Ala Asp His Asp Ser Met  
385 390 395 400  
Ile Ser Gly Arg Gly Glu Glu Phe Ala Glu Lys Leu Glu Ser Ile Trp  
405 410 415  
Cys Ser Phe Lys Glu Ser Gly  
420

(2) INFORMATION FOR SEQ ID NO:598:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 344 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..344
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567407

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:598:

Met Trp Phe Leu Gly Phe Ala Arg Glu Phe Lys Ser Lys Leu Ser Arg  
1 5 10 15  
Lys Leu Arg Lys Ser Lys Ile His Gln Glu Ser Val Asn Arg Trp Ser  
20 25 30  
Asp Cys Gly Cys Lys Ser Cys Lys Ser Trp Thr Lys Asn Glu Asp Gly  
35 40 45  
Asn Leu His Val Val Val Lys Asp Ser Thr Ser Arg Glu Thr Glu Tyr  
50 55 60  
Ser Val Gln Glu Pro Ser Glu Asn Val Ile Phe Ile His Gly Phe Met  
65 70 75 80  
Gly Ser Ser His Phe Trp Thr Glu Thr Val Phe Glu His Ile Gln Lys  
85 90 95  
Asp Asp Tyr Arg Leu Leu Ala Ile Asp Leu Leu Gly Phe Gly Glu Ser  
100 105 110  
Pro Lys Pro Arg Asp Ser Leu Tyr Thr Leu Lys Asp His Val Asp Thr  
115 120 125  
Ile Glu Arg Ser Val Ile Lys Pro Tyr Gln Leu Asp Ser Phe His Val  
130 135 140  
Val Ala His Ser Met Gly Cys Leu Ile Ala Leu Ala Leu Ala Lys  
145 150 155 160  
His Ser Asn Ile Val Lys Ser Val Thr Leu Val Ala Pro Pro Tyr Phe  
165 170 175  
Pro Ser Ser Val Asp Gly Ser Val Leu Asn Arg Ile Ala Arg Lys Arg  
180 185 190  
Leu Trp Pro Pro Leu Ala Phe Gly Thr Ala Val Met Ser Trp Tyr Glu  
195 200 205  
His Ile Gly Arg Cys Val Cys Phe Ile Ile Cys Lys His His Lys Ile  
210 215 220  
Trp Glu Trp Leu Ile Lys Leu Cys Ile Gly Lys Arg Glu Ile His Trp  
225 230 235 240  
Lys Ile Lys Asp Ile Thr Arg His Thr His His Ser Ala Trp His Ser  
245 250 255  
Met His Asn Val Ile Cys Gly Gly Ser Lys Val Ala Asp Glu His Leu  
260 265 270  
Glu Thr Leu Ile Lys Ser Gly Val Lys Ile His Leu Met Gln Gly Asp  
275 280 285  
Cys Asp Gln Ile Val Pro Ser His Cys Ser Gly Asn Met Lys Arg Thr

340

(1) SEQUENCE CHARACTERISTICS:

- (ii) MOLECULE TYPE: peptide

- (A) NAME/KEY: peptide

- (B) LOCATION: 1..265

- (D) OTHER INFORMATION: / Ceres Seq. ID 1567408

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:599:

(2) INFORMATION FOR SEQ ID NO:600:

- ```
(i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 1054 base pairs
      (B) TYPE: nucleic acid
      (C) STRANDEDNESS: single
      (D) TOPOLOGY: linear
```

- (ii) MOLECULE TYPE: DNA (genomic)

- (ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1054

(D) OTHER INFORMATION: / Ceres Seq. ID 1567417

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:600:

gaggctcggtt	gtctgtgtga	tttctcttct	ccttcttctc	tcatttttct	catctgttct	60
ctcaacacaaa	agctcatcat	ttcaaaaaact	tcgggtgcc	ggaacagaa	caggccctga	120
agctttcgct	tttgattcca	cgggaaaagg	attctacacc	ggagtcaccc	gcggtaaaaa	180
cctcaaatat	cttccaaga	aaggttatgt	cgactttgcc	cagatcacaa	actcttcgaa	240
gtctctgttg	tgcgacggag	cacttggaaac	cactaacgtc	gaaaaatgtg	gtcgaccacg	300
cggaatagcc	ttcaacacga	aaacaggtga	tccttacgtc	gtagatgctg	cattgggtct	360
ccacgtcacc	cctgcgcgtg	ggggtttggc	taagaagatc	gccgacagtg	tcggCggcaa	420
gcctcttttg	ttctttgacg	ggcTtgacGt	agatcccact	accggcgctg	tcattttcac	480
ttctctcagc	ccaactattg	gccctaggga	tgtgttgaaa	gcagtgcgaa	caaaagactc	540
gaocggtaag	ttcttcaaat	acgatccatc	aaaaaaggtc	gtgactgtat	tgatggaagg	600
ttttagcggc	tcagccggat	gtgccgttag	ctcagatggt	tcattgtgct	tggttggtca	660
gttcaacaaa	agtaacatca	agaggtattg	gatcaaaagg	tcacaagctg	gtactttctg	720
agactttcac	aactcggctc	cgaaccctga	caacatcaag	aggatcggtt	ctactggaaa	780
cttttggggt	gcttcggctg	tgaactcagc	caccggaccg	acaaaCccct	cggcggttaa	840
agtcagttct	gcgggtaaa	tgcttcagac	cattccctca	aaagacaaagt	ttgggggatac	900
tttgcttagt	gaagttaaac	aatacaaaag	acagctttat	atcggaagctc	tttttggctc	960
tttgcgggR	aattcttaag	ctttaaagtg	aacatgttat	tagtatgggt	tagaattaaa	1020
gtgattgaat	cgaaataaat	atggttacaa	aggc			

(2) INFORMATION FOR SEQ ID NO:601:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 325 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..325

(D) OTHER INFORMATION: / Ceres Seq. ID 1567418

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:601:

Arg	Ser	Phe	Val	Ser	Leu	Ile	Ser	Leu	Leu	Leu	Leu	Ser	Phe	Ser
1			5						10				15	
Ser	Ser	Val	Leu	Ser	Thr	Lys	Lys	Ser	Ser	Phe	Gln	Lys	Leu	Pro Val
		20						25				30		
Pro	Gly	Asn	Arg	Thr	Gly	Pro	Glu	Ala	Phe	Ala	Phe	Asp	Ser	Thr Gly
		35					40					45		
Lys	Gly	Phe	Tyr	Thr	Gly	Val	Thr	Gly	Gly	Lys	Ile	Leu	Lys	Tyr Leu
		50				55					60			
Pro	Lys	Lys	Gly	Tyr	Val	Asp	Phe	Ala	Gln	Ile	Thr	Asn	Ser	Ser Lys
65					70				75					80
Ser	Ser	Leu	Cys	Asp	Gly	Ala	Leu	Gly	Thr	Asn	Val	Glu	Lys	Cys
			85						90					95
Gly	Arg	Pro	Ala	Gly	Ile	Ala	Phe	Asn	Thr	Lys	Thr	Gly	Asp	Leu Tyr
		100						105					110	
Val	Val	Asp	Ala	Ala	Leu	Gly	Leu	His	Val	Ile	Pro	Arg	Arg	Gly Gly
		115				120						125		
Leu	Ala	Lys	Lys	Ile	Ala	Asp	Ser	Val	Gly	Gly	Lys	Pro	Phe	Leu Phe
		130				135					140			
Leu	Asp	Gly	Leu	Asp	Val	Asp	Pro	Thr	Thr	Gly	Val	Val	Tyr	Phe Thr
145					150				155					160
Ser	Phe	Ser	Ser	Thr	Phe	Gly	Pro	Arg	Asp	Val	Leu	Lys	Ala	Val Ala
				165					170					175
Thr	Lys	Asp	Ser	Thr	Gly	Lys	Phe	Phe	Lys	Tyr	Asp	Pro	Ser	Lys Lys
				180				185					190	
Val	Val	Thr	Val	Leu	Met	Glu	Gly	Leu	Ser	Gly	Ser	Ala	Gly	Cys Ala
		195				200					205			
Val	Ser	Ser	Asp	Gly	Ser	Phe	Val	Leu	Val	Gly	Gln	Phe	Thr	Lys Ser

210	215	220
Asn Ile Lys Arg Tyr Trp	Ile Lys Gly Ser Lys	Ala Gly Thr Ser Glu
225	230	240
Asp Phe Thr Asn Ser Val	Ser Asn Pro Asp Asn	Ile Lys Arg Ile Gly
245	250	255
Ser Thr Gly Asn Phe Trp	Val Ala Ser Val Val	Asn Ser Ala Thr Gly
260	265	270
Pro Thr Asn Pro Ser Ala	Val Lys Val Ser Ser	Ala Gly Lys Val Leu
275	280	285
Gln Thr Ile Pro Leu Lys	Asp Lys Phe Gly Asp	Thr Leu Val Ser Glu
290	295	300
Val Asn Glu Tyr Lys Gly	Gln Leu Tyr Ile Gly	Ala Leu Phe Gly Pro
305	310	315
Phe Ala Xaa Asn Ser		
325		

(2) INFORMATION FOR SEQ ID NO:602:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1469 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1469

(D) OTHER INFORMATION: / Ceres Seq. ID 1567419

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:602:

atcaatagtt	caataactaag	aaacccggcct	atatatatat	ttgtgggtcac	taattttctcc	60
aaaaaacagtt	tgcccttcggt	aaaaagatgg	aaacctcagag	aaaacactcgt	acagccctctc	120
acacgtgtca	tccctgcccgt	cgaaccattc	catacagaa	ctacgccgtg	tttctactgtt	180
gtggcatcat	agctctcatg	tatcaccatg	tacactcaact	tgtaaacgca	aacaacactc	240
taataaacat	tctctctctc	ctctccgata	tgtttctcgc	cttcatgtgg	gcaaccacaa	300
cttccctccg	cttaaacccg	gttcatcgga	cggagtacc	tgaaaaatat	gctgctaacc	360
cgagGactt	tccaaagctg	gaogttttta	tatgcacggc	tgatccgtac	aaggagcctc	420
cgatgatggt	ggttaacacc	gctttatcgg	tgatggctta	cgatgatccg	tctcataaga	480
tctcagtgta	cgtatccggc	gatggaggat	cttccctgac	tttgtttgct	cttatggagg	540
ctgccaaagt	ctctaagcat	tggttgccct	tttgcaagaa	taacaatgtt	caagatcgct	600
ctccctgaagt	tattttttct	tcaaaagtac	attcttggag	tgatgaagct	gaaaaactta	660
agatgatgta	cgaagacatg	agaagttaga	tgcaacatgt	ggttgagagt	ggaaaagtgt	720
agBactcgct	tatttgcatt	cgatcaattt	agttgtgtgt	tcgactctgtg	gacagataaa	780
ttoactcgtc	atgaccattc	taccattatt	aaagtgctac	aacataacga	aacagagatg	840
atgccaaacc	tatatatagt	ttaagagaaa	aagagttaa	tttaccacca	ctatttcaaa	900
gcgggtgctc	ttaatacttt	gtttacagta	ctgcgcgtga	tgacaaactc	accaactcatt	960
ctaacactag	actgtgacat	gtactcaaac	aatctctacag	caccacttca	tgctctgtgc	1020
tatttttttag	accctaaagt	caattttggt	ttaggatttg	tgcaattttc	tcaaaaattt	1080
caaggaataa	acaaaaatga	tatttatgca	tccgagctca	aaagcccat	tgacatcaac	1140
acggttgggt	ttgatggact	tatgggacca	gttcatatgg	gaactgggtg	tttcttcaat	1200
cgacggcgct	tttatgggoc	tccgactagt	ttgaacttgc	ctgaCgatg	aaaaacttgg	1260
gccaaatcgg	attgcgcata	aaccatttaa	aaccocaaat	attttggcgt	tggtcacacga	1320
gtgtagcagg	tgtaactacg	agtgcaaac	caatttggga	tccaaggtta	gattaaattg	1380
aactttagct	tattttttat	tatgtgtatt	ttttgtttat	gtttacagat	tttgtttctt	1440
ttacatcaac	tagctctctc	aaaatccat				

(2) INFORMATION FOR SEQ ID NO:603:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 221 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..221

(D) OTHER INFORMATION: / Ceres Seq. ID 1567420

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:603:

Met Glu Pro Gln Arg Lys His Ser Thr Ala Leu His Thr Cys His Pro
1 5 10 15
Cys Arg Arg Thr Ile Pro Tyr Arg Ile Tyr Ala Val Phe His Leu Cys
20 25 30
Gly Ile Ile Ala Leu Met Tyr His His Val His Ser Leu Val Asn Ala
35 40 45
Asn Asn Thr Leu Ile Thr Cys Leu Leu Leu Ser Asp Ile Val Leu
50 55 60
Ala Phe Met Trp Ala Thr Thr Thr Ser Leu Arg Leu Asn Pro Val His
65 70 75 80
Arg Thr Glu Tyr Pro Glu Lys Tyr Ala Ala Lys Pro Glu Asp Phe Pro
85 90 95
Lys Leu Asp Val Phe Ile Cys Thr Ala Asp Pro Tyr Lys Glu Pro Pro
100 105 110
Met Met Val Val Asn Thr Ala Leu Ser Val Met Ala Tyr Glu Tyr Pro
115 120 125
Ser His Lys Ile Ser Val Tyr Val Ser Asp Asp Gly Gly Ser Ser Leu
130 135 140
Thr Leu Phe Ala Leu Met Glu Ala Ala Lys Phe Ser Lys His Trp Leu
145 150 155 160
Pro Phe Cys Lys Asn Asn Asn Val Gln Asp Arg Ser Pro Glu Val Tyr
165 170 175
Phe Ser Ser Lys Ser His Ser Trp Ser Asp Glu Ala Glu Asn Leu Lys
180 185 190
Met Met Tyr Glu Asp Met Lys Ser Arg Val Glu His Val Val Glu Ser
195 200 205
Gly Lys Val Glu Xaa Cys Val Tyr Cys Met Arg Ser Ile
210 215 220

(2) INFORMATION FOR SEQ ID NO:604:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 184 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..184

(D) OTHER INFORMATION: / Ceres Seq. ID 1567421

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:604:

Met Tyr His His Val His Ser Leu Val Asn Ala Asn Asn Thr Leu Ile
1 5 10 15
Thr Cys Leu Leu Leu Leu Ser Asp Ile Val Leu Ala Phe Met Trp Ala
20 25 30
Thr Thr Thr Ser Leu Arg Leu Asn Pro Val His Arg Thr Glu Tyr Pro
35 40 45
Glu Lys Tyr Ala Ala Lys Pro Glu Asp Phe Pro Lys Leu Asp Val Phe
50 55 60
Ile Cys Thr Ala Asp Pro Tyr Lys Glu Pro Pro Met Met Val Val Asn
65 70 75 80
Thr Ala Leu Ser Val Met Ala Tyr Glu Tyr Pro Ser His Lys Ile Ser
85 90 95
Val Tyr Val Ser Asp Asp Gly Gly Ser Ser Leu Thr Leu Phe Ala Leu
100 105 110
Met Glu Ala Ala Lys Phe Ser Lys His Trp Leu Pro Phe Cys Lys Asn
115 120 125
Asn Asn Val Gln Asp Arg Ser Pro Glu Val Tyr Phe Ser Ser Lys Ser
130 135 140

His Ser Trp Ser Asp Glu Ala Glu Asn Leu Lys Met Met Tyr Glu Asp
145 150 155 160
Met Lys Ser Arg Val Glu His Val Val Glu Ser Gly Lys Val Glu Xaa
165 170 175
Cys Val Tyr Cys Met Arg Ser Ile
180

(2) INFORMATION FOR SEQ ID NO:605:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 194 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..194

(D) OTHER INFORMATION: / Ceres Seq. ID 1567422

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:605:

Met Trp Leu Arg Val Glu Lys Leu Xaa Thr Ala Phe Ile Ala Cys Asp
1 5 10 15
Gln Phe Ser Cys Val Phe Asp Leu Trp Thr Asp Lys Phe Thr Arg His
20 25 30
Asp His Pro Thr Ile Ile Lys Val Leu Gln His Asn Glu Thr Glu Met
35 40 45
Met Pro Asn Leu Ile Tyr Val Ser Arg Glu Lys Ser Lys Val Ser Pro
50 55 60
His His Phe Lys Ala Gly Ala Leu Asn Thr Leu Leu Arg Val Ser Ala
65 70 75 80
Val Met Thr Asn Ser Pro Ile Ile Leu Thr Leu Asp Cys Asp Met Tyr
85 90 95
Ser Asn Asn Pro Thr Ala Pro Leu His Ala Leu Cys Tyr Phe Leu Asp
100 105 110
Pro Lys Ile Asn Phe Gly Leu Gly Phe Val Gln Phe Pro Gln Lys Phe
115 120 125
Gln Gly Ile Asn Lys Asn Asp Ile Tyr Ala Ser Glu Leu Lys Arg Pro
130 135 140
Phe Asp Ile Asn Thr Val Gly Phe Asp Gly Leu Met Gly Pro Val His
145 150 155 160
Met Gly Thr Gly Cys Phe Phe Asn Arg Arg Ala Phe Tyr Gly Pro Pro
165 170 175
Thr Ser Leu Thr Leu Pro Asp Asp Arg Lys Thr Trp Ala Lys Ser Asp
180 185 190
Cys Arg

(2) INFORMATION FOR SEQ ID NO:606:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1865 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1865

(D) OTHER INFORMATION: / Ceres Seq. ID 1567445

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:606:

ctgattattt ccaatgacct tttctctgt ctgattcgtt tgtttcggcg attcaactct 60
tcttcaacgc cctgagagtc acgcacgaga attggattga tggtttttca cacgcaggag 120
aggcgattcg ttgtcttctt ctgtcccgct tgacctgttt cgaatcgaaga tggtagattat 180
gcagcagctg attctaaatt agggcattta aatccgcctt ccaggtgaat ttttgaanaa 240
taattaaagg gtgttcttga atggacttga aaatggataa tgttatattgg ggaagattta 300


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aacttggtcg gaagatcggt ggtggctctt ttggagaact tttcttggc gtaagtttgc 360
aaaccggaga ggaagcagct gtttaagctg agcctgcgaa aactaagcat ccccaacttc 420
attatgagtc gaagatatac atgctctctc aaggagggaag tggcatcccc agccttaagt 480
ggtttggggt tcaaggagac tacaatgcga ttgtcattga tctgcttggg ccaggtttgg 540
aagacttgtt caactactgc aataggaggc ttactttgaa ggcagttttg atgcttgcag 600
atcaactgat tagcagagtt gaatatatgc attcaagggg gtttcttcac cgtgacatca 660
aacctgcaca tttcttgatg ggacttggtc gcaaaagcaa ccaggttgat atcatgtatt 720
ttgggcttgc aaagaagtat agggatctcc aaacacatag gcatactccc tatagagaaa 780
acaagaacct tacgggcaca gctcggtatg ctagtgtcaa cactcaccta ggagtggagc 840
aaagttaggag ggatgactcg gagtctcttg gttacgtact catgtatttc ctgagaggaa 900
gcttaccgtg gcaggagact aaagctggca caaagaagca aaagtatgac agaattagcg 960
agaagaagt atcaactctc atagaggtct tgtgcaagtc atatccaccc gaattctgat 1020
catactttca atactgcaga tctctgcgat tcgaagacAa accagactac tcatacttaa 1080
agagactttt ccagagactg tttatccgtg aaggttatca gtttgattat gtattgcaat 1140
ggactgcatt gaaacacctc cagagttagt ccaggtccca ttccagtaca catgaaagggc 1200
atcgtaaccg taaaccaggg atgggtgcgg gaccgtctgc tgaaaaacct gaaagggatt 1260
cagtagggaa catcccgcat aaattctcag tgcggctcga agcattttggc gaaaggaacg 1320
ttagaggacc cagtcoccat caaaaccata ccagacatcg aactcttgac gaaattccct 1380
caatgaaacc tgctgtgaat atggtatctg agaaaggaa aaacacttcc agatacggga 1440
gtgcttgcag gagagcagta gcctcaggaa gttagaccaag ctcatcaggt gaacaagggg 1500
agagccggga ctgcagccgc gtgacctcaa gcggtggcgg tgtccgacca tcagctttcc 1560
aaagaaccca agcagcagct gctgtgagtg gatacagatc aaagacagca tctgccttta 1620
accgcgaccg agtagccgtc tcaagaacag caccgagcga ggctctcaga agctctgagc 1680
ttctttcgat ccgcaaatga agccttcac aattggctct ttgctgtaa ttggattott 1740
ctttacatat gttgtttgt cctttgttcc caagaaactc ccaatttttc atgtattatt 1800
aaattctctg gattttgtat caatttttcc acactttatt gtaactcatga caatttgtg 1860
agttt

```

(2) INFORMATION FOR SEQ ID NO:607:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 479 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..479
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567446

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:607:

```

Met Asp Leu Lys Met Asp Asn Val Ile Gly Gly Lys Phe Lys Leu Gly
1      5      10      15
Arg Lys Ile Gly Gly Gly Ser Phe Gly Glu Leu Phe Leu Ala Val Ser
      20      25      30
Leu Gln Thr Gly Glu Glu Ala Ala Val Lys Leu Glu Pro Ala Lys Thr
      35      40      45      50
Lys His Pro Gln Leu His Tyr Glu Ser Lys Ile Tyr Met Leu Leu Gln
      55      60      65
Gly Gly Ser Gly Ile Pro Ser Leu Lys Trp Phe Gly Val Gln Gly Asp
      70      75      80
Tyr Asn Ala Met Val Ile Asp Leu Leu Gly Pro Ser Leu Glu Asp Leu
      85      90      95
Phe Asn Tyr Cys Asn Arg Leu Thr Leu Lys Ala Val Leu Met Leu
      100      105      110
Ala Asp Gln Leu Ile Ser Arg Val Glu Tyr Met His Ser Arg Gly Phe
      115      120      125
Leu His Arg Asp Ile Lys Pro Asp Asn Phe Leu Met Gly Leu Gly Arg
      130      135      140
Lys Ala Asn Gln Val Tyr Ile Ile Asp Phe Gly Leu Ala Lys Lys Tyr
      145      150      155      160
Arg Asp Leu Gln Thr His Arg His Ile Pro Tyr Arg Glu Asn Lys Asn
      165      170      175

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Leu Thr Gly Thr Ala Arg Tyr Ala Ser Val Asn Thr His Leu Gly Val
180 185 190
Glu Gln Ser Arg Arg Asp Asp Leu Glu Ser Leu Gly Tyr Val Leu Met
195 200 205
Tyr Phe Leu Arg Gly Ser Leu Pro Trp Gln Gly Leu Lys Ala Gly Thr
210 215 220
Lys Lys Gln Lys Tyr Asp Arg Ile Ser Glu Lys Lys Val Ser Thr Pro
225 230 235 240
Ile Glu Val Leu Cys Lys Ser Tyr Pro Pro Glu Phe Val Ser Tyr Phe
245 250 255
Gln Tyr Cys Arg Ser Leu Arg Phe Glu Asp Lys Pro Asp Tyr Ser Tyr
260 265 270
Leu Lys Arg Leu Phe Arg Asp Leu Phe Ile Arg Glu Gly Tyr Gln Phe
275 280 285
Asp Tyr Val Phe Asp Trp Thr Ala Leu Lys His Pro Gln Ser Ser Ala
290 295 300
Arg Ser His Ser Ser Thr His Glu Arg His Arg Thr Gly Lys Pro Gly
305 310 315 320
Met Gly Ala Gly Pro Ser Ala Glu Lys Pro Glu Arg Ile Ser Val Gly
325 330 335
Asn Ile Arg Asp Lys Phe Ser Gly Ala Val Glu Ala Phe Ala Arg Arg
340 345 350
Asn Val Arg Gly Pro Ser Pro His Gln Asn His Thr Arg His Arg Thr
355 360 365
Leu Asp Glu Ile Pro Ser Met Lys Pro Ala Val Asn Met Val Ser Glu
370 375 380
Lys Gly Arg Asn Thr Ser Arg Tyr Gly Ser Ala Ser Arg Arg Ala Val
385 390 395 400
Ala Ser Gly Ser Arg Pro Ser Ser Ser Gly Glu Gln Arg Glu Ser Arg
405 410 415
Asp Ser Ser Arg Val Ala Ser Ser Gly Gly Val Arg Pro Ser Val
420 425 430
Phe Gln Arg Thr Gln Ala Ala Ala Val Ser Gly Tyr Glu Ser Lys
435 440 445
Thr Ala Ser Ala Phe Asn Arg Asp Arg Val Ala Ala Ser Arg Thr Ala
450 455 460
Arg Asp Glu Ala Leu Arg Ser Phe Glu Leu Leu Ser Ile Arg Lys
465 470 475

(2) INFORMATION FOR SEQ ID NO:608:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 475 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..475

(D) OTHER INFORMATION: / Ceres Seq. ID 1567447

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:608:

Met Asp Asn Val Ile Gly Gly Lys Phe Lys Leu Gly Arg Lys Ile Gly
1 5 10 15
Gly Gly Ser Phe Gly Glu Leu Phe Leu Ala Val Ser Leu Gln Thr Gly
20 25 30
Glu Glu Ala Ala Val Lys Leu Glu Pro Ala Lys Thr Lys His Pro Gln
35 40 45
Leu His Tyr Glu Ser Lys Ile Tyr Met Leu Leu Gln Gly Gly Ser Gly
50 55 60
Ile Pro Ser Leu Lys Trp Phe Gly Val Gln Gly Asp Tyr Asn Ala Met
65 70 75 80
Val Ile Asp Leu Leu Gly Pro Ser Leu Glu Asp Leu Phe Asn Tyr Cys

[illegible]

(i) SEQUENCE CHARACTERISTICS:

- (ii) MOLECULE TYPE: peptide

- (A) NAME/KEY: peptide

- (B) LOCATION: 1..419

- (D) OTHER INFORMATION: / Ceres Seq. ID 1567448

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:609:

```

Met Leu Leu Gln Gly Gly Ser Gly Ile Pro Ser Leu Lys Trp Phe Gly
1      5      10      15
Val Gln Gly Asp Tyr Asn Ala Met Val Ile Asp Leu Leu Gly Pro Ser
20      25      30
Leu Glu Asp Leu Phe Asn Tyr Cys Asn Arg Arg Leu Thr Lys Ala
35      40      45
Val Leu Met Leu Ala Asp Gln Leu Ile Ser Arg Val Glu Tyr Met His
50      55      60
Ser Arg Gly Phe Leu His Arg Asp Ile Lys Pro Asp Asn Phe Leu Met
65      70      75      80
Gly Leu Gly Arg Lys Ala Asn Gln Val Tyr Ile Ile Asp Phe Gly Leu
85      90      95
Ala Lys Lys Tyr Arg Asp Leu Gln Thr His Arg His Ile Pro Tyr Arg
100     105     110
Glu Asn Lys Asn Leu Thr Gly Thr Ala Arg Tyr Ala Ser Val Asn Thr
115     120     125
His Leu Gly Val Glu Gln Ser Arg Arg Asp Asp Leu Glu Ser Leu Gly
130     135     140
Tyr Val Leu Met Tyr Phe Leu Arg Gly Ser Leu Pro Trp Gln Gly Leu
145     150     155     160
Lys Ala Gly Thr Lys Lys Gln Lys Tyr Asp Arg Ile Ser Glu Lys Lys
165     170     175
Val Ser Thr Pro Ile Glu Val Leu Cys Lys Ser Tyr Pro Pro Glu Phe
180     185     190
Val Ser Tyr Phe Gln Tyr Cys Arg Ser Leu Arg Phe Glu Asp Lys Pro
195     200     205
Asp Tyr Ser Tyr Leu Lys Arg Leu Phe Arg Asp Leu Phe Ile Arg Glu
210     215     220
Gly Tyr Gln Phe Asp Tyr Val Phe Asp Trp Thr Ala Leu Lys His Pro
225     230     235     240
Gln Ser Ser Ala Arg Ser His Ser Ser Thr His Glu Arg His Arg Thr
245     250     255
Gly Lys Pro Gly Met Gly Ala Gly Pro Ser Ala Glu Lys Pro Glu Arg
260     265     270
Ile Ser Val Gly Asn Ile Arg Asp Lys Phe Ser Gly Ala Val Glu Ala
275     280     285
Phe Ala Arg Arg Asn Val Arg Gly Pro Ser Pro His Gln Asn His Thr
290     295     300
Arg His Arg Thr Leu Asp Glu Ile Pro Ser Met Lys Pro Ala Val Asn
305     310     315     320
Met Val Ser Glu Lys Gly Arg Asn Thr Ser Arg Tyr Gly Ser Ala Ser
325     330     335
Arg Arg Ala Val Ala Ser Gly Ser Arg Pro Ser Ser Ser Gly Glu Gln
340     345     350
Arg Glu Ser Arg Asp Ser Ser Arg Val Ala Ser Ser Gly Gly Val
355     360     365
Arg Pro Ser Val Phe Gln Arg Thr Gln Ala Ala Ala Val Ser Gly
370     375     380
Tyr Glu Ser Lys Thr Ala Ser Ala Phe Asn Arg Asp Arg Val Ala Ala
385     390     395     400
Ser Arg Thr Ala Arg Asp Glu Ala Leu Arg Ser Phe Glu Leu Leu Ser
405     410     415
Ile Arg Lys

```

(2) INFORMATION FOR SEQ ID NO:610:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 697 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..697
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567449

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:610:

aacgaatctt	gtttagtaaa	aagcgcaGct	gcaaaaaaaaa	tcgagtagag	aagaagtagg	60
cagacaaaga	agaagaagaa	gaagttctcg	gcgtgcttca	atggcgatat	cagtagcagc	120
ttcgtctctt	atggccgtga	tggttccacg	tggtcccgcc	gtatccaccc	gttgctccgc	180
cgtcccttat	cttctctctc	gctcctttgg	ccgatcctct	ttcaccgttc	cgttgaagct	240
tgtttcaggg	aatggattgc	aaaaaagtga	attgtagaag	acaagagctt	cttcagaaga	300
gaacctcgcc	attgatacca	acgaactcat	cacagatttg	aaggaaaagt	gggatggctt	360
tgagaacaaa	tctactgtac	ttatatatgg	aggaggagcc	attgttgctg	tttggttatc	420
ttccattgtt	gttggtgcca	tcaactctgt	tcctctgctt	ccgaaaagta	tggaaactgt	480
cgtctcggg	tacactggat	ggtttgtota	cagatacctt	ctcttcaagt	caagcagaaa	540
ggaaattggct	gaggatattg	aatccttgaa	gaagaagatg	gcaggaaagc	aatagattca	600
ttttcaaaaa	aaacagagtt	tctctctgta	tgttttctcg	taatatcgtg	ttatattata	660
caatgtctct	gtttcaacat	tgtatctggt	gcattctc			

(2) INFORMATION FOR SEQ ID NO:611:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..58
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567450

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:611:

Met	Ala	Ile	Ser	Val	Ala	Ala	Ser	Ser	Ser	Met	Ala	Val	Met	Val	Pro	
1			5						10				15			
Arg	Val	Pro	Ala	Val	Ser	Thr	Arg	Cys	Ser	Ala	Val	Pro	Tyr	Leu	Pro	
		20						25					30			
Pro	Arg	Ser	Phe	Gly	Arg	Ser	Ser	Phe	Thr	Val	Pro	Leu	Lys	Leu	Val	
		35					40					45				
Ser	Gly	Asn	Gly	Leu	Gln	Lys	Val	Glu	Leu							
		50				55										

(2) INFORMATION FOR SEQ ID NO:612:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..71
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567451

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:612:

Met	Val	Leu	Arg	Thr	Asn	Leu	Leu	Tyr	Leu	Tyr	Met	Glu	Glu	Glu	Pro	
1			5					10					15			
Leu	Leu	Leu	Phe	Gly	Tyr	Leu	Pro	Leu	Leu	Val	Pro	Ser	Thr	Leu		
		20					25					30				
Phe	Leu	Cys	Phe	Arg	Lys	Leu	Trp	Asn	Leu	Ser	Val	Ser	Gly	Thr	Leu	
		35				40					45					
Asp	Gly	Leu	Ser	Thr	Asp	Thr	Phe	Ser	Ser	Ser	Gln	Ala	Glu	Arg	Asn	
		50				55					60					
Trp	Leu	Arg	Ile	Leu	Asn	Pro										
		65				70										

(2) INFORMATION FOR SEQ ID NO:613:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 60 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..60
(D) OTHER INFORMATION: / Ceres Seq. ID 1567452
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:613:
Met Glu Glu Glu Pro Leu Leu Leu Phe Gly Tyr Leu Pro Leu Leu Leu
1 5 10 15
Val Pro Ser Thr Leu Phe Leu Cys Phe Arg Lys Leu Trp Asn Leu Ser
20 25 30
Val Ser Gly Thr Leu Asp Gly Leu Ser Thr Asp Thr Phe Ser Ser Ser
35 40 45
Gln Ala Glu Arg Asn Trp Leu Arg Ile Leu Asn Pro
50 55 60

(2) INFORMATION FOR SEQ ID NO:614:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1122 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -
(B) LOCATION: 1..1122
(D) OTHER INFORMATION: / Ceres Seq. ID 1567453

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:614:

atatttttgat	atgtaaaaatt	tatcgaaaac	gttccatttc	aatatgtaga	caaaagcggag	60
aagtatattg	tggaggcgccg	aagcaaggga	gcagagctag	tggtgttccc	ggaggggttt	120
atcgggtgtc	atcctcgagg	ttttaggttc	gggttagcgg	ttggcggtca	taacgaagaa	180
gggcgtgatg	agtttcggaa	gtaccatgct	tctgctatc	atgttctctg	ccctgaagta	240
gcaagattgg	ctgacgtggc	taggaaaaac	catgtgtact	tggtaatggg	agccatagag	300
aagggaaggg	ataccctcta	tgcacacagt	cttttcttta	gtccacaggg	tcagttcttg	360
ggcaagcacc	gtaaaactcat	gcccacaagt	tgggaacgtt	gcatttgggg	ccaaggggac	420
ggatacacca	tcgccgttta	cgacactccc	attggaaaac	tcgggtctgc	tatttctgtg	480
gagaatagga	tgccctctcta	cagaactgca	ttgtacgcc	aaggcattga	gctttattgt	540
gcacctactg	ctgatgggttc	gaaagaatgg	caatcgtcga	tgcttcacat	tcgcgatcgaa	600
ggtggaatgt	tgctctgttc	ggcttgccaa	ttctgccagc	gtaaaacatt	ccctgatcat	660
ctcgactact	tgtttaacga	ttggtacgac	gacaaaagac	atgattctat	tgcttcccaa	720
ggtggaagtg	tcattatttc	acctttggga	caagttctcg	ccggaccaaa	ctttgaatca	780
gaagggtctg	tcacagctga	tattgatctt	ggtgatatag	caagagccaa	gttatacttc	840
gattcggttg	gacattactc	gagaccagat	gttttacaat	tgaccgtaaa	tgagcacccg	900
aggaaaatcg	ttacattcgt	gacgaaggtg	gagaaaagctg	aggatgactc	aaacaaatag	960
taagagacct	gaagttcgta	tctgctggag	ttatgtcaat	cgtatggagt	caagtcacaa	1020
atgtttctgt	gcgttttcat	tttatgttca	agtttatatta	cttttctct	tcaatggtaa	1080
gatcatatga	gtcaagtaat	aatggtaaga	cttatgttgt	tg		

(2) INFORMATION FOR SEQ ID NO:615:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 224 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1..224
(D) OTHER INFORMATION: / Ceres Seq. ID 1567454

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:615:

```

Met Gly Ala Ile Glu Lys Glu Gly Tyr Thr Leu Tyr Cys Thr Val Leu
1      5      10      15
Phe Phe Ser Pro Gln Gly Gln Phe Leu Gly Lys His Arg Lys Leu Met
20     25     30
Pro Thr Ser Leu Glu Arg Cys Ile Trp Gly Gln Gly Asp Gly Ser Thr
35     40     45
Ile Pro Val Tyr Asp Thr Pro Ile Gly Lys Leu Gly Ala Ala Ile Cys
50     55     60
Trp Glu Asn Arg Met Pro Leu Tyr Arg Thr Ala Leu Tyr Ala Lys Gly
65     70     75     80
Ile Glu Leu Tyr Cys Ala Pro Thr Ala Asp Gly Ser Lys Glu Trp Gln
85     90     95
Ser Ser Met Leu His Ile Ala Ile Glu Gly Gly Cys Phe Val Leu Ser
100    105    110
Ala Cys Gln Phe Cys Gln Arg Lys His Phe Pro Asp His Pro Asp Tyr
115    120    125
Leu Phe Thr Asp Trp Tyr Asp Asp Lys Glu His Asp Ser Ile Val Ser
130    135    140
Gln Gly Gly Ser Val Ile Ile Ser Pro Leu Gly Gln Val Leu Ala Gly
145    150    155    160
Pro Asn Phe Glu Ser Glu Gly Leu Val Thr Ala Asp Ile Asp Leu Gly
165    170    175
Asp Ile Ala Arg Ala Lys Leu Tyr Phe Asp Ser Val Gly His Tyr Ser
180    185    190
Arg Pro Asp Val Leu His Leu Thr Val Asn Glu His Pro Arg Lys Ser
195    200    205
Val Thr Phe Val Thr Lys Val Glu Lys Ala Glu Asp Asp Ser Asn Lys
210    215    220

```

(2) INFORMATION FOR SEQ ID NO:616:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 193 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..193

(D) OTHER INFORMATION: / Ceres Seq. ID 1567455

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:616:

```

Met Pro Thr Ser Leu Glu Arg Cys Ile Trp Gly Gln Gly Asp Gly Ser
1      5      10      15
Thr Ile Pro Val Tyr Asp Thr Pro Ile Gly Lys Leu Gly Ala Ala Ile
20     25     30
Cys Trp Glu Asn Arg Met Pro Leu Tyr Arg Thr Ala Leu Tyr Ala Lys
35     40     45
Gly Ile Glu Leu Tyr Cys Ala Pro Thr Ala Asp Gly Ser Lys Glu Trp
50     55     60
Gln Ser Ser Met Leu His Ile Ala Ile Glu Gly Gly Cys Phe Val Leu
65     70     75     80
Ser Ala Cys Gln Phe Cys Gln Arg Lys His Phe Pro Asp His Pro Asp
85     90     95
Tyr Leu Phe Thr Asp Trp Tyr Asp Asp Lys Glu His Asp Ser Ile Val
100    105    110
Ser Gln Gly Gly Ser Val Ile Ile Ser Pro Leu Gly Gln Val Leu Ala
115    120    125
Gly Pro Asn Phe Glu Ser Glu Gly Leu Val Thr Ala Asp Ile Asp Leu
130    135    140
Gly Asp Ile Ala Arg Ala Lys Leu Tyr Phe Asp Ser Val Gly His Tyr

```

145		150		155		160
Ser	Arg	Pro	Asp	Val	Leu	His
			165		170	
Ser	Val	Thr	Phe	Val	Thr	Lys
			180		185	
						190
						195
						200
						205
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						590
						595
						600

(2) INFORMATION FOR SEQ ID NO:617:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 156 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..156
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567456

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:617:

Met	Pro	Leu	Tyr	Arg	Thr	Ala	Leu	Tyr	Ala	Lys	Gly	Ile	Glu	Leu	Tyr
1			5					10					15		
Cys	Ala	Pro	Thr	Ala	Asp	Gly	Ser	Lys	Glu	Trp	Gln	Ser	Ser	Met	Leu
			20				25					30			
His	Ile	Ala	Ile	Glu	Gly	Gly	Cys	Phe	Val	Leu	Ser	Ala	Cys	Gln	Phe
			35				40					45			
Cys	Gln	Arg	Lys	His	Phe	Pro	Asp	His	Pro	Asp	Tyr	Leu	Phe	Thr	Asp
			50				55				60				
Trp	Tyr	Asp	Asp	Lys	Glu	His	Asp	Ser	Ile	Val	Ser	Gln	Gly	Gly	Ser
			65				70			75			80		
Val	Ile	Ile	Ser	Pro	Leu	Gly	Gln	Val	Leu	Ala	Gly	Pro	Asn	Phe	Glu
			85				90					95			
Ser	Glu	Gly	Leu	Val	Thr	Ala	Asp	Ile	Asp	Leu	Gly	Asp	Ile	Ala	Arg
			100				105					110			
Ala	Lys	Leu	Tyr	Phe	Asp	Ser	Val	Gly	His	Tyr	Ser	Arg	Pro	Asp	Val
			115				120					125			
Leu	His	Leu	Thr	Val	Asn	Glu	His	Pro	Arg	Lys	Ser	Val	Thr	Phe	Val
			130				135					140			
Thr	Lys	Val	Glu	Lys	Ala	Glu	Asp	Asp	Ser	Asn	Lys				
			145				150				155				

(2) INFORMATION FOR SEQ ID NO:618:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1811 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1811
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567463

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:618:

agctatcaat	ttaactggaga	agagatgggt	ggatcagagg	ttttggagga	atgtggagaa	60
aaaaaagca	agaaagagtc	aaagaagcga	gcgcgtaaac	tggagaagtt	gtcccgtaaa	120
cagtaacgag	aagaagccac	atcatcatct	ctttctctgg	aggaggagga	tgaatcgtgt	180
tcacgcaact	acggtgacgt	gactactaac	gagttgcagt	cggtctgtta	gggaaaagag	240
ctcaactgat	tgagcaactt	ggttgaagag	attgtggggt	cagaggtttc	gatcagaggt	300
cgactgcaca	agaatcgctt	agtcggtacc	aaattgtttg	tgatcttgag	ggaaaagtga	360
ttcacggttc	aatgcgtggg	ggaggagacc	agagttgggt	caaacatgat	taaatattgtc	420
aagcagctga	gtcgtgtaac	tgttgttgag	cttatcggtg	tcgtctctca	ccctaagaag	480
cctctcacag	gaaccaccca	gcaggttgaa	atacatgtca	gaaaaatgta	ctgcctcagc	540
agatccttgc	caaatattacc	acttgtttgt	gaggatgctg	ctcgtagtga	atcagatatt	600

gaaaaatctg	gcaaggatgg	caaacaagct	gctcgtgtcc	ttcaggacac	acgtttgaat	660
aataagggttc	ttgacatcag	aacaccggct	aatcaagcca	tcttcogtat	tcagtgccaa	720
gtccaaattg	cgttcagaga	atacttacaa	tccaaggggt	ttcttgaat	ccacacaccg	780
aaatgtatcg	ctggcagtag	tgaaggaggt	tctgctgtgt	ttaggttgga	ctacaaaagg	840
cagcctgctt	gtctggctca	gtctcctcag	cttcataaag	agatggcgat	atgtgggtgac	900
atgcgacgcg	tctttgaggt	tggtcctgtt	ttcagagctg	aagactcctt	cactcataga	960
cacctgtgtg	aattcgttgg	tcttgatgtg	gagatggaga	ttcgaatgca	ctactctgtg	1020
ataatggatc	ttgtggggaga	gttgtttccg	ttcatattca	caaaaataga	agaaaagggtc	1080
ccaaaggaaac	ttgaatctgt	cagaaaagcaa	taccttttcc	aatctttgaa	gtttcttccg	1140
caaacattga	ggctaaccctt	tgacagaagg	attcaaatgc	ttaagggaagc	tggcgaggag	1200
gttgatctct	ttggtgatct	aaatacagaa	tctgagagga	aacttggcca	gcttgctgtc	1260
gaaaagtaca	agacggagtt	ctacatgctg	catcgctatc	catcgctctt	cagacccgtc	1320
tacacatgac	cctatgaaaa	tgatttctaac	tacagcaact	ctttcgtatg	cttcatcaga	1380
ggagaggaga	tcactgtcag	agctcaacgt	atccatgacc	cagaactctt	ggagaagcgc	1440
gcaagagaaat	gcggcattga	tgtcaagaca	atatccacgt	acattgatgc	attcagggtac	1500
ggtgcNaccA	cctcacgggt	gattcggagt	ggggctggag	cgtgtggttaa	tgctctattg	1560
tgccctcaat	aacatccgca	aaacttcgct	attccctcgt	gactctcaaa	ggctcactcc	1620
ctaataatcat	tgctcttccc	tggcgactct	caaaaggctcg	ctcccttaat	atctatcttt	1680
gataaattgtc	cccgctcccg	atttctaagt	tatttttttg	gtgcagttcg	ttagtggttt	1740
agttatcttt	aaaactatgta	tgtgttgtaa	cctttaaatt	attaaggagc	agtactattt	1800
gggctttttc	g					

(2) INFORMATION FOR SEQ ID NO:619:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 388 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..388

(D) OTHER INFORMATION: / Ceres Seq. ID 1567464

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:619:

Met	Ile	Lys	Phe	Val	Lys	Gln	Leu	Ser	Arg	Glu	Ser	Val	Glu	Leu
1				5				10					15	
Ile	Gly	Val	Val	Ser	His	Pro	Lys	Lys	Pro	Leu	Thr	Gly	Thr	Gln
			20					25					30	
Gln	Val	Glu	Ile	His	Val	Arg	Lys	Met	Tyr	Cys	Leu	Ser	Arg	Ser
			35					40					45	
Pro	Asn	Leu	Pro	Leu	Val	Val	Glu	Asp	Ala	Ala	Arg	Ser	Glu	Ser
			50					55					60	
Ile	Glu	Lys	Ser	Gly	Lys	Asp	Gly	Lys	Gln	Ala	Ala	Arg	Val	Leu
			65					70					75	
Asp	Thr	Arg	Leu	Asn	Asn	Arg	Val	Leu	Asp	Ile	Arg	Thr	Pro	Ala
				85					90				95	
Gln	Ala	Ile	Phe	Arg	Ile	Gln	Cys	Gln	Val	Gln	Ile	Ala	Phe	Arg
				100					105				110	
Tyr	Leu	Gln	Ser	Lys	Gly	Phe	Leu	Glu	Ile	His	Thr	Pro	Lys	Leu
				115				120					125	
Ala	Gly	Ser	Ser	Glu	Gly	Gly	Ser	Ala	Val	Phe	Arg	Leu	Asp	Tyr
				130				135					140	
Gly	Gln	Pro	Ala	Cys	Leu	Ala	Gln	Ser	Pro	Gln	Leu	His	Lys	Gln
				145					150				155	
Ala	Ile	Cys	Gly	Asp	Met	Arg	Arg	Val	Phe	Glu	Val	Gly	Pro	Val
				165					170				175	
Arg	Ala	Glu	Asp	Ser	Phe	Thr	His	Arg	His	Leu	Cys	Glu	Phe	Val
				180				185					190	
Leu	Asp	Val	Glu	Met	Glu	Ile	Arg	Met	His	Tyr	Ser	Glu	Ile	Met
				195				200					205	
Leu	Val	Gly	Glu	Leu	Phe	Pro	Phe	Ile	Phe	Thr	Lys	Ile	Glu	Glu
				210				215					220	

Cys Pro Lys Glu Leu Glu Ser Val Arg Lys Gln Tyr Pro Phe Gln Ser
225 230 235 240
Leu Lys Phe Leu Pro Gln Thr Leu Arg Leu Thr Phe Ala Glu Gly Ile
245 250 255
Gln Met Leu Lys Glu Ala Gly Glu Glu Val Asp Pro Leu Gly Asp Leu
260 265 270
Asn Thr Glu Ser Glu Arg Lys Leu Gly Gln Leu Val Leu Glu Lys Tyr
275 280 285
Lys Thr Glu Phe Tyr Met Leu His Arg Tyr Pro Ser Ala Val Arg Pro
290 295 300
Phe Tyr Thr Met Pro Tyr Glu Asn Asp Ser Asn Tyr Ser Asn Ser Phe
305 310 315 320
Asp Val Phe Ile Arg Gly Glu Glu Ile Met Ser Gly Ala Gln Arg Ile
325 330 335
His Asp Pro Glu Leu Leu Glu Lys Arg Ala Arg Glu Cys Gly Ile Asp
340 345 350
Val Lys Thr Ile Ser Thr Tyr Ile Asp Ala Phe Arg Tyr Gly Xaa Thr
355 360 365
Thr Ser Arg Trp Ile Arg Ser Gly Ala Cys Gly Asn Ala Leu
370 375 380
Met Cys Pro Gln
385

(2) INFORMATION FOR SEQ ID NO:620:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 348 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..348

(D) OTHER INFORMATION: / Ceres Seq. ID 1567465

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:620:

Met Tyr Cys Leu Ser Arg Ser Leu Pro Asn Leu Pro Leu Val Val Glu
1 5 10 15
Asp Ala Ala Arg Ser Glu Ser Asp Ile Glu Lys Ser Gly Lys Asp Gly
20 25 30
Lys Gln Ala Ala Arg Val Leu Gln Asp Thr Arg Leu Asn Asn Arg Val
35 40 45
Leu Asp Ile Arg Thr Pro Ala Asn Gln Ala Ile Phe Arg Ile Gln Cys
50 55 60
Gln Val Gln Ile Ala Phe Arg Glu Tyr Leu Gln Ser Lys Gly Phe Leu
65 70 75 80
Glu Ile His Thr Pro Lys Leu Ile Ala Gly Ser Ser Glu Gly Gly Ser
85 90 95
Ala Val Phe Arg Leu Asp Tyr Lys Gly Gln Pro Ala Cys Leu Ala Gln
100 105 110
Ser Pro Gln Leu His Lys Gln Met Ala Ile Cys Gly Asp Met Arg Arg
115 120 125
Val Phe Glu Val Gly Pro Val Phe Arg Ala Glu Asp Ser Phe Thr His
130 135 140
Arg His Leu Cys Glu Phe Val Gly Leu Asp Val Glu Met Glu Ile Arg
145 150 155 160
Met His Tyr Ser Glu Ile Met Asp Leu Val Gly Glu Leu Phe Pro Phe
165 170 175
Ile Phe Thr Lys Ile Glu Glu Arg Cys Pro Lys Glu Leu Glu Ser Val
180 185 190
Arg Lys Gln Tyr Pro Phe Gln Ser Leu Lys Phe Leu Pro Gln Thr Leu
195 200 205
Arg Leu Thr Phe Ala Glu Gly Ile Gln Met Leu Lys Glu Ala Gly Glu

210	215	220
Glu Val Asp Pro Leu Gly Asp Leu Asn Thr Glu Ser Glu Arg Lys Leu		
225	230	235
Gly Gln Leu Val Leu Glu Lys Tyr Lys Thr Glu Phe Tyr Met Leu His		240
	245	250
Arg Tyr Pro Ser Ala Val Arg Pro Phe Tyr Thr Met Pro Tyr Glu Asn		255
	260	265
Asp Ser Asn Tyr Ser Asn Ser Phe Asp Val Phe Ile Arg Gly Glu Glu		270
	275	280
Ile Met Ser Gly Ala Gln Arg Ile His Asp Pro Glu Leu Leu Glu Lys		285
	290	295
Arg Ala Arg Glu Cys Gly Ile Asp Val Lys Thr Ile Ser Thr Tyr Ile		300
305	310	315
Asp Ala Phe Arg Tyr Gly Xaa Thr Thr Ser Arg Trp Ile Arg Ser Gly		320
	325	330
Ala Gly Ala Cys Gly Asn Ala Leu Met Cys Pro Gln		335
	340	345

(2) INFORMATION FOR SEQ ID NO:621:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 229 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..229

(D) OTHER INFORMATION: / Ceres Seq. ID 1567466

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:621:

Met Ala Ile Cys Gly Asp Met Arg Arg Val Phe Glu Val Gly Pro Val		
1	5	10
Phe Arg Ala Glu Asp Ser Phe Thr His Arg His Leu Cys Glu Phe Val		15
	20	25
Gly Leu Asp Val Glu Met Glu Ile Arg Met His Tyr Ser Glu Ile Met		30
	35	40
Asp Leu Val Gly Glu Leu Phe Pro Phe Ile Phe Thr Lys Ile Glu Glu		45
	50	55
Arg Cys Pro Lys Glu Leu Glu Ser Val Arg Lys Gln Tyr Pro Phe Gln		60
65	70	75
Ser Leu Lys Phe Leu Pro Gln Thr Leu Arg Leu Thr Phe Ala Glu Gly		80
	85	90
Ile Gln Met Leu Lys Glu Ala Gly Glu Glu Val Asp Pro Leu Gly Asp		95
	100	105
Leu Asn Thr Glu Ser Glu Arg Lys Leu Gly Gln Leu Val Leu Glu Lys		110
	115	120
Tyr Lys Thr Glu Phe Tyr Met Leu His Arg Tyr Pro Ser Ala Val Arg		125
	130	135
Pro Phe Tyr Thr Met Pro Tyr Glu Asn Asp Ser Asn Tyr Ser Asn Ser		140
145	150	155
Phe Asp Val Phe Ile Arg Gly Glu Glu Ile Met Ser Gly Ala Gln Arg		160
	165	170
Ile His Asp Pro Glu Leu Leu Glu Lys Arg Ala Arg Glu Cys Gly Ile		175
	180	185
Asp Val Lys Thr Ile Ser Thr Tyr Ile Asp Ala Phe Arg Tyr Gly Xaa		190
	195	200
Thr Thr Ser Arg Trp Ile Arg Ser Gly Ala Gly Ala Cys Gly Asn Ala		205
	210	215
Leu Met Cys Pro Gln		220
225		

(2) INFORMATION FOR SEQ ID NO:622:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 759 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..759
(D) OTHER INFORMATION: / Ceres Seq. ID 1567489

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:622:

gaccacaaatc	tgacgccttct	ctctctcttt	ctggtatctg	cgtttgattc	ggagaaKdaa	60
aaaTaahhaa	aaMaaaaag	caaagagaga	gcttcaatgg	agttagcttc	atccttggtta	120
gagctctgtt	tgtttccgta	tttcttctct	ccgcatggca	agagttcaat	gattttgggtg	180
aaagatgggtg	ccgactcaet	aaattcttga	aaccaaattt	caatgccttt	gtaaaccatg	240
tgacaactca	cactggccag	caattgccac	cagtcgatat	gaagattctt	gttgctgctg	300
ctatagcctt	gaaggggtat	gggggactat	tgtttgtctt	tgccagctca	ttggggagctt	360
atctcttgct	tctgcataca	gccgttgcca	ccccaaattt	gtatgatttc	tacaactaag	420
atgttgacag	aaaggaattc	ggccaaactat	tttcaaaatt	tacacagagc	ttggctcttc	480
ttggaggact	gctctctctc	attggaatga	aaaactcaag	gaacacaggt	aggcaactca	540
ggaaaaaggg	tccaaaaggca	aaagcaaaact	gaagaagcca	tatctttcat	cggttttatt	600
cggtctgtat	tttatattca	ttttggaatc	caggatgggt	ttaaagagtc	tatctgatga	660
ggccattgaa	aggcaaaatc	tctgcaaatc	attttgctta	cttcaagaag	cttttatgac	720
actttttgtg	agaaataatt	atggattatt	gtttcttag			

(2) INFORMATION FOR SEQ ID NO:623:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 97 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..97
(D) OTHER INFORMATION: / Ceres Seq. ID 1567490

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:623:

Met	Lys	Ile	Leu	Val	Ala	Ala	Ala	Ile	Ala	Leu	Lys	Gly	Ile	Gly	
1				5				10					15		
Leu	Leu	Phe	Val	Phe	Gly	Ser	Ser	Leu	Gly	Ala	Tyr	Leu	Leu	Leu	
			20					25					30		
His	Gln	Ala	Val	Ala	Thr	Pro	Ile	Leu	Tyr	Asp	Phe	Tyr	Asn	Tyr	Asp
		35					40					45			
Val	Asp	Arg	Lys	Glu	Phe	Gly	Gln	Leu	Phe	Ser	Lys	Phe	Thr	Gln	Ser
		50				55					60				
Leu	Ala	Leu	Leu	Gly	Gly	Leu	Leu	Phe	Phe	Ile	Gly	Met	Lys	Asn	Ser
				65			70			75				80	
Arg	Lys	His	Gly	Arg	Gln	Leu	Arg	Lys	Lys	Ala	Pro	Lys	Ala	Lys	Ala
			85				90					95			

Asn

(2) INFORMATION FOR SEQ ID NO:624:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 397 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..397
(D) OTHER INFORMATION: / Ceres Seq. ID 1567501

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:624:

aaaaacgcaa cgaagaacaa aatgggttca aagtcaccaa atattgtcgc acttggttta 60
ccctacttc ttactttta cactotttcc tctcaagttg aagtcgtgga atctacaggg 120
cgcaaacatt cgttttgggg aaatcctatc gtgtggactc cacactcaa ttcatgtgga 180
ggttctcaag catcagattt tgcttcttcc aagtggacga caggccgacc atgcagacgt 240
agtCgtNcct ccaggaacta atattcctgt ttctgatcaa tctccatagt actttaattt 300
gagtttgagt tactctgtgt tcgaatttta aagtatatgt ggttttctgt tttagtttgc 360
tgtotcaact ctcaagtgtg gaggaataat ataaact

(2) INFORMATION FOR SEQ ID NO:625:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 86 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..86
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567502

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:625:

Lys Asn Ala Thr Lys Asn Lys Met Gly Ser Lys Ser Pro Asn Ile Val
1 5 10 15
Ala Leu Val Leu Pro Leu Leu Leu Ile Leu Tyr Thr Leu Ser Ser Gln
20 25 30
Val Glu Val Val Glu Ser Thr Gly Arg Lys Leu Ser Phe Trp Gly Asn
35 40 45
Pro Ile Val Trp Thr Pro His Ser Asn Ser Cys Gly Gly Ser Pro Ala
50 55 60
Ser Val Phe Ala Ser Ser Lys Trp Thr Thr Gly Arg Pro Cys Arg Arg
65 70 75 80
Ser Arg Xaa Ser Arg Asn
85

(2) INFORMATION FOR SEQ ID NO:626:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 95 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..95
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567503

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:626:

Lys Thr Gln Arg Arg Thr Lys Trp Val Gln Ser His Gln Ile Leu Ser
1 5 10 15
His Leu Cys Tyr Pro Tyr Phe Leu Tyr Phe Thr Leu Phe Pro Leu Lys
20 25 30
Leu Lys Ser Trp Asn Leu Gln Gly Ala Asn Phe Arg Phe Gly Glu Ile
35 40 45
Leu Ser Cys Gly Leu His Thr Gln Ile His Val Glu Val Leu Gln His
50 55 60
Gln Tyr Leu Leu Leu Pro Ser Gly Arg Gln Ala Asp His Ala Asp Val
65 70 75 80
Val Xaa Pro Pro Gly Thr Asn Ile Pro Val Ser Asp Gln Ser Pro
85 90 95

(2) INFORMATION FOR SEQ ID NO:627:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 79 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..79

(D) OTHER INFORMATION: / Ceres Seq. ID 1567504

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:627:

```
Met Gly Ser Lys Ser Pro Asn Ile Val Ala Leu Val Leu Pro Leu Leu
1           5           10          15
Leu Ile Leu Tyr Thr Leu Ser Ser Gln Val Glu Val Val Glu Ser Thr
20          25          30
Gly Arg Lys Leu Ser Phe Trp Gly Asn Pro Ile Val Trp Thr Pro His
35          40          45
Ser Asn Ser Cys Gly Gly Ser Pro Ala Ser Val Phe Ala Ser Ser Lys
50          55          60
Trp Thr Thr Gly Arg Pro Cys Arg Arg Ser Arg Xaa Ser Arg Asn
65          70          75
```

(2) INFORMATION FOR SEQ ID NO:628:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 750 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..750

(D) OTHER INFORMATION: / Ceres Seq. ID 1567513

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:628:

```
taataaaaaa ataaaaagta attagtgaga gaattaaagaa aaacaaagtc tattccatac      60
gaagaagagc ctcagggttaa ttttttataa gatgggttat tggaaagtcga aggtgtgtcc      120
aaggatgaag aaattgttgc agaagagtcg agcaaaaaag gaagttgttg agggaggagaa      180
gccacgagag gtggaagtcg tggaggaggt gtcgtgaaaa ccgaagaacc ggccaaggaa      240
ggagaaacta aaccggagga aataattgca accggcgaga aagagataga aatagttgaa      300
gagaagaaag aagaggctaa accgggtgag gttccggtcc tgcgactgac ggaggagaag      360
aagccagccg tagaagagga gaagaagacg gcgcccgttg aagagaagaa gccagctgtg      420
gaagaggaga agaagcctgc cgtggaagag aagaaacctg tggaggagga gaaaaaagaa      480
gttggttcgc ctgttccggg ggtgaaact ccttcgacta aggcctccga aactccggtg      540
gttgaactc cggcccaagg tccggaaact ccgcgGCGtg cgccacaaa ggcttgaatt      600
ttcttcattg tacatttttc taaaaaaata ttgattgtct ttgtgtgat aatttatttt      660
ctttgtttat ttgtcttatt atccatgtga atttcctcta taaattaatt tgcttgcttg      720
```

(2) INFORMATION FOR SEQ ID NO:629:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 41 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..41

(D) OTHER INFORMATION: / Ceres Seq. ID 1567514

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:629:

```
Met Gly Tyr Trp Lys Ser Lys Val Val Pro Arg Met Lys Lys Leu Phe
1           5           10          15
Glu Lys Ser Pro Ala Lys Lys Glu Val Val Glu Glu Glu Lys Pro Arg
20          25          30
Glu Val Glu Val Val Glu Glu Val Ser
35          40
```

(2) INFORMATION FOR SEQ ID NO:630:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..30
(D) OTHER INFORMATION: / Ceres Seq. ID 1567515
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:630:
Met Lys Lys Leu Phe Glu Lys Ser Pro Ala Lys Lys Glu Val Val Glu
1 5 10 15
Glu Glu Lys Pro Arg Glu Val Glu Val Val Glu Glu Val Ser
20 25 30
(2) INFORMATION FOR SEQ ID NO:631:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 591 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..591
(D) OTHER INFORMATION: / Ceres Seq. ID 1567520
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:631:
actcgggtccc atcatgccaag tagataaaca ctgaatcacc aaatcttggt tgagatttag 60
aaaaaaagga agctccaaga gatggcaaga gttgttaaaa tcgattctgc agagtcatgg 120
gatttctatg tgagccaagc caagaatcag aattgtccca ttgtggctca ttctactgca 180
ttaatggtga ttcttctgtg gtttatgaac tccttcttcg aagagcttgc gtttaactat 240
aaggatgctc tgtttctaat agttgatggt gatgaagtta aggaagtggc aagtcaacta 300
gaggtaaagg cgatgccaac ttcttctgtt ttgaaggatg gtaatgcgat gcacaaactc 360
gtgggcgcaa accctgatga gattaagaaa cgggtcgatg gtttcgttca gtctctacgt 420
gtgtttcata ttgcttaaga gagatttata gatacgagca gaatactaaa taaagtttgt 480
gtgaagtgtg attagtttgt aactttggta tttggtttgt gtgaaAtatc aagtgttaagt 540
gtaaattttt ataaaaagca gtttgttat aaacaagaac tggatttatt c
(2) INFORMATION FOR SEQ ID NO:632:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 118 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..118
(D) OTHER INFORMATION: / Ceres Seq. ID 1567521
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:632:
Met Ala Arg Val Val Lys Ile Asp Ser Ala Glu Ser Trp Asp Phe Tyr
1 5 10 15
Val Ser Gln Ala Lys Asn Gln Asn Cys Pro Ile Val Ala His Phe Thr
20 25 30
Ala Leu Trp Cys Ile Pro Ser Val Phe Met Asn Ser Phe Phe Glu Glu
35 40 45
Leu Ala Phe Asn Tyr Lys Asp Ala Leu Phe Leu Ile Val Asp Val Asp
50 55 60
Glu Val Lys Glu Val Ala Ser Gln Leu Glu Val Lys Ala Met Pro Thr
65 70 75 80
Phe Leu Phe Leu Lys Asp Gly Asn Ala Met Asp Lys Leu Val Gly Ala
85 90 95
Asn Pro Asp Glu Ile Lys Lys Arg Val Asp Gly Phe Val Gln Ser Ser

100 105 110

Arg Val Val His Ile Ala
115

(2) INFORMATION FOR SEQ ID NO:633:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 77 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..77
(D) OTHER INFORMATION: / Ceres Seq. ID 1567522
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:633:

Met	Asn	Ser	Phe	Phe	Glu	Glu	Leu	Ala	Phe	Asn	Tyr	Lys	Asp	Ala	Leu
1				5					10					15	
Phe	Leu	Ile	Val	Asp	Val	Asp	Glu	Val	Lys	Glu	Val	Ala	Ser	Gln	Leu
			20				25					30			
Glu	Val	Lys	Ala	Met	Pro	Thr	Phe	Leu	Phe	Leu	Lys	Asp	Gly	Asn	Ala
	35					40					45				
Met	Asp	Lys	Leu	Val	Gly	Ala	Asn	Pro	Asp	Glu	Ile	Lys	Lys	Arg	Val
	50				55					60					
Asp	Gly	Phe	Val	Gln	Ser	Ser	Arg	Val	Val	His	Ile	Ala			
65				70					75						

(2) INFORMATION FOR SEQ ID NO:634:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1352 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..1352
(D) OTHER INFORMATION: / Ceres Seq. ID 1567526
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:634:

aatcagtaaaa	acgaaaaagct	aatccaaaac	tctttaatta	ttgttaacaa	ctgatcaatg	60
gctgttaacaa	gctcttcttc	tacttgtgat	ggttttcttc	tcatcagcct	tattgttgct	120
gttttctcat	tggttggggc	atcatctgct	cagttaaacg	caacgtttta	ctcagggaacg	180
tgccctaacg	catctgccat	cgttcgcagc	actattcagc	aaagctcttca	atccgatgca	240
agaatcggag	gcagcctaata	cgccttccat	tttcacgact	gttttgttaa	tggttgcgat	300
gggtgcgtct	tgcttgacga	cacttcaaac	atccagagcg	agaagaacgc	tcctgccaat	360
gcaaaactcaa	ctagaggatt	caatgttgct	gatagtatca	agacagccct	cgagaatgct	420
tgctccggca	tgctttcttg	ctctgacatt	ttagctcttg	cttcagagcg	ctctgtgctt	480
ttggcaggag	gactctcatg	gactgtgtta	ttaggaaaga	gagatgggtc	caccgcaaac	540
ttgtctggag	ccaattcgct	tcttccctct	cccttcgaag	gccttaacaa	catcacatca	600
aaatttttag	ctgtcgggct	aaatacaacc	gatgtagtat	cttgtctcgg	agcgatcaag	660
tttggcgtcg	gtcaatgcgt	aacCgttcaa	caatagaacta	ttcaacttca	acgggacagg	720
aaaccgccac	ccgactctga	actcaaacct	tctcagcagt	cttcaaacgc	tatgtctcca	780
aaacggcagc	aatacaggga	tcaccaatct	cgatctgagc	acacctgatg	cgttcgataa	840
caattactac	acgaaacctc	agagtaacaa	tggtcttctc	cagtcagacc	aggaactgtt	900
ctcaaacacc	ggttcagcca	cgtcccgat	tggttaattcc	tttgcaagta	accagacctt	960
gttttttgag	gcgtttgttc	agctctatg	caagatgggg	aacattagtc	ccttgactgg	1020
gagtagtgga	gagattagac	aagactgtaa	ggtggttaat	ggacagtcac	cagccaactga	1080
agcaggggac	attcagttac	aatctgaagg	accagtgagt	gtagcagata	tgtgaacaa	1140
gagtagatca	gtttccacgt	ttgtttatca	tataatgaat	ataactccta	ggccgaatca	1200
tttttgtaga	aaaaataagt	ttggttgagg	agaaaaatag	tgagtgtagt	ggttgtggtt	1260
tacacttttg	aaaattttta	tattctaaaa	cattattatg	cctaaatata	tgcatgcatg	1320
tataacgtct	atcgttttga	tacattttgt	gg			

(2) INFORMATION FOR SEQ ID NO:635:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 212 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..212
(D) OTHER INFORMATION: / Ceres Seq. ID 1567527
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:635:

Met	Ala	Val	Thr	Ser	Ser	Ser	Ser	Thr	Cys	Asp	Gly	Phe	Phe	Ile	Ile
1				5				10					15		
Ser	Leu	Ile	Val	Val	Ser	Ser	Leu	Phe	Gly	Ala	Ser	Ser	Ala	Gln	
		20					25					30			
Leu	Asn	Ala	Thr	Phe	Tyr	Ser	Gly	Thr	Cys	Pro	Asn	Ala	Ser	Ala	Ile
		35					40				45				
Val	Arg	Ser	Thr	Ile	Gln	Gln	Ala	Leu	Gln	Ser	Asp	Ala	Arg	Ile	Gly
	50				55				60						
Gly	Ser	Leu	Ile	Arg	Leu	His	Phe	His	Asp	Cys	Phe	Val	Asn	Gly	Cys
65				70					75					80	
Asp	Gly	Ser	Leu	Leu	Asp	Asp	Thr	Ser	Ser	Ile	Gln	Ser	Glu	Lys	
			85				90						95		
Asn	Ala	Pro	Ala	Asn	Ala	Asn	Ser	Thr	Arg	Gly	Phe	Asn	Val	Val	Asp
		100					105					110			
Ser	Ile	Lys	Thr	Ala	Leu	Glu	Asn	Ala	Cys	Pro	Gly	Ile	Val	Ser	Cys
		115					120					125			
Ser	Asp	Ile	Leu	Ala	Leu	Ala	Ser	Glu	Ala	Ser	Val	Ser	Leu	Ala	Gly
	130					135					140				
Gly	Pro	Ser	Trp	Thr	Val	Leu	Leu	Gly	Arg	Arg	Asp	Gly	Leu	Thr	Ala
145				150					155					160	
Asn	Leu	Ser	Gly	Ala	Asn	Ser	Ser	Leu	Pro	Pro	Phe	Glu	Gly	Leu	
			165				170						175		
Asn	Asn	Ile	Thr	Ser	Lys	Phe	Val	Ala	Val	Gly	Leu	Asn	Thr	Thr	Asp
		180					185						190		
Val	Val	Ser	Leu	Ser	Gly	Ala	His	Thr	Phe	Gly	Arg	Gly	Gln	Cys	Val
	195						200						205		
Thr	Val	Gln	Gln												
	210														

(2) INFORMATION FOR SEQ ID NO:636:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 716 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..716

(D) OTHER INFORMATION: / Ceres Seq. ID 1567532

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:636:

aagaattagg	gtttctcttt	gtcttcagca	gtcagtgccg	atccgtagGa	gaaaagtgtg	60
agaatctgcc	acocatgggtc	gtatgcacag	tgcaggaaag	ggatatttcag	ccctctgogtt	120
gccttacaag	agatcgtctc	caagctggct	caagaccacc	tctcaggatg	ttgatgaatc	180
aattctgaaa	tttgccaaaa	agggtattgac	cccttccacg	attgggtgtga	ttctccgtga	240
ctctcacggt	atccctcagg	tcaagagtgt	tactggaagc	aagatcttga	ggatactcaa	300
agctcatggc	cttgctcctg	agatccctga	ggatctgtac	cattctaata	agaaggctgt	360
tgccatccgt	aaacatctcg	agagggaacg	gaaggacaag	gattccaagt	tcaggctcat	420
cttggtttag	agcaggattc	accgcctcgc	tgcgtattac	aagaagacca	agaagctccc	480
tcccgtctgg	aagtacgaat	ccactaccgc	gagcaccctt	gtgggttaag	ctggagctct	540
gaggaggatt	ctactagtct	gttgctctcc	tttggtttga	tgaattctca	actttagtct	600

taatgtttca gcaggatttt tgtgtttgcc tctcttcttt ttcggaatc ttatgctccc 660
ttgtttaaga gaatcgtatg atcttgaatt tactattgaa tatgcttttg catccc

(2) INFORMATION FOR SEQ ID NO:637:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 151 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..151
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567533

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:637:

Met	Gly	Arg	Met	His	Ser	Arg	Gly	Lys	Gly	Ile	Ser	Ala	Ser	Ala	Leu
1			5				10					15			
Pro	Tyr	Lys	Arg	Ser	Ser	Pro	Ser	Trp	Leu	Lys	Thr	Thr	Ser	Gln	Asp
		20					25					30			
Val	Asp	Glu	Ser	Ile	Cys	Lys	Phe	Ala	Lys	Lys	Gly	Leu	Thr	Pro	Ser
	35					40					45				
Gln	Ile	Gly	Val	Ile	Leu	Arg	Asp	Ser	His	Gly	Ile	Pro	Gln	Val	Lys
	50				55					60					
Ser	Val	Thr	Gly	Ser	Lys	Ile	Leu	Arg	Ile	Leu	Lys	Ala	His	Gly	Leu
65				70					75				80		
Ala	Pro	Glu	Ile	Pro	Glu	Asp	Leu	Tyr	His	Leu	Ile	Lys	Lys	Ala	Val
		85					90						95		
Ala	Ile	Arg	Lys	His	Leu	Glu	Arg	Asn	Arg	Lys	Asp	Lys	Asp	Ser	Lys
		100					105						110		
Phe	Arg	Leu	Ile	Leu	Val	Glu	Ser	Arg	Ile	His	Arg	Leu	Ala	Arg	Tyr
		115					120					125			
Tyr	Lys	Lys	Thr	Lys	Lys	Leu	Pro	Pro	Val	Trp	Lys	Tyr	Glu	Ser	Thr
	130					135						140			
Thr	Ala	Ser	Thr	Leu	Val	Ala									
145						150									

(2) INFORMATION FOR SEQ ID NO:638:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 148 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..148
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567534

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:638:

Met	His	Ser	Arg	Gly	Lys	Gly	Ile	Ser	Ala	Ser	Ala	Leu	Pro	Tyr	Lys
1				5			10					15			
Arg	Ser	Ser	Pro	Ser	Trp	Leu	Lys	Thr	Thr	Ser	Gln	Asp	Val	Asp	Glu
			20				25					30			
Ser	Ile	Cys	Lys	Phe	Ala	Lys	Lys	Gly	Leu	Thr	Pro	Ser	Gln	Ile	Gly
		35					40					45			
Val	Ile	Leu	Arg	Asp	Ser	His	Gly	Ile	Pro	Gln	Val	Lys	Ser	Val	Thr
	50					55					60				
Gly	Ser	Lys	Ile	Leu	Arg	Ile	Leu	Lys	Ala	His	Gly	Leu	Ala	Pro	Glu
65					70					75				80	
Ile	Pro	Glu	Asp	Leu	Tyr	His	Leu	Ile	Lys	Lys	Ala	Val	Ala	Ile	Arg
			85						90				95		
Lys	His	Leu	Glu	Arg	Asn	Arg	Lys	Asp	Lys	Asp	Ser	Lys	Phe	Arg	Leu
			100				105						110		
Ile	Leu	Val	Glu	Ser	Arg	Ile	His	Arg	Leu	Ala	Arg	Tyr	Tyr	Lys	Lys

115 120 125
Thr Lys Lys Leu Pro Pro Val Trp Lys Tyr Glu Ser Thr Thr Ala Ser
130 135 140
Thr Leu Val Ala
145

(2) INFORMATION FOR SEQ ID NO:639:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 675 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..675
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567544

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:639:

aattcgacgt	ctctcttttcg	tctctgtatc	gatttttttcg	ccgcgaattt	cgaataggtt	60
cttcaccata	agcttgagat	cttatttctc	tactgtttct	tgcttcttct	ctatcgatat	120
ggctggtaaa	gggtgggaaag	ggcttctagc	tgcggaagacg	acggcagcag	ctgcaaaacaa	180
agacagtgtt	aagaagaaat	ccatctctcg	ctcttctcgt	gctgggtatc	agtttccagt	240
gggtcgtatt	catcgctcaac	tcaagcaaag	agtttcagca	catggaagag	ttggtgccac	300
tgctcgtgtt	tacactcgat	caattctaga	atacttgact	gctgaagtac	tcgagttagc	360
tggaatgcg	agcaaggatc	tcaaagttaa	gagaattaca	ccaagacatt	tcgacgttgc	420
aatcagagga	gatgaggaac	ttgacactct	catcaaaagg	accattgcag	gaggaggtgt	480
gatccctcac	atccacaagt	cccttgtcaa	caaagtcaac	aaggattgag	tttcgtcttc	540
tgagtcctaa	gtctctatta	tactatgtgc	ctcttttcta	gacgcctcta	tggtatatag	600
ggttcaattg	atctcttagg	tctctcgttt	tagactcata	ctcttgttat	tttgctaatt	660
cttaccatgat	tgagg					

(2) INFORMATION FOR SEQ ID NO:640:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 175 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..175
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567545

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:640:

Ile	Arg	Arg	Leu	Ser	Phe	Val	Ser	Val	Ser	Ile	Phe	Ser	Pro	Arg	Ile
1			5						10				15		
Ser	Asn	Arg	Phe	Phe	Thr	Ile	Ser	Leu	Arg	Ser	Tyr	Phe	Ser	Thr	Val
			20					25					30		
Leu	Cys	Phe	Phe	Ser	Ile	Asp	Met	Ala	Gly	Lys	Gly	Gly	Lys	Gly	Leu
			35				40						45		
Leu	Ala	Ala	Lys	Thr	Thr	Ala	Ala	Ala	Asn	Lys	Asp	Ser	Val	Lys	
			50			55				60					
Lys	Lys	Ser	Ile	Ser	Arg	Ser	Ser	Arg	Ala	Gly	Ile	Gln	Phe	Pro	Val
			65			70			75					80	
Gly	Arg	Ile	His	Arg	Gln	Leu	Lys	Gln	Arg	Val	Ser	Ala	His	Gly	Arg
			85					90					95		
Val	Gly	Ala	Thr	Ala	Ala	Val	Tyr	Thr	Ala	Ser	Ile	Leu	Glu	Tyr	Leu
			100				105					110			
Thr	Ala	Glu	Val	Leu	Glu	Leu	Ala	Gly	Asn	Ala	Ser	Lys	Asp	Leu	Lys
			115			120						125			
Val	Lys	Arg	Ile	Thr	Pro	Arg	His	Leu	Gln	Leu	Ala	Ile	Arg	Gly	Asp
			130			135					140				
Glu	Glu	Leu	Asp	Thr	Leu	Ile	Lys	Gly	Thr	Ile	Ala	Gly	Gly	Gly	Val
			145			150				155					160

Ile Pro His Ile His Lys Ser Leu Val Asn Lys Val Thr Lys Asp
165 170 175

(2) INFORMATION FOR SEQ ID NO:641:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 136 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..136
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567546

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:641:

```
Met Ala Gly Lys Gly Gly Lys Gly Leu Leu Ala Ala Lys Thr Thr Ala
1      5      10
Ala Ala Ala Asn Lys Asp Ser Val Lys Lys Lys Ser Ile Ser Arg Ser
20     25     30
Ser Arg Ala Gly Ile Gln Phe Pro Val Gly Arg Ile His Arg Gln Leu
35     40     45
Lys Gln Arg Val Ser Ala His Gly Arg Val Gly Ala Thr Ala Ala Val
50     55     60
Tyr Thr Ala Ser Ile Leu Glu Tyr Leu Thr Ala Glu Val Leu Glu Leu
65     70     75     80
Ala Gly Asn Ala Ser Lys Asp Leu Lys Val Lys Arg Ile Thr Pro Arg
85     90     95
His Leu Gln Leu Ala Ile Arg Gly Asp Glu Glu Leu Asp Thr Leu Ile
100    105    110
Lys Gly Thr Ile Ala Gly Gly Gly Val Ile Pro His Ile His Lys Ser
115    120    125
Leu Val Asn Lys Val Thr Lys Asp
130    135
```

(2) INFORMATION FOR SEQ ID NO:642:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 566 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..566
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567547

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:642:

```
tcaagccgtc aacaatgtcg aagcgaggcg gtggaggtac ctctggtaac aaattcagga      60
tgtcactggg tcttccgggt gcggcgacgg tgaactgtgc cgataacacc ggtgctaaga      120
atctctacat catttccgtg aaaggatcac aaggctgtct taatcgatta cctcttgcgtt      180
gcgtcgagga catggtgatg gccaccgtca aaaagggtaa gcctgatctc agggaaaaagg      240
ttcttctctc cgtcatcggt aggcacgcga aaccatggcg ccgaaaggat ggtgtttctg      300
tgtacttcga agataatgct ggagtcattg tcaaccoccaa gggagaaatg aaaggttctg      360
caattactgg tcttattggg aaagagtggt ctgatctttg gccaaaggatt gctagtgtcg      420
ccaatgccat tgtctaatga tcagatcaat caattgcttg tatttgatgg atatgtctag      480
atacaaatgt gagaattttg gtacgaagat atttttttt tctgacaata tgtatctgac      540
attcaaatga ttggctatt ttTgac
```

(2) INFORMATION FOR SEQ ID NO:643:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 144 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..144

(D) OTHER INFORMATION: / Ceres Seq. ID 1567548

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:643:

Lys	Pro	Ser	Thr	Met	Ser	Lys	Arg	Gly	Arg	Gly	Gly	Thr	Ser	Gly	Asn	
1				5					10					15		
Lys	Phe	Arg	Met	Ser	Leu	Gly	Leu	Pro	Val	Ala	Ala	Thr	Val	Asn	Cys	
			20					25					30			
Ala	Asp	Asn	Thr	Gly	Ala	Lys	Asn	Leu	Tyr	Ile	Ile	Ser	Val	Lys	Gly	
		35					40					45				
Ile	Lys	Gly	Arg	Leu	Asn	Arg	Leu	Pro	Ser	Ala	Cys	Val	Gly	Asp	Met	
	50				55						60					
Val	Met	Ala	Thr	Val	Lys	Gly	Lys	Pro	Asp	Leu	Arg	Lys	Lys	Val		
65				70					75					80		
Leu	Pro	Ala	Val	Ile	Val	Arg	Gln	Arg	Lys	Pro	Trp	Arg	Arg	Lys	Asp	
			85					90						95		
Gly	Val	Phe	Met	Tyr	Phe	Glu	Asp	Asn	Ala	Gly	Val	Ile	Val	Asn	Pro	
			100					105					110			
Lys	Gly	Glu	Met	Lys	Gly	Ser	Ala	Ile	Thr	Gly	Pro	Ile	Gly	Lys	Glu	
		115					120					125				
Cys	Ala	Asp	Leu	Trp	Pro	Arg	Ile	Ala	Ser	Ala	Ala	Asn	Ala	Ile	Val	
130						135						140				

(2) INFORMATION FOR SEQ ID NO:644:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 140 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..140

(D) OTHER INFORMATION: / Ceres Seq. ID 1567549

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:644:

Met	Ser	Lys	Arg	Gly	Arg	Gly	Gly	Thr	Ser	Gly	Asn	Lys	Phe	Arg	Met	
1				5				10					15			
Ser	Leu	Gly	Leu	Pro	Val	Ala	Ala	Thr	Val	Asn	Cys	Ala	Asp	Asn	Thr	
			20					25					30			
Gly	Ala	Lys	Asn	Leu	Tyr	Ile	Ile	Ser	Val	Lys	Gly	Ile	Lys	Gly	Arg	
		35					40					45				
Leu	Asn	Arg	Leu	Pro	Ser	Ala	Cys	Val	Gly	Asp	Met	Val	Met	Ala	Thr	
	50				55						60					
Val	Lys	Lys	Gly	Lys	Pro	Asp	Leu	Arg	Lys	Lys	Val	Leu	Pro	Ala	Val	
65				70					75					80		
Ile	Val	Arg	Gln	Arg	Lys	Pro	Trp	Arg	Arg	Lys	Asp	Gly	Val	Phe	Met	
			85					90						95		
Tyr	Phe	Glu	Asp	Asn	Ala	Gly	Val	Ile	Val	Asn	Pro	Lys	Gly	Glu	Met	
			100					105					110			
Lys	Gly	Ser	Ala	Ile	Thr	Gly	Pro	Ile	Gly	Lys	Glu	Cys	Ala	Asp	Leu	
		115					120					125				
Trp	Pro	Arg	Ile	Ala	Ser	Ala	Ala	Asn	Ala	Ile	Val					
130						135					140					

(2) INFORMATION FOR SEQ ID NO:645:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 125 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..125
 (D) OTHER INFORMATION: / Ceres Seq. ID 1567550
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:645:
Met Ser Leu Gly Leu Pro Val Ala Ala Thr Val Asn Cys Ala Asp Asn
1 5 10 15
Thr Gly Ala Lys Asn Leu Tyr Ile Ile Ser Val Lys Gly Ile Lys Gly
 20 25 30
Arg Leu Asn Arg Leu Pro Ser Ala Cys Val Gly Asp Met Val Met Ala
 35 40 45
Thr Val Lys Lys Gly Lys Pro Asp Leu Arg Lys Lys Val Leu Pro Ala
 50 55 60
Val Ile Val Arg Gln Arg Lys Pro Trp Arg Arg Lys Asp Gly Val Phe
65 70 75 80
Met Tyr Phe Glu Asp Asn Ala Gly Val Ile Val Asn Pro Lys Gly Glu
 85 90 95
Met Lys Gly Ser Ala Ile Thr Gly Pro Ile Gly Lys Glu Cys Ala Asp
 100 105 110
Leu Trp Pro Arg Ile Ala Ser Ala Ala Asn Ala Ile Val
 115 120 125
(2) INFORMATION FOR SEQ ID NO:646:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 352 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: DNA (genomic)
 (ix) FEATURE:
 (A) NAME/KEY: -
 (B) LOCATION: 1..352
 (D) OTHER INFORMATION: / Ceres Seq. ID 1567555
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:646:
cctagaaatt ttgtctctct cgccgccttg cgaaaagcat ttctgatctt actcttagga 60
taaaaaaatg tcgacagttg gagagcttgc ttgcagctac gctgttatga tctctgagga 120
cgagggtatc gctatcacgg ctgacaaaat cgcgaccttg gtgaaagctg ctggtgttag 180
tattgagtca tactggccaa tgctattcgc caagatggct gagaaaacgta acgtgactga 240
tctcatcatg aacgttggtg ctggtgtgtg aggtgtgtgc ccggttgacg ctgtgtctcc 300
agctgctggc ggtgtgtcgg caSctgcaac cggagcacca ctctccacca cc
(2) INFORMATION FOR SEQ ID NO:647:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 95 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..95
 (D) OTHER INFORMATION: / Ceres Seq. ID 1567556
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:647:
Met Ser Thr Val Gly Glu Leu Ala Cys Ser Tyr Ala Val Met Ile Leu
1 5 10 15
Glu Asp Glu Gly Ile Ala Ile Thr Ala Asp Lys Ile Ala Thr Leu Val
 20 25 30
Lys Ala Ala Gly Val Ser Ile Glu Ser Tyr Trp Pro Met Leu Phe Ala
 35 40 45
Lys Met Ala Glu Lys Arg Asn Val Thr Asp Leu Ile Met Asn Val Gly
 50 55 60
Ala Gly Gly Gly Gly Gly Ala Pro Val Ala Ala Ala Pro Ala Ala

(2) INFORMATION FOR SEQ ID NO:648:

(ii) MOLECULE TYPE: peptide

(A) NAME/KEY: peptide

(B) LOCATION: 1..82

(D) OTHER INFORMATION: / Ceres Seq. ID 1567557

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:648:

(2) INFORMATION FOR SEQ ID NO:649:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..51

(D) OTHER INFORMATION: / Ceres Seq. ID 1567558

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:649:

(2) INFORMATION FOR SEQ ID NO:650:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1465 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1465

(D) OTHER INFORMATION: / Ceres Seq. ID 1567563

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:650:

agattaaaaa ctctttaaaa actttttgtc ataaatcagg caaagaagta aaagaggctt 60
aaaactctct ctctctcttg gtcttctctc ctcttaacga aaatggactc tctaactctc 120

ttcttcacgcg	gcgcactcgt	cgccgtcggt	atctactggt	tcctctcggt	tcctcggtcca	180
gcagagcgta	aaggcaaacg	agccgtagat	ctctctggcg	gctcaatctc	gcgcgagaaa	240
gtccaaagaca	actacaaaac	gtactggctc	ttcttcgcgc	gtccaaaaga	aatcgaaacc	300
gcgcgagaaag	ttccagactt	cgtcgacaca	ttctacaatt	tcgtccaccga	catatcacgag	360
tggggatggg	gacaatccct	ccactttctca	ccatcaatcc	ccggaaaatc	tcacaaaagac	420
gcacgcgcgc	tcacgaaga	gatggccgta	gatctgatcc	aagtcaaac	tggtcaaaag	480
atcttagacg	tcggatdcgg	cgtcgccggt	bcgatgcgag	cgattgcac	tcactcgaga	540
gtcaacgtag	tcgggattac	gataaacgag	tatcagggtg	acagagctcg	ttccacaaat	600
aagaaagctg	gtctcgacgc	gcctttgcgag	gtcgtctgtg	gtaacttcct	ccagatgcgc	660
ttcgatgaca	acagtttcga	cggtgcttat	tcacatcgaag	ccacgtgtca	gcgcgcgaag	720
ctggaggaag	tgtagcgaga	gatctacagg	gtgtgaaac	ccggatctat	gtatgtgtcg	780
tacgagtggtg	ttacgacgga	gaaattttaag	gcggaggatg	acgaaAcacg	tgagggtaat	840
ccaaggtGatt	gagagaggtg	atgcgttacc	tgggcttagg	cttacgtgga	tattgctgag	900
acggctaaaa	gggttgggtt	tgagatagt	aaggagaagg	atctggcgag	tcaccgcgct	960
gagccgtggt	ggctagggt	taagatgggt	agggttgctt	attggaggaa	tcacattgtg	1020
gttcagattt	tgtagcggt	tggaattgct	cctaaaggaa	ctgttgatgt	tcattgagatg	1080
ttgtttaaga	ctgctgatta	tttgaccaga	ggaggtgaaa	ccggaataatt	ctctccgatg	1140
catatgattc	tcgtcagaaa	accggagtca	ccggaggaga	gttcttgaga	aaggtagaaa	1200
ggaacacatca	ccggaaaaaag	tatggagaat	tttctcaatt	tggttttatt	tttaagttaa	1260
atcaacttgg	ttattgtact	atttttgtgt	tttaatttgg	ttgtgttttc	aagaattatt	1320
agtttttttt	tggttttttg	catatgagaa	tcttactctt	gatttctccg	ccgtagtgcc	1380
gcgcgagcat	agggattatt	tagtattttt	aagtgtgttt	aagattgatt	aacaagttag	1440
tgaataaaaa	tgtagttagg	tgctgc				

(2) INFORMATION FOR SEQ ID NO:651:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 249 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..249

(D) OTHER INFORMATION: / Ceres Seq. ID 1567564

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:651:

Met	Asp	Ser	Leu	Thr	Leu	Phe	Phe	Thr	Gly	Ala	Leu	Val	Ala	Val	Gly
1				5					10					15	
Ile	Tyr	Trp	Phe	Leu	Cys	Val	Leu	Gly	Pro	Ala	Glu	Arg	Lys	Gly	Lys
				20				25					30		
Arg	Ala	Val	Asp	Leu	Ser	Gly	Gly	Ser	Ile	Ser	Ala	Glu	Lys	Val	Gln
				35				40					45		
Asp	Asn	Tyr	Lys	Gln	Tyr	Trp	Ser	Phe	Phe	Arg	Arg	Pro	Lys	Glu	Ile
				50				55				60			
Glu	Thr	Ala	Glu	Lys	Val	Pro	Asp	Phe	Val	Asp	Thr	Phe	Tyr	Asn	Leu
				65				70				75		80	
Val	Thr	Asp	Ile	Tyr	Glu	Trp	Gly	Trp	Gly	Gln	Ser	Phe	His	Phe	Ser
				85				90					95		
Pro	Ser	Ile	Pro	Gly	Lys	Ser	His	Lys	Asp	Ala	Thr	Arg	Leu	His	Glu
				100				105					110		
Glu	Met	Ala	Val	Asp	Leu	Ile	Gln	Val	Lys	Pro	Gly	Gln	Lys	Ile	Leu
				115				120				125			
Asp	Val	Gly	Xaa	Gly	Val	Gly	Gly	Xaa	Met	Arg	Ala	Ile	Ala	Ser	His
				130				135				140			
Ser	Arg	Ala	Asn	Val	Val	Gly	Ile	Thr	Ile	Asn	Glu	Tyr	Gln	Val	Asn
				145				150				155		160	
Arg	Ala	Arg	Leu	His	Asn	Lys	Lys	Ala	Gly	Leu	Asp	Ala	Leu	Cys	Glu
				165				170					175		
Val	Val	Cys	Gly	Asn	Phe	Leu	Gln	Met	Pro	Phe	Asp	Asp	Asn	Ser	Phe
				180				185					190		
Asp	Gly	Ala	Tyr	Ser	Ile	Glu	Ala	Thr	Cys	His	Ala	Pro	Lys	Leu	Glu
				195				200					205		

Glu Val Tyr Ala Glu Ile Tyr Arg Val Leu Lys Pro Gly Ser Met Tyr
210 215 220
Val Ser Tyr Glu Trp Val Thr Thr Glu Lys Phe Lys Ala Glu Asp Asp
225 230 235 240
Glu Thr Arg Gly Gly Asn Pro Arg Asp
245

(2) INFORMATION FOR SEQ ID NO:652:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 136 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..136

(D) OTHER INFORMATION: / Ceres Seq. ID 1567565

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:652:

Met Ala Val Asp Leu Ile Gln Val Lys Pro Gly Gln Lys Ile Leu Asp
1 5 10 15
Val Gly Xaa Gly Val Gly Gly Xaa Met Arg Ala Ile Ala Ser His Ser
20 25 30
Arg Ala Asn Val Val Gly Ile Thr Ile Asn Glu Tyr Gln Val Asn Arg
35 40 45
Ala Arg Leu His Asn Lys Lys Ala Gly Leu Asp Ala Leu Cys Glu Val
50 55 60
Val Cys Gly Asn Phe Leu Gln Met Pro Phe Asp Asn Ser Phe Asp
65 70 75 80
Gly Ala Tyr Ser Ile Glu Ala Thr Cys His Ala Pro Lys Leu Glu Glu
85 90 95
Val Tyr Ala Glu Ile Tyr Arg Val Leu Lys Pro Gly Ser Met Tyr Val
100 105 110
Ser Tyr Glu Trp Val Thr Thr Glu Lys Phe Lys Ala Glu Asp Asp Glu
115 120 125
Thr Arg Gly Gly Asn Pro Arg Asp
130 135

(2) INFORMATION FOR SEQ ID NO:653:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1629 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1629

(D) OTHER INFORMATION: / Ceres Seq. ID 1567581

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:653:

aatttthtTC gaacaccgaa aacactttcg aacctataaa gacagaacac tgtgtcaatt 60
ttcattacct ggggaacaaaa cgcaaaatca aagacaataa tttttccccc gagagagaaa 120
atgcagaggt tgaagcagca gcagcagcag caacaagtta tgatgcagca agctcttatg 180
cagcaacagt ctctctacca tcttggtctc cttgccccgc cacagataga accaatccca 240
agtggaaatc tccccctcg ttttgatcca agtacttgcc gcagtgtgta cgttggaaac 300
atccatattc aggtgacgga acctctgctt caagagggtt ttgctggcac tggctcctgta 360
gaaagctgta aactaatatg gaaagaaaag tcttcttatg ggtttgtgca ctactttgat 420
cgaagatctg ctggtcttgc aatcctttct ctcaatggaa ggcatattgt ttggcaacct 480
atcaagggtta actgggctta tgcgagtgcc cagagggagg atacatcaag tcaactcaat 540
ataatttgta gggattttag tccggagggtt actgatgcaa tgcgtgttac ttgcttctct 600
gtctaccgga cttgctcgga tgcaagagtt atgtgggagc agaaaaactgg gcgttcaaga 660
ggatttggat ttgtttccct cgttaaccaa caggatgcc agactgcaat agatgagata 720
actgggaaat ggcttgggtc caggcagata cgttgcaact gggcgacaaa gggagccact 780

tcctgtgtgagg	acaaacagag	ctctgattcc	aaaagcgtcg	tggaacttac	cagtggtgtgc	840
tcgggaggatg	gtaaaagatac	tactaatggt	gaagctcctg	agaacaatgc	tcagtacaca	900
actgttttacg	tcggttaactc	tgctccacag	gtgtccacag	ttgatcttca	ccgccacttc	960
cattccctctg	gtcgtgggggt	catagaggaa	gtccgtgttc	aaagagacaa	aggtttcgga	1020
tttgtgagat	actctactca	tgtagaggca	gccctcgcta	ttcagatggg	aaacacacat	1080
tcctacctta	gtggcaggca	aatgaagtgt	tcttggggaa	gcaagccaac	tccagcagga	1140
acagettcaa	acccgcttcc	tcaccagct	cctgcaccaa	tcccgggatt	ctcagccagat	1200
gatctcttgg	cttacgagag	gcaactagcg	atgagcaaga	ttgcagggaat	gaatccgatg	1260
atgcatcacc	cgcagggaca	acatgtcttt	aaacaagctg	caatggggagc	cactgtgttca	1320
aaccaggcaa	tatatgacgg	tggttaccag	aacgcgcagc	agctcatgta	ctaccagtaa	1380
gatctctctc	ggagccgtta	cttgagcgaa	gagttcttct	ttttctctct	ttttgttatg	1440
taacgtctctt	attgtatctt	tttctttctt	tctaacttat	gttctgttta	taatgttatc	1500
atgtagctgt	gggtttgtgg	tttgtgttcc	acgttttttc	ttttgttaac	tactacgggt	1560
tacgtttttg	cacatcttca	actctttctt	ctttctcttt	ctctaactta	atcttatatta	1620
ttgggtcgc						

(2) INFORMATION FOR SEQ ID NO:654:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 459 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..459

(D) OTHER INFORMATION: / Ceres Seq. ID 1567582

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:654:

Asn	Xaa	Ser	Arg	Thr	Pro	Lys	Thr	Leu	Ser	Asn	Pro	Lys	Arg	Gln	Asn
1						5					10			15	
Thr	Val	Ser	Ile	Phe	Ile	Thr	Trp	Glu	Gln	Asn	Ala	Lys	Ser	Lys	Thr
						20				25			30		
Ile	Ile	Phe	Ser	Pro	Arg	Glu	Lys	Met	Gln	Arg	Leu	Lys	Gln	Gln	Gln
						35				40			45		
Gln	Gln	Gln	Gln	Val	Met	Met	Gln	Gln	Ala	Leu	Met	Gln	Gln	Gln	Ser
						50				55			60		
Leu	Tyr	His	Pro	Gly	Leu	Leu	Ala	Pro	Pro	Gln	Ile	Glu	Pro	Ile	Pro
						65				70			75		80
Ser	Gly	Asn	Leu	Pro	Pro	Gly	Phe	Asp	Pro	Ser	Thr	Cys	Arg	Ser	Val
						85				90			95		
Tyr	Val	Gly	Asn	Ile	His	Ile	Gln	Val	Thr	Glu	Pro	Leu	Leu	Gln	Glu
						100				105			110		
Val	Phe	Ala	Gly	Thr	Gly	Pro	Val	Glu	Ser	Cys	Lys	Leu	Ile	Arg	Lys
						115				120			125		
Glu	Lys	Ser	Ser	Tyr	Gly	Phe	Val	His	Tyr	Phe	Asp	Arg	Arg	Ser	Ala
						130				135			140		
Gly	Leu	Ala	Ile	Leu	Ser	Leu	Asn	Gly	Arg	His	Leu	Phe	Gly	Gln	Pro
						145				150			155		160
Ile	Lys	Val	Asn	Trp	Ala	Tyr	Ala	Ser	Gly	Gln	Arg	Glu	Asp	Thr	Ser
						165				170			175		
Ser	His	Phe	Asn	Ile	Phe	Val	Gly	Asp	Leu	Ser	Pro	Glu	Val	Thr	Asp
						180				185			190		
Ala	Met	Leu	Phe	Thr	Cys	Phe	Ser	Val	Tyr	Pro	Thr	Cys	Ser	Asp	Ala
						195				200			205		
Arg	Val	Met	Trp	Asp	Gln	Lys	Thr	Gly	Arg	Ser	Arg	Gly	Phe	Gly	Phe
						210				215			220		
Val	Ser	Phe	Arg	Asn	Gln	Gln	Asp	Ala	Gln	Thr	Ala	Ile	Asp	Glu	Ile
						225				230			235		240
Thr	Gly	Lys	Trp	Leu	Gly	Ser	Arg	Gln	Ile	Arg	Cys	Asn	Trp	Ala	Thr
						245				250			255		
Lys	Gly	Ala	Thr	Ser	Gly	Glu	Asp	Lys	Gln	Ser	Ser	Asp	Ser	Lys	Ser
						260				265			270		

(2) INFORMATION FOR SEO ID NO:655:

{A} LENGTH: 419 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..419

(D) OTHER INFORMATION: / Ceres Seq. ID 1567583

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:655:

1	Gln	Arg	Leu	5	Gln	Gln	Gln	Gln	10	Gln	Gln	Val	Met	15	Gln					
1	Gln	Ala	Leu	20	Gln	Gln	Gln	Leu	25	Tyr	His	Pro	Gly	Leu	30	Ala				
Pro	Pro	Gln	Ile	35	Glu	Pro	Ile	Pro	40	Ser	Gly	Asn	Leu	45	Pro	Gly	Phe			
Asp	Pro	Ser	Thr	50	Cys	Arg	Ser	Val	55	Tyr	Val	Gly	Asn	60	Ile	His	Ile	Gln		
Val	Thr	Glu	Pro	65	Leu	Leu	Gln	Glu	70	Val	Phe	Ala	Gly	75	Thr	Gly	Pro	80	Val	
Glu	Ser	Cys	Lys	85	Leu	Ile	Arg	Lys	90	Glu	Lys	Ser	Ser	95	Tyr	Gly	Phe	95	Val	
His	Tyr	Phe	Asp	100	Arg	Arg	Ser	Ala	105	Gly	Leu	Ala	Ile	110	Leu	Ser	Leu	110	Asn	
Gly	Arg	His	Leu	115	Phe	Gly	Gln	Pro	120	Ile	Lys	Val	Asn	125	Trp	Ala	Tyr	125	Ala	
Ser	Gly	Gln	Arg	130	Glu	Asp	Thr	Ser	135	Ser	Ser	His	Phe	140	Asn	Ile	Phe	140	Val	Gly
Asp	Leu	Ser	Pro	145	Glu	Val	Thr	Asp	150	Ala	Met	Leu	Phe	155	Thr	Cys	Phe	155	Ser	160
Val	Tyr	Pro	Thr	165	Cys	Ser	Asp	Ala	170	Arg	Val	Met	Trp	175	Asp	Gln	Lys	175	Thr	180
Gly	Arg	Ser	Arg	180	Gly	Phe	Gly	Phe	185	Val	Ser	Phe	Arg	190	Asn	Gln	Gln	190	Asp	195
Ala	Gln	Thr	Ala	200	Ile	Asp	Glu	Ile	205	Thr	Gly	Lys	Trp	210	Leu	Gly	Ser	210	Arg	215

Met	Met	Gln	Gln	Ala	Leu	Met	Gln	Gln	Gln	Ser	Leu	Tyr	His	Pro	Gly
1				5				10						15	
Leu	Leu	Ala	Pro	Pro	Gln	Ile	Glu	Pro	Ile	Pro	Ser	Gly	Asn	Leu	Pro
			20					25					30		
Pro	Gly	Phe	Asp	Pro	Ser	Thr	Cys	Arg	Ser	Val	Tyr	Val	Gly	Asn	Ile
		35					40					45			
His	Ile	Gln	Val	Thr	Glu	Pro	Leu	Gln	Glu	Val	Phe	Ala	Gly	Thr	
	50					55				60					
Gly	Pro	Val	Glu	Ser	Cys	Lys	Leu	Ile	Arg	Lys	Glu	Lys	Ser	Ser	Tyr
65					70					75					80
Gly	Phe	Val	His	Tyr	Phe	Asp	Arg	Ser	Ala	Gly	Leu	Ala	Ile	Leu	
			85					90					95		
Ser	Leu	Asn	Gly	Arg	His	Leu	Phe	Gly	Gln	Pro	Ile	Lys	Val	Asn	Trp
			100					105					110		
Ala	Tyr	Ala	Ser	Gly	Gln	Arg	Glu	Asp	Thr	Ser	Ser	His	Phe	Asn	Ile
		115					120					125			
Phe	Val	Gly	Asp	Leu	Ser	Pro	Glu	Val	Thr	Asp	Ala	Met	Leu	Phe	Thr
	130					135					140				
Cys	Phe	Ser	Val	Tyr	Pro	Thr	Cys	Ser	Asp	Ala	Arg	Val	Met	Trp	Asp
145					150					155					160

Gln Lys Thr Gly Arg Ser Arg Gly Phe Gly Phe Val Ser Phe Arg Asn
165 170 175
Gln Gln Asp Ala Gln Thr Ala Ile Asp Glu Ile Thr Gly Lys Trp Leu
180 185 190
Gly Ser Arg Gln Ile Arg Cys Asn Trp Ala Thr Lys Gly Ala Thr Ser
195 200 205
Gly Glu Asp Lys Gln Ser Ser Asp Ser Lys Ser Val Val Glu Leu Thr
210 215 220
Ser Gly Val Ser Glu Asp Gly Lys Asp Thr Trp Asn Gly Glu Ala Pro
225 230 235
Glu Asn Asn Ala Gln Tyr Thr Thr Val Tyr Val Gly Asn Leu Ala Pro
245 250 255
Glu Val Ser Gln Val Asp Leu His Arg His Phe His Ser Leu Gly Ala
260 265 270
Gly Val Ile Glu Glu Val Arg Val Gln Arg Asp Lys Gly Phe Gly Phe
275 280 285
Val Arg Tyr Ser Thr His Val Glu Ala Ala Leu Ala Ile Gln Met Gly
290 295 300
Asn Thr His Ser Tyr Leu Ser Gly Arg Gln Met Lys Cys Ser Trp Gly
305 310 315
Ser Lys Pro Thr Pro Ala Gly Thr Ala Ser Asn Pro Leu Pro Pro Pro
325 330 335
Ala Pro Ala Pro Ile Pro Gly Phe Ser Ala Ser Asp Leu Leu Ala Tyr
340 345 350
Glu Arg Gln Leu Ala Met Ser Lys Met Ala Gly Met Asn Pro Met Met
355 360 365
His His Pro Gln Gly Gln His Ala Phe Lys Gln Ala Ala Met Gly Ala
370 375 380
Thr Gly Ser Asn Gln Ala Ile Tyr Asp Gly Gly Tyr Gln Asn Ala Gln
385 390 395
Gln Leu Met Tyr Tyr Gln
405

(2) INFORMATION FOR SEQ ID NO:657:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1190 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1190

(D) OTHER INFORMATION: / Ceres Seq. ID 1567589

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:657:

agaaaccctga	aaaatccttta	ttgtagcagc	tgagagcaata	tatatcccaa	tttgcgcgcaa	60
ctagggtttt	ctcttcctca	cgcaaaagcaa	tacatcgagc	tctcccaactg	attcagcagc	120
tctttgaact	actcttcgac	aatggcgaggaa	cgttggtggag	aacgtgtggtg	tgagcgtggtg	180
ggagaaactg	gtgatttcgg	acgaggattc	ggaggcccg	gaggtcgctgg	agatcgttga	240
gggctgtggc	gtggaggccg	tggttggtcgt	cgtggaggcg	gtgccagtga	agaagagaaaa	300
tggtttccag	tgaccaagct	tggttcgtcac	gtggcggtcg	gtcatatcaa	gcagatagag	360
cagatctcat	ttcattcaact	cccgggttaag	gagtaccaga	tcattgatat	gctcatcggt	420
ccaacattga	aggatgaggt	aatgaaaaatc	atgccgggtc	agaaaaaac	caggcgctggt	480
caaaaggcata	gattcaaggc	ctttgttgtc	gttgagagatg	gtaattgtcoa	tggttggttgg	540
ggagtgaagt	gctctaagga	agttgctacg	gccattagag	gagcgattat	tctcgctaa	600
ctgtctgttg	ttccagtgag	gagaggttac	tggttgtaaca	agattgggaa	gccacatacg	660
gttccttgta	aggtgactgg	gaagtgtgga	tctgtgacag	tgagagaggt	tcacgctcct	720
agaggttctg	gtattgtggc	tgctagaggt	cctaagaag	ttcttcaatt	cgctggaatt	780
gatgatgttt	gcactctctc	caggggatcc	acaaaaactc	ttggaaaCtt	cgctcagggt	840
acattcgatt	tccttcagaa	gacttacgga	ttccttacc	cagaggtctg	gaaggagaca	900
agattctcta	gatcaccata	ccaagagcac	actgatttcc	tggtgtccaa	ggctctttcg	960
accagcaaac	ccgaccaggt	ggttgaagac	caagcctaaa	caatgcttcc	accttgtgtt	1020

ctttttggat tataatcctt catgagttaa ttttggttga acctttggta gtatatgttg 1080
ctggattgtg cacccttctgt tttcatctcc tcttccaac tactttattt ttgcttatgg 1140
atcttaatgt tctagttttg cttttacttt tgttgagaaa agttaaatcc

(2) INFORMATION FOR SEQ ID NO:658:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 285 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..285

(D) OTHER INFORMATION: / Ceres Seq. ID 1567590

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:658:

Met Ala Glu Arg Gly Gly Glu Arg Gly Val Glu Arg Gly Gly Glu Arg
1 5 10 15
Gly Asp Phe Gly Arg Gly Phe Gly Gly Arg Gly Gly Arg Gly Asp Arg
20 25 30
Gly Gly Arg Gly Arg Gly Gly Arg Gly Gly Arg Gly Gly Arg Ala
35 40 45
Ser Glu Glu Glu Lys Trp Val Pro Val Thr Lys Leu Gly Arg His Val
50 55 60
Ala Ala Gly His Ile Lys Gln Ile Glu Gln Ile Tyr Leu His Ser Leu
65 70 75 80
Pro Val Lys Glu Tyr Gln Ile Ile Asp Met Leu Ile Gly Pro Thr Leu
85 90 95
Lys Asp Glu Val Met Lys Ile Met Pro Val Gln Lys Gln Thr Arg Ala
100 105 110
Gly Gln Arg Thr Arg Phe Lys Ala Phe Val Val Val Gly Asp Gly Asn
115 120 125
Gly His Val Gly Leu Gly Val Lys Cys Ser Lys Glu Val Ala Thr Ala
130 135 140
Ile Arg Gly Ala Ile Ile Leu Ala Lys Leu Ser Val Val Pro Val Arg
145 150 155 160
Arg Gly Tyr Trp Gly Asn Lys Ile Gly Lys Pro His Thr Val Pro Cys
165 170 175
Lys Val Thr Gly Lys Cys Gly Ser Val Thr Val Arg Met Val Pro Ala
180 185 190
Pro Arg Gly Ser Gly Ile Val Ala Ala Arg Val Pro Lys Lys Val Leu
195 200 205
Gln Phe Ala Gly Ile Asp Asp Val Phe Thr Ser Ser Arg Gly Ser Thr
210 215 220
Lys Thr Leu Gly Asn Phe Val Lys Ala Thr Phe Asp Cys Leu Gln Lys
225 230 235 240
Thr Tyr Gly Phe Leu Thr Pro Glu Phe Trp Lys Glu Thr Arg Phe Ser
245 250 255
Arg Ser Pro Tyr Gln Glu His Thr Asp Phe Leu Ala Ser Lys Ala Leu
260 265 270
Ser Thr Ser Lys Pro Asp Pro Val Val Glu Asp Gln Ala
275 280 285

(2) INFORMATION FOR SEQ ID NO:659:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 196 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..196

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:659:

(2) INFORMATION FOR SEO ID NO:660:

(A) LENGTH: 185 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..185

(D) OTHER INFORMATION: / Ceres Seq. ID 1567592

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:660:

Met	Lys	Ile	Met	Pro	Val	Gln	Lys	Gln	Thr	Arg	Ala	Gly	Gln	Arg	Thr
1			5					10					15		
Arg	Phe	Lys	Ala	Phe	Val	Val	Val	Gly	Asp	Gly	Asn	Gly	His	Val	Gly
			20					25					30		
Leu	Gly	Val	Lys	Cys	Ser	Lys	Glu	Val	Ala	Thr	Ala	Ile	Arg	Gly	Ala
			35				40					45			
Ile	Ile	Leu	Ala	Lys	Leu	Ser	Val	Val	Pro	Val	Arg	Arg	Gly	Tyr	Trp
			50			55					60				
Gly	Asn	Lys	Ile	Gly	Lys	Pro	His	Thr	Val	Pro	Cys	Lys	Val	Thr	Gly
					70					75					80
Lys	Cys	Gly	Ser	Val	Thr	Val	Arg	Met	Val	Pro	Ala	Pro	Arg	Gly	Ser
				85					90					95	
Gly	Ile	Val	Ala	Ala	Arg	Val	Pro	Lys	Lys	Val	Leu	Gln	Phe	Ala	Gly
				100				105					110		
Ile	Asp	Asp	Val	Phe	Thr	Ser	Ser	Arg	Gly	Ser	Thr	Lys	Thr	Leu	Gly
			115					120				125			
Asn	Phe	Val	Lys	Ala	Thr	Phe	Asp	Cys	Leu	Gln	Lys	Thr	Tyr	Gly	Phe
						135					140				
Leu	Thr	Pro	Glu	Phe	Trp	Lys	Glu	Thr	Arg	Phe	Ser	Arg	Ser	Pro	Tyr
					150					155					160
Gln	Glu	His	Thr	Asp	Phe	Leu	Ala	Ser	Lys	Ala	Leu	Ser	Thr	Ser	Lys

165 170 175

Pro Asp Pro Val Val Glu Asp Gln Ala
180 185

(2) INFORMATION FOR SEQ ID NO:661:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1236 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..1236
(D) OTHER INFORMATION: / Ceres Seq. ID 1567593
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:661:

aaaccaca	acataatttc	acatatctct	ctttctttct	cttgaaggaa	agacgaagat	60
ctccaagtcc	caagttgtta	acacaagacg	taaacatggg	tcactctggg	ttcttagtta	120
tgattatggt	aggagtcagt	gcttctctcg	tgagcgtcta	cgggtggcgt	tgatccaacg	180
ctcacgccc	ttttacggt	gggtggtgat	cttcgggcac	aatgggtggt	gcttgtggat	240
atggttaatt	atatagccaa	ggctacggga	cgagcacggc	ggctctaagc	acagScctct	300
ttcaacaagt	gacttagctg	tggttcttgc	tttgagataa	gatgtgaaaa	cgatggtaaa	360
tggtgtttac	ctggctcaat	cggtgtaacc	gctacaaact	tcgtcccgcc	aaataacggc	420
ttagcgaaac	ataatggcgg	ttggtgtaat	ctcctcttgc	aacactttga	ccttgctcac	480
cctgtttttc	aacgcattgc	tcagtacaga	gctggaaatc	tcctgttttc	ctacagaagg	540
gttctcttgc	ggagaaagg	aggaataaga	ttcacgataa	acggccactc	atactcaac	600
cttgtgtcga	tcacaaactg	cggtggtgcc	ggagacgttc	actcgccggc	gatcaagggt	660
tcaagaacag	tgtggcaagc	taigtcaagg	aactgggggc	aaaattggca	aagcaactct	720
tacctcaacg	gtcaagcact	ttcctttaag	gtcaccacca	cgacggccgc	cacagtgtgc	780
tccttcaacg	cgctctctgc	cggtctggtc	tatggccaga	cttttgcggc	tgagacagttc	840
cggtaaaaag	ggcaagttgg	ttaactcttc	ttccatttat	ctaaagtaaa	ctcattttgtg	900
tggttatatt	gysctcttga	aaaaactcgg	ttattgagag	agtgatgcgt	cgagggtctg	960
gttttgcaga	aggccttgat	gacgtctaatt	cttttttggg	acctctttat	ttttctttct	1020
tgaaactagt	ttttgttaag	aaagaaaaaa	caagttatag	tagttaattg	attactgatg	1080
cagaggtgga	gttttaacta	ccaccgcgta	gtagtagtta	tgagtttttt	attttaaggt	1140
gtgagagaga	gttagattat	caagatttgt	caattttatt	atgtttgttt	gtaataatag	1200
aatcttttac	ttcagttta	gaaaattggg	ggattg			

(2) INFORMATION FOR SEQ ID NO:662:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 104 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..104
(D) OTHER INFORMATION: / Ceres Seq. ID 1567594
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:662:

Thr	Gln	Gln	His	Asn	Phe	Thr	Tyr	Leu	Ser	Phe	Phe	Leu	Leu	Lys	Glu
1			5					10				15			
Arg	Arg	Arg	Ser	Pro	Ser	Pro	Lys	Leu	Leu	Thr	Gln	Asp	Val	Asn	Met
			20				25					30			
Gly	His	Leu	Gly	Phe	Leu	Val	Met	Ile	Met	Val	Gly	Val	Met	Ala	Ser
	35					40					45				
Ser	Val	Ser	Val	Tyr	Gly	Gly	Gly	Trp	Ile	Asn	Ala	His	Ala	Thr	Phe
	50				55					60					
Tyr	Gly	Gly	Gly	Asp	Ala	Ser	Gly	Thr	Met	Gly	Gly	Ala	Cys	Gly	Tyr
65				70				75					80		
Gly	Asn	Leu	Tyr	Ser	Gln	Gly	Tyr	Gly	Thr	Ser	Thr	Ala	Ala	Leu	Ser
				85				90					95		
Thr	Xaa	Ser	Leu	Gln	Gln	Trp	Thr								

Case 1:07-cv-00000-000

100

(2) INFORMATION FOR SEQ ID NO:663:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 73 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..73
(D) OTHER INFORMATION: / Ceres Seq. ID 1567595

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:663:

Met	Gly	His	Leu	Gly	Phe	Leu	Val	Met	Ile	Met	Val	Gly	Val	Met	Ala
1			5						10						15
Ser	Ser	Val	Ser	Val	Tyr	Gly	Gly	Gly	Trp	Ile	Asn	Ala	His	Ala	Thr
			20					25					30		
Phe	Tyr	Gly	Gly	Gly	Asp	Ala	Ser	Gly	Thr	Met	Gly	Gly	Ala	Cys	Gly
			35					40					45		
Tyr	Gly	Asn	Leu	Tyr	Ser	Gln	Gly	Tyr	Gly	Thr	Ser	Thr	Ala	Ala	Leu
			50			55					60				
Ser	Thr	Xaa	Ser	Leu	Gln	Trp	Thr								
65					70										

(2) INFORMATION FOR SEQ ID NO:664:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 65 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..65
(D) OTHER INFORMATION: / Ceres Seq. ID 1567596

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:664:

Met	Ile	Met	Val	Gly	Val	Met	Ala	Ser	Ser	Val	Ser	Val	Tyr	Gly	Gly
1				5					10					15	
Gly	Trp	Ile	Asn	Ala	His	Ala	Thr	Phe	Tyr	Gly	Gly	Gly	Asp	Ala	Ser
			20					25					30		
Gly	Thr	Met	Gly	Gly	Ala	Cys	Gly	Tyr	Gly	Asn	Leu	Tyr	Ser	Gln	Gly
			35				40					45			
Tyr	Gly	Thr	Ser	Thr	Ala	Ala	Leu	Ser	Thr	Xaa	Ser	Leu	Gln	Gln	Trp
			50			55					60				
Thr															
65															

(2) INFORMATION FOR SEQ ID NO:665:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 606 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..606
(D) OTHER INFORMATION: / Ceres Seq. ID 1567605

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:665:

cagttccacg	gaacacatggt	ggaaggaagt	ttctttgaag	acttgaacat	cccaaacaga	60
gcaaacacaa	acaacagcag	caacaatcaa	acgttttttc	aaggggaacaa	caacaacaac	120
aatgtgttta	agttcgacac	tcgagatcac	aacaactttg	aagctgcaca	taacaacaac	180
aataacagta	gcggcaacag	gttcacagctt	gtgttttgatt	ccacaccggt	cgacatggcg	240

tcattcgatt acagagatga tatgtcgtatg ccaggagtag taggaacgat ggatggaatg	300
cagcagaagc agcaagatgt atccatatgg ttctaaagtc ttggtagtag atttcattctt	360
ctcttatttt tatctttttg ttctttacat tcaactcaacc atgtaatat ttttctctggg	420
tctctctgtc tctatcgtctt gttatgatgt gtctgtgaaga gtctctaaaa actctctgtt	480
actgtgtgtc tttgtctcgg cttggtgaat ctctctgtca tcatcagctt ttagttaacac	540
acccgacttg gggatgaacg aacactaaat gtaagttttc ataataataa tatatttgca	600

Agctcc

(2) INFORMATION FOR SEQ ID NO:666:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..111
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567606

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:666:

Gln	Phe	Pro	Gly	Asn	Met	Val	Glu	Gly	Ser	Phe	Phe	Glu	Asp	Leu	Asn
1			5						10					15	
Ile	Pro	Asn	Arg	Ala	Asn	Asn	Asn	Asn	Ser	Ser	Asn	Asn	Gln	Thr	Phe
			20						25					30	
Phe	Gln	Gly	Asn	Asn	Asn	Asn	Asn	Val	Phe	Lys	Phe	Asp	Thr	Ala	
			35						40					45	
Asp	His	Asn	Asn	Phe	Glu	Ala	Ala	His	Asn	Asn	Asn	Asn	Asn	Ser	Ser
			50						55					60	
Gly	Asn	Arg	Phe	Gln	Leu	Val	Phe	Asp	Ser	Thr	Pro	Phe	Asp	Met	Ala
			65						70					80	
Ser	Phe	Asp	Tyr	Arg	Asp	Asp	Met	Ser	Met	Pro	Gly	Val	Val	Gly	Thr
			85						90					95	
Met	Asp	Gly	Met	Gln	Gln	Lys	Gln	Gln	Asp	Val	Ser	Ile	Trp	Phe	
			100						105					110	

(2) INFORMATION FOR SEQ ID NO:667:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 106 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..106
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567607

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:667:

Met	Val	Glu	Gly	Ser	Phe	Phe	Glu	Asp	Leu	Asn	Ile	Pro	Asn	Arg	Ala
1				5					10					15	
Asn	Asn	Asn	Asn	Ser	Ser	Asn	Asn	Gln	Thr	Phe	Phe	Gln	Gly	Asn	Asn
				20					25					30	
Asn	Asn	Asn	Asn	Val	Phe	Lys	Phe	Asp	Thr	Ala	Asp	His	Asn	Asn	Phe
				35					40					45	
Glu	Ala	Ala	His	Asn	Asn	Asn	Asn	Asn	Ser	Ser	Gly	Asn	Arg	Phe	Gln
				50					55					60	
Leu	Val	Phe	Asp	Ser	Thr	Pro	Phe	Asp	Met	Ala	Ser	Phe	Asp	Tyr	Arg
				65					70					80	
Asp	Asp	Met	Ser	Met	Pro	Gly	Val	Val	Gly	Thr	Met	Asp	Gly	Met	Gln
				85					90					95	
Gln	Lys	Gln	Gln	Asp	Val	Ser	Ile	Trp	Phe						
				100					105						

(2) INFORMATION FOR SEQ ID NO:668:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1448 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1448

(D) OTHER INFORMATION: / Ceres Seq. ID 1567608

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:668:

```
aaaaagatgg  tgcacttcag  atgcttgcca  caaatattga  gtatgatgag  cataaaggac  60
gcattgtcat  tggcagcata  cagcagggg  tactgcgcaa  aggaatggat  gtcagggtgt  120
gcacttctga  agattcctgt  agattttcaa  gagtttagta  gctttttgta  tatgagaaat  180
tctacagagt  acctactgat  tcaagtgaag  ctggagatat  ttgcgctgta  tgtggcatag  240
acaacattca  gattggggag  actattgctg  ataaagtaca  tgggaagcct  ctacctacaa  300
tcaaagttag  agagccaact  gtgaaaatgt  ccttctctgt  aaacacctct  ccattttctg  360
tcctgtgagg  gaagtattga  acaagcagga  acttacgaga  tcgttttaac  ctggaacttg  420
aaagaaatct  agctatgaaa  gtggaagatg  gtgagacagc  agacacattc  attgttagtg  480
ccgtggtaca  ttacacatta  ccattcctgt  agaaaaatgt  cgaagagaag  gatattgaatt  540
tatggttgcc  cccccgaag  ttatcaacaa  aagggttaac  gataaattgc  tggagccata  600
tgagatagca  actgttgaag  taccagagcg  tcacatgggg  cctgttgttg  aacttcttgg  660
caaaaggcgt  ggacagatgt  ttgatatgca  ggggtgttgg  tcggaaggaa  caactttctt  720
gcggtacaaa  atccccacac  gtggacttct  tggattgagg  aacgcaattt  taacagcttc  780
tcgctgggaca  cgtatcctta  acactgtatt  tgacagttta  tggaccttgg  cgcggtgata  840
ttagcccgag  cgatctaggt  tcgctggttg  cctttgaaga  tggaaacata  acatcatatg  900
ccctggccag  tcgctcaggag  agagggcaca  tgtttgttag  ttctggagtg  gatgtataca  960
aaggctcagat  agttgggatc  caccGagaga  cccggcgact  tgggtcttaa  tatctgcgaag  1020
aagaaggcag  cgacaacaac  aagatccaac  aaagatgtaa  cagtgattct  tgacactccc  1080
ttaacatata  gtctggacga  ctgcatcgaa  tacattgaag  aggatgagtt  ggtggaggtt  1140
acaccttcta  gtattaggat  gtgcaagaat  cagaaaaatg  caagaaaagg  caggcagtaa  1200
aacccatttt  tgcaagctgg  gtttggagga  aattgaagaa  agctctctac  taaaaaaaaa  1260
gaaagctagt  ttctagtgtt  atttatagcg  ttgtttgatt  gttatacata  gctttattct  1320
tatagcaaa  ggtgagtcct  gatgttatcc  aattaatggt  tttttggaat  atctccatgc  1380
cctttgatca  tctgatactt  aaagctgtac  aactctgaa  gttgtgcact  agcagatatt  1440
aaagtgtg
```

(2) INFORMATION FOR SEQ ID NO:669:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 168 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..168

(D) OTHER INFORMATION: / Ceres Seq. ID 1567609

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:669:

```
Lys Asp Gly Ala Leu Gln Met Leu Ala Thr Asn Ile Glu Tyr Asp Glu
1      5      10      15
His Lys Gly Arg Ile Ala Ile Gly Arg Leu His Ala Gly Val Leu Arg
20      25      30
Lys Gly Met Asp Val Arg Val Cys Thr Ser Glu Asp Ser Cys Arg Phe
35      40      45
Ala Arg Val Ser Glu Leu Phe Val Tyr Glu Lys Phe Tyr Arg Val Pro
50      55      60
Thr Asp Ser Val Glu Ala Gly Asp Ile Cys Ala Val Cys Gly Ile Asp
65      70      75      80
Asn Ile Gln Ile Gly Glu Thr Ile Ala Asp Lys Val His Gly Lys Pro
85      90      95
Leu Pro Thr Ile Lys Val Glu Glu Pro Thr Val Lys Met Ser Phe Ser
100      105      110
```

Val Asn Thr Ser Pro Phe Ser Gly Arg Glu Gly Lys Tyr Val Thr Ser
115 120 125
Arg Asn Leu Arg Asp Arg Leu Asn Arg Glu Leu Glu Arg Asn Leu Ala
130 135 140
Met Lys Val Glu Asp Gly Glu Thr Ala Asp Thr Phe Ile Val Ser Ala
145 150 155 160
Val Val His Tyr Thr Leu Pro Ser
165

(2) INFORMATION FOR SEQ ID NO:670:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 162 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..162
(D) OTHER INFORMATION: / Ceres Seq. ID 1567610

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:670:

Met Leu Ala Thr Asn Ile Glu Tyr Asp Glu His Lys Gly Arg Ile Ala
1 5 10 15
Ile Gly Arg Leu His Ala Gly Val Leu Arg Lys Gly Met Asp Val Arg
20 25 30
Val Cys Thr Ser Glu Asp Ser Cys Arg Phe Ala Arg Val Ser Glu Leu
35 40 45
Phe Val Tyr Glu Lys Phe Tyr Arg Val Pro Thr Asp Ser Val Glu Ala
50 55 60
Gly Asp Ile Cys Ala Val Cys Gly Ile Asp Asn Ile Gln Ile Gly Glu
65 70 75 80
Thr Ile Ala Asp Lys Val His Gly Lys Pro Leu Pro Thr Ile Lys Val
85 90 95
Glu Glu Pro Thr Val Lys Met Ser Phe Ser Val Asn Thr Ser Pro Phe
100 105 110
Ser Gly Arg Glu Gly Lys Tyr Val Thr Ser Arg Asn Leu Arg Asp Arg
115 120 125
Leu Asn Arg Glu Leu Glu Arg Asn Leu Ala Met Lys Val Glu Asp Gly
130 135 140
Glu Thr Ala Asp Thr Phe Ile Val Ser Ala Val His Tyr Thr Leu
145 150 155 160
Pro Ser

(2) INFORMATION FOR SEQ ID NO:671:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 134 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..134
(D) OTHER INFORMATION: / Ceres Seq. ID 1567611

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:671:

Met Asp Val Arg Val Cys Thr Ser Glu Asp Ser Cys Arg Phe Ala Arg
1 5 10 15
Val Ser Glu Leu Phe Val Tyr Glu Lys Phe Tyr Arg Val Pro Thr Asp
20 25 30
Ser Val Glu Ala Gly Asp Ile Cys Ala Val Cys Gly Ile Asp Asn Ile
35 40 45
Gln Ile Gly Glu Thr Ile Ala Asp Lys Val His Gly Lys Pro Leu Pro

(2) INFORMATION FOR SEO ID NO:672:

(A) LENGTH: 1143 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..1143
(D) OTHER INFORMATION: / Ceres Seq. ID 1567622

gaaaatggat	caagcaaaag	gaaaagtctgt	tgttaactggt	gcttcaagct	tcttgggtctc	60
tgtgcttgta	aagaggcttc	tctctgaag	atataagtt	atgcgaaac	tcagatattc	120
atggaataag	aagaaacttg	caccactat	gaagttagaa	atggcaaaag	agagactacc	180
tgtggtgga	gctgatttaa	tggaaagag	aagtttgat	acgccttaa	tgggtgagta	240
aggaggtgt	catactgctt	ctccggtgt	taaacctacc	tctaattcag	aggaggaagt	300
tctgagacca	gctatagaag	gaacctcca	tgtactcga	tactgaaag	agaatccttc	360
ctcgaagcgc	gctgtttcca	ctctactcct	tctcaacgt	aggatcagag	atgatttga	420
tcccataatc	gctcttcacg	aatcaatttt	gacgtctgtg	gaactctgca	agcgcttcca	480
gtctctggat	cccttatcag	agcatatgc	ggacaacgt	gcatggaatt	tctctgaaga	540
aaatggttat	gacctgcctc	ctgtttcaac	atctctctc	tgtggaccca	gtctgctcc	600
tgtattttgt	tctcacgctt	ccgattgctt	cggaattact	aaaggagaaa	cagagaagtt	660
ccaatggcat	ggacaaatg	ggtatgttca	tatcgatgac	Gttgcagaa	cccacatgt	720
cgttttcgaa	cagcaagcag	ctccagcgag	atatacttgt	agctctaac	ttataagct	780
aggaagaa	gtttcattcc	tctatcgctg	taccocata	ctccctatc	ccaagagtt	840
tgagaactca	aataggttgc	atatacgact	tgcacctctg	aagatcacga	tctctcggtg	900
caagctcaag	tcctctgaag	agatgttcga	tgaactgatt	cgctcattag	tcgacgaagg	960
ctattttat	actgtctctc	cataactctg	ggactagaga	atattgtcca	ataagattgt	1020
tctgaaatg	tagtcatctg	gattccaat	gaagaatagg	gattgtgaaa	catgaaatca	1080
aagattacaa	acgatataat	ctttacttgt	ttatgaacca	aatcataaca	tatttctctc	1140
cag						

(2) INFORMATION FOR SEQ ID NO:673:

(A) LENGTH: 327 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

```
(ix) FEATURE:
```

- (A) NAME/KEY: peptide
(B) LOCATION: 1..327
(D) OTHER INFORMATION: / Ceres Seq. ID 1567623

Lys	Met	Asp	Gln	Ala	Lys	Gly	Lys	Val	Cys	Val	Thr	Gly	Ala	Ser	Gly
1			5					10						15	
Phe	Leu	Ala	Ser	Trp	Leu	Val	Lys	Arg	Leu	Leu	Leu	Glu	Gly	Tyr	Glu
		20						25					30		
Val	Ile	Gly	Thr	Val	Arg	Asp	Pro	Gly	Asn	Glu	Lys	Lys	Leu	Ala	His
	35					40						45			

```

Leu Trp Lys Leu Glu Gly Ala Lys Glu Arg Leu Arg Leu Val Lys Ala
50 55 60
Asp Leu Met Glu Glu Gly Ser Phe Asp Asn Ala Ile Met Gly Cys Gln
65 70 75 80
Gly Val Phe His Thr Ala Ser Pro Val Leu Lys Pro Thr Ser Asn Pro
85 90 95
Glu Glu Glu Ile Leu Arg Pro Ala Ile Glu Gly Thr Leu Asn Val Leu
100 105 110
Arg Ser Cys Arg Lys Asn Pro Ser Leu Lys Arg Val Val Leu Thr Ser
115 120 125
Ser Ser Ser Thr Val Arg Ile Arg Asp Asp Phe Asp Pro Lys Ile Pro
130 135 140
Leu Asp Glu Ser Ile Trp Thr Ser Val Glu Leu Cys Lys Arg Phe Gln
145 150 155 160
Val Trp Tyr Ala Leu Ser Lys Thr Leu Ala Glu Gln Ala Ala Trp Lys
165 170 175
Phe Ser Glu Glu Asn Gly Ile Asp Leu Val Thr Val Leu Pro Ser Phe
180 185 190
Leu Val Gly Pro Ser Leu Pro Pro Asp Leu Cys Ser Thr Ala Ser Asp
195 200 205
Val Leu Gly Leu Leu Lys Gly Glu Thr Glu Lys Phe Gln Trp His Gly
210 215 220
Gln Met Gly Tyr Val His Ile Asp Asp Val Ala Arg Thr His Ile Val
225 230 235 240
Val Phe Glu His Glu Ala Ala Gln Gly Arg Tyr Ile Cys Ser Ser Asn
245 250 255
Val Ile Ser Leu Glu Glu Leu Val Ser Phe Leu Ser Ala Arg Tyr Pro
260 265 270
Ser Leu Pro Ile Pro Lys Arg Phe Glu Lys Leu Asn Arg Leu His Tyr
275 280 285
Asp Phe Asp Thr Ser Lys Ile Gln Ser Leu Gly Leu Lys Phe Lys Ser
290 295 300
Leu Glu Glu Met Phe Asp Asp Cys Ile Ala Ser Leu Val Glu Gln Gly
305 310 315 320
Tyr Leu Ser Thr Val Leu Pro
325

```

(2) INFORMATION FOR SEQ ID NO:674:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 326 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..326

- (D) OTHER INFORMATION: / Ceres Seq. ID 1567624

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:674:

```

Met Asp Gln Ala Lys Gly Lys Val Cys Val Thr Gly Ala Ser Gly Phe
1 5 10 15
Leu Ala Ser Trp Leu Val Lys Arg Leu Leu Leu Glu Gly Tyr Glu Val
20 25 30
Ile Gly Thr Val Arg Asp Pro Gly Asn Glu Lys Lys Leu Ala His Leu
35 40 45
Trp Lys Leu Glu Gly Ala Lys Glu Arg Leu Arg Leu Val Lys Ala Asp
50 55 60
Leu Met Glu Glu Gly Ser Phe Asp Asn Ala Ile Met Gly Cys Gln Gly
65 70 75 80
Val Phe His Thr Ala Ser Pro Val Leu Lys Pro Thr Ser Asn Pro Glu
85 90 95
Glu Glu Ile Leu Arg Pro Ala Ile Glu Gly Thr Leu Asn Val Leu Arg

```

(2) INFORMATION FOR SEQ ID NO:675:

(A) LENGTH: 261 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..261

(D) OTHER INFORMATION: / Ceres Seq. ID 1567625

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:675:

Met	Glu	Glu	Gly	Ser	Phe	Asp	Asn	Ala	Ile	Met	Gly	Cys	Gln	Gly	Val
1				5					10				15		
Phe	His	Thr	Ala	Ser	Pro	Val	Leu	Lys	Pro	Thr	Ser	Asn	Pro	Glu	Glu
			20					25					30		
Glu	Ile	Leu	Arg	Pro	Ala	Ile	Glu	Gly	Thr	Leu	Asn	Val	Leu	Arg	Ser
		35				40					45				
Cys	Arg	Lys	Asn	Pro	Ser	Leu	Lys	Arg	Val	Val	Leu	Thr	Ser	Ser	Ser
	50					55				60					
Ser	Thr	Val	Arg	Ile	Arg	Asp	Asp	Phe	Asp	Pro	Lys	Ile	Pro	Leu	Asp
65				70						75				80	
Glu	Ser	Ile	Trp	Thr	Ser	Val	Glu	Leu	Cys	Lys	Arg	Phe	Gln	Val	Trp
			85					90					95		
Tyr	Ala	Leu	Ser	Lys	Thr	Leu	Ala	Glu	Gln	Ala	Ala	Trp	Lys	Phe	Ser
			100					105					110		
Glu	Glu	Asn	Gly	Ile	Asp	Leu	Val	Thr	Val	Leu	Pro	Ser	Phe	Leu	Val
		115				120					125				
Gly	Pro	Ser	Leu	Pro	Pro	Asp	Leu	Cys	Ser	Thr	Ala	Ser	Asp	Val	Leu
	130					135					140				
Gly	Leu	Leu	Lys	Gly	Glu	Thr	Glu	Lys	Phe	Gln	Trp	His	Gly	Gln	Met
145					150					155				160	

Gly Tyr Val His Ile Asp Asp Val Ala Arg Thr His Ile Val Val Phe
165 170 175
Glu His Glu Ala Ala Gln Gly Arg Tyr Ile Cys Ser Ser Asn Val Ile
180 185 190
Ser Leu Glu Glu Leu Val Ser Phe Leu Ser Ala Arg Tyr Pro Ser Leu
195 200 205
Pro Ile Pro Lys Arg Phe Glu Lys Leu Asn Arg Leu His Tyr Asp Phe
210 215 220
Asp Thr Ser Lys Ile Gln Ser Leu Gly Leu Lys Phe Lys Ser Leu Glu
225 230 235 240
Glu Met Phe Asp Asp Cys Ile Ala Ser Leu Val Glu Gln Gly Tyr Leu
245 250 255
Ser Thr Val Leu Pro
260

(2) INFORMATION FOR SEQ ID NO:676:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1160 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1160

(D) OTHER INFORMATION: / Ceres Seq. ID 1567629

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:676:

aaagtggagc	gacgtgcgtc	tgcttcgtct	cattacaaaag	cagaagaaac	acaaacagag	60
tcagagatct	taagagttaa	agactaatcc	caacaatggc	gtctctcaaa	gtcccaagca	120
atgttctctc	tcccgaaagt	gacgccgagc	aactccacaa	ggctttttca	ggatggggta	180
ccaacgagaa	gctgatacata	tcaataactag	ctcacaggaa	cgcagcacaa	cgcagcttga	240
tcgcgacgct	ttatgcagct	acotacaatg	aggatcttct	caaagcatta	gacaaagagc	300
ttttctagcga	ctttgagaga	gctgtgatgt	tgtggactct	tgatccacca	gagagagatg	360
cttattttggc	taaagaatcc	accaagatgt	tcaccaagaa	caattggggtt	cttgttgaaa	420
tcgcttgcac	aaggcctgct	cttgagotta	tcaaggtcaa	gcaagcttac	caagctcgat	480
acaagaaatc	aatcgaggaa	gatgtcgcgc	aacacacatc	tggtgacott	cgtaagctct	540
tgcttctctc	tgtgagcact	ttcaggatgt	aaggagatga	tgtgaacatg	atgcttgcaa	600
gatctgaagc	taagatactt	cacgagaagg	tctcagagaa	atctctacgt	gacgatgact	660
tcacatcaga	attgacaaca	agaagcaaa	cacagctcgg	tgcaaacactc	aaccactaca	720
acaacgagta	tggaaacgac	attaacaaga	acttgaagga	agagtccgac	gacaatgact	780
acatgaaact	actaagagct	gtaatcacat	gtttgacata	ccctgagaag	cattttgaga	840
aggttctctc	tctatcaatc	aacaaaatgg	gaacagacga	atggggacta	acccgagctc	900
tgactacacg	aactgaaagt	gacatggaac	gcacaaaga	ggaatatcag	cgaagaaaac	960
gcattctctt	ggaccgtGct	atcgccaag	acacttctgg	tgactatgag	gacatgcttg	1020
ttgctcttct	cggacatggc	gatgcttgaa	actgtttcaa	cttctcgagt	cctctcttct	1080
cttaactgcat	ggtttgtttt	aaataaaaga	gttgtgaaac	tggttctgca	actatttatc	1140
aatgatcggt	tgagtgtgtc					

(2) INFORMATION FOR SEQ ID NO:677:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 317 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..317

(D) OTHER INFORMATION: / Ceres Seq. ID 1567630

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:677:

Met Ala Ser Leu Lys Val Pro Ser Asn Val Pro Leu Pro Glu Asp Asp						
1	5	10	15			
Ala Glu Gln Leu His Lys Ala Phe Ser Gly Trp Gly Thr Asn Glu Lys						

20	25	30
Leu Ile Ile Ser Ile Leu Ala His Arg Asn Ala Ala Gln Arg Ser Leu		
35	40	45
Ile Arg Ser Val Tyr Ala Ala Thr Tyr Asn Glu Asp Leu Leu Lys Ala		
50	55	60
Leu Asp Lys Glu Leu Ser Ser Asp Phe Glu Arg Ala Val Met Leu Trp		
65	70	75
Thr Leu Asp Pro Pro Glu Arg Asp Ala Tyr Leu Ala Lys Glu Ser Thr		
85	90	95
Lys Met Phe Thr Lys Asn Asn Trp Val Leu Val Glu Ile Ala Cys Thr		
100	105	110
Arg Pro Ala Leu Glu Leu Ile Lys Val Lys Gln Ala Tyr Gln Ala Arg		
115	120	125
Tyr Lys Lys Ser Ile Glu Glu Asp Val Ala Gln His Thr Ser Gly Asp		
130	135	140
Leu Arg Lys Leu Leu Leu Pro Leu Val Ser Thr Phe Arg Tyr Glu Gly		
145	150	155
Asp Asp Val Asn Met Met Leu Ala Arg Ser Glu Ala Lys Ile Leu His		
165	170	175
Glu Lys Val Ser Glu Lys Ser Tyr Ser Asp Asp Phe Ile Arg Ile		
180	185	190
Leu Thr Thr Arg Ser Lys Ala Gln Leu Gly Ala Thr Leu Asn His Tyr		
195	200	205
Asn Asn Glu Tyr Gly Asn Ala Ile Asn Lys Asn Leu Lys Glu Glu Ser		
210	215	220
Asp Asp Asn Asp Tyr Met Lys Leu Leu Arg Ala Val Ile Thr Cys Leu		
225	230	235
Thr Tyr Pro Glu Lys His Phe Glu Lys Val Leu Arg Leu Ser Ile Asn		
245	250	255
Lys Met Gly Thr Asp Glu Trp Gly Leu Thr Arg Val Val Thr Arg		
260	265	270
Thr Glu Val Asp Met Glu Arg Ile Lys Glu Glu Tyr Gln Arg Arg Asn		
275	280	285
Ser Ile Pro Leu Asp Arg Ala Ile Ala Lys Asp Thr Ser Gly Asp Tyr		
290	295	300
Glu Asp Met Leu Val Ala Leu Leu Gly His Gly Asp Ala		
305	310	315

(2) INFORMATION FOR SEQ ID NO:678:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 240 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..240

(D) OTHER INFORMATION: / Ceres Seq. ID 1567631

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:678:

Met Leu Trp Thr Leu Asp Pro Pro Glu Arg Asp Ala Tyr Leu Ala Lys		
1	5	10
Glu Ser Thr Lys Met Phe Thr Lys Asn Asn Trp Val Leu Val Glu Ile		
20	25	30
Ala Cys Thr Arg Pro Ala Leu Glu Leu Ile Lys Val Lys Gln Ala Tyr		
35	40	45
Gln Ala Arg Tyr Lys Lys Ser Ile Glu Glu Asp Val Ala Gln His Thr		
50	55	60
Ser Gly Asp Leu Arg Lys Leu Leu Leu Pro Leu Val Ser Thr Phe Arg		
65	70	75
Tyr Glu Gly Asp Asp Val Asn Met Met Leu Ala Arg Ser Glu Ala Lys		
85	90	95

```

Ile Leu His Glu Lys Val Ser Glu Lys Ser Tyr Ser Asp Asp Asp Phe
      100                      105                      110
Ile Arg Ile Leu Thr Thr Arg Ser Lys Ala Gln Leu Gly Ala Thr Leu
      115                      120                      125
Asn His Tyr Asn Asn Glu Tyr Gly Asn Ala Ile Asn Lys Asn Leu Lys
      130                      135                      140
Glu Glu Ser Asp Asp Asn Asp Tyr Met Lys Leu Leu Arg Ala Val Ile
      145                      150                      155                      160
Thr Cys Leu Thr Tyr Pro Glu Lys His Phe Glu Lys Val Leu Arg Leu
      165                      170                      175
Ser Ile Asn Lys Met Gly Thr Asp Glu Trp Gly Leu Thr Arg Val Val
      180                      185                      190
Thr Thr Arg Thr Glu Val Asp Met Glu Arg Ile Lys Glu Glu Tyr Gln
      195                      200                      205
Arg Arg Asn Ser Ile Pro Leu Asp Arg Ala Ile Ala Lys Asp Thr Ser
      210                      215                      220
Gly Asp Tyr Glu Asp Met Leu Val Ala Leu Leu Gly His Gly Asp Ala
      225                      230                      235                      240

```

(2) INFORMATION FOR SEQ ID NO:679:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 220 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..220

(D) OTHER INFORMATION: / Ceres Seq. ID 1567632

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:679:

```

Met Phe Thr Lys Asn Asn Trp Val Leu Val Glu Ile Ala Cys Thr Arg
 1      5      10      15
Pro Ala Leu Glu Leu Ile Lys Val Lys Gln Ala Tyr Gln Ala Arg Tyr
 20      25      30
Lys Lys Ser Ile Glu Glu Asp Val Ala Gln His Thr Ser Gly Asp Leu
 35      40      45
Arg Lys Leu Leu Leu Pro Leu Val Ser Thr Phe Arg Tyr Glu Gly Asp
 50      55      60
Asp Val Asn Met Met Leu Ala Arg Ser Glu Ala Lys Ile Leu His Glu
 65      70      75      80
Lys Val Ser Glu Lys Ser Tyr Ser Asp Asp Phe Ile Arg Ile Leu
 85      90      95
Thr Thr Arg Ser Lys Ala Gln Leu Gly Ala Thr Leu Asn His Tyr Asn
100      105      110
Asn Glu Tyr Gly Asn Ala Ile Asn Lys Asn Leu Lys Glu Glu Ser Asp
115      120      125
Asp Asn Asp Tyr Met Lys Leu Leu Arg Ala Val Ile Thr Cys Leu Thr
130      135      140
Tyr Pro Glu Lys His Phe Glu Lys Val Leu Arg Leu Ser Ile Asn Lys
145      150      155      160
Met Gly Thr Asp Glu Trp Gly Leu Thr Arg Val Val Thr Thr Arg Thr
165      170      175
Glu Val Asp Met Glu Arg Ile Lys Glu Glu Tyr Gln Arg Arg Asn Ser
180      185      190
Ile Pro Leu Asp Arg Ala Ile Ala Lys Asp Thr Ser Gly Asp Tyr Glu
195      200      205
Asp Met Leu Val Ala Leu Leu Gly His Gly Asp Ala
210      215      220

```

(2) INFORMATION FOR SEQ ID NO:680:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 628 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:

(A) NAME/KEY: -
(B) LOCATION: 1..628
(D) OTHER INFORMATION: / Ceres Seq. ID 1567661

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:680:

ttgtctcttt	ctcaaacata	tctcaactta	ttgtttgaat	ataaaaagag	atatcaaaaa	60
gaagagaga	ccaaaaacaa	aacaaaatc	tctaataaaa	atggcttcca	aagctatctt	120
cttctctttt	tttgtctgtc	cgcgcgtgtg	tttgtcttct	ctggcaggtt	tcgcgcgcgc	180
tgatgctgac	gacttcgac	gtttccagat	tcaaggatca	gtttactgtg	acaactgccc	240
tgtccaattc	gttaccgcgc	tcagcaaat	cctcgaaggc	gcgaaaagta	agttggagtg	300
caggagcaga	acaaacggaa	ccataacatt	gaccaaaaga	gctgttaccg	acaaaacagg	360
aagctacaaa	atggaagtaa	ccggtgacca	cgaggaagaa	gtttgcgagc	ttgttttgg	420
ccaatcacca	gacagtgggt	gcagtgatgt	cagcacagag	gcttacttac	gtaacgcgcg	480
taagatcagt	ttaacggcga	atgacggaat	cgtctccac	gagacacgta	ttgttaacc	540
tctcggtttc	atggttcaga	ctcMATTggc	tgattgtcct	gctgcctcca	aggagcttgg	600
tattgtccct	gacgtaacat	ctc	taagcg			

(2) INFORMATION FOR SEQ ID NO:681:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 207 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1..207
(D) OTHER INFORMATION: / Ceres Seq. ID 1567662

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:681:

Cys	Pro	Leu	Leu	Lys	His	Ile	Ser	Thr	Tyr	Cys	Leu	Asn	Ile	Lys	Arg	
1				5					10					15		
Asp	Ile	Lys	Lys	Lys	Arg	Arg	Pro	Lys	Thr	Lys	Gln	Lys	Ser	Leu	Ile	
				20					25					30		
Lys	Met	Ala	Ser	Ser	Lys	Ala	Ile	Phe	Phe	Ser	Phe	Phe	Val	Val	Ser	Ala
				35					40					45		
Val	Cys	Leu	Ser	Ser	Leu	Ala	Gly	Phe	Ala	Ala	Ala	Asp	Ala	Asp	Asp	
				50					55					60		
Phe	Asp	Arg	Phe	Gln	Ile	Gln	Gly	Ser	Val	Tyr	Cys	Asp	Thr	Cys	Arg	
				65					70					75		
Val	Gln	Phe	Val	Thr	Arg	Leu	Ser	Lys	Phe	Leu	Glu	Gly	Ala	Lys	Val	
				85					90					95		
Lys	Leu	Glu	Cys	Arg	Ser	Arg	Thr	Asn	Gly	Thr	Ile	Thr	Leu	Thr	Lys	
				100					105					110		
Glu	Ala	Val	Thr	Asp	Lys	Thr	Gly	Ser	Tyr	Lys	Met	Glu	Val	Thr	Gly	
				115					120					125		
Asp	His	Glu	Glu	Glu	Val	Cys	Glu	Leu	Val	Leu	Val	Gln	Ser	Pro	Asp	
				130					135					140		
Ser	Gly	Cys	Ser	Asp	Val	Ser	Thr	Glu	Ala	Tyr	Leu	Arg	Asn	Ala	Ala	
				145					150					155		
Lys	Ile	Ser	Leu	Thr	Ala	Asn	Asp	Gly	Ile	Val	Ser	His	Glu	Thr	Arg	
				165					170					175		
Ile	Val	Asn	Pro	Leu	Gly	Phe	Met	Val	Gln	Thr	Xaa	Leu	Ala	Asp	Cys	
				180					185					190		
Pro	Ala	Ala	Phe	Lys	Glu	Leu	Gly	Ile	Val	Pro	Asp	Val	Thr	Phe		
				195					200					205		

(2) INFORMATION FOR SEQ ID NO:682:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 174 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..174
 (D) OTHER INFORMATION: / Ceres Seq. ID 1567663
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:682:

Met	Ala	Ser	Lys	Ala	Ile	Phe	Phe	Ser	Phe	Val	Val	Ser	Ala	Val
1			5					10				15		
Cys	Leu	Ser	Ser	Leu	Ala	Gly	Phe	Ala	Ala	Asp	Ala	Asp	Asp	Phe
			20				25				30			
Asp	Arg	Phe	Gln	Ile	Gln	Gly	Ser	Val	Tyr	Cys	Asp	Thr	Cys	Arg
			35				40				45			
Gln	Phe	Val	Thr	Arg	Leu	Ser	Lys	Phe	Leu	Glu	Gly	Ala	Lys	Val
			50				55				60			
Leu	Glu	Cys	Arg	Ser	Arg	Thr	Asn	Gly	Thr	Ile	Thr	Leu	Thr	Lys
			65				70			75				80
Ala	Val	Thr	Asp	Lys	Thr	Gly	Ser	Tyr	Lys	Met	Glu	Val	Thr	Gly
			85						90			95		
His	Glu	Glu	Glu	Val	Cys	Glu	Leu	Val	Leu	Val	Gln	Ser	Pro	Asp
			100					105				110		
Gly	Cys	Ser	Asp	Val	Ser	Thr	Glu	Ala	Tyr	Leu	Arg	Asn	Ala	Ala
			115				120				125			
Ile	Ser	Leu	Thr	Ala	Asn	Asp	Gly	Ile	Val	Ser	His	Glu	Thr	Arg
			130				135				140			
Val	Asn	Pro	Leu	Gly	Phe	Met	Val	Gln	Thr	Xaa	Leu	Ala	Asp	Cys
			145				150			155				160
Ala	Ala	Phe	Lys	Glu	Leu	Gly	Ile	Val	Pro	Asp	Val	Thr	Phe	
			165					170						

(2) INFORMATION FOR SEQ ID NO:683:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 569 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: DNA (genomic)
 (ix) FEATURE:
 (A) NAME/KEY: -
 (B) LOCATION: 1..569
 (D) OTHER INFORMATION: / Ceres Seq. ID 1567674
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:683:

aaaatctcga	aacctctaatt	attctaagat	tctaatttgt	gaagtttgtg	aggttttagg	60
gatgggttac	aatttctaca	tgagagtgtg	tgaggttgtt	gatgatgctt	caacggatgc	120
aatcatatcg	tggagcgaaa	gcaacaacag	tttcattatc	tggaaagtgt	gagagtttta	180
cagaaggatt	ctgcctaaat	atgtagactt	gggcacaaac	ctctcacggt	ttttctccaa	240
ccttcgttct	catgggttca	aaatagttaa	aggaagaact	ggagtattgg	aatttggaac	300
tgaagatttt	gtcagagata	aactggagct	tatgaagaag	atggttagcg	ataaacgtaa	360
agcaaggaaa	gcagctaaat	ccaaagcaag	gaaagctaga	gttcaagtcg	agttctcttt	420
ccaacacttg	caaatttgat	ccattaaatc	agttctcttt	tttatgtata	tattcatctc	480
caagtagatc	aagtcttaaga	acttttccaat	agtatgtatc	tctctttata	ggaaccCtct	540
tttatgctct	agttcttgat	Tcttctctc				

(2) INFORMATION FOR SEQ ID NO:684:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 145 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..145

(D) OTHER INFORMATION: / Ceres Seq. ID 1567675

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:684:

Lys	Ser	Arg	Asn	Pro	Asn	Tyr	Ser	Lys	Ile	Leu	Ile	Cys	Glu	Val	Cys
1			5					10						15	
Glu	Val	Leu	Gly	Met	Gly	Tyr	Asn	Phe	Tyr	Met	Arg	Val	Tyr	Glu	Val
			20					25					30		
Val	Asp	Asp	Ala	Ser	Thr	Asp	Ala	Ile	Ile	Ser	Trp	Ser	Glu	Ser	Asn
		35					40					45			
Asn	Ser	Phe	Ile	Ile	Trp	Asn	Val	Gly	Glu	Phe	Tyr	Arg	Arg	Ile	Leu
	50					55					60				
Pro	Lys	Tyr	Val	Asp	Leu	Gly	Thr	Asn	Leu	Ser	Arg	Phe	Phe	Ser	Asn
	65				70					75				80	
Leu	Arg	Ser	His	Gly	Phe	Lys	Ile	Val	Lys	Gly	Arg	Thr	Gly	Val	Leu
			85						90					95	
Glu	Phe	Gly	His	Glu	Asp	Phe	Val	Arg	Asp	Lys	Leu	Glu	Leu	Met	Lys
			100					105					110		
Lys	Met	Val	Ser	Asp	Lys	Arg	Lys	Ala	Arg	Lys	Ala	Ala	Lys	Ser	Lys
		115				120						125			
Ala	Arg	Lys	Ala	Arg	Val	Gln	Val	Glu	Phe	Leu	Phe	Gln	His	Leu	Gln
	130					135					140				

Ile
145

(2) INFORMATION FOR SEQ ID NO:685:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 125 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..125

(D) OTHER INFORMATION: / Ceres Seq. ID 1567676

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:685:

Met	Gly	Tyr	Asn	Phe	Tyr	Met	Arg	Val	Tyr	Glu	Val	Val	Asp	Asp	Ala
1			5					10						15	
Ser	Thr	Asp	Ala	Ile	Ile	Ser	Trp	Ser	Glu	Ser	Asn	Asn	Ser	Phe	Ile
			20					25					30		
Ile	Trp	Asn	Val	Gly	Glu	Phe	Tyr	Arg	Arg	Ile	Leu	Pro	Lys	Tyr	Val
		35					40					45			
Asp	Leu	Gly	Thr	Asn	Leu	Ser	Arg	Phe	Phe	Ser	Asn	Leu	Arg	Ser	His
	50					55					60				
Gly	Phe	Lys	Ile	Val	Lys	Gly	Arg	Thr	Gly	Val	Leu	Glu	Phe	Gly	His
	65				70				75					80	
Glu	Asp	Phe	Val	Arg	Asp	Lys	Leu	Glu	Leu	Met	Lys	Lys	Met	Val	Ser
			85						90					95	
Asp	Lys	Arg	Lys	Ala	Arg	Lys	Ala	Ala	Lys	Ser	Lys	Ala	Arg	Lys	Ala
			100				105						110		
Arg	Val	Gln	Val	Glu	Phe	Leu	Phe	Gln	His	Leu	Gln	Ile			
		115				120									

(2) INFORMATION FOR SEQ ID NO:686:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 119 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..119

(D) OTHER INFORMATION: / Ceres Seq. ID 1567677

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:686:

```
Met Arg Val Tyr Glu Val Val Asp Asp Ala Ser Thr Asp Ala Ile Ile
1           5           10           15
Ser Trp Ser Glu Ser Asn Asn Ser Phe Ile Ile Trp Asn Val Gly Glu
20           25           30
Phe Tyr Arg Arg Ile Leu Pro Lys Tyr Val Asp Leu Gly Thr Asn Leu
35           40           45
Ser Arg Phe Phe Ser Asn Leu Arg Ser His Gly Phe Lys Ile Val Lys
50           55           60
Gly Arg Thr Gly Val Leu Glu Phe Gly His Glu Asp Phe Val Arg Asp
65           70           75           80
Lys Leu Glu Leu Met Lys Lys Met Val Ser Asp Lys Arg Lys Ala Arg
85           90           95
Lys Ala Ala Lys Ser Lys Ala Arg Lys Ala Arg Val Gln Val Glu Phe
100          105          110
Leu Phe Gln His Leu Gln Ile
115
```

(2) INFORMATION FOR SEQ ID NO:687:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1133 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1133

(D) OTHER INFORMATION: / Ceres Seq. ID 1567687

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:687:

```
aacagatcaa ggaatgaatta gatgtgtttt ccaaggaagc tgtgtctttc gaagccaagc      60
gcatcaaaag tctaagagca gtgtttggag aagtctaccc cgatcccgtc agagtgggtg      120
caattgggag gaaggttgag gatctcttgg ctgatactga aaacaatgaa tgggtcattgc      180
tttcttcoga gttttgtgga ggaaccacac taacaaacac ccgcgaagcc aaagcatttg      240
ctctctatc ggagaagggg attgctaaag gtattcgtag ggtaactgct gtgactactg      300
aatgtgtctt tgatgcattg aatgcggcgt ccttacttga aagagaagta gaggtagcct      360
ccagagcgga ggggaagtga ttggaaaaa aagtttctgc ttgaaaaagc cgagttagatg      420
cagcaattat cccagcagct aaaaagcgag atattaggac taagattgct tcgcttcaga      480
atgaagtta gaaaagctcag aaaaaaatag cggaaacaaa cctgaaaaaa tctgtcaaat      540
tagcaacaga ggcagctgag tccgcagcat cagatgggaa gactttctgc ataattccagc      600
tggatgtggg tcttgatgca gcagctgtgc gagaggccgt ttcaaaagtc atggaaaaaa      660
agggtagtgc gataatggtg ttcagcacag atgaagcac atgaagcgcg gttgtgtgtg      720
caggagtgcc agaaaaatca gaccagtta agccgttaga cgtcactgaa tgggtgacaa      780
ctgcatctgg tctctataaa ggaaggtgcg ggaaagggaa aggtgtgtct gcatcaggcg      840
agggaaacga tgctctccaa gtgcaggcgg ctttgatata ggcttcatca ttgcatcaaa      900
tgaagctcaa ctgatttggt cgaggagtta cataatctgt gaggtcagaa taacctctac      960
ttaatttgct ttcatttgta accgttttac acatgtttta agaatctgtt aaatttctct      1020
gtttcttgta tggaatttgt ggtatgacac tcttttagtc aaagttaaca atgctgttta      1080
taattccttg tgaaatgata tcttcccgct tgcgttgaaa ttggtatttt ttt
```

(2) INFORMATION FOR SEQ ID NO:688:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 303 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..303

(D) OTHER INFORMATION: / Ceres Seq. ID 1567688

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:688:

Gln	Ile	Lys	Asp	Glu	Leu	Asp	Val	Phe	Ser	Lys	Glu	Ala	Val	Leu	Ser
1		5							10					15	
Glu	Ala	Lys	Arg	Ile	Lys	Gly	Leu	Arg	Ala	Val	Phe	Gly	Glu	Val	Tyr
		20						25					30		
Pro	Asp	Pro	Val	Arg	Val	Val	Ser	Ile	Gly	Arg	Lys	Val	Glu	Asp	Leu
		35					40					45			
Leu	Ala	Asp	Pro	Glu	Asn	Asn	Glu	Trp	Ser	Leu	Leu	Ser	Ser	Glu	Phe
		50				55					60				
Cys	Gly	Gly	Thr	His	Ile	Thr	Asn	Thr	Arg	Glu	Ala	Lys	Ala	Phe	Ala
			70						75					80	
Leu	Leu	Ser	Glu	Lys	Gly	Ile	Ala	Lys	Gly	Ile	Arg	Arg	Val	Thr	Ala
			85						90				95		
Val	Thr	Thr	Glu	Cys	Ala	Phe	Asp	Ala	Leu	Asn	Ala	Ala	Ser	Leu	Leu
			100				105						110		
Glu	Arg	Glu	Val	Glu	Asp	Ala	Ser	Arg	Ala	Glu	Gly	Ser	Ala	Leu	Glu
			115				120					125			
Lys	Lys	Val	Ser	Ala	Leu	Lys	Ser	Arg	Val	Asp	Ala	Ala	Ile	Ile	Pro
			130			135					140				
Ala	Ala	Lys	Lys	Ala	Asp	Ile	Arg	Thr	Lys	Ile	Ala	Ser	Leu	Gln	Asn
			145			150				155				160	
Glu	Val	Arg	Lys	Ala	Gln	Lys	Lys	Ile	Ala	Glu	Gln	Asn	Leu	Lys	Lys
			165						170					175	
Ser	Val	Lys	Leu	Ala	Thr	Glu	Ala	Ala	Glu	Ser	Ala	Ala	Ser	Asp	Gly
			180						185				190		
Lys	Thr	Phe	Cys	Ile	Ile	Gln	Leu	Asp	Val	Gly	Leu	Asp	Ala	Ala	Ala
			195				200					205			
Val	Arg	Glu	Ala	Val	Ser	Lys	Val	Met	Glu	Lys	Lys	Gly	Met	Ser	Ile
			210			215					220				
Met	Val	Phe	Ser	Thr	Asp	Glu	Ser	Thr	Asn	Lys	Ala	Val	Val	Cys	Ala
			225			230				235				240	
Gly	Val	Pro	Glu	Lys	Ser	Asp	Gln	Phe	Lys	Pro	Leu	Asp	Val	Thr	Glu
			245						250					255	
Trp	Leu	Thr	Thr	Ala	Leu	Gly	Pro	Leu	Lys	Gly	Arg	Cys	Gly	Lys	Gly
			260			265							270		
Lys	Gly	Gly	Leu	Ala	Ser	Gly	Gln	Gly	Thr	Asp	Ala	Ser	Gln	Val	Gln
			275			280						285			
Ala	Ala	Leu	Asp	Met	Ala	Ser	Ser	Phe	Ala	Ser	Met	Lys	Leu	Asn	
			290			295					300				

(2) INFORMATION FOR SEQ ID NO:689:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1326 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1326

(D) OTHER INFORMATION: / Ceres Seq. ID 1567700

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:689:

aaaaagcact	ctgtgtgcct	ctgc aaatta	acaatttcct	cagaacaatt	acatttcgat	60
tcgatttcgat	tctcttatct	tcttgatctc	tggtttgttca	tctgtgtgtg	atctccagat	120
gttggtttgt	agaattttgt	cgcgagtaac	cgcgaacgcg	ggcatacgc	catctctatc	180
cgccgtcact	cttcgcgcga	ggaatcacac	tctctgtttc	tcgagccggt	ttcactccct	240
agctcacgat	ttctgcgata	agcttgttcc	agctcagatg	tctatgatgg	attcgtttgc	300
actgc aaagg	tccaattttt	cttctctcac	ctcgcctgaa	tcagatgaga	agaagaccca	360
cactgaggcc	tcaaaagcaa	gtgaagagaa	acctacagct	gaggcaaac	aaccaggctc	420
tgactctgaa	tctaagatt	ctgtgacaga	tcttgcaaaa	agaaagcgga	aggtgtctaa	480

aggagctgca	tcttcatctt	ctgaatcaga	tcttgagagt	gatgatgatg	aattgtcagc	540
cgatgatttg	gtgaagctcg	tagctgagaa	ggaagagcta	ctgtctcgaga	aggaagaaga	600
gattaagcag	ttgaaagaca	aagttctctg	cacttatgct	gagatggaga	atgtcatgga	660
cagaacaaga	cgtgatgctg	aaaacaccaa	aaagatgccc	gtacagaatt	ttgcaaaagc	720
ccatttggat	gtggcggaata	atcttggaa	agcttctctg	gttgctcaaa	aaagcttctc	780
aaagcttgac	acctcagaag	attctgctgg	agcagctcca	ctattaaaga	ccctttttaga	840
aggagtggag	atgactgaga	aacagctctg	tgaggtattt	aagaaatttg	gtatggagaa	900
gtatgatccg	ataaacgagc	catttgatcc	aaacagacat	aacgcagtgt	tcacagtccc	960
tgatgcttct	aagccagaag	gcacagttgc	tcattgtctg	aagtctggat	acacgctgta	1020
tgaccgagtt	ataagaccag	ctgaggtttg	tgttaccacg	ggaggagaga	accaagaaga	1080
aaagaagaag	tctgatgctt	aagaagaagt	cagctggttt	tcataaaatt	tgtaacgggt	1140
ctatgtttcc	attaacatct	tctcgagtct	tcagatcata	gtthtctttt	gtggtttggt	1200
tTatcattta	gatgaacaag	atctcccata	agttTgctgg	acatggcatt	tgcaagggaa	1260
atctcgcttb	tgtgtctgtt	tTctctcttc	tccatgctat	aattgaacga	ggaaaatctc	1320
atctt						

(2) INFORMATION FOR SEQ ID NO:690:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 327 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..327

(D) OTHER INFORMATION: / Ceres Seq. ID 1567701

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:690:

Met	Leu	Val	Leu	Arg	Ile	Leu	Ser	Arg	Val	Thr	Arg	Asn	Ala	Gly	Ile
1			5						10					15	
Arg	Ser	Ser	Leu	Ser	Ala	Val	Thr	Leu	Pro	Ala	Arg	Asn	Gln	Thr	Pro
			20					25					30		
Val	Phe	Ser	Ser	Arg	Phe	His	Ser	Leu	Ala	His	Asp	Phe	Ser	His	Lys
			35				40				45				
Leu	Val	Pro	Ala	Gln	Met	Ser	Met	Met	Asp	Ser	Phe	Ala	Leu	Gln	Arg
			50			55					60				
Phe	Asn	Phe	Ser	Ser	Ser	Thr	Ser	Pro	Glu	Ser	Asp	Glu	Lys	Lys	Thr
			65			70			75					80	
His	Thr	Glu	Ala	Ser	Lys	Thr	Ser	Glu	Glu	Lys	Pro	Thr	Ala	Glu	Ala
			85						90				95		
Asn	Gln	Pro	Gly	Leu	Asp	Ser	Glu	Ser	Lys	Asp	Ser	Val	Thr	Asp	Ser
			100				105						110		
Ala	Lys	Arg	Lys	Arg	Lys	Gly	Ala	Lys	Gly	Ala	Ala	Ser	Ser	Ser	Ser
			115				120				125				
Glu	Ser	Asp	Ser	Glu	Ser	Asp	Asp	Asp	Glu	Leu	Ser	Ala	Asp	Asp	Leu
			130			135					140				
Val	Lys	Leu	Val	Ala	Glu	Lys	Glu	Glu	Leu	Leu	Ser	Glu	Lys	Glu	Glu
			145			150			155					160	
Glu	Ile	Lys	Gln	Leu	Lys	Asp	Lys	Val	Leu	Arg	Thr	Tyr	Ala	Glu	Met
			165						170				175		
Glu	Asn	Val	Met	Asp	Arg	Thr	Arg	Arg	Asp	Ala	Glu	Asn	Thr	Lys	Lys
			180				185						190		
Tyr	Ala	Val	Gln	Asn	Phe	Ala	Lys	Ser	Leu	Leu	Asp	Val	Ala	Asp	Asn
			195				200				205				
Leu	Gly	Arg	Ala	Ser	Ser	Val	Val	Lys	Glu	Ser	Phe	Ser	Lys	Leu	Asp
			210			215					220				
Thr	Ser	Glu	Asp	Ser	Ala	Gly	Ala	Ala	Pro	Leu	Leu	Lys	Thr	Leu	Leu
			225			230			235					240	
Glu	Gly	Val	Glu	Met	Thr	Glu	Lys	Gln	Leu	Ala	Glu	Val	Phe	Lys	Lys
			245						250				255		
Phe	Gly	Met	Glu	Lys	Tyr	Asp	Pro	Ile	Asn	Glu	Pro	Phe	Asp	Pro	Asn
			260				265					270			

Arg His Asn Ala Val Phe Gln Val Pro Asp Ala Ser Lys Pro Glu Gly
275 280 285
Thr Val Ala His Val Leu Lys Ser Gly Tyr Thr Leu Tyr Asp Arg Val
290 295 300
Ile Arg Pro Ala Glu Val Gly Val Thr Gln Gly Gly Glu Asn Gln Glu
305 310 315 320
Glu Lys Lys Glu Ser Asp Ala
325

(2) INFORMATION FOR SEQ ID NO:691:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 274 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..274

(D) OTHER INFORMATION: / Ceres Seq. ID 1567702

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:691:

Met Ser Met Met Asp Ser Phe Ala Leu Gln Arg Phe Asn Phe Ser Ser
1 5 10 15
Ser Thr Ser Pro Glu Ser Asp Glu Lys Lys Thr His Thr Glu Ala Ser
20 25 30
Lys Thr Ser Glu Glu Lys Pro Thr Ala Glu Ala Asn Gln Pro Gly Leu
35 40 45
Asp Ser Glu Ser Lys Asp Ser Val Thr Asp Ser Ala Lys Arg Lys Arg
50 55 60
Lys Gly Ala Lys Gly Ala Ala Ser Ser Ser Ser Glu Ser Asp Ser Glu
65 70 75 80
Ser Asp Asp Asp Glu Leu Ser Ala Asp Asp Leu Val Lys Leu Val Ala
85 90 95
Glu Lys Glu Glu Leu Leu Ser Glu Lys Glu Glu Glu Ile Lys Gln Leu
100 105 110
Lys Asp Lys Val Leu Arg Thr Tyr Ala Glu Met Glu Asn Val Met Asp
115 120 125
Arg Thr Arg Arg Asp Ala Glu Asn Thr Lys Lys Tyr Ala Val Gln Asn
130 135 140
Phe Ala Lys Ser Leu Leu Asp Val Ala Asp Asn Leu Gly Arg Ala Ser
145 150 155 160
Ser Val Val Lys Glu Ser Phe Ser Lys Leu Asp Thr Ser Glu Asp Ser
165 170 175
Ala Gly Ala Ala Pro Leu Leu Lys Thr Leu Leu Glu Gly Val Glu Met
180 185 190
Thr Glu Lys Gln Leu Ala Glu Val Phe Lys Lys Phe Gly Met Glu Lys
195 200 205
Tyr Asp Pro Ile Asn Glu Pro Phe Asp Pro Asn Arg His Asn Ala Val
210 215 220
Phe Gln Val Pro Asp Ala Ser Lys Pro Glu Gly Thr Val Ala His Val
225 230 235 240
Leu Lys Ser Gly Tyr Thr Leu Tyr Asp Arg Val Ile Arg Pro Ala Glu
245 250 255
Val Gly Val Thr Gln Gly Gly Glu Asn Gln Glu Glu Lys Lys Glu Ser
260 265 270
Asp Ala

(2) INFORMATION FOR SEQ ID NO:692:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 272 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..272
(D) OTHER INFORMATION: / Ceres Seq. ID 1567703
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:692:

Met	Met	Asp	Ser	Phe	Ala	Leu	Gln	Arg	Phe	Asn	Phe	Ser	Ser	Ser	Thr	
1				5				10						15		
Ser	Pro	Glu	Ser	Asp	Glu	Lys	Lys	Thr	His	Thr	Glu	Ala	Ser	Lys	Thr	
			20					25					30			
Ser	Glu	Glu	Lys	Pro	Thr	Ala	Glu	Ala	Asn	Gln	Pro	Gly	Leu	Asp	Ser	
			35				40					45				
Glu	Ser	Lys	Asp	Ser	Val	Thr	Asp	Ser	Ala	Lys	Arg	Lys	Arg	Lys	Gly	
			50				55				60					
Ala	Lys	Gly	Ala	Ala	Ser	Ser	Ser	Ser	Glu	Ser	Asp	Ser	Glu	Ser	Asp	
65				70					75					80		
Asp	Asp	Glu	Leu	Ser	Ala	Asp	Asp	Leu	Val	Lys	Leu	Val	Ala	Glu	Lys	
			85					90					95			
Glu	Glu	Leu	Leu	Ser	Glu	Lys	Glu	Glu	Glu	Ile	Lys	Gln	Leu	Lys	Asp	
			100					105					110			
Lys	Val	Leu	Arg	Thr	Tyr	Ala	Glu	Met	Glu	Asn	Val	Met	Asp	Arg	Thr	
			115				120					125				
Arg	Arg	Asp	Ala	Glu	Asn	Thr	Lys	Lys	Tyr	Ala	Val	Gln	Asn	Phe	Ala	
			130				135					140				
Lys	Ser	Leu	Leu	Asp	Val	Ala	Asp	Asn	Leu	Gly	Arg	Ala	Ser	Ser	Val	
			145				150				155				160	
Val	Lys	Glu	Ser	Phe	Ser	Lys	Leu	Asp	Thr	Ser	Glu	Asp	Ser	Ala	Gly	
			165					170					175			
Ala	Ala	Pro	Leu	Leu	Lys	Thr	Leu	Leu	Glu	Gly	Val	Glu	Met	Thr	Glu	
			180				185						190			
Lys	Gln	Leu	Ala	Glu	Val	Phe	Lys	Lys	Phe	Gly	Met	Glu	Lys	Tyr	Asp	
			195				200					205				
Pro	Ile	Asn	Glu	Pro	Phe	Asp	Pro	Asn	Arg	His	Asn	Ala	Val	Phe	Gln	
			210			215					220					
Val	Pro	Asp	Ala	Ser	Lys	Pro	Glu	Gly	Thr	Val	Ala	His	Val	Leu	Lys	
			225			230				235				240		
Ser	Gly	Tyr	Thr	Leu	Tyr	Asp	Arg	Val	Ile	Arg	Pro	Ala	Glu	Val	Gly	
			245					250					255			
Val	Thr	Gln	Gly	Gly	Glu	Asn	Gln	Glu	Glu	Lys	Lys	Glu	Ser	Asp	Ala	
			260					265					270			

(2) INFORMATION FOR SEQ ID NO:693:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1418 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1418

(D) OTHER INFORMATION: / Ceres Seq. ID 1567704

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:693:

ataggaactcg	acaaatagaa	gaagcagatt	cgttgctaac	gaaGtaaagg	attcttaacttt	60
tttagtcttt	gctttagaaa	taacttataa	ctacaagtca	gagagggggcc	gagtaaatcg	120
gaaagatgac	ggcgccgatg	atcctgaccg	gaagtgatc	ggcgccggag	agagacgctc	180
ggatggcgca	cactgctatg	gcgtttgttc	agctctttaa	tggtggatgc	catgtgattc	240
ctaaagtatc	tcttaagtgt	ggagtcacac	agcttgtctt	ctgtgtatgc	cgtgatcttc	300
ttgtctctc	tattctcgct	cctcttgctt	acttcgcgca	aagaaagatc	agaactccaa	360

tgaataaaaag	ccttctcttgg	tcattcttctt	ttctgggctt	agcaggggga	tttgggaacc	420
agttgttatt	ttctatcggt	cttacatata	caaataccac	ttatgctgct	ggcattcaac	480
catccatccc	ggctttccac	ttctcttggg	ctgtcatgat	gggtacagaa	agagtgtaatt	540
tggttgagaat	cgaagggtcaa	actaagggtg	gaggcacact	tggtgtgtgt	atgggtgctg	600
tcctcatggt	tgattttcga	ggtccggcct	tgtaggaga	taaagatgca	gactttgcga	660
tgaacaatga	aaatcagtgct	aaagggtcaac	ctgagcctac	tggttggtta	gtctctgggt	720
ttctcgatct	tggaatttgag	caatggcaca	ttggagtttt	atgcttgatt	ggaaactgca	780
tggtgtatggc	tacttttctt	gccattcagg	cggcactttt	gaagaagtat	ccggcaaatc	840
ttctctgttg	tgcaattatca	tactYcttgg	gcacagtact	aatgtgcaca	acagctttct	900
ttatggtaaa	ggagcccatg	gattgggaagc	taacacaatc	tgaggttctt	gcagttatat	960
atgcaggagt	tatcgcatca	gcactaaact	atggactctt	gactttgtcc	aataagatta	1020
ttggtctctgc	cttgggtgct	ctctacaatc	ctcttcaacc	cgtctgcata	gctttcctat	1080
cgagatactt	ttctcggtagc	cccatttato	tcggaagcgt	tggtgggtgga	ttcttcatca	1140
ttctaggaact	ctatatggtc	acttgggcac	cgttttagaga	gcgaaaaaca	gcggtttccg	1200
ggatttgggat	tgccgccccat	gggtctaaaaa	cctcagagcc	cttgatattt	aatgggacag	1260
ttaacagact	aggacagttg	ttttctggat	taaccagttc	ctctgtgaaa	ttcgcagact	1320
aaaaagatac	caaaaagtta	agattccagac	gagatcccat	tttacaacag	ctataacttt	1380
tggttaactt	tcactctctta	ttaatatctt	cttcgatt			

(2) INFORMATION FOR SEQ ID NO:694:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 398 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..398

(D) OTHER INFORMATION: / Ceres Seq. ID 1567705

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:694:

Met	Thr	Ala	Pro	Met	Ile	Leu	Thr	Gly	Ser	Gly	Ser	Ala	Ala	Glu	Arg
1			5					10						15	
Asp	Ala	Arg	Met	Ala	His	Thr	Ala	Met	Ala	Phe	Val	Gln	Leu	Phe	Asn
			20					25						30	
Gly	Gly	Tyr	His	Val	Ile	Thr	Lys	Val	Ala	Leu	Asn	Val	Gly	Val	Asn
			35					40						45	
Gln	Leu	Val	Phe	Cys	Val	Cys	Arg	Asp	Leu	Leu	Ala	Leu	Ser	Ile	Leu
			50					55						60	
Ala	Pro	Leu	Ala	Tyr	Phe	Arg	Glu	Arg	Lys	Ile	Arg	Thr	Pro	Met	Asn
			65							75				80	
Lys	Ser	Leu	Leu	Leu	Ser	Phe	Phe	Phe	Leu	Gly	Leu	Ala	Gly	Val	Phe
			85						90					95	
Gly	Asn	Gln	Leu	Leu	Phe	Leu	Ile	Gly	Leu	Thr	Tyr	Thr	Asn	Pro	Thr
			100					105						110	
Tyr	Ala	Ala	Ile	Gln	Pro	Ser	Ile	Pro	Val	Phe	Thr	Phe	Leu	Leu	
			115					120						125	
Ala	Val	Met	Met	Gly	Thr	Glu	Arg	Val	Asn	Leu	Leu	Arg	Ile	Glu	Gly
			130					135						140	
Gln	Thr	Lys	Val	Gly	Gly	Thr	Leu	Val	Cys	Val	Met	Gly	Ala	Val	Phe
			145					150						155	
Met	Val	Val	Phe	Arg	Gly	Pro	Ala	Leu	Leu	Gly	Asp	Lys	Asp	Ala	Asp
			165						170					175	
Phe	Ala	Met	Asn	Asn	Glu	Ile	Ser	Ala	Lys	Gly	Gln	Pro	Glu	Pro	Thr
			180					185						190	
Gly	Trp	Leu	Val	Ser	Gly	Phe	Leu	Asp	Leu	Gly	Phe	Glu	Gln	Trp	His
			195					200						205	
Ile	Gly	Val	Leu	Cys	Leu	Ile	Gly	Asn	Cys	Met	Cys	Met	Ala	Thr	Phe
			210					215						220	
Leu	Ala	Ile	Gln	Ala	Pro	Leu	Leu	Lys	Lys	Tyr	Pro	Ala	Asn	Leu	Ser
			225					230						235	
Val	Ala	Ala	Leu	Ser	Tyr	Xaa	Phe	Gly	Thr	Val	Leu	Met	Cys	Thr	Thr

(2) INFORMATION FOR SEO ID NO:695:

(A) LENGTH: 394 amino acids

(C) STRANDEDNESS:

(D) TOPOLOGY: lin

MOLECULE TYPE: peptid

(ix) FEATURE:

(A) NAM

(B) LOCATION: 1..394

(D) OTHER INFORMATION

SEQUENCE DESCRIPTION: SEQ ID NO:695:

Ile Leu Thr Gly Ser Gly Ser Ala Ala Glu A

Ala	His	Thr	20	Ala	Met	Ala	Phe	Val	Gln	Leu	Phe	Asn	Gly	Gly	Tyr	His
Val	Ile	Thr	35	Val	Ala	Leu	Asn	Val	Gly	Val	Asn	Gln	Leu	Val	Phe	
Cys	Val	Cys	50	Arg	Asp	Leu	Ala	Leu	Ser	Ile	Leu	Ala	Pro	Leu	Ala	
Tyr	Phe	Arg	65	Glu	Arg	Gly	Ile	Arg	Thr	Pro	Met	Asn	Lys	Ser	Leu	
Leu	Ser	Phe	85	Phe	Leu	Gly	Leu	Ala	Gly	Val	Phe	Gly	Asn	Gln	Leu	
Leu	Phe	Leu	100	Ile	Gly	Leu	Thr	Tyr	Thr	Asn	Pro	Thr	Tyr	Ala	Ala	
Ile	Gln	Pro	115	Ser	Ile	Pro	Val	Phe	Thr	Phe	Leu	Leu	Ala	Val	Met	
Gly	Thr	Glu	130	Arg	Val	Asn	Leu	Leu	Arg	Ile	Glu	Gly	Gln	Thr	Lys	
Gly	Gly	Thr	145	Leu	Val	Cys	Val	Met	Gly	Ala	Val	Phe	Met	Val	Val	
Arg	Gly	Pro	165	Ala	Leu	Gly	Asp	Lys	Asp	Ala	Asp	Phe	Ala	Met	Asn	
Asn	Glu	Ile	180	Ser	Ala	Lys	Gly	Gln	Pro	Glu	Pro	Thr	Gly	Trp	Leu	
Ser	Gly	Phe	195	Leu	Asp	Leu	Gly	Phe	Glu	Gln	Trp	His	Ile	Gly	Val	
Cys	Leu	Ile	210	Gly	Asn	Cys	Met	Cys	Met	Ala	Thr	Phe	Leu	Ala	Ile	
Ala	Pro	Leu	225	Leu	Lys	Tyr	Pro	Ala	Asn	Leu	Ser	Val	Ala	Ala	Leu	

Ser Tyr Xaa Phe Gly Thr Val Leu Met Cys Thr Thr Ala Phe Phe Met
245 250 255
Val Lys Glu Pro Leu Asp Trp Lys Leu Thr Gln Ser Glu Val Leu Ala
260 265 270
Val Ile Tyr Ala Gly Val Ile Ala Ser Ala Leu Asn Tyr Gly Leu Leu
275 280 285
Thr Trp Ser Asn Lys Ile Ile Gly Pro Ala Leu Val Ala Leu Tyr Asn
290 295 300
Pro Leu Gln Pro Ala Ala Ser Ala Phe Leu Ser Arg Ile Phe Leu Gly
305 310 315 320
Ser Pro Ile Tyr Leu Gly Ser Val Val Gly Gly Phe Phe Ile Ile Leu
325 330 335
Gly Leu Tyr Met Val Thr Trp Ala Ser Phe Arg Glu Arg Lys Thr Ala
340 345 350
Val Ser Gly Ile Gly Ile Ala Pro His Gly Leu Lys Thr Ser Glu Pro
355 360 365
Leu Ile Phe Asn Gly Thr Val Asn Arg Leu Gly Gln Leu Phe Ser Gly
370 375 380
Leu Pro Ser Ser Ser Val Lys Ser Ala Asp
385 390

(2) INFORMATION FOR SEQ ID NO:696:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 379 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..379

(D) OTHER INFORMATION: / Ceres Seq. ID 1567707

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:696:

Met Ala His Thr Ala Met Ala Phe Val Gln Leu Phe Asn Gly Gly Tyr
1 5 10 15
His Val Ile Thr Lys Val Ala Leu Asn Val Gly Val Asn Gln Leu Val
20 25 30
Phe Cys Val Cys Arg Asp Leu Leu Ala Leu Ser Ile Leu Ala Pro Leu
35 40 45
Ala Tyr Phe Arg Glu Arg Lys Ile Arg Thr Pro Met Asn Lys Ser Leu
50 55 60
Leu Leu Ser Phe Phe Phe Leu Gly Leu Ala Gly Val Phe Gly Asn Gln
65 70 75 80
Leu Leu Phe Leu Ile Gly Leu Thr Tyr Thr Asn Pro Thr Tyr Ala Ala
85 90 95
Ala Ile Gln Pro Ser Ile Pro Val Phe Thr Phe Leu Leu Ala Val Met
100 105 110
Met Gly Thr Glu Arg Val Asn Leu Leu Arg Ile Glu Gly Gln Thr Lys
115 120 125
Val Gly Gly Thr Leu Val Cys Val Met Gly Ala Val Phe Met Val Val
130 135 140
Phe Arg Gly Pro Ala Leu Leu Gly Asp Lys Asp Ala Asp Phe Ala Met
145 150 155 160
Asn Asn Glu Ile Ser Ala Lys Gly Gln Pro Glu Pro Thr Gly Trp Leu
165 170 175
Val Ser Gly Phe Leu Asp Leu Gly Phe Glu Gln Trp His Ile Gly Val
180 185 190
Leu Cys Leu Ile Gly Asn Cys Met Cys Met Ala Thr Phe Leu Ala Ile
195 200 205
Gln Ala Pro Leu Leu Lys Lys Tyr Pro Ala Asn Leu Ser Val Ala Ala
210 215 220
Leu Ser Tyr Xaa Phe Gly Thr Val Leu Met Cys Thr Thr Ala Phe Phe

225 230 235 240
Met Val Lys Glu Pro Leu Asp Trp Lys Leu Thr Gln Ser Glu Val Leu
245 250 255
Ala Val Ile Tyr Ala Gly Val Ile Ala Ser Ala Leu Asn Tyr Gly Leu
260 265 270
Leu Thr Trp Ser Asn Lys Ile Ile Gly Pro Ala Leu Val Ala Leu Tyr
275 280 285
Asn Pro Leu Gln Pro Ala Ala Ser Ala Phe Leu Ser Arg Ile Phe Leu
290 295 300
Gly Ser Pro Ile Tyr Leu Gly Ser Val Val Gly Gly Phe Phe Ile Ile
305 310 315 320
Leu Gly Leu Tyr Met Val Thr Trp Ala Ser Phe Arg Glu Arg Lys Thr
325 330 335
Ala Val Ser Gly Ile Gly Ile Ala Pro His Gly Leu Lys Thr Ser Glu
340 345 350
Pro Leu Ile Phe Asn Gly Thr Val Asn Arg Leu Gly Gln Leu Phe Ser
355 360 365
Gly Leu Pro Ser Ser Ser Val Lys Ser Ala Asp
370 375

(2) INFORMATION FOR SEQ ID NO:697:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 713 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..713

(D) OTHER INFORMATION: / Ceres Seq. ID 1567711

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:697:

atcaagataa gcttatagtt atcactaaga gttttgtcta cgtacatttt gtgatcaaac 60
aagttaataca tcaaaagatg gaaggcaaaa ctgtgatctc aagtctgctc ataataagtc 120
ttgtctttagc acagattcaa gtagaagcaa aaatctgctg tctaccacag gatgatatag 180
ctgtgtattt tgtatgcatg ctttcogtgt catccaatt ttattgtcta ttaagagata 240
aatgcaaaaa tacatctcag acgatatgtc ctcggggata tactaatgac attctcgaaa 300
attctgtgtga tgcgtgcaat gaattattgca agctagggtg tgcattcctt gtgtgtggtg 360
ccttgaccac tctccaaaac tttagcgcga gtaaaagtatt gagtgaaagc gttgaacaat 420
gcaccaagggc atgtttctct gtcgtgcacc gagGatctac cgcgcgagtt aaaaagtgcct 480
aaacaagtat attttaaagt gaagggtggt catcattcag agtggcgcta ctgtttttac 540
ggaataattg tcgtctatcg atgtatgttg taaaaaaaaa tgctagacta tgggtgctagt 600
actgttttaat aagttgtttc cggtttgcca atgtgtcatg agagtttttg atcctagatt 660
gtatatccct tctacttctc ttctcttaaa taaataataa tgtgtccttc tgc

(2) INFORMATION FOR SEQ ID NO:698:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 159 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..159

(D) OTHER INFORMATION: / Ceres Seq. ID 1567712

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:698:

Gln Asp Lys Leu Ile Val Ile Thr Lys Ser Phe Val Tyr Val His Phe
1 5 10 15
Val Ile Lys Gln Val Ile Asn Gln Lys Met Glu Gly Lys Thr Val Ile
20 25 30
Ser Ser Leu Leu Ile Ile Ser Leu Val Leu Ala Gln Ile Gln Val Glu
35 40 45

Ala Lys Ile Cys Cys Pro Thr Lys Asp Asp Arg Ser Val Tyr Phe Val
50 55 60
Cys Met Leu Ser Val Ser Ser Gln Phe Tyr Cys Leu Lys Ser Lys
65 70 75 80
Cys Lys Asn Thr Ser Ser Gln Thr Ile Cys Pro Gly Tyr Thr Asn Asp
85 90 95
Ile Leu Glu Asn Ser Gly Asp Ala Val Asn Glu Tyr Cys Lys Leu Gly
100 105 110
Cys Ala Ser Ser Val Cys Gly Ala Leu Thr Thr Leu Gln Asn Phe Asp
115 120 125
Ala Ser Lys Val Leu Ser Glu Ala Val Glu Gln Cys Thr Lys Ala Cys
130 135 140
Ser Ser Val Cys Thr Gly Gly Ser Thr Ala Ala Val Lys Ser Ala
145 150 155

(2) INFORMATION FOR SEQ ID NO:699:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 134 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..134
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567713

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:699:

Met Glu Gly Lys Thr Val Ile Ser Ser Leu Leu Ile Ile Ser Leu Val
1 5 10 15
Leu Ala Gln Ile Gln Val Glu Ala Lys Ile Cys Cys Pro Thr Lys Asp
20 25 30
Asp Arg Ser Val Tyr Phe Val Cys Met Leu Ser Val Ser Ser Gln Phe
35 40 45
Tyr Cys Leu Leu Lys Ser Lys Cys Lys Asn Thr Ser Gln Thr Ile Cys
50 55 60
Pro Pro Gly Tyr Thr Asn Asp Ile Leu Glu Asn Ser Gly Asp Ala Val
65 70 75 80
Asn Glu Tyr Cys Lys Leu Gly Cys Ala Ser Ser Val Cys Gly Ala Leu
85 90 95
Thr Thr Leu Gln Asn Phe Asp Ala Ser Lys Val Leu Ser Glu Ala Val
100 105 110
Glu Gln Cys Thr Lys Ala Cys Ser Ser Val Cys Thr Gly Gly Ser Thr
115 120 125
Ala Ala Val Lys Ser Ala
130

(2) INFORMATION FOR SEQ ID NO:700:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 94 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..94
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567714

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:700:

Met Leu Ser Val Ser Ser Gln Phe Tyr Cys Leu Leu Lys Ser Lys Cys
1 5 10 15
Lys Asn Thr Ser Gln Thr Ile Cys Pro Gly Tyr Thr Asn Asp Ile
20 25 30
Leu Glu Asn Ser Gly Asp Ala Val Asn Glu Tyr Cys Lys Leu Gly Cys

35 40 45
Ala Ser Ser Val Cys Gly Ala Leu Thr Thr Leu Gln Asn Phe Asp Ala
50 55 60
Ser Lys Val Leu Ser Glu Ala Val Glu Gln Cys Thr Lys Ala Cys Ser
65 70 75 80
Ser Val Cys Thr Gly Gly Ser Thr Ala Ala Val Lys Ser Ala
85 90

(2) INFORMATION FOR SEQ ID NO:701:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 587 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..587
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567715

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:701:

atatataaca	ataacacttt	gggtttttaga	ctttagatcac	gaatcaaaaa	catttgagat	60
aaaaatcaga	aaagtaaaaga	gacgaaaaatg	gcggatcaaac	aagcaggaac	aatcgtcgga	120
ggagttcgcg	atatgtatgc	aaatgctaata	gatcttcaag	tcgagagtct	cgctcgtttc	180
gctgtcgaag	agcataacaa	gaacgagaac	ttgactctgg	agtacaagag	gctccttggg	240
gcgaaaacac	aggttgtggc	aggaacaatg	caccatctaa	ctgtggagggt	ggctgatggt	300
gagaccaata	aggtctatga	ggccaagggt	ttggagaaa	cttggggagaa	tctcaagcag	360
ttggagaggt	tcaaccacct	tcacgatggt	taatccgatg	ccttgagctt	tctctgcggc	420
ttgagtgaag	tccttgtgtg	ctctcagacc	acgtgataag	agttctgggt	taaccaagtt	480
aactctctta	ataagtgaaa	tccagtcaca	tgtgtttgaa	ctggatttgt	gtgtatctct	540
tgactctcgt	ttgtgtattg	ctattagcaa	actctcactt	tttatcc		

(2) INFORMATION FOR SEQ ID NO:702:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 70 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..70
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567716

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:702:

Tyr	Ile	Thr	Ile	Thr	Leu	Trp	Val	Leu	Asp	Phe	Arg	Tyr	Glu	Ser	Lys	
1				5				10					15			
Thr	Phe	Glu	Ile	Lys	Ile	Arg	Lys	Val	Lys	Arg	Arg	Lys	Trp	Arg	Ile	
				20				25					30			
Asn	Lys	Gln	Glu	Gln	Ser	Ser	Glu	Glu	Phe	Ala	Ile	Leu	Met	Gln	Met	
				35				40					45			
Leu	Met	Ile	Phe	Lys	Ser	Arg	Val	Ser	Leu	Val	Ser	Leu	Ser	Met	Ser	
				50				55					60			
Ile	Thr	Arg	Thr	Arg	Thr											
65				70												

(2) INFORMATION FOR SEQ ID NO:703:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 101 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..101

(D) OTHER INFORMATION: / Ceres Seq. ID 1567717

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:703:

Met Ala Asp Gln Gln Ala Gly Thr Ile Val Gly Gly Val Arg Asp Ile
1 5 10 15
Asp Ala Asn Ala Asn Asp Leu Gln Val Glu Ser Leu Ala Arg Phe Ala
20 25 30
Val Asp Glu His Asn Lys Asn Glu Asn Leu Thr Leu Glu Tyr Lys Arg
35 40 45
Leu Leu Gly Ala Lys Thr Gln Val Val Ala Gly Thr Met His His Leu
50 55 60
Thr Val Glu Val Ala Asp Gly Glu Thr Asn Lys Val Tyr Glu Ala Lys
65 70 75 80
Val Leu Glu Lys Ala Trp Glu Asn Leu Lys Gln Leu Glu Ser Phe Asn
85 90 95
His Leu His Asp Val
100

(2) INFORMATION FOR SEQ ID NO:704:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 587 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..587

(D) OTHER INFORMATION: / Ceres Seq. ID 1567721

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:704:

cttcgctctt atgtgtctct gcccaaat aaaaactcag aaaccttaga aaattccgat 60
tcatacaactg agagagaaga agaattgaga aatgatgaag cgctcgatcc caacgttcaa 120
ccgcactctg gtgcagagag tcattccagcc cgctaaaacc gaaagcgcca ttctcttacc 180
tgagaaatcc tccaagtctg actcaggcaa ggtgatagct gttggacctg gatcaaggga 240
taaggacggg aaattgattc cggtctctgt gaaggaaggc gacactgttc ttcttccaga 300
gtacggtggt acacaggctca agctcggcga gaacgagtac catctcttcc gggacgagga 360
tgttttggga actttgcaag aggattgaaa aggctaagct tgccaactta accacgaggg 420
ttcatgttgg tgtttgggt atgaggagaa gtcatttata aattagttaa tcttgaagat 480
gtggttggac ttgttggct ttatcattg aatctacctt tatgaacctg tcttgaatt 540
tttacaatat ggcataatc acatggataa ccCaagtgtt gcatctt

(2) INFORMATION FOR SEQ ID NO:705:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..51

(D) OTHER INFORMATION: / Ceres Seq. ID 1567722

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:705:

Leu Pro Ser Tyr Val Ser Leu Pro Gln Ile Lys Asn Ser Glu Thr Leu
1 5 10 15
Glu Asn Ser Asp Ser Ser Thr Glu Arg Glu Glu Glu Leu Arg Asn Asp
20 25 30
Glu Ala Ser Asp Pro Asn Val Gln Pro His Leu Gly Ala Glu Ser His
35 40 45
Pro Ala Arg
50

(2) INFORMATION FOR SEQ ID NO:706:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 98 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..98
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1567723
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:706:

Met	Met	Lys	Arg	Leu	Ile	Pro	Thr	Phe	Asn	Arg	Ile	Leu	Val	Gln	Arg
1				5				10						15	
Val	Ile	Gln	Pro	Ala	Lys	Thr	Glu	Ser	Gly	Ile	Leu	Leu	Pro	Glu	Lys
			20				25				30				
Ser	Ser	Lys	Leu	Asn	Ser	Gly	Lys	Val	Ile	Ala	Val	Gly	Pro	Gly	Ser
		35				40					45				
Arg	Asp	Lys	Asp	Gly	Lys	Leu	Ile	Pro	Val	Ser	Val	Lys	Glu	Gly	Asp
	50				55					60					
Thr	Val	Leu	Leu	Pro	Glu	Tyr	Gly	Gly	Thr	Gln	Val	Lys	Leu	Gly	Glu
65				70					75					80	
Asn	Glu	Tyr	His	Leu	Phe	Arg	Asp	Glu	Asp	Val	Leu	Gly	Thr	Leu	His
			85					90						95	

Glu Asp

- (2) INFORMATION FOR SEQ ID NO:707:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 97 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..97
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1567724
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:707:

Met	Lys	Arg	Leu	Ile	Pro	Thr	Phe	Asn	Arg	Ile	Leu	Val	Gln	Arg	Val
1			5					10					15		
Ile	Gln	Pro	Ala	Lys	Thr	Glu	Ser	Gly	Ile	Leu	Leu	Pro	Glu	Lys	Ser
			20				25				30				
Ser	Lys	Leu	Asn	Ser	Gly	Lys	Val	Ile	Ala	Val	Gly	Pro	Gly	Ser	Arg
		35			40						45				
Asp	Lys	Asp	Gly	Lys	Leu	Ile	Pro	Val	Ser	Val	Lys	Glu	Gly	Asp	Thr
	50			55						60					
Val	Leu	Leu	Pro	Glu	Tyr	Gly	Gly	Thr	Gln	Val	Lys	Leu	Gly	Glu	Asn
65				70					75					80	
Glu	Tyr	His	Leu	Phe	Arg	Asp	Glu	Asp	Val	Leu	Gly	Thr	Leu	His	Glu
			85					90						95	

Asp

- (2) INFORMATION FOR SEQ ID NO:708:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1209 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..1209
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1567738
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:708:

ataccctcat	ttaaatggcg	gagattacaa	gggaaagaga	caactccaat	tcaaagctct	60
gattttttcc	accaatcccc	attttttccc	ttttacaatt	cttaagctag	ttttatactt	120
ttctttctcc	tttcatttgg	gttaagagaa	gccatggata	ccgagtttct	ccgaacccta	180
gatcgctcaga	ttcttttggg	tgtcttcggt	gcttttcgtc	ccgttggtgc	tggtgctgct	240
tatttttcta	catctctcaa	gaacgcgaga	gtgtgttttg	atccagagaa	tttcaaggag	300
ttcaagcttg	ttaagagaca	tcagcttagt	cacaatgtgg	ccaagtctgt	ttttgaactc	360
ccaactttcta	ctctctgtgt	gggtcttccc	attggaccaac	acatcagttg	caggggaaag	420
gatggctcaag	gagaggatgt	tattaagcca	tacaccgccga	ctacgttaga	ctctgacgtt	480
ggacgttttcg	aacttgtcat	taagatgtat	cgcgaaggac	ggatgtctca	tcatttcagg	540
gagatgcgtg	ttggagacca	tcttgccgta	aagggaacca	agggtaggtt	caagtatcaa	600
ccaggtcagt	ttaggggcatt	tggaaatgctt	gctggaggtt	caggcatcac	tcctatgttc	660
caagtggcca	gagcaattct	agaaaaacca	acagacaaga	caaaggtgca	ttctattttac	720
gccaacgtca	catcacgaca	cattctcttg	aaggagaagt	tgagggtctc	tactaccaat	780
taccctgaac	aattttaaaat	ctctctatgt	ttgaaccagc	ctcgggaagt	atgggtatggt	840
gggtgtggat	ttgtatcaaa	ggaaatgatt	cagactcatt	gccctgcacc	tgcactctgat	900
atcagatccc	taagatcgcg	accaccgccca	atgaacaagg	ccatggctgc	aaaccttgaa	960
gctctgggat	actctccgga	gatgcaattc	cagttctgat	ctgaatatct	ttcttttggt	1020
gctctgaaac	ggaactcata	ataatttagt	tacaatccca	actacgagag	ttgtgtcttta	1080
actgagttag	agttgtatct	ctgttgtgtg	tCtgtttagc	ccactgaaa	gtttccattg	1140
attggtttac	gaattgttta	Ygacattttg	gttcacatat	accggttttg	tgcaaacact	1200
ttgtgctgc						

(2) INFORMATION FOR SEQ ID NO:709:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 281 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..281

(D) OTHER INFORMATION: / Ceres Seq. ID 1567739

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:709:

Met	Asp	Thr	Glu	Phe	Leu	Arg	Thr	Leu	Asp	Arg	Gln	Ile	Leu	Leu	Gly
1					5					10				15	
Val	Phe	Val	Ala	Phe	Val	Ala	Val	Gly	Ala	Gly	Ala	Ala	Tyr	Phe	Leu
					20					25				30	
Thr	Ser	Ser	Lys	Lys	Arg	Arg	Val	Cys	Leu	Asp	Pro	Glu	Asn	Phe	Lys
					35					40				45	
Glu	Phe	Lys	Leu	Val	Lys	Arg	His	Gln	Leu	Ser	His	Asn	Val	Ala	Lys
					50					55				60	
Phe	Val	Phe	Glu	Leu	Pro	Thr	Ser	Thr	Ser	Val	Leu	Gly	Leu	Pro	Ile
65					70					75				80	
Gly	Gln	His	Ile	Ser	Cys	Arg	Gly	Lys	Asp	Gly	Gln	Gly	Glu	Asp	Val
					85					90				95	
Ile	Lys	Pro	Tyr	Thr	Pro	Thr	Thr	Leu	Asp	Ser	Asp	Val	Gly	Arg	Phe
					100					105				110	
Glu	Leu	Val	Ile	Lys	Met	Tyr	Pro	Gln	Gly	Arg	Met	Ser	His	His	Phe
					115					120				125	
Arg	Glu	Met	Arg	Val	Gly	Asp	His	Leu	Ala	Val	Lys	Gly	Pro	Lys	Gly
					130					135				140	
Arg	Phe	Lys	Tyr	Gln	Pro	Gly	Gln	Phe	Arg	Ala	Phe	Gly	Met	Leu	Ala
145					150					155				160	
Gly	Gly	Ser	Gly	Ile	Thr	Pro	Met	Phe	Gln	Val	Ala	Arg	Ala	Ile	Leu
					165					170				175	
Glu	Asn	Pro	Thr	Asp	Lys	Thr	Lys	Val	His	Leu	Ile	Tyr	Ala	Asn	Val
					180					185				190	
Thr	Tyr	Asp	Asp	Ile	Leu	Leu	Lys	Glu	Glu	Leu	Glu	Gly	Leu	Thr	Thr
					195					200				205	
Asn	Tyr	Pro	Glu	Gln	Phe	Lys	Ile	Phe	Tyr	Val	Leu	Asn	Gln	Pro	Pro
					210					215				220	

Glu Val Trp Asp Gly Gly Val Gly Phe Val Ser Lys Glu Met Ile Gln
225 230 235 240
Thr His Cys Pro Ala Pro Ala Ser Asp Ile Gln Ile Leu Arg Cys Gly
245 250 255
Pro Pro Pro Met Asn Lys Ala Met Ala Ala Asn Leu Glu Ala Leu Gly
260 265 270
Tyr Ser Pro Glu Met Gln Phe Gln Phe
275 280

(2) INFORMATION FOR SEQ ID NO:710:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 164 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..164

(D) OTHER INFORMATION: / Ceres Seq. ID 1567740

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:710:

Met Tyr Pro Gln Gly Arg Met Ser His His Phe Arg Glu Met Arg Val
1 5 10 15
Gly Asp His Leu Ala Val Lys Gly Pro Lys Gly Arg Phe Lys Tyr Gln
20 25 30
Pro Gly Gln Phe Arg Ala Phe Gly Met Leu Ala Gly Gly Ser Gly Ile
35 40 45
Thr Pro Met Phe Gln Val Ala Arg Ala Ile Leu Glu Asn Pro Thr Asp
50 55 60
Lys Thr Lys Val His Leu Ile Tyr Ala Asn Val Thr Tyr Asp Asp Ile
65 70 75 80
Leu Leu Lys Glu Glu Leu Glu Gly Leu Thr Thr Asn Tyr Pro Glu Gln
85 90 95
Phe Lys Ile Phe Tyr Val Leu Asn Gln Pro Pro Glu Val Trp Asp Gly
100 105 110
Gly Val Gly Phe Val Ser Lys Glu Met Ile Gln Thr His Cys Pro Ala
115 120 125
Pro Ala Ser Asp Ile Gln Ile Leu Arg Cys Gly Pro Pro Pro Met Asn
130 135 140
Lys Ala Met Ala Ala Asn Leu Glu Ala Leu Gly Tyr Ser Pro Glu Met
145 150 155 160
Gln Phe Gln Phe

(2) INFORMATION FOR SEQ ID NO:711:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 158 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..158

(D) OTHER INFORMATION: / Ceres Seq. ID 1567741

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:711:

Met Ser His His Phe Arg Glu Met Arg Val Gly Asp His Leu Ala Val
1 5 10 15
Lys Gly Pro Lys Gly Arg Phe Lys Tyr Gln Pro Gly Gln Phe Arg Ala
20 25 30
Phe Gly Met Leu Ala Gly Gly Ser Gly Ile Thr Pro Met Phe Gln Val
35 40 45
Ala Arg Ala Ile Leu Glu Asn Pro Thr Asp Lys Thr Lys Val His Leu

50	55	60
Ile Tyr Ala Asn Val Thr Tyr Asp Asp Ile Leu Leu Lys Glu Glu Leu		
65	70	75
Glu Gly Leu Thr Thr Asn Tyr Pro Glu Gln Phe Lys Ile Phe Tyr Val		80
	85	90
Leu Asn Gln Pro Pro Glu Val Trp Asp Gly Gly Val Gly Phe Val Ser		95
	100	105
Lys Glu Met Ile Gln Thr His Cys Pro Ala Pro Ala Ser Asp Ile Gln		110
	115	120
Ile Leu Arg Cys Gly Pro Pro Pro Met Asn Lys Ala Met Ala Ala Asn		125
	130	135
Leu Glu Ala Leu Gly Tyr Ser Pro Glu Met Gln Phe Gln Phe		140
145	150	155

(2) INFORMATION FOR SEQ ID NO:712:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1203 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1203
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567750

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:712:

ataaaaaaaa	aaacaaaaat	ataatgtgga	cttctaaaaa	cataagcttc	actttcttcca	60
tcacacaact	acttctcgcg	tctgtcaacg	catccgcaaa	ggccaaaaac	caaccgctgt	120
tcccagcgat	tctaactctt	ggtgattcaa	cagtcgacac	aggcaacaat	aactaccctt	180
cacaaacact	cttcagagct	aaacatgttc	cttacgggat	tgatctccca	aaccactcac	240
ctaacgggaag	attctcaaac	ggaaaaattt	tctccgacat	aatcgcaacc	aaactcaaca	300
ctaaacaggtt	tgttctctcc	ttcttacaac	caaatctcac	cgaccaagaa	attgtaaccg	360
gagtcgtgttt	tgcattcacga	ggtgccgggt	acgatgacca	aaccagtctc	acgacacaag	420
cgattcgtgt	ctcgggaacaa	ccaaatatgt	tcaagagtta	ctttgctcgt	cttaagagta	480
tcgtaggaga	caagaaagcc	atgaagatca	taaacaaatgc	tttggtggtt	gtgagtcgag	540
ggcctaataga	tttcaatett	aattattacg	agggtccccc	atggcgctcg	atgtatcccta	600
gcatttctga	ttaccaagat	tttgttctta	ataagcttaa	caatttcgtg	atggagcttt	660
acagcctagg	ttgccggaaa	attttggtcg	gaggtttacc	gccaatggga	tgtttaccga	720
ttcaaatgac	tgtctcaattc	cgcaacgtcc	taaggttttc	cttggaacaa	gagacacagag	780
actctgttttt	atacaactcag	aaacttcaga	agctctttacc	tcagacacaaa	gcactctctta	840
caggaagcaaa	gatcctttac	tctgatgtct	atgaccttat	gtgggagatg	ctccaaaacc	900
ctagcaataa	cgggttttaa	gagacgcaga	gaggtgtgtg	tggaaacagg	ttcttgagaga	960
cgagcttcat	gtgtaatgct	tattcttcca	tgtgtgagaa	tcgctcgagg	ttctgtttct	1020
ttgactcgat	tcatccatct	gaagctacct	acaattacat	tggtaatgtt	cttgataacta	1080
agattcgtgg	gtggccttaa	gcttaagtta	tcaagatttg	caaagattga	acaaaattat	1140
ctgttYtcat	aatgtgacta	tttgtggact	Tcgtttgtta	atcaactatt	aactttggct	1200
ctt						

(2) INFORMATION FOR SEQ ID NO:713:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 367 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..367
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567751

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:713:

Lys Asn Lys Asn Lys Asn Ile Met Trp Thr Ser Lys Thr Ile Ser Phe		
1	5	10
Thr Phe Phe Ile Thr Thr Ile Leu Leu Ala Ser Cys Asn Ala Ser Ala		15

	20		25		30
Lys Ala Lys Thr Gln Pro Leu Phe Pro Ala Ile Leu Ile Phe Gly Asp	35	40	45		
Ser Thr Val Asp Thr Gly Asn Asn Tyr Pro Ser Gln Thr Ile Phe	50	55	60		
Arg Ala Lys His Val Pro Tyr Gly Ile Asp Leu Pro Asn His Ser Pro	65	70	75		80
Asn Gly Arg Phe Ser Asn Gly Lys Ile Phe Ser Asp Ile Ile Ala Thr	85	90	95		
Lys Leu Asn Ile Lys Gln Phe Val Pro Pro Phe Leu Gln Pro Asn Leu	100	105	110		
Thr Asp Gln Glu Ile Val Thr Gly Val Cys Phe Ala Ser Ala Gly Ala	115	120	125		
Gly Tyr Asp Asp Gln Thr Ser Leu Thr Thr Gln Ala Ile Arg Val Ser	130	135	140		
Glu Gln Pro Asn Met Phe Lys Ser Tyr Ile Ala Arg Leu Lys Ser Ile	145	150	155		160
Val Gly Asp Lys Lys Ala Met Lys Ile Ile Asn Asn Ala Leu Val Val	165	170	175		
Val Ser Ala Gly Pro Asn Asp Phe Ile Leu Asn Tyr Tyr Glu Val Pro	180	185	190		
Thr Trp Arg Arg Met Tyr Pro Ser Ile Ser Asp Tyr Gln Asp Phe Val	195	200	205		
Leu Asn Lys Leu Asn Asn Phe Val Met Glu Leu Tyr Ser Leu Gly Cys	210	215	220		
Arg Lys Ile Leu Val Gly Gly Leu Pro Pro Met Gly Cys Leu Pro Ile	225	230	235		240
Gln Met Thr Ala Gln Phe Arg Asn Val Leu Arg Phe Cys Leu Glu Gln	245	250	255		
Glu Asn Arg Asp Ser Val Leu Tyr Asn Gln Lys Leu Gln Lys Leu Leu	260	265	270		
Pro Gln Thr Gln Ala Ser Leu Thr Gly Ser Lys Ile Leu Tyr Ser Asp	275	280	285		
Val Tyr Asp Pro Met Met Glu Met Leu Gln Asn Pro Ser Lys Tyr Gly	290	295	300		
Phe Lys Glu Thr Thr Arg Gly Cys Cys Gly Thr Gly Phe Leu Glu Thr	305	310	315		320
Ser Phe Met Cys Asn Ala Tyr Ser Ser Met Cys Glu Asn Arg Ser Glu	325	330	335		
Phe Leu Phe Phe Asp Ser Ile His Pro Ser Glu Ala Thr Tyr Asn Tyr	340	345	350		
Ile Gly Asn Val Leu Asp Thr Lys Ile Arg Gly Trp Leu Lys Ala	355	360	365		

(2) INFORMATION FOR SEQ ID NO:714:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 360 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..360
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567752

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:714:

Met Trp Thr Ser Lys Thr Ile Ser Phe Thr Phe Phe Ile Thr Thr Ile	5	10	15
Leu Leu Ala Ser Cys Asn Ala Ser Ala Lys Ala Lys Thr Gln Pro Leu	20	25	30
Phe Pro Ala Ile Leu Ile Phe Gly Asp Ser Thr Val Asp Thr Gly Asn	35	40	45

Asn Asn Tyr Pro Ser Gln Thr Ile Phe Arg Ala Lys His Val Pro Tyr
50 55 60
Gly Ile Asp Leu Pro Asn His Ser Pro Asn Gly Arg Phe Ser Asn Gly
65 70 75 80
Lys Ile Phe Ser Asp Ile Ile Ala Thr Lys Leu Asn Ile Lys Gln Phe
85 90 95
Val Pro Pro Phe Leu Gln Pro Asn Leu Thr Asp Gln Glu Ile Val Thr
100 105 110
Gly Val Cys Phe Ala Ser Ala Gly Ala Gly Tyr Asp Asp Gln Thr Ser
115 120 125
Leu Thr Thr Gln Ala Ile Arg Val Ser Glu Gln Pro Asn Met Phe Lys
130 135 140
Ser Tyr Ile Ala Arg Leu Lys Ser Ile Val Gly Asp Lys Lys Ala Met
145 150 155 160
Lys Ile Ile Asn Asn Ala Leu Val Val Val Ser Ala Gly Pro Asn Asp
165 170 175
Phe Ile Leu Asn Tyr Tyr Glu Val Pro Thr Trp Arg Arg Met Tyr Pro
180 185 190
Ser Ile Ser Asp Tyr Gln Asp Phe Val Leu Asn Lys Leu Asn Asn Phe
195 200 205
Val Met Glu Leu Tyr Ser Leu Gly Cys Arg Lys Ile Leu Val Gly Gly
210 215 220
Leu Pro Pro Met Gly Cys Leu Pro Ile Gln Met Thr Ala Gln Phe Arg
225 230 235 240
Asn Val Leu Arg Phe Cys Leu Glu Gln Glu Asn Arg Asp Ser Val Leu
245 250 255
Tyr Asn Gln Lys Leu Gln Lys Leu Leu Pro Gln Thr Gln Ala Ser Leu
260 265 270
Thr Gly Ser Lys Ile Leu Tyr Ser Asp Val Tyr Asp Pro Met Met Glu
275 280 285
Met Leu Gln Asn Pro Ser Lys Tyr Gly Phe Lys Glu Thr Thr Arg Gly
290 295 300
Cys Cys Gly Thr Gly Phe Leu Glu Thr Ser Phe Met Cys Asn Ala Tyr
305 310 315 320
Ser Ser Met Cys Glu Asn Arg Ser Glu Phe Leu Phe Phe Asp Ser Ile
325 330 335
His Pro Ser Glu Ala Thr Tyr Asn Tyr Ile Gly Asn Val Leu Asp Thr
340 345 350
Lys Ile Arg Gly Trp Leu Lys Ala
355 360

(2) INFORMATION FOR SEQ ID NO:715:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 219 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..219

(D) OTHER INFORMATION: / Ceres Seq. ID 1567753

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:715:

Met Phe Lys Ser Tyr Ile Ala Arg Leu Lys Ser Ile Val Gly Asp Lys
1 5 10 15
Lys Ala Met Lys Ile Ile Asn Asn Ala Leu Val Val Val Ser Ala Gly
20 25 30
Pro Asn Asp Phe Ile Leu Asn Tyr Tyr Glu Val Pro Thr Trp Arg Arg
35 40 45
Met Tyr Pro Ser Ile Ser Asp Tyr Gln Asp Phe Val Leu Asn Lys Leu
50 55 60
Asn Asn Phe Val Met Glu Leu Tyr Ser Leu Gly Cys Arg Lys Ile Leu

65	70	75	80
Val Gly Gly Leu Pro	Pro Met Gly Cys	Leu Pro Ile Gln Met	Thr Ala
	85	90	95
Gln Phe Arg Asn Val Leu Arg Phe Cys Leu Glu Gln Glu Asn Arg Asp	100	105	110
Ser Val Leu Tyr Asn Gln Lys Leu Gln Lys Leu Leu Pro Gln Thr Gln	115	120	125
Ala Ser Leu Thr Gly Ser Lys Ile Leu Tyr Ser Asp Val Tyr Asp Pro	130	135	140
Met Met Glu Met Leu Gln Asn Pro Ser Lys Tyr Gly Phe Lys Glu Thr	145	150	155
Thr Arg Gly Cys Cys Gly Thr Gly Phe Leu Glu Thr Ser Phe Met Cys	165	170	175
Asn Ala Tyr Ser Ser Met Cys Glu Asn Arg Ser Glu Phe Leu Phe Phe	180	185	190
Asp Ser Ile His Pro Ser Glu Ala Thr Tyr Asn Tyr Ile Gly Asn Val	195	200	205
Leu Asp Thr Lys Ile Arg Gly Trp Leu Lys Ala	210	215	

(2) INFORMATION FOR SEQ ID NO:716:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 678 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..678
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567762

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:716:

aatcgatttc	tccgatacga	tagccgacgg	agaaatgacc	aagttcagga	agctcggcgg	60
cccagcaggt	caccgtatgt	ccatgctcag	gactatgggt	tctcaattgg	tgcaacacga	120
gcgaattgag	accactgtta	caaaggctat	agaagttcgt	cgtcttgctg	ataatgat	180
tcaactcgga	aaagagggtt	cactagctgc	agcaagaaga	gctgctgggt	ttgttagagg	240
agatgatgta	cttcacaaga	ttttacaga	attggckcat	cgatacaaa	atagagctgg	300
tggtatacaca	agaatgcttc	gtactcgcat	tcgtgttggt	gatgctgccc	caatggccta	360
tatcgagttt	atcgatagag	agaacgagct	aaggcaatca	aaaccagcta	ctctcaacc	420
tcacactcga	gtgccacttg	atccatgggc	tagatcccg	ctcaccaggc	agtatgctcc	480
accaaaggag	gCaaaaaact	tctgattctg	acctataaat	agaagaagat	ctctctcgct	540
ctctcacacc	agaagatcat	gttttttttc	ccctggccca	tggtgtttct	ccctcaaccc	600
atagctttgt	atgtctggca	cettattcat	cactgcat	cacaatgtgt	ttaaaccagt	660
ttaaatgtag	tttctctg					

(2) INFORMATION FOR SEQ ID NO:717:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 167 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..167
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567763

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:717:

Ile Ala Phe Ser Asp Arg Ile Ala Asp Gly Glu Met Thr Lys Phe Arg	5	10	15
Lys Leu Gly Arg Pro Ala Gly His Arg Met Ser Met Leu Arg Thr Met	20	25	30
Val Ser Gln Leu Val Gln His Glu Arg Ile Glu Thr Thr Val Thr Lys	35	40	45

Ala Ile Glu Val Arg Arg Leu Ala Asp Asn Met Ile Gln Leu Gly Lys
50 55 60
Glu Gly Ser Leu Ala Ala Ala Arg Arg Ala Ala Gly Phe Val Arg Gly
65 70 75 80
Asp Asp Val Leu His Lys Ile Phe Thr Glu Leu Xaa His Arg Tyr Lys
85 90 95
Asp Arg Ala Gly Tyr Thr Arg Met Leu Arg Thr Arg Ile Arg Val
100 105 110
Gly Asp Ala Ala Pro Met Ala Tyr Ile Glu Phe Ile Asp Arg Glu Asn
115 120 125
Glu Leu Arg Gln Ser Lys Pro Ala Thr Pro Gln Pro Pro Arg Val
130 135 140
Pro Leu Asp Pro Trp Ala Arg Ser Arg Leu Thr Arg Gln Tyr Ala Pro
145 150 155 160
Pro Lys Glu Ala Lys Asn Phe
165

(2) INFORMATION FOR SEQ ID NO:718:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 156 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..156

(D) OTHER INFORMATION: / Ceres Seq. ID 1567764

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:718:

Met Thr Lys Phe Arg Lys Leu Gly Arg Pro Ala Gly His Arg Met Ser
1 5 10 15
Met Leu Arg Thr Met Val Ser Gln Leu Val Gln His Glu Arg Ile Glu
20 25 30
Thr Thr Val Thr Lys Ala Ile Glu Val Arg Arg Leu Ala Asp Asn Met
35 40 45
Ile Gln Leu Gly Lys Glu Gly Ser Leu Ala Ala Ala Arg Arg Ala Ala
50 55 60
Gly Phe Val Arg Gly Asp Asp Val Leu His Lys Ile Phe Thr Glu Leu
65 70 75 80
Xaa His Arg Tyr Lys Asp Arg Ala Gly Gly Tyr Thr Arg Met Leu Arg
85 90 95
Thr Arg Ile Arg Val Gly Asp Ala Ala Pro Met Ala Tyr Ile Glu Phe
100 105 110
Ile Asp Arg Glu Asn Glu Leu Arg Gln Ser Lys Pro Ala Thr Pro Gln
115 120 125
Pro Pro Arg Val Pro Leu Asp Pro Trp Ala Arg Ser Arg Leu Thr
130 135 140
Arg Gln Tyr Ala Pro Pro Lys Glu Ala Lys Asn Phe
145 150 155

(2) INFORMATION FOR SEQ ID NO:719:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 142 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..142

(D) OTHER INFORMATION: / Ceres Seq. ID 1567765

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:719:

Met Ser Met Leu Arg Thr Met Val Ser Gln Leu Val Gln His Glu Arg

1	5	10	15
Ile Glu Thr Thr Val Thr Lys Ala Ile Glu Val Arg Arg Leu Ala Asp			
	20	25	30
Asn Met Ile Gln Leu Gly Lys Glu Gly Ser Leu Ala Ala Arg Arg			
	35	40	45
Ala Ala Gly Phe Val Arg Gly Asp Asp Val Leu His Lys Ile Phe Thr			
	50	55	60
Glu Leu Xaa His Arg Tyr Lys Asp Arg Ala Gly Gly Tyr Thr Arg Met			
	65	70	75
Leu Arg Thr Arg Ile Arg Val Gly Asp Ala Ala Pro Met Ala Tyr Ile			
	85	90	95
Glu Phe Ile Asp Arg Glu Asn Glu Leu Arg Gln Ser Lys Pro Ala Thr			
	100	105	110
Pro Gln Pro Pro Pro Arg Val Pro Leu Asp Pro Trp Ala Arg Ser Arg			
	115	120	125
Leu Thr Arg Gln Tyr Ala Pro Pro Lys Glu Ala Lys Asn Phe			
	130	135	140

(2) INFORMATION FOR SEQ ID NO:720:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1251 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1251

(D) OTHER INFORMATION: / Ceres Seq. ID 1567773

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:720:

acgcaggcaa	agtgctcgta	atttaattcta	tagaagaaac	agagctctct	gtttgtgttt	60
aatctctgttc	tgcttccctt	accggttttg	cgctagaaac	acgcggagg	cgamcaatc	120
cacagcaaaa	gcaactcaaa	taatacacgt	cagcaattcc	acgtggcatg	attctctctg	180
ctctgtagat	gtccaaatag	gtagccacgt	cagcggcgta	tcagagctca	aaagatacct	240
ccacoggatc	gggtacgtca	aggatggctc	cgaataattt	tcgcagctgt	tcgatgggtc	300
ctctggaatcg	gcaatctctc	tgatatcaaga	aaatctcgtt	ttaccaataa	ccggaagact	360
cgacacgagt	acagttactc	tcattgtcgt	accgcgatgt	ggcggttagSg	atacgcacat	420
gaccatcaac	aacgatttcc	tcacacacaac	ggcgatttat	acgtatttca	acggtaaacc	480
gaaatggaac	cgtgatacgc	taacctacgc	tatctccaaa	actcaacaa	tcgatttact	540
gaactcagaa	gacgtcaaaa	ccgttttccg	gcgagctttt	tcacagtgtt	caagcgtgat	600
tcctgtgagt	ttcgaggaga	tcgacgattt	cacgacggct	gattttaaag	tcggatttca	660
cgctggtagc	cacggtagcg	ggcttccgtt	tgacgggtga	ottggaactt	tagcacacgc	720
ttttgocccg	gagaacggga	ggcttcacct	cgacgcggcg	gagacgtgga	tcgtcgacga	780
tgacttgaaa	ggatcttcaag	aggtggccgt	tgacttggag	ctctgtggcg	ctcagagagt	840
cggtcaactt	ttgggattag	gacatagctc	gcaggagctg	gcggttatgt	atccgagctt	900
ccgacccgag	accaaagaaa	ttgatcttac	ggttgatgac	gtggcagggt	tacttaagct	960
atatgggtcg	aatctctaac	tacggttgga	ttcactaacg	cagtcggaag	attctattaa	1020
aaacggcacc	gtatcacata	gattcttgtc	ggggaaattt	atcggtttat	ttctgttggt	1080
tgttgggttc	attcttttcc	tataggttta	taggcataaa	aaatactgtt	tttattcaat	1140
tatttttaat	taaatgtaca	tatattttcc	aactatgtaa	atgtaaatat	atagtgaac	1200
aaaaaaagat	gtacatatat	agttaggctt	ataattaggt	ttatgtgtct	g	

(2) INFORMATION FOR SEQ ID NO:721:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 367 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..367

(D) OTHER INFORMATION: / Ceres Seq. ID 1567774

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:721:

Arg	Arg	Gln	Met	Ser	Arg	Asn	Leu	Ile	Tyr	Arg	Arg	Asn	Arg	Ala	Leu
1			5						10					15	
Cys	Phe	Val	Leu	Ile	Leu	Phe	Cys	Phe	Pro	Tyr	Arg	Phe	Gly	Ala	Arg
			20					25					30		
Asn	Thr	Pro	Glu	Ala	Xaa	Gln	Ser	Thr	Ala	Lys	Ala	Thr	Gln	Ile	Ile
			35					40					45		
His	Val	Ser	Asn	Ser	Thr	Trp	His	Asp	Phe	Ser	Arg	Leu	Val	Asp	Val
			50				55				60				
Gln	Ile	Gly	Ser	His	Val	Ser	Gly	Val	Ser	Glu	Leu	Lys	Arg	Tyr	Leu
			65				70			75				80	
His	Arg	Phe	Gly	Tyr	Val	Lys	Asp	Gly	Ser	Glu	Ile	Phe	Ser	Asp	Val
			85					90					95		
Phe	Asp	Gly	Pro	Leu	Glu	Ser	Ala	Ile	Ser	Leu	Tyr	Gln	Glu	Asn	Leu
			100					105					110		
Gly	Leu	Pro	Ile	Thr	Gly	Arg	Leu	Asp	Thr	Ser	Thr	Val	Thr	Leu	Met
			115				120					125			
Ser	Leu	Pro	Arg	Cys	Gly	Val	Xaa	Asp	Thr	His	Met	Thr	Ile	Asn	Asn
			130				135				140				
Asp	Phe	Leu	His	Thr	Thr	Ala	His	Tyr	Thr	Tyr	Phe	Asn	Gly	Lys	Pro
			145				150			155				160	
Lys	Trp	Asn	Arg	Asp	Thr	Leu	Thr	Tyr	Ala	Ile	Ser	Lys	Thr	His	Lys
			165					170					175		
Leu	Asp	Tyr	Leu	Thr	Ser	Glu	Asp	Val	Lys	Thr	Val	Phe	Arg	Arg	Ala
			180					185					190		
Phe	Ser	Gln	Trp	Ser	Ser	Val	Ile	Pro	Val	Ser	Phe	Glu	Glu	Val	Asp
			195				200					205			
Asp	Phe	Thr	Thr	Ala	Asp	Leu	Lys	Ile	Gly	Phe	Tyr	Ala	Gly	Asp	His
			210				215				220				
Gly	Asp	Gly	Leu	Pro	Phe	Asp	Gly	Val	Leu	Gly	Thr	Leu	Ala	His	Ala
			225				230			235				240	
Phe	Ala	Pro	Glu	Asn	Gly	Arg	Leu	His	Leu	Asp	Ala	Ala	Glu	Thr	Trp
			245					250					255		
Ile	Val	Asp	Asp	Leu	Lys	Gly	Ser	Ser	Glu	Val	Ala	Val	Asp	Leu	
			260				265					270			
Glu	Ser	Val	Ala	Thr	His	Glu	Ile	Gly	His	Leu	Leu	Gly	Leu	Gly	His
			275				280					285			
Ser	Ser	Gln	Glu	Ser	Ala	Val	Met	Tyr	Pro	Ser	Leu	Arg	Pro	Arg	Thr
			290				295				300				
Lys	Lys	Val	Asp	Leu	Thr	Val	Asp	Asp	Val	Ala	Gly	Val	Leu	Lys	Leu
			305				310			315				320	
Tyr	Gly	Pro	Asn	Pro	Lys	Leu	Arg	Leu	Asp	Ser	Leu	Thr	Gln	Ser	Glu
			325					330					335		
Asp	Ser	Ile	Lys	Asn	Gly	Thr	Val	Ser	His	Arg	Phe	Leu	Ser	Gly	Asn
			340					345					350		
Phe	Ile	Gly	Tyr	Val	Leu	Leu	Val	Val	Gly	Leu	Ile	Leu	Phe	Leu	
			355				360					365			

(2) INFORMATION FOR SEQ ID NO:722:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 364 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..364
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567775

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:722:

Met	Ser	Arg	Asn	Leu	Ile	Tyr	Arg	Arg	Asn	Arg	Ala	Leu	Cys	Phe	Val
1			5					10					15		

Leu Ile Leu Phe Cys Phe Pro Tyr Arg Phe Gly Ala Arg Asn Thr Pro
20 25 30
Glu Ala Xaa Gln Ser Thr Ala Lys Ala Thr Gln Ile Ile His Val Ser
35 40 45
Asn Ser Thr Trp His Asp Phe Ser Arg Leu Val Asp Val Gln Ile Gly
50 55 60
Ser His Val Ser Gly Val Ser Glu Leu Lys Arg Tyr Leu His Arg Phe
65 70 75 80
Gly Tyr Val Lys Asp Gly Ser Glu Ile Phe Ser Asp Val Phe Asp Gly
85 90 95
Pro Leu Glu Ser Ala Ile Ser Leu Tyr Gln Glu Asn Leu Gly Leu Pro
100 105 110
Ile Thr Gly Arg Leu Asp Thr Ser Thr Val Thr Leu Met Ser Leu Pro
115 120 125
Arg Cys Gly Val Xaa Asp Thr His Met Thr Ile Asn Asn Asp Phe Leu
130 135 140
His Thr Thr Ala His Tyr Thr Tyr Phe Asn Gly Lys Pro Lys Trp Asn
145 150 155 160
Arg Asp Thr Leu Thr Tyr Ala Ile Ser Lys Thr His Lys Leu Asp Tyr
165 170 175
Leu Thr Ser Glu Asp Val Lys Thr Val Phe Arg Arg Ala Phe Ser Gln
180 185 190
Trp Ser Ser Val Ile Pro Val Ser Phe Glu Glu Val Asp Asp Phe Thr
195 200 205
Thr Ala Asp Leu Lys Ile Gly Phe Tyr Ala Gly Asp His Gly Asp Gly
210 215 220
Leu Pro Phe Asp Gly Val Leu Gly Thr Leu Ala His Ala Phe Ala Pro
225 230 235 240
Glu Asn Gly Arg Leu His Leu Asp Ala Ala Glu Thr Trp Ile Val Asp
245 250 255
Asp Asp Leu Lys Gly Ser Ser Glu Val Ala Val Asp Leu Glu Ser Val
260 265 270
Ala Thr His Glu Ile Gly His Leu Leu Gly Leu Gly His Ser Ser Gln
275 280 285
Glu Ser Ala Val Met Tyr Pro Ser Leu Arg Pro Arg Thr Lys Lys Val
290 295 300
Asp Leu Thr Val Asp Asp Val Ala Gly Val Leu Lys Leu Tyr Gly Pro
305 310 315 320
Asn Pro Lys Leu Arg Leu Asp Ser Leu Thr Gln Ser Glu Asp Ser Ile
325 330 335
Lys Asn Gly Thr Val Ser His Arg Phe Leu Ser Gly Asn Phe Ile Gly
340 345 350
Tyr Val Leu Leu Val Val Gly Leu Ile Leu Phe Leu
355 360

(2) INFORMATION FOR SEQ ID NO:723:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 240 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..240
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567776

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:723:

Met Ser Leu Pro Arg Cys Gly Val Xaa Asp Thr His Met Thr Ile Asn
1 5 10 15
Asn Asp Phe Leu His Thr Thr Ala His Tyr Thr Tyr Phe Asn Gly Lys
20 25 30
Pro Lys Trp Asn Arg Asp Thr Leu Thr Tyr Ala Ile Ser Lys Thr His

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(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..241

(D) OTHER INFORMATION: / Ceres Seq. ID 1567778

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:725:

Ser Glu Lys Arg Ile Phe Phe Trp Gln Met Leu Arg Ser Ser Ile Arg
1 5 10 15
Leu Leu Tyr Ile Arg Arg Thr Ser Pro Leu Leu Arg Ser Leu Ser Ser
20 25 30
Ser Ser Ser Leu Ser Ser Lys Arg Phe Asp Ser Ala Lys Pro Ile Phe
35 40 45
Asn Ser His Arg Thr Phe Cys Leu Pro Pro Ile Ser Thr Thr Gly Ala
50 55 60
Lys Leu Ser Arg Ser Glu His Ser Met Ala Ala Ser Ser Glu Pro Lys
65 70 75 80
Ser Leu Tyr Asp Phe Thr Val Lys Asp Ala Lys Gly Asn Asp Val Asp
85 90 95
Leu Ser Ile Tyr Lys Gly Lys Val Leu Leu Ile Val Asn Val Ala Ser
100 105 110
Gln Cys Gly Leu Thr Asn Ser Asn Tyr Thr Glu Leu Ala Gln Leu Tyr
115 120 125
Glu Lys Tyr Lys Gly His Gly Phe Glu Ile Leu Ala Phe Pro Cys Asn
130 135 140
Gln Phe Gly Asn Gln Glu Pro Gly Thr Asn Glu Ile Val Gln Phe
145 150 155 160
Ala Cys Thr Arg Phe Lys Ala Glu Tyr Pro Ile Phe Asp Lys Val Asp
165 170 175
Val Asn Gly Asp Lys Ala Ala Pro Val Tyr Lys Phe Leu Lys Ser Ser
180 185 190
Lys Gly Gly Leu Phe Gly Asp Gly Ile Lys Trp Asn Phe Ala Lys Phe
195 200 205
Leu Val Asp Lys Asp Gly Asn Val Val Asp Arg Phe Ala Pro Thr Thr
210 215 220
Ser Pro Leu Ser Ile Glu Lys Asp Leu Lys Lys Leu Leu Gly Val Thr
225 230 235 240
Ala

(2) INFORMATION FOR SEQ ID NO:726:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 232 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..232

(D) OTHER INFORMATION: / Ceres Seq. ID 1567779

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:726:

Met Leu Arg Ser Ser Ile Arg Leu Leu Tyr Ile Arg Arg Thr Ser Pro
1 5 10 15
Leu Leu Arg Ser Leu Ser Ser Ser Ser Ser Leu Ser Ser Lys Arg Phe
20 25 30
Asp Ser Ala Lys Pro Ile Phe Asn Ser His Arg Thr Phe Cys Leu Pro
35 40 45
Pro Ile Ser Thr Thr Gly Ala Lys Leu Ser Arg Ser Glu His Ser Met
50 55 60
Ala Ala Ser Ser Glu Pro Lys Ser Leu Tyr Asp Phe Thr Val Lys Asp
65 70 75 80
Ala Lys Gly Asn Asp Val Asp Leu Ser Ile Tyr Lys Gly Lys Val Leu

(ix) FEATURE:

(A) NAME/KEY: -
(B) LOCATION: 1..1418
(D) OTHER INFORMATION: / Ceres Seq. ID 1567785

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:728:

atccattgat	gagtatataa	ttttgtttgt	gggtattgct	ttgtttgatc	tgctaagtgc	60
tttactcttt	ctggaagaaa	gcttttgaag	atcagcctaa	aagtgatctc	tcataactgc	120
ttaaaagatt	gttgaacctc	gaagatgtct	ttggccgaga	taaacaagaa	tgaagtgcag	180
attgtttatt	gggctcttaa	tgctgacctt	acacagtttt	tgaccagctg	gaggcctttc	240
ttctccgat	tccatctgat	tgttgtcaaa	gatcctgagc	tcaaggagga	actcaacata	300
ccagaagcct	ttgacgtaga	tgtctactct	aagactgaca	tggaaaaagg	tgtgggcgca	360
tccaattcca	ccatgtttct	tggtctattt	tgcatatatt	tcgggtatct	cgatatacaa	420
aagaagtaca	ttgtctctat	tgatgatgat	tgtgtccctg	ctaaagatcc	gaagggtttc	480
ctagtggatg	ctgttaactca	gcacgtgatc	aaccttgaaa	accacgccac	gcctctcttc	540
ttcaacaccc	tttatgatcc	ttactgcgag	ggagcggatt	ttgtccgtgg	ataccctttc	600
agcctcagaa	gtgggtgtcc	ttgtgctgca	tcttgtgggc	tttggcttaa	tctagctgat	660
cttgatgctc	caacacaagc	ttctcaagaca	gagaaaagga	acactgcata	tgtttgatgcg	720
gttatgactg	ttccggccaa	ggctatgcta	cccataagcg	gaatcaacat	tgcttttaac	780
cgcgagtggg	tggttccagc	tttggctgct	gcactcagat	tggctggaga	agggaaaagt	840
agatgggaaa	caacttgaaga	tggttgggtg	gggatgtgtc	tgaacacata	ctctgatcat	900
ttgggttatg	tggtgaaaac	cggactgcct	tatgtgtgga	gaaacgagag	aggagatgca	960
gtggagagtt	tgaggaaagc	aatgggaagg	aatgaagctg	atggagaaaa	gtgttccatt	1020
tttcgattca	gtgaaattgc	cggagactgc	gcttaaaagt	gaagatttgg	tgattgagct	1080
tgctaaagcg	gtgaaagagc	agtttagttc	agatgatcct	gcctttacgc	aaagctgctga	1140
tgctatgtgt	aagttgggtc	agctctgtaa	ttctgttaat	tctagcgctt	gaagttgaa	1200
aatctcttga	ggttagggtc	ctttatcact	tctaagcata	ttatcatgtc	tcagagattt	1260
accacaagtc	ttttctttct	tttagtaca	tcatgtttat	tttctctttt	tatctaaatt	1320
ataagcatgt	gttttttga	caactcaata	tgtaacctga	tgaaccccat	ctgctttgac	1380
tcgatgatat	taatatctat	tgcttagctt	tttacttt			

(2) INFORMATION FOR SEQ ID NO:729:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 303 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1..303
(D) OTHER INFORMATION: / Ceres Seq. ID 1567786

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:729:

Met	Ser	Leu	Ala	Glu	Ile	Asn	Lys	Asn	Glu	Val	Asp	Ile	Val	Ile	Gly
1				5					10					15	
Ala	Leu	Asn	Ala	Asp	Leu	Thr	Gln	Phe	Leu	Thr	Ser	Trp	Arg	Pro	Phe
			20					25					30		
Phe	Ser	Gly	Phe	His	Leu	Ile	Val	Val	Lys	Asp	Pro	Glu	Leu	Lys	Glu
			35				40					45			
Glu	Leu	Asn	Ile	Pro	Glu	Gly	Phe	Asp	Val	Asp	Val	Tyr	Ser	Lys	Thr
			50			55					60				
Asp	Met	Glu	Lys	Val	Val	Gly	Ala	Ser	Asn	Ser	Thr	Met	Phe	Ser	Gly
			65			70				75				80	
Tyr	Ser	Cys	Arg	Tyr	Phe	Gly	Tyr	Leu	Val	Ser	Lys	Lys	Lys	Tyr	Ile
			85						90					95	
Val	Ser	Ile	Asp	Asp	Asp	Cys	Val	Pro	Ala	Lys	Asp	Pro	Lys	Gly	Phe
			100					105					110		
Leu	Val	Asp	Ala	Val	Thr	Gln	His	Val	Ile	Asn	Leu	Glu	Asn	Pro	Ala
			115				120					125			
Thr	Pro	Leu	Phe	Phe	Asn	Thr	Leu	Tyr	Asp	Pro	Tyr	Cys	Glu	Gly	Ala
			130			135					140				
Asp	Phe	Val	Arg	Gly	Tyr	Pro	Phe	Ser	Leu	Arg	Ser	Gly	Val	Pro	Cys
			145			150				155				160	
Ala	Ala	Ser	Cys	Gly	Leu	Trp	Leu	Asn	Leu	Ala	Asp	Leu	Asp	Ala	Pro

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(2) INFORMATION FOR SEO ID NO:730:

(A) LENGTH: 238 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..238

(D) OTHER INFORMATION: / Ceres Seq. ID 1567787

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:730:

(2) INFORMATION FOR SEQ ID NO:731:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 227 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..227
(D) OTHER INFORMATION: / Ceres Seq. ID 1567788
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:731:
Met Phe Ser Gly Tyr Ser Cys Arg Tyr Phe Gly Tyr Leu Val Ser Lys
1 5 10 15
Lys Lys Tyr Ile Val Ser Ile Asp Asp Asp Cys Val Pro Ala Lys Asp
20 25 30
Pro Lys Gly Phe Leu Val Asp Ala Val Thr Gln His Val Ile Asn Leu
35 40 45
Glu Asn Pro Ala Thr Pro Leu Phe Phe Asn Thr Leu Tyr Asp Pro Tyr
50 55 60
Cys Glu Gly Ala Asp Phe Val Arg Gly Tyr Pro Phe Ser Leu Arg Ser
65 70 75 80
Gly Val Pro Cys Ala Ala Ser Cys Gly Leu Trp Leu Asn Leu Ala Asp
85 90 95
Leu Asp Ala Pro Thr Gln Ala Leu Lys Thr Glu Lys Arg Asn Thr Ala
100 105 110
Tyr Val Asp Ala Val Met Thr Val Pro Ala Lys Ala Met Leu Pro Ile
115 120 125
Ser Gly Ile Asn Ile Ala Phe Asn Arg Glu Leu Val Gly Pro Ala Leu
130 135 140
Val Pro Ala Leu Arg Leu Ala Gly Glu Gly Lys Val Arg Trp Glu Thr
145 150 155 160
Leu Glu Asp Val Trp Cys Gly Met Cys Leu Lys His Ile Ser Asp His
165 170 175
Leu Gly Tyr Gly Val Lys Thr Gly Leu Pro Tyr Val Trp Arg Asn Glu
180 185 190
Arg Gly Asp Ala Val Glu Ser Leu Arg Lys Gln Met Gly Arg Asn Glu
195 200 205
Ala Asp Gly Glu Lys Cys Ser Ile Phe Arg Phe Ile Glu Ile Ala Arg
210 215 220
Asp Cys Ala
225

(2) INFORMATION FOR SEQ ID NO:732:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1304 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..1304
(D) OTHER INFORMATION: / Ceres Seq. ID 1567789

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:732:

atctttcttc	tctctctatc	tctctctttt	gaacctataa	aactctttct	ttacaaggat	60
tgatcttttt	gtatttttga	ttttgacatt	tgcttttgtg	tcgatctctg	ttttgatgcg	120
atttctctgt	ttttaaagcc	atttgataga	tgttttccgg	taaagctcag	cgagagaaga	180
agaagaacaa	caatggagtt	tacagatttc	tcaaagacga	gttttttacta	cccgctcgta	240
caaaagcggtt	gggatttcgg	agattttacg	gcggcgagga	ggcattcttt	agggttcgat	300
gagttattaa	gtttctcagca	gcattcaagac	tttgctactg	tttctctctca	ttctctcatt	360
ctccaaacgt	ctccaaccgca	cagcaaacg	caaccatcgg	cgaaagctgt	ttcaagatga	420
attcaagctc	caccgtcaga	gcaattagt	acgtcaaaag	tggagtcctt	gtgttcgat	480
catttgttga	taaaccCacc	ggcgactcct	aactcgtcat	cgatttcgtc	tgcttcaagc	540

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gaggctctaa atgaagagaa accgaaaaca gaagacaatg aagaagaagg aggtgaagat    600
caacaagaga agagtcatac taagaaacag ttgaagacaa agaagaataa tcagaagaga    660
cagagagagg caagagtgcg attcatgaca aagagtgaag ttgatcatc cgaagatggt    720
tatcgctggc gaaaatatgg tcaaaaagct gtcaaaaaca gtccttttcc caggagtgtac    780
taccgttgca caacggcttc atgtaacgtg aagaagagag tggagagatc attcagagat    840
ccaagcactg tggttacaac ctacgaaggt caacacactc acattagtcc actcagctct    900
cgctctattt ccactggagg ttctttcgga tcgtcaggag ctgcttcgag tctcggtaat    960
ggttgctttg ggtttcctat tgatggctcc acgttaatct ctctcagtt ccaacagctt   1020
gtccaatacc atcaccaca gacgcaacaa gaactcatgt cttgttttgg aggagtcac   1080
gagtaccotta atagccaagc taatgagtat ggtgatgata atcgtgtgaa gaagagtgcg   1140
gttttggtta aagataatgg actttctgca gatgtgttgc cgtatcatat gttgaaggaa   1200
gagtagtagt atatatatg tcttatagtt ttYaactcag tttttttttg tataattgtc   1260
taaaagaaac ggatcttttg tctgatgaa gaagatgttt tctc

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(2) INFORMATION FOR SEQ ID NO:733:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 337 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..337
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567790

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:733:

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Met Gln Phe Thr Asp Phe Ser Lys Thr Ser Phe Tyr Tyr Pro Ser Ser
1      5      10      15
Gln Ser Val Trp Asp Phe Gly Asp Leu Ala Ala Glu Arg His Ser
20      25      30
Leu Gly Phe Met Glu Leu Leu Ser Ser Gln Gln His Gln Asp Phe Ala
35      40      45
Thr Val Ser Pro His Ser Phe Leu Leu Gln Thr Ser Gln Pro Gln Thr
50      55      60
Gln Thr Gln Pro Ser Ala Lys Leu Ser Ser Ser Ile Ile Gln Ala Pro
65      70      75
Pro Ser Glu Gln Leu Val Thr Ser Lys Val Glu Ser Leu Cys Ser Asp
85      90      95
His Leu Leu Ile Asn Pro Pro Ala Thr Pro Asn Ser Ser Ser Ile Ser
100      105      110
Ser Ala Ser Ser Glu Ala Leu Asn Glu Glu Lys Pro Lys Thr Glu Asp
115      120      125
Asn Gln Glu Glu Gly Gly Glu Asp Gln Gln Glu Lys Ser His Thr Lys
130      135      140
Lys Gln Leu Lys Ala Lys Lys Asn Asn Gln Lys Arg Gln Arg Glu Ala
145      150      155
Arg Val Ala Phe Met Thr Lys Ser Glu Val Asp His Leu Glu Asp Gly
165      170      175
Tyr Arg Trp Arg Lys Tyr Gly Gln Lys Ala Val Lys Asn Ser Pro Phe
180      185      190
Pro Arg Ser Tyr Tyr Arg Cys Thr Thr Ala Ser Cys Asn Val Lys Lys
195      200      205
Arg Val Glu Arg Ser Phe Arg Asp Pro Ser Thr Val Val Thr Thr Tyr
210      215      220
Glu Gly Gln His Thr His Ile Ser Pro Leu Thr Ser Arg Pro Ile Ser
225      230      235
Thr Gly Gly Phe Phe Gly Ser Ser Gly Ala Ala Ser Ser Leu Gly Asn
245      250      255
Gly Cys Phe Gly Phe Pro Ile Asp Gly Ser Thr Leu Ile Ser Pro Gln
260      265      270
Phe Gln Gln Leu Val Gln Tyr His His Gln Gln Gln Gln Glu Leu
275      280      285

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Met Ser Cys Phe Gly Gly Val Asn Glu Tyr Leu Asn Ser His Ala Asn
290 295 300
Glu Tyr Gly Asp Asn Arg Val Lys Lys Ser Arg Val Leu Val Lys
305 310 315 320
Asp Asn Gly Leu Leu Gln Asp Val Val Pro Tyr His Met Leu Lys Glu
325 330 335
Glu

(2) INFORMATION FOR SEQ ID NO:734:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 302 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..302

(D) OTHER INFORMATION: / Ceres Seq. ID 1567791

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:734:

Met Glu Leu Leu Ser Ser Gln Gln His Gln Asp Phe Ala Thr Val Ser
1 5 10 15
Pro His Ser Phe Leu Leu Gln Thr Ser Gln Pro Gln Thr Gln Gln
20 25 30
Pro Ser Ala Lys Leu Ser Ser Ser Ile Ile Gln Ala Pro Pro Ser Glu
35 40 45
Gln Leu Val Thr Ser Lys Val Glu Ser Leu Cys Ser Asp His Leu Leu
50 55 60
Ile Asn Pro Pro Ala Thr Pro Asn Ser Ser Ser Ile Ser Ser Ala Ser
65 70 75 80
Ser Glu Ala Leu Asn Glu Glu Lys Pro Lys Thr Glu Asp Asn Glu Glu
85 90 95
Glu Gly Gly Glu Asp Gln Gln Glu Lys Ser His Thr Lys Lys Gln Leu
100 105 110
Lys Ala Lys Lys Asn Asn Gln Lys Arg Gln Arg Glu Ala Arg Val Ala
115 120 125
Phe Met Thr Lys Ser Glu Val Asp His Leu Glu Asp Gly Tyr Arg Trp
130 135 140
Arg Lys Tyr Gly Gln Lys Ala Val Lys Asn Ser Pro Phe Pro Arg Ser
145 150 155 160
Tyr Tyr Arg Cys Thr Thr Ala Ser Cys Asn Val Lys Lys Arg Val Glu
165 170 175
Arg Ser Phe Arg Asp Pro Ser Thr Val Val Thr Thr Tyr Glu Gly Gln
180 185 190
His Thr His Ile Ser Pro Leu Thr Ser Arg Pro Ile Ser Thr Gly Gly
195 200 205
Phe Phe Gly Ser Ser Gly Ala Ala Ser Ser Leu Gly Asn Gly Cys Phe
210 215 220
Gly Phe Pro Ile Asp Gly Ser Thr Leu Ile Ser Pro Gln Phe Gln Gln
225 230 235 240
Leu Val Gln Tyr His His Gln Gln Gln Gln Gln Glu Leu Met Ser Cys
245 250 255
Phe Gly Gly Val Asn Glu Tyr Leu Asn Ser His Ala Asn Glu Tyr Gly
260 265 270
Asp Asp Asn Arg Val Lys Lys Ser Arg Val Leu Val Lys Asp Asn Gly
275 280 285
Leu Leu Gln Asp Val Val Pro Tyr His Met Leu Lys Glu Glu
290 295 300

(2) INFORMATION FOR SEQ ID NO:735:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 173 amino acids

(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..173
(D) OTHER INFORMATION: / Ceres Seq. ID 1567792
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:735:
Met Thr Lys Ser Glu Val Asp His Leu Glu Asp Gly Tyr Arg Trp Arg
1 5 10 15
Lys Tyr Gly Gln Lys Ala Val Lys Asn Ser Pro Phe Pro Arg Ser Tyr
20 25 30
Tyr Arg Cys Thr Thr Ala Ser Cys Asn Val Lys Lys Arg Val Glu Arg
35 40 45
Ser Phe Arg Asp Pro Ser Thr Val Val Thr Thr Tyr Glu Gly Gln His
50 55 60
Thr His Ile Ser Pro Leu Thr Ser Arg Pro Ile Ser Thr Gly Gly Phe
65 70 75 80
Phe Gly Ser Ser Gly Ala Ala Ser Ser Leu Gly Asn Gly Cys Phe Gly
85 90 95
Phe Pro Ile Asp Gly Ser Thr Leu Ile Ser Pro Gln Phe Gln Gln Leu
100 105 110
Val Gln Tyr His His Gln Gln Gln Gln Glu Leu Met Ser Cys Phe
115 120 125
Gly Gly Val Asn Glu Tyr Leu Asn Ser His Ala Asn Glu Tyr Gly Asp
130 135 140
Asp Asn Arg Val Lys Lys Ser Arg Val Leu Val Lys Asp Asn Gly Leu
145 150 155 160
Leu Gln Asp Val Val Pro Tyr His Met Leu Lys Glu Glu
165 170

(2) INFORMATION FOR SEQ ID NO:736:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 853 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..853
(D) OTHER INFORMATION: / Ceres Seq. ID 1567797

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:736:

agaatttgag attgcctctg caaagagtaa aatggcgaat cctaaagtct tcttcgacat 60
cttgattggg aagatgaagg cagggcgtgt tctaattggag ttatttgcag atgtgactcc 120
gagaacagct aataatttcc gtgctttgtg cactggggag aatggatttg gaaagcagg 180
gaaggcttta cactacaagg gctcagcctt tcaccgtata atcccagggt tcatgtgtca 240
aggtggagat ttactctcgt ggaatggaac tggaggagaa tctattttac ggtctaaaatt 300
tgaagatgag aaactcaagt tgaagcacac tgggtccagg attttgtcta tggctaactc 360
tgggtcccaac actagtgggt ctcagttctt catctgcaca gagaagactt cgtgcttga 420
tgggaataac gtgttttttc ggaaagtgtg tgatggatac aatgtgggtca aggcaatgga 480
ggatgttgGg ctctgacatg ggaatccctt ctgaacgagt tgtgattgaa gattgtgggt 540
agctcaagaa cccaagtcca taagtcttta aaacattggg tgggttgatc ttgacaggtt 600
attctatcat atgctgtgaa gcagagacag catcttagcg ttaagggtcaa tctagtctgt 660
gatgcactac ttgtgttttg actatatcat atgaacctta ggaagtggtc catcctttga 720
agttgttttc ttaaaaactc tgtgtgagac taggtgggat gataataatg gttagtcttc 780
ttatgaagac atttggtttt gtactcttct tattttgggt tagttaatat gaatgaacca 840
aactcttctt agg

(2) INFORMATION FOR SEQ ID NO:737:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 164 amino acids

(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..164
 (D) OTHER INFORMATION: / Ceres Seq. ID 1567798
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:737:
Glu Phe Glu Ile Ala Ser Ala Lys Ser Lys Met Ala Asn Pro Lys Val
1 5 10 15
Phe Phe Asp Ile Leu Ile Gly Lys Met Lys Ala Gly Arg Val Val Met
 20 25 30
Glu Leu Phe Ala Asp Val Thr Pro Arg Thr Ala Asn Asn Phe Arg Ala
 35 40 45
Leu Cys Thr Gly Glu Asn Gly Ile Gly Lys Ala Gly Lys Ala Leu His
 50 55 60
Tyr Lys Gly Ser Ala Phe His Arg Ile Ile Pro Gly Phe Met Cys Gln
65 70 75 80
Gly Gly Asp Phe Thr Arg Gly Asn Gly Thr Gly Gly Glu Ser Ile Tyr
 85 90 95
Gly Ser Lys Phe Glu Asp Glu Asn Phe Lys Leu Lys His Thr Gly Pro
 100 105 110
Gly Ile Leu Ser Met Ala Asn Ser Gly Pro Asn Thr Ser Gly Ser Gln
 115 120 125
Phe Phe Ile Cys Thr Glu Lys Thr Ser Trp Leu Asp Gly Lys His Val
 130 135 140
Val Phe Gly Lys Val Val Asp Gly Tyr Asn Val Val Lys Ala Met Glu
145 150 155 160
Asp Val Gly Leu

(2) INFORMATION FOR SEQ ID NO:738:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 154 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..154
 (D) OTHER INFORMATION: / Ceres Seq. ID 1567799
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:738:
Met Ala Asn Pro Lys Val Phe Phe Asp Ile Leu Ile Gly Lys Met Lys
1 5 10 15
Ala Gly Arg Val Val Met Glu Leu Phe Ala Asp Val Thr Pro Arg Thr
 20 25 30
Ala Asn Asn Phe Arg Ala Leu Cys Thr Gly Glu Asn Gly Ile Gly Lys
 35 40 45
Ala Gly Lys Ala Leu His Tyr Lys Gly Ser Ala Phe His Arg Ile Ile
 50 55 60
Pro Gly Phe Met Cys Gln Gly Gly Asp Phe Thr Arg Gly Asn Gly Thr
65 70 75 80
Gly Gly Glu Ser Ile Tyr Gly Ser Lys Phe Glu Asp Glu Asn Phe Lys
 85 90 95
Leu Lys His Thr Gly Pro Gly Ile Leu Ser Met Ala Asn Ser Gly Pro
 100 105 110
Asn Thr Ser Gly Ser Gln Phe Phe Ile Cys Thr Glu Lys Thr Ser Trp
 115 120 125
Leu Asp Gly Lys His Val Val Phe Gly Lys Val Val Asp Gly Tyr Asn
130 135 140

Val Val Lys Ala Met Glu Asp Val Gly Leu
145 150

(2) INFORMATION FOR SEQ ID NO:739:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 140 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..140
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567800

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:739:

```
Met Lys Ala Gly Arg Val Val Met Glu Leu Phe Ala Asp Val Thr Pro
1      5      10      15
Arg Thr Ala Asn Asn Phe Arg Ala Leu Cys Thr Gly Glu Asn Gly Ile
20     25     30
Gly Lys Ala Gly Lys Ala Leu His Tyr Lys Gly Ser Ala Phe His Arg
35     40     45
Ile Ile Pro Gly Phe Met Cys Gln Gly Gly Asp Phe Thr Arg Gly Asn
50     55     60
Gly Thr Gly Gly Glu Ser Ile Tyr Gly Ser Lys Phe Glu Asp Glu Asn
65     70     75     80
Phe Lys Leu Lys His Thr Gly Pro Gly Ile Leu Ser Met Ala Asn Ser
85     90     95
Gly Pro Asn Thr Ser Gly Ser Gln Phe Phe Ile Cys Thr Glu Lys Thr
100    105    110
Ser Trp Leu Asp Gly Lys His Val Val Phe Gly Lys Val Val Asp Gly
115    120    125
Tyr Asn Val Val Lys Ala Met Glu Asp Val Gly Leu
130    135    140
```

(2) INFORMATION FOR SEQ ID NO:740:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1033 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1033
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567812

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:740:

```
ctcaatttct tttttttctt cagaaatttc ctccgatttc aaaattttcc ggtgaaatcg      60
aaaaaaaaag cgagatcttc ttctctaagt cgcgacgacct taagcagaga tcaatatgtc      120
taactggcga aGctcgccga gcaagccgag cggtacgaag agatggttca attcatggaa      180
cagctcgtaa gtggagctac accggccggt gagctgaccg tagaagagag gaactttctc      240
tcggtcgcgt ataaaaacct gattggatct ctctgctgcg catggagaaat cgtgtctttc      300
attgagcaaa aggaagagag caggaaagaac gaagaacacg tgcgcttgt taaggattac      360
agatctaaag ttgagactga gctttcttcg atctgttctg ggattctcag gttacttgat      420
tcgcatctga ttctcttcag taactgccagt gactctaagg ttttttaact gaagatgaaa      480
ggagattatc atcgttatatt ggctgagttt aaatctggtg atgagaggaa aactgcgtct      540
gaagatacta tgatcgctta caaagctgct caggacgttg cagttgtctga tctagcactc      600
aacatccoga tcaggtcttg ttggctctt aactcttcag tgttttacta cgagattctc      660
aactcttcag agaaagcttg tagcatggcg aaacaggctt ttgaagaagc cattgctgag      720
ctggacacat tgggagagga gacatacaag gacagtactc tcatcatgca gtgtctaagg      780
gacaatctaa cctctttgac cctccgatat caggagcaga tggatgagcc ctgaaggtct      840
aatggaagaa aagacggtta tgaatgtac atcgcaacct aacgcaaaaa ctgagttcaa      900
cctcctttgc tgaataaact gTtcgaaaag aaaagtttgt ttttttatga cagatttatg      960
gcacagcttt ggtgttatct gctgctctgt atcaactctg tttttgtttg gtaattttat      1020
```

ctcatctttg etc

(2) INFORMATION FOR SEQ ID NO:741:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 277 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..277
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567813

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:741:

Leu Asn Phe Phe Phe Ser Ser Arg Asn Phe Leu Arg Phe Gln Asn Phe
1 5 10 15
Pro Val Lys Ser Lys Lys Lys Ala Arg Ser Ser Ser Leu Met Ala Thr
20 25 30
Thr Leu Ser Arg Asp Gln Tyr Val Tyr Met Ala Lys Leu Ala Glu Gln
35 40 45
Ala Glu Arg Tyr Glu Glu Met Val Gln Phe Met Glu Gln Leu Val Ser
50 55 60
Gly Ala Thr Pro Ala Gly Glu Leu Thr Val Glu Glu Arg Asn Leu Leu
65 70 75 80
Ser Val Ala Tyr Lys Asn Val Ile Gly Ser Leu Arg Ala Ala Trp Arg
85 90 95
Ile Val Ser Ser Ile Glu Gln Lys Glu Glu Ser Arg Lys Asn Glu Glu
100 105 110
His Val Ser Leu Val Lys Asp Tyr Arg Ser Lys Val Glu Thr Glu Leu
115 120 125
Ser Ser Ile Cys Ser Gly Ile Leu Arg Leu Leu Asp Ser His Leu Ile
130 135 140
Pro Ser Ala Thr Ala Ser Glu Ser Lys Val Phe Tyr Leu Lys Met Lys
145 150 155 160
Gly Asp Tyr His Arg Tyr Leu Ala Glu Phe Lys Ser Gly Asp Glu Arg
165 170 175
Lys Thr Ala Ala Glu Asp Thr Met Ile Ala Tyr Lys Ala Ala Gln Asp
180 185 190
Val Ala Val Ala Asp Leu Ala Pro Thr His Pro Ile Arg Leu Gly Leu
195 200 205
Ala Leu Asn Phe Ser Val Phe Tyr Tyr Glu Ile Leu Asn Ser Ser Glu
210 215 220
Lys Ala Cys Ser Met Ala Lys Gln Ala Phe Glu Glu Ala Ile Ala Glu
225 230 235 240
Leu Asp Thr Leu Gly Glu Glu Ser Tyr Lys Asp Ser Thr Leu Ile Met
245 250 255
Gln Leu Leu Arg Asp Asn Leu Thr Leu Trp Thr Ser Asp Met Gln Glu
260 265 270
Gln Met Asp Glu Ala
275

(2) INFORMATION FOR SEQ ID NO:742:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 248 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..248
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567814

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:742:

Met Ala Thr Thr Leu Ser Arg Asp Gln Tyr Val Tyr Met Ala Lys Leu
1 5 10 15
Ala Glu Gln Ala Glu Arg Tyr Glu Glu Met Val Gln Phe Met Glu Gln
20 25 30
Leu Val Ser Gly Ala Thr Pro Ala Gly Glu Leu Thr Val Glu Glu Arg
35 40 45
Asn Leu Leu Ser Val Ala Tyr Lys Asn Val Ile Gly Ser Leu Arg Ala
50 55 60
Ala Trp Arg Ile Val Ser Ser Ile Glu Gln Lys Glu Glu Ser Arg Lys
65 70 75 80
Asn Glu Glu His Val Ser Leu Val Lys Asp Tyr Arg Ser Lys Val Glu
85 90 95
Thr Glu Leu Ser Ser Ile Cys Ser Gly Ile Leu Arg Leu Leu Asp Ser
100 105 110
His Leu Ile Pro Ser Ala Thr Ala Ser Glu Ser Lys Val Phe Tyr Leu
115 120 125
Lys Met Lys Gly Asp Tyr His Arg Tyr Leu Ala Glu Phe Lys Ser Gly
130 135 140
Asp Glu Arg Lys Thr Ala Ala Glu Asp Thr Met Ile Ala Tyr Lys Ala
145 150 155 160
Ala Gln Asp Val Ala Val Ala Asp Leu Ala Pro Thr His Pro Ile Arg
165 170 175
Leu Gly Leu Ala Leu Asn Phe Ser Val Phe Tyr Tyr Glu Ile Leu Asn
180 185 190
Ser Ser Glu Lys Ala Cys Ser Met Ala Lys Gln Ala Phe Glu Glu Ala
195 200 205
Ile Ala Glu Leu Asp Thr Leu Gly Glu Glu Ser Tyr Lys Asp Ser Thr
210 215 220
Leu Ile Met Gln Leu Leu Arg Asp Asn Leu Thr Leu Trp Thr Ser Asp
225 230 235 240
Met Gln Glu Gln Met Asp Glu Ala
245

(2) INFORMATION FOR SEQ ID NO:743:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 236 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..236
(D) OTHER INFORMATION: / Ceres Seq. ID 1567815

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:743:

Met Ala Lys Leu Ala Glu Gln Ala Glu Arg Tyr Glu Glu Met Val Gln
1 5 10 15
Phe Met Glu Gln Leu Val Ser Gly Ala Thr Pro Ala Gly Glu Leu Thr
20 25 30
Val Glu Glu Arg Asn Leu Leu Ser Val Ala Tyr Lys Asn Val Ile Gly
35 40 45
Ser Leu Arg Ala Ala Trp Arg Ile Val Ser Ser Ile Glu Gln Lys Glu
50 55 60
Glu Ser Arg Lys Asn Glu Glu His Val Ser Leu Val Lys Asp Tyr Arg
65 70 75 80
Ser Lys Val Glu Thr Glu Leu Ser Ser Ile Cys Ser Gly Ile Leu Arg
85 90 95
Leu Leu Asp Ser His Leu Ile Pro Ser Ala Thr Ala Ser Glu Ser Lys
100 105 110
Val Phe Tyr Leu Lys Met Lys Gly Asp Tyr His Arg Tyr Leu Ala Glu
115 120 125
Phe Lys Ser Gly Asp Glu Arg Lys Thr Ala Ala Glu Asp Thr Met Ile

(C) STRANDEDNESS:

(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..392

(D) OTHER INFORMATION: / Ceres Seq. ID 1567836

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:745:

Phe	Leu	Asp	Lys	Gln	Arg	Ala	Arg	Asp	Gly	Ser	His	Ile	Ile	Thr	Arg	
1			5						10					15		
Ser	Ile	Phe	Ser	Arg	Lys	Arg	Lys	Cys	Asp	Tyr	Pro	Phe	Asp	Phe	Phe	
			20					25					30			
Ala	Glu	Glu	Asp	Glu	Arg	Glu	Lys	Lys	Arg	Lys	Arg	Phe	Glu	Ile	Met	
		35					40					45				
Ala	Asn	Val	Val	Gly	Gln	Leu	Lys	Arg	Gly	Ile	Ser	Arg	Gln	Phe	Ser	
	50					55					60					
Thr	Gly	Ser	Leu	Arg	Arg	Thr	Leu	Ser	Arg	Gln	Phe	Thr	Arg	Gln	Ala	
65				70					75					80		
Ser	His	Asp	Pro	Arg	Arg	Asn	Asn	Met	Arg	Phe	Ser	Phe	Gly	Arg	Gln	
			85					90						95		
Ser	Ser	Leu	Asp	Pro	Ile	Arg	Arg	Ser	Pro	Asp	Gly	Ser	Asn	Gly	Pro	
		100						105					110			
Gln	Leu	Ala	Val	Pro	Asp	Asn	Leu	Asp	Ala	Thr	Met	Gln	Leu	Leu	Phe	
	115						120					125				
Val	Ala	Cys	Arg	Gly	Asp	Val	Glu	Gly	Val	Gln	Asp	Leu	Leu	Asp	Glu	
	130					135					140					
Gly	Ile	Asp	Val	Asn	Ser	Ile	Asp	Leu	Asp	Gly	Arg	Thr	Ala	Leu	His	
	145			150						155				160		
Ile	Ala	Ala	Cys	Glu	Gly	His	Val	Asp	Val	Val	Lys	Leu	Leu	Leu	Thr	
		165						170					175			
Arg	Lys	Ala	Asn	Ile	Asp	Ala	Arg	Asp	Arg	Trp	Gly	Ser	Thr	Ala	Ala	
		180					185						190			
Ala	Asp	Ala	Lys	Tyr	Tyr	Gly	Asn	Met	Asp	Val	Phe	Asn	Ile	Leu	Lys	
	195						200					205				
Ala	Arg	Gly	Ala	Lys	Val	Pro	Lys	Thr	Lys	Arg	Thr	Pro	Met	Val	Val	
	210					215					220					
Ala	Asn	Pro	Arg	Glu	Val	Pro	Glu	Tyr	Glu	Leu	Asn	Pro	Gln	Glu	Leu	
225				230					235					240		
Gln	Val	Arg	Lys	Ala	Asp	Gly	Ile	Ser	Lys	Gly	Ile	Tyr	Gln	Val	Ala	
		245							250				255			
Lys	Trp	Asn	Gly	Thr	Lys	Val	Ser	Val	Lys	Ile	Leu	Asp	Lys	Asp	Leu	
	260						265					270				
Tyr	Lys	Asp	Ser	Asp	Thr	Ile	Asn	Ala	Phe	Lys	His	Glu	Leu	Thr	Leu	
	275						280					285				
Phe	Glu	Lys	Val	Arg	His	Pro	Asn	Val	Val	Gln	Phe	Val	Gly	Ala	Val	
	290					295					300					
Thr	Gln	Asn	Val	Pro	Met	Met	Ile	Val	Ser	Glu	Tyr	His	Pro	Lys	Gly	
305				310						315				320		
Asp	Leu	Gly	Ser	Tyr	Leu	Gln	Lys	Lys	Gly	Arg	Leu	Ser	Pro	Ala	Lys	
		325							330					335		
Val	Leu	Arg	Phe	Ala	Leu	Asp	Ile	Ala	Arg	Gly	Met	Asn	Tyr	Leu	His	
		340					345						350			
Glu	Cys	Lys	Pro	Glu	Pro	Val	Ile	His	Cys	Asp	Leu	Lys	Pro	Lys	Asn	
	355					360					365					
Ile	Met	Leu	Asp	Ser	Gly	Gly	His	Leu	Lys	Val	Ala	Gly	Ile	Trp	Phe	
	370					375					380					
Asp	Lys	Phe	Cys	Lys	Val	Ile	Ile									
385					390											

(2) INFORMATION FOR SEQ ID NO:746:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 345 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..345
(D) OTHER INFORMATION: / Ceres Seq. ID 1567837
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:746:
Met Ala Asn Val Val Gly Gln Leu Lys Arg Gly Ile Ser Arg Gln Phe
1 5 10 15
Ser Thr Gly Ser Leu Arg Arg Thr Leu Ser Arg Gln Phe Thr Arg Gln
20 25 30
Ala Ser His Asp Pro Arg Arg Asn Asn Met Arg Phe Ser Phe Gly Arg
35 40 45
Gln Ser Ser Leu Asp Pro Ile Arg Arg Ser Pro Asp Gly Ser Asn Gly
50 55 60
Pro Gln Leu Ala Val Pro Asp Asn Leu Asp Ala Thr Met Gln Leu Leu
65 70 75 80
Phe Val Ala Cys Arg Gly Asp Val Glu Gly Val Gln Asp Leu Leu Asp
85 90 95
Glu Gly Ile Asp Val Asn Ser Ile Asp Leu Asp Gly Arg Thr Ala Leu
100 105 110
His Ile Ala Ala Cys Glu Gly His Val Asp Val Val Lys Leu Leu Leu
115 120 125
Thr Arg Lys Ala Asn Ile Asp Ala Arg Asp Arg Trp Gly Ser Thr Ala
130 135 140
Ala Ala Asp Ala Lys Tyr Tyr Gly Asn Met Asp Val Phe Asn Ile Leu
145 150 155 160
Lys Ala Arg Gly Ala Lys Val Pro Lys Thr Lys Arg Thr Pro Met Val
165 170 175
Val Ala Asn Pro Arg Glu Val Pro Glu Tyr Glu Leu Asn Pro Gln Glu
180 185 190
Leu Gln Val Arg Lys Ala Asp Gly Ile Ser Lys Gly Ile Tyr Gln Val
195 200 205
Ala Lys Trp Asn Gly Thr Lys Val Ser Val Lys Ile Leu Asp Lys Asp
210 215 220
Leu Tyr Lys Asp Ser Asp Thr Ile Asn Ala Phe Lys His Glu Leu Thr
225 230 235 240
Leu Phe Glu Lys Val Arg His Pro Asn Val Val Gln Phe Val Gly Ala
245 250 255
Val Thr Gln Asn Val Pro Met Met Ile Val Ser Glu Tyr His Pro Lys
260 265 270
Gly Asp Leu Gly Ser Tyr Leu Gln Lys Lys Gly Arg Leu Ser Pro Ala
275 280 285
Lys Val Leu Arg Phe Ala Leu Asp Ile Ala Arg Gly Met Asn Tyr Leu
290 295 300
His Glu Cys Lys Pro Glu Pro Val Ile His Cys Asp Leu Lys Pro Lys
305 310 315 320
Asn Ile Met Leu Asp Ser Gly Gly His Leu Lys Val Ala Gly Ile Trp
325 330 335
Phe Asp Lys Phe Cys Lys Val Ile Ile
340 345

(2) INFORMATION FOR SEQ ID NO:747:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 304 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide

(B) LOCATION: 1..304

(D) OTHER INFORMATION: / Ceres Seq. ID 1567838

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:747:

```
Met Arg Phe Ser Phe Gly Arg Gln Ser Ser Leu Asp Pro Ile Arg Arg
1      5      10      15
Ser Pro Asp Gly Ser Asn Gly Pro Gln Leu Ala Val Pro Asp Asn Leu
20      25      30
Asp Ala Thr Met Gln Leu Leu Phe Val Ala Cys Arg Gly Asp Val Glu
35      40      45
Gly Val Gln Asp Leu Leu Asp Glu Gly Ile Asp Val Asn Ser Ile Asp
50      55      60
Leu Asp Gly Arg Thr Ala Leu His Ile Ala Ala Cys Glu Gly His Val
65      70      75      80
Asp Val Val Lys Leu Leu Thr Arg Lys Ala Asn Ile Asp Ala Arg
85      90      95
Asp Arg Trp Gly Ser Thr Ala Ala Asp Ala Lys Tyr Tyr Gly Asn
100     105     110
Met Asp Val Phe Asn Ile Leu Lys Ala Arg Gly Ala Lys Val Pro Lys
115     120     125
Thr Lys Arg Thr Pro Met Val Val Ala Asn Pro Arg Glu Val Pro Glu
130     135     140
Tyr Glu Leu Asn Pro Gln Glu Leu Gln Val Arg Lys Ala Asp Gly Ile
145     150     155     160
Ser Lys Gly Ile Tyr Gln Val Ala Lys Trp Asn Gly Thr Lys Val Ser
165     170     175
Val Lys Ile Leu Asp Lys Asp Leu Tyr Lys Asp Ser Asp Thr Ile Asn
180     185     190
Ala Phe Lys His Glu Leu Thr Leu Phe Glu Lys Val Arg His Pro Asn
195     200     205
Val Val Gln Phe Val Gly Ala Val Thr Gln Asn Val Pro Met Met Ile
210     215     220
Val Ser Glu Tyr His Pro Lys Gly Asp Leu Gly Ser Tyr Leu Gln Lys
225     230     235     240
Lys Gly Arg Leu Ser Pro Ala Lys Val Leu Arg Phe Ala Leu Asp Ile
245     250     255
Ala Arg Gly Met Asn Tyr Leu His Glu Cys Lys Pro Glu Pro Val Ile
260     265     270
His Cys Asp Leu Lys Pro Lys Asn Ile Met Leu Asp Ser Gly Gly His
275     280     285
Leu Lys Val Ala Gly Ile Trp Phe Asp Lys Phe Cys Lys Val Ile Ile
290     295     300
```

(2) INFORMATION FOR SEQ ID NO:748:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1884 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1884

(D) OTHER INFORMATION: / Ceres Seq. ID 1567843

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:748:

```
acagcttctg atctcaactag tgttcgtcat cttgttctga ttgaagtttg ggaagtgggtg 60
atggtaatat gagcagcagc gcgtgtagcc atcggcggtt tgcgaaagc tcgtctcgtc 120
acatacctcc ctctctctcg tctcttctca gtgtcgccag atgagtatgg acgcacaaag 180
cgttttctgaa aagcttagga gttctggtct attacgaact caaggtcttaa ttggaggcaa 240
gtggcttgac tcgtatgaca ataagacaat caaggttaac aatccagcaa ccggtgaaat 300
tatagctgat gttgcattga tgggaacaaa agagacaaat gatgctattg cttcttctta 360
```

tgaagcattt	acctcttgga	gcagattgac	tgctggagag	aggagtaaa	ttttcggag	420
atggtatgac	ctcctgattg	cacacaagga	agaacttgga	caacttataa	ctttggagca	480
aggaaaaacca	ctcaaggaa	ccatcggaga	ggtagcatat	ggggcaagtt	ttatttgatg	540
ctatggcggag	gaggcaaaa	gtgtatatgg	tgatataatt	cctccgaatc	tgcttgatcg	600
ccgactgttg	gttctaaaaa	agcctgtcgg	tattgttggt	gcaattacc	cttggaactt	660
ccccttagcc	atgattactc	ggaaggtcgg	ccctgctctt	gcttctggat	gcacgggtgt	720
tgttaaacca	tctgaactta	cgcccttaac	agcacttgct	gcggctgaac	ttgcaacttca	780
agctggagtt	cctccggggg	cacttaattg	ggtcatggga	aatgctccctg	aatttgggga	840
tgctttgctt	acgagctcac	aggtgagaaa	aatcacgttc	acgggatcaa	cagcagttgg	900
gaagaaattg	atggcagctg	ctgcacctac	cgtaagaag	gtttctctag	aacttggcgg	960
caacgcacc	tctatagtat	ttgatgatgc	agacctggat	gtagctgtaa	aaggaaagct	1020
tgcagcgaaa	tttaggaata	gtggtcagac	atgtgtttgt	gcgaacagag	tactttgtga	1080
agatggtatc	tatgataaat	ttgctgaggg	ctttctgaa	gcggttcaca	aattagaagt	1140
aggagatggg	tttaggggat	ggacaaccca	gggtccactt	ataaatgatg	cagcagttga	1200
aaaagttagag	acatttgtac	aaagtgctgt	ttctaaggga	gcaaaaatca	tcattgggtg	1260
caaaagggcac	agtcctaggga	tgactttcta	tgagcctact	gttatccggc	atgtttcggg	1320
taacatgatc	atgtctaagg	aggagatttt	tggacctgta	gttcccttta	ttcgggttcaa	1380
aaccgaggag	gcgcgtatca	gaattgtctaa	tgacacaatt	gcaggacttg	ctgcttatat	1440
attcacaaac	agtgctccaaa	gatcttggcg	tgattttgaa	gcacttgaat	atggaactgt	1500
aggggtgaac	gaaggactca	tatcaacaga	ggtggctcca	ttcgggggag	tgaagcagtc	1560
tggtcttggg	aggggaagat	ccaagtatgg	tatggacgaa	taccttgaga	tcaaatagct	1620
atgcttctga	gatattgaata	gacactgatt	tggtttgttt	gaaaagcttt	agaaaattgt	1680
agtttttttc	ctccactcgt	atccttcttaa	taaaagctta	ctgtggaaca	taataagagt	1740
tcggaggata	cttcttaaga	aataagatt	tggtctacga	ccaattgtta	gcattgattt	1800
tagataataa	tttgggggtt	ccattttatt	tatctttgtt	tacgttattt	ttttctttgt	1860
tttactgttaa	tttttgtaat	tcgg				

(2) INFORMATION FOR SEQ ID NO:749:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 495 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..495

(D) OTHER INFORMATION: / Ceres Seq. ID 1567844

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:749:

Met	Ser	Met	Asp	Ala	Gln	Ser	Val	Ser	Glu	Lys	Leu	Arg	Ser	Ser	Gly
1				5						10				15	
Leu	Leu	Arg	Thr	Gln	Gly	Leu	Ile	Gly	Gly	Lys	Trp	Leu	Asp	Ser	Tyr
			20					25					30		
Asp	Asn	Lys	Thr	Ile	Lys	Val	Asn	Asn	Pro	Ala	Thr	Gly	Glu	Ile	Ile
		35					40					45			
Ala	Asp	Val	Ala	Cys	Met	Gly	Thr	Lys	Glu	Thr	Asn	Asp	Ala	Ile	Ala
		50				55					60				
Ser	Ser	Tyr	Glu	Ala	Phe	Thr	Ser	Trp	Ser	Arg	Leu	Thr	Ala	Gly	Glu
		65			70				75					80	
Arg	Ser	Lys	Val	Leu	Arg	Arg	Trp	Tyr	Asp	Leu	Leu	Ile	Ala	His	Lys
		85						90						95	
Glu	Glu	Leu	Gly	Gln	Leu	Ile	Thr	Leu	Glu	Gln	Gly	Lys	Pro	Leu	Lys
		100						105					110		
Glu	Ala	Ile	Gly	Glu	Val	Ala	Tyr	Gly	Ala	Ser	Phe	Ile	Glu	Tyr	Tyr
		115				120					125				
Ala	Glu	Glu	Ala	Lys	Arg	Val	Tyr	Gly	Asp	Ile	Ile	Pro	Pro	Asn	Leu
		130				135					140				
Ser	Asp	Arg	Arg	Leu	Leu	Val	Leu	Lys	Gln	Pro	Val	Gly	Ile	Val	Gly
		145			150				155					160	
Ala	Ile	Thr	Pro	Trp	Asn	Phe	Pro	Leu	Ala	Met	Ile	Thr	Arg	Lys	Val
		165						170						175	
Gly	Pro	Ala	Leu	Ala	Ser	Gly	Cys	Thr	Val	Val	Val	Lys	Pro	Ser	Glu

Met	Asp	Ala	Gln	Ser	Val	Ser	Glu	Lys	Leu	Arg	Ser	Ser	Gly	Leu	Leu
1				5				10						15	
Lys	Thr	Gln	Gly	Leu	Ile	Gly	Gly	Lys	Trp	Leu	Asp	Ser	Thr	Asp	Asn
		20						25					30		
Lys	Thr	Ile	Lys	Val	Asn	Asn	Pro	Ala	Thr	Gly	Glu	Ile	Ile	Ala	Asp
		35					40					45			
Val	Ala	Cys	Met	Gly	Thr	Lys	Glu	Thr	Asn	Asp	Ala	Ile	Ala	Ser	Ser
	50					55				60					
Tyr	Glu	Ala	Phe	Thr	Ser	Trp	Ser	Arg	Leu	Thr	Ala	Gly	Glu	Arg	Ser
65				70					75					80	

Lys Val Leu Arg Arg Trp Tyr Asp Leu Leu Ile Ala His Lys Glu Glu
85 90 95
Leu Gly Gln Leu Ile Thr Leu Glu Gln Gly Lys Pro Leu Lys Glu Ala
100 105 110
Ile Gly Glu Val Ala Tyr Gly Ala Ser Phe Ile Glu Tyr Tyr Ala Glu
115 120 125
Glu Ala Lys Arg Val Tyr Gly Asp Ile Ile Pro Pro Asn Leu Ser Asp
130 135 140
Arg Arg Leu Leu Val Leu Lys Gln Pro Val Gly Ile Val Gly Ala Ile
145 150 155 160
Thr Pro Trp Asn Phe Pro Leu Ala Met Ile Thr Arg Lys Val Gly Pro
165 170 175
Ala Leu Ala Ser Gly Cys Thr Val Val Val Lys Pro Ser Glu Leu Thr
180 185 190
Pro Leu Thr Ala Leu Ala Ala Glu Leu Ala Leu Gln Ala Gly Val
195 200 205
Pro Pro Gly Ala Leu Asn Val Val Met Gly Asn Ala Pro Glu Ile Gly
210 215 220
Asp Ala Leu Leu Thr Ser Pro Gln Val Arg Lys Ile Thr Phe Thr Gly
225 230 235 240
Ser Thr Ala Val Gly Lys Lys Leu Met Ala Ala Ala Pro Thr Val
245 250 255
Lys Lys Val Ser Leu Glu Leu Gly Gly Asn Ala Pro Ser Ile Val Phe
260 265 270
Asp Asp Ala Asp Leu Asp Val Ala Val Lys Gly Thr Leu Ala Ala Lys
275 280 285
Phe Arg Asn Ser Gly Gln Thr Cys Val Cys Ala Asn Arg Val Leu Val
290 295 300
Gln Asp Gly Ile Tyr Asp Lys Phe Ala Glu Ala Phe Ser Glu Ala Val
305 310 315 320
Gln Lys Leu Glu Val Gly Asp Gly Phe Arg Asp Gly Thr Thr Gln Gly
325 330 335
Pro Leu Ile Asn Asp Ala Ala Val Gln Lys Val Glu Thr Phe Val Gln
340 345 350
Asp Ala Val Ser Lys Gly Ala Lys Ile Ile Ile Gly Gly Lys Arg His
355 360 365
Ser Leu Gly Met Thr Phe Tyr Glu Pro Thr Val Ile Arg Asp Val Ser
370 375 380
Asp Asn Met Ile Met Ser Lys Glu Glu Ile Phe Gly Pro Val Ala Pro
385 390 395 400
Leu Ile Arg Phe Lys Thr Glu Glu Asp Ala Ile Arg Ile Ala Asn Asp
405 410 415
Thr Ile Ala Gly Leu Ala Ala Tyr Ile Phe Thr Asn Ser Val Gln Arg
420 425 430
Ser Trp Arg Val Phe Glu Ala Leu Glu Tyr Gly Leu Val Gly Val Asn
435 440 445
Glu Gly Leu Ile Ser Thr Glu Val Ala Pro Phe Gly Gly Val Lys Gln
450 455 460
Ser Gly Leu Gly Arg Glu Gly Ser Lys Tyr Gly Met Asp Glu Tyr Leu
465 470 475 480
Glu Ile Lys Tyr Val Cys Leu Gly Asp Met Asn Arg His
485 490

(2) INFORMATION FOR SEQ ID NO:751:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 442 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide

(B) LOCATION: 1..442

(D) OTHER INFORMATION: / Ceres Seq. ID 1567846

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:751:

Met Gly Thr Lys Glu Thr Asn Asp Ala Ile Ala Ser Ser Tyr Glu Ala
1 5 10 15
Phe Thr Ser Trp Ser Arg Leu Thr Ala Gly Glu Arg Ser Lys Val Leu
20 25 30
Arg Arg Trp Tyr Asp Leu Leu Ile Ala His Lys Glu Glu Leu Gly Gln
35 40 45
Leu Ile Thr Leu Glu Gln Gly Lys Pro Leu Lys Glu Ala Ile Gly Glu
50 55 60
Val Ala Tyr Gly Ala Ser Phe Ile Glu Tyr Tyr Ala Glu Glu Ala Lys
65 70 75 80
Arg Val Tyr Gly Asp Ile Ile Pro Pro Asn Leu Ser Asp Arg Arg Leu
85 90 95
Leu Val Leu Lys Gln Pro Val Gly Ile Val Gly Ala Ile Thr Pro Trp
100 105 110
Asn Phe Pro Leu Ala Met Ile Thr Arg Lys Val Gly Pro Ala Leu Ala
115 120 125
Ser Gly Cys Thr Val Val Val Lys Pro Ser Glu Leu Thr Pro Leu Thr
130 135 140
Ala Leu Ala Ala Ala Glu Leu Ala Leu Gln Ala Gly Val Pro Pro Gly
145 150 155 160
Ala Leu Asn Val Val Met Gly Asn Ala Pro Glu Ile Gly Asp Ala Leu
165 170 175
Leu Thr Ser Pro Gln Val Arg Lys Ile Thr Phe Thr Gly Ser Thr Ala
180 185 190
Val Gly Lys Lys Leu Met Ala Ala Ala Pro Thr Val Lys Lys Val
195 200 205
Ser Leu Glu Leu Gly Gly Asn Ala Pro Ser Ile Val Phe Asp Asp Ala
210 215 220
Asp Leu Asp Val Ala Val Lys Gly Thr Leu Ala Ala Lys Phe Arg Asn
225 230 235 240
Ser Gly Gln Thr Cys Val Cys Ala Asn Arg Val Leu Val Gln Asp Gly
245 250 255
Ile Tyr Asp Lys Phe Ala Glu Ala Phe Ser Glu Ala Val Gln Lys Leu
260 265 270
Glu Val Gly Asp Gly Phe Arg Asp Gly Thr Thr Gln Gly Pro Leu Ile
275 280 285
Asn Asp Ala Ala Val Gln Lys Val Glu Thr Phe Val Gln Asp Ala Val
290 295 300
Ser Lys Gly Ala Lys Ile Ile Ile Gly Gly Lys Arg His Ser Leu Gly
305 310 315 320
Met Thr Phe Tyr Glu Pro Thr Val Ile Arg Asp Val Ser Asp Asn Met
325 330 335
Ile Met Ser Lys Glu Glu Ile Phe Gly Pro Val Ala Pro Leu Ile Arg
340 345 350
Phe Lys Thr Glu Glu Asp Ala Ile Arg Ile Ala Asn Asp Thr Ile Ala
355 360 365
Gly Leu Ala Ala Tyr Ile Phe Thr Asn Ser Val Gln Arg Ser Trp Arg
370 375 380
Val Phe Glu Ala Leu Glu Tyr Gly Leu Val Gly Val Asn Glu Gly Leu
385 390 395 400
Ile Ser Thr Glu Val Ala Pro Phe Gly Gly Val Lys Gln Ser Gly Leu
405 410 415
Gly Arg Glu Gly Ser Lys Tyr Gly Met Asp Glu Tyr Leu Glu Ile Lys
420 425 430
Tyr Val Cys Leu Gly Asp Met Asn Arg His
435 440

(2) INFORMATION FOR SEQ ID NO:752:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1386 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..1386
(D) OTHER INFORMATION: / Ceres Seq. ID 1567877

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:752:

aaacctttct	ctttctgtgt	aacgagaaaa	caaaagctat	cgtcttttct	actactacta	60
ctgctattat	tacattgaat	ccctttgtgt	ctttcttctt	agotgctact	ttgttcgagt	120
gctttcttac	atgcgcgtcg	agattgttga	caggaaaaag	aagtctctgt	gaacacGaga	180
Ntgtagctga	gattctaaag	caatggagag	agtacaatga	gcagattgag	gcagaactct	240
gtatcgatgg	tgggtgtcca	aaatcaatcc	gaaagccctc	tccaaaaaggt	tcgaggaagg	300
gttgtatgaa	aggtaaaggt	ggacctgaaa	acgggatttg	tgactataga	gaagttagac	360
agaggagatg	gggtaaaatg	gttgcgtgag	tcogtgagcc	agacggaggt	gctaggttgt	420
ggctcggtac	tttctccagt	tcatatgaag	ctgcattggc	ttatgacgag	gcggccaaag	480
ctatatatgg	tcagttctgc	agactcaatc	ttcccgagat	cacaaatcgc	tctttctoga	540
ctgctgccac	tgccactgtg	tcaggctcgg	ttactgcatt	ttctgatgaa	tctgaagttt	600
gtgcacgtga	ggatacaaat	gcaagttcag	gttttggtca	ggtgaaacta	gaggattgta	660
gcgatgaata	tgttctctta	gatagttctc	agtgatttaa	agaggagctg	aaaggaaaaag	720
aggaagttag	ggaagaacat	aacttggctg	ttggttttgg	aattggacag	gactcgaaaa	780
gggagacttt	ggatgcttgg	ttgatgggaa	atggcaatga	acaagaacca	ttggaagtgt	840
gtgtggatga	aacgtttgat	attaatgagc	tattgggtat	attaaacgac	aaaatgtgt	900
ctgtccaaga	gacaatgcag	tatcaagtgg	atagacaccc	aaatttcagt	taccaaacgc	960
agtttccaaa	ttctaacctg	ctcgggagcc	tcaacctcat	ggagattgct	caaccaggag	1020
ttgattatgg	atgtccctta	gtgcagccca	gtgatatgga	gaactatgat	attgatttag	1080
accatccgag	gttcaatgat	cttgacatac	aggacttgga	ttttggagga	gacaaagatg	1140
ttcatggatc	tacataagat	ttcaaattto	gtttgactgt	ccctaagttg	tgtattctgt	1200
ccgagacgggt	gtagctgtta	ctagctagaa	gctgcctctc	tttgaagcta	ctgatacttt	1260
ctgatattaa	tggttgtgag	acgtagtaca	tgtatttagg	taatgtagga	caagttcaaa	1320
tatgattcct	tctttctttt	tcttgtgaat	acatatgaca	tatgaagaag	ttcaaacgtt	1380
gggtcc						

(2) INFORMATION FOR SEQ ID NO:753:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 384 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..384
(D) OTHER INFORMATION: / Ceres Seq. ID 1567878

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:753:

Thr	Phe	Leu	Phe	Ser	Ala	Asn	Glu	Lys	Thr	Lys	Ala	Ile	Val	Phe	Ala
1			5						10				15		
Thr	Thr	Thr	Thr	Thr	Ala	Ile	Ile	Thr	Leu	Asn	Pro	Leu	Cys	Ser	Ser
					20				25				30		
Ser	Ala	Ala	Ala	Thr	Leu	Phe	Glu	Cys	Phe	Leu	Thr	Cys	Arg	Arg	Leu
					35				40				45		
Leu	Thr	Gly	Lys	Gly	Ser	Leu	Val	Glu	His	Glu	Xaa	Val	Ala	Glu	Ile
					50				55				60		
Leu	Arg	Gln	Trp	Arg	Glu	Tyr	Asn	Glu	Gln	Ile	Glu	Ala	Glu	Ser	Cys
					65				70				75		
Ile	Asp	Gly	Gly	Gly	Pro	Lys	Ser	Ile	Arg	Lys	Pro	Pro	Pro	Lys	Gly
					85				90				95		
Ser	Arg	Lys	Gly	Cys	Met	Lys	Gly	Lys	Gly	Gly	Pro	Glu	Asn	Gly	Ile
					100				105				110		
Cys	Asp	Tyr	Arg	Glu	Val	Arg	Gln	Arg	Arg	Trp	Gly	Lys	Trp	Val	Ala

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      115              120              125
Glu Ile Arg Glu Pro Asp Gly Gly Ala Arg Leu Trp Leu Gly Thr Phe
130              135              140
Ser Ser Ser Tyr Glu Ala Ala Leu Ala Tyr Asp Glu Ala Ala Lys Ala
145              150              155              160
Ile Tyr Gly Gln Ser Ala Arg Leu Asn Leu Pro Glu Ile Thr Asn Arg
      165              170              175
Ser Ser Ser Thr Ala Ala Thr Ala Thr Val Ser Gly Ser Val Thr Ala
      180              185              190
Phe Ser Asp Glu Ser Glu Val Cys Ala Arg Glu Asp Thr Asn Ala Ser
      195              200              205
Ser Gly Phe Gly Gln Val Lys Leu Glu Asp Cys Ser Asp Glu Tyr Val
      210              215              220
Leu Leu Asp Ser Ser Gln Cys Ile Lys Glu Glu Leu Lys Gly Lys Glu
      225              230              235              240
Glu Val Arg Glu Glu His Asn Leu Ala Val Gly Phe Gly Ile Gly Gln
      245              250              255
Asp Ser Lys Arg Glu Thr Leu Asp Ala Trp Leu Met Gly Asn Gly Asn
      260              265              270
Glu Gln Glu Pro Leu Glu Phe Gly Val Asp Glu Thr Phe Asp Ile Asn
      275              280              285
Glu Leu Leu Gly Ile Leu Asn Asp Asn Asn Val Ser Gly Gln Glu Thr
      290              295              300
Met Gln Tyr Gln Val Asp Arg His Pro Asn Phe Ser Tyr Gln Thr Gln
      305              310              315
Phe Pro Asn Ser Asn Leu Leu Gly Ser Leu Asn Pro Met Glu Ile Ala
      320              325              330              335
Gln Pro Gly Val Asp Tyr Gly Cys Pro Tyr Val Gln Pro Ser Asp Met
      340              345              350
Glu Asn Tyr Gly Ile Asp Leu Asp His Arg Arg Phe Asn Asp Leu Asp
      355              360              365
Ile Gln Asp Leu Asp Phe Gly Gly Asp Lys Asp Val His Gly Ser Thr
      370              375              380

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(2) INFORMATION FOR SEQ ID NO:754:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 283 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..283
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567879

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:754:

```

Met Lys Gly Lys Gly Gly Pro Glu Asn Gly Ile Cys Asp Tyr Arg Glu
1      5      10      15
Val Arg Gln Arg Arg Trp Gly Lys Trp Val Ala Glu Ile Arg Glu Pro
      20      25      30
Asp Gly Gly Ala Arg Leu Trp Leu Gly Thr Phe Ser Ser Ser Tyr Glu
      35      40      45
Ala Ala Leu Ala Tyr Asp Glu Ala Ala Lys Ala Ile Tyr Gly Gln Ser
      50      55      60
Ala Arg Leu Asn Leu Pro Glu Ile Thr Asn Arg Ser Ser Ser Thr Ala
      65      70      75      80
Ala Thr Ala Thr Val Ser Gly Ser Val Thr Ala Phe Ser Asp Glu Ser
      85      90      95
Glu Val Cys Ala Arg Glu Asp Thr Asn Ala Ser Ser Gly Phe Gly Gln
      100      105      110

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Val Lys Leu Glu Asp Cys Ser Asp Glu Tyr Val Leu Leu Asp Ser Ser
115 120 125
Gln Cys Ile Lys Glu Glu Leu Lys Gly Lys Glu Glu Val Arg Glu Glu
130 135 140
His Asn Leu Ala Val Gly Phe Gly Ile Gly Gln Asp Ser Lys Arg Glu
145 150 155 160
Thr Leu Asp Ala Trp Leu Met Gly Asn Gly Asn Glu Gln Glu Pro Leu
165 170 175
Glu Phe Gly Val Asp Glu Thr Phe Asp Ile Asn Glu Leu Leu Gly Ile
180 185 190
Leu Asn Asp Asn Asn Val Ser Gly Gln Glu Thr Met Gln Tyr Gln Val
195 200 205
Asp Arg His Pro Asn Phe Ser Tyr Gln Thr Gln Phe Pro Asn Ser Asn
210 215 220
Leu Leu Gly Ser Leu Asn Pro Met Glu Ile Ala Gln Pro Gly Val Asp
225 230 235 240
Tyr Gly Cys Pro Tyr Val Gln Pro Ser Asp Met Glu Asn Tyr Gly Ile
245 250 255
Asp Leu Asp His Arg Arg Phe Asn Asp Leu Asp Ile Gln Asp Leu Asp
260 265 270
Phe Gly Gly Asp Lys Asp Val His Gly Ser Thr
275 280

(2) INFORMATION FOR SEQ ID NO:755:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 572 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..572
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567884

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:755:

aaaatagctg atcattttgg aggggaagcct cacttgggtt acatgctgat ccgcgacaaa	60
ttggcagagc ttccaggagga gaagaacaaa gtccacaagg aacgggtcga agaaaggaga	120
tcaaaggaga ggagtagaga gcgagaatca agtaaaagaca gagacggagg agatagccgt	180
gaccgaggaa gagatgttga ccgcagGagt agagatcgtg acaggcacca tgaccaccga	240
gaacatgaca gaaactataa ccagtcacgt ggctatgact caagaagccg gcgcagttca	300
cggtcccggt ctagggaaag accgagggat catgatcgcc gcagacgcca tgaccgctac	360
taagaccctg ccaagagctgg ttgcacctgg tttaaagagt tttaacagat gcgttttagga	420
tctatttggG agttacaac acctttcttt ttctttgctc aagtgtttta aggatttttg	480
agattgtaac ttactttaag ttgttaAgag gagcttcttc agatatcttt aatttgtttt	540
ttatgttgtt gacatcaaa acttgcgagt ag	

(2) INFORMATION FOR SEQ ID NO:756:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..120
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567885

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:756:

Lys Ile Ala Asp His Phe Gly Gly Lys Leu His Leu Gly Tyr Met Leu	
1 5 10 15	
Ile Arg Asp Lys Leu Ala Glu Leu Gln Glu Lys Asn Lys Val His	
20 25 30	
Lys Glu Arg Val Glu Glu Arg Arg Ser Lys Glu Arg Ser Arg Glu Arg	

35 40 45
Glu Ser Ser Lys Asp Arg Asp Gly Gly Asp Ser Arg Asp Arg Gly Arg
50 55 60
Asp Val Asp Arg Arg Ser Arg Asp Arg Asp Arg His His Asp His Arg
65 70 75
Glu His Asp Arg Asn Tyr Asn Gln Ser Arg Gly Tyr Asp Ser Arg Ser
85 90 95
Arg Arg Ser Ser Arg Ser Arg Ser Arg Glu Arg Pro Arg Asp His Asp
100 105 110
Arg Arg Arg Arg His Asp Arg Tyr
115 120

(2) INFORMATION FOR SEQ ID NO:757:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 106 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..106
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567886

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:757:

Met Leu Ile Arg Asp Lys Leu Ala Glu Leu Gln Glu Glu Lys Asn Lys
1 5 10 15
Val His Lys Glu Arg Val Glu Glu Arg Arg Ser Lys Glu Arg Ser Arg
20 25 30
Glu Arg Glu Ser Ser Lys Asp Arg Asp Gly Gly Asp Ser Arg Asp Arg
35 40 45
Gly Arg Asp Val Asp Arg Arg Ser Arg Asp Arg Asp Arg His His Asp
50 55 60
His Arg Glu His Asp Arg Asn Tyr Asn Gln Ser Arg Gly Tyr Asp Ser
65 70 75 80
Arg Ser Arg Arg Ser Ser Arg Ser Arg Ser Arg Glu Arg Pro Arg Asp
85 90 95
His Asp Arg Arg Arg Arg His Asp Arg Tyr
100 105

(2) INFORMATION FOR SEQ ID NO:758:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 74 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..74
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567887

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:758:

Met Leu Thr Ala Gly Val Glu Ile Val Thr Gly Thr Met Thr Thr Glu
1 5 10 15
Asn Met Thr Glu Thr Ile Thr Ser His Val Ala Met Thr Gln Glu Ala
20 25 30
Gly Ala Val His Gly Pro Gly Leu Gly Lys Asp Arg Gly Ile Met Ile
35 40 45
Ala Ala Asp Ala Met Thr Ala Thr Lys Thr Leu Pro Lys Met Val Ala
50 55 60
Pro Gly Leu Arg Gly Ser Tyr Arg Cys Val
65 70

(2) INFORMATION FOR SEQ ID NO:759:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1148 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..1148
(D) OTHER INFORMATION: / Ceres Seq. ID 1567896

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:759:

caaaggtttt	caatgaatc	catgacaagt	aaactcaagt	acgggtctgtg	tcccccttctt	60
aatcattttg	ctgaggaagc	aacaactctt	gacttgcaaa	gcgtcttcgg	gaggttcaact	120
ttcgatacaa	ttttcattcg	tataactggg	tctgattccta	gatctctctc	cattgaaatg	180
ctcgaagcag	aatttgcata	agctctcgac	gatgttggag	aagggtattct	ttataggcat	240
tttaaaccaa	ggttcttggg	gaagctgcaa	aactggatag	gattcggaca	agagaagaag	300
ctcactgaag	ctaagtcaac	ttttgaccgc	gtgtgtgccca	aatacatatc	agccaagaga	360
gaagagatta	aaagatcaca	agggactttc	aatggaggaa	gtcaggatct	tttaacttcc	420
ttcataaagc	tagacacgac	caagtacaag	ctcttgaatc	cgagtgcaga	taagtctctt	480
agagacaaca	tcttagcttt	cattctagcg	ggaagagaca	caacagccac	cgctctctct	540
gtggttctct	ggcttctctc	tgaaaaatcca	catgtggtag	ccaagattca	tcaagagatc	600
aaatcaacaa	ctgatctatc	aagaacagga	aatagccaa	agaatgtaga	caagtgtgtg	660
tatttacatg	gtgcgttgtg	tgaagcaatg	agactctacc	caccagtctc	Cttcggacgc	720
aagtctccaa	tcaaatcaga	tgtgcttcca	agtggccata	aagttgatgc	aaactctaa	780
attattatct	gtctttatgc	attggggagg	atgcccagcg	tttggggaga	agatgcattc	840
cagttcaagc	cagagagatg	gatttcggag	aatggaggca	taaaacatga	gcctctcttc	900
aagtttttgt	cggttcaatg	cggttcaatg	actgtctag	gtaaacatct	agcttagact	960
caaatgaaga	tagtgccagt	ggagatatta	cgaaactacg	acattaaagt	ttctcaagga	1020
cagaagattg	tgccagctct	tggttttata	ttgtcaatga	aaacatggct	tcaaatcact	1080
gttactaaga	gatgttctgc	ttgaatttat	tcattgtatta	aataaaaaaa	tcattttggg	1140
ttggtttt						

(2) INFORMATION FOR SEQ ID NO:760:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 367 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..367
(D) OTHER INFORMATION: / Ceres Seq. ID 1567897

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:760:

Gln	Arg	Phe	Ser	Met	Ser	Thr	Met	Thr	Ser	Lys	Leu	Lys	Tyr	Gly	Leu
1			5							10				15	
Val	Pro	Leu	Leu	Asn	His	Phe	Ala	Glu	Gly	Thr	Thr	Leu	Asp	Leu	
			20					25				30			
Gln	Ser	Val	Phe	Gly	Arg	Phe	Thr	Phe	Asp	Thr	Ile	Phe	Ile	Leu	Ile
			35				40				45				
Thr	Gly	Ser	Asp	Pro	Arg	Ser	Leu	Ser	Ile	Glu	Met	Pro	Glu	Asp	Glu
			50			55				60					
Phe	Ala	Lys	Ala	Leu	Asp	Asp	Val	Gly	Glu	Gly	Ile	Leu	Tyr	Arg	His
65			70					75						80	
Phe	Lys	Pro	Arg	Phe	Leu	Trp	Lys	Leu	Gln	Asn	Trp	Ile	Gly	Phe	Gly
			85					90			95				
Gln	Glu	Lys	Lys	Leu	Thr	Glu	Ala	Asn	Ala	Thr	Phe	Asp	Arg	Val	Cys
			100				105					110			
Ala	Lys	Tyr	Ile	Ser	Ala	Lys	Arg	Glu	Glu	Ile	Lys	Arg	Ser	Gln	Gly
			115			120					125				
Thr	Ser	Asn	Gly	Gly	Ser	Gln	Asp	Leu	Leu	Thr	Ser	Phe	Ile	Lys	Leu
			130			135					140				
Asp	Thr	Thr	Lys	Tyr	Lys	Leu	Leu	Asn	Pro	Ser	Asp	Asp	Lys	Phe	Leu

```

145          150          155          160
Arg Asp Asn Ile Leu Ala Phe Ile Leu Ala Gly Arg Asp Thr Thr Ala
          165          170          175
Thr Ala Leu Ser Trp Phe Phe Trp Leu Leu Ser Glu Asn Pro His Val
          180          185          190
Val Ala Lys Ile His Gln Glu Ile Asn Ile Asn Thr Asp Leu Ser Arg
          195          200          205
Thr Gly Asn Ser Gln Glu Asn Val Asp Lys Leu Val Tyr Leu His Gly
          210          215          220
Ala Leu Cys Glu Ala Met Arg Leu Tyr Pro Pro Val Ser Phe Gly Arg
225          230          235          240
Lys Ser Pro Ile Lys Ser Asp Val Leu Pro Ser Gly His Lys Val Asp
          245          250          255
Ala Asn Ser Lys Ile Ile Ile Cys Leu Tyr Ala Leu Gly Arg Met Arg
          260          265          270
Ala Val Trp Gly Glu Asp Ala Ser Gln Phe Lys Pro Glu Arg Trp Ile
          275          280          285
Ser Glu Asn Gly Gly Ile Lys His Glu Pro Ser Phe Lys Phe Leu Ser
          290          295          300
Phe Asn Ala Gly Pro Arg Thr Cys Leu Gly Lys His Leu Ala Met Thr
305          310          315          320
Gln Met Lys Ile Val Ala Val Glu Ile Leu Arg Asn Tyr Asp Ile Lys
          325          330          335
Val Leu Gln Gly Gln Lys Ile Val Pro Ala Leu Gly Phe Ile Leu Ser
          340          345          350
Met Lys His Gly Leu Gln Ile Thr Val Thr Lys Arg Cys Ser Ala
          355          360          365

```

(2) INFORMATION FOR SEQ ID NO:761:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 363 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..363
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567898

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:761:

```

Met Ser Thr Met Thr Ser Lys Leu Lys Tyr Gly Leu Val Pro Leu Leu
1          5          10          15
Asn His Phe Ala Glu Glu Gly Thr Thr Leu Asp Leu Gln Ser Val Phe
          20          25          30
Gly Arg Phe Thr Phe Asp Thr Ile Phe Ile Leu Ile Thr Gly Ser Asp
          35          40          45
Pro Arg Ser Leu Ser Ile Glu Met Pro Glu Asp Glu Phe Ala Lys Ala
          50          55          60
Leu Asp Asp Val Gly Glu Gly Ile Leu Tyr Arg His Phe Lys Pro Arg
65          70          75          80
Phe Leu Trp Lys Leu Gln Asn Trp Ile Gly Phe Gly Gln Glu Lys Lys
          85          90          95
Leu Thr Glu Ala Asn Ala Thr Phe Asp Arg Val Cys Ala Lys Tyr Ile
          100          105          110
Ser Ala Lys Arg Glu Glu Ile Lys Arg Ser Gln Gly Thr Ser Asn Gly
          115          120          125
Gly Ser Gln Asp Leu Leu Thr Ser Phe Ile Lys Leu Asp Thr Thr Lys
          130          135          140
Tyr Lys Leu Leu Asn Pro Ser Asp Asp Lys Phe Leu Arg Asp Asn Ile
145          150          155          160
Leu Ala Phe Ile Leu Ala Gly Arg Asp Thr Thr Ala Thr Ala Leu Ser
          165          170          175

```

Trp Phe Phe Trp Leu Leu Ser Glu Asn Pro His Val Val Ala Lys Ile
180 185 190
His Gln Glu Ile Asn Ile Asn Thr Asp Leu Ser Arg Thr Gly Asn Ser
195 200 205
Gln Glu Asn Val Asp Lys Leu Val Tyr Leu His Gly Ala Leu Cys Glu
210 215 220
Ala Met Arg Leu Tyr Pro Pro Val Ser Phe Gly Arg Lys Ser Pro Ile
225 230 235 240
Lys Ser Asp Val Leu Pro Ser Gly His Lys Val Asp Ala Asn Ser Lys
245 250 255
Ile Ile Ile Cys Leu Tyr Ala Leu Gly Arg Met Arg Ala Val Trp Gly
260 265 270
Glu Asp Ala Ser Gln Phe Lys Pro Glu Arg Trp Ile Ser Glu Asn Gly
275 280 285
Gly Ile Lys His Glu Pro Ser Phe Lys Phe Leu Ser Phe Asn Ala Gly
290 295 300
Pro Arg Thr Cys Leu Gly Lys His Leu Ala Met Thr Gln Met Lys Ile
305 310 315 320
Val Ala Val Glu Ile Leu Arg Asn Tyr Asp Ile Lys Val Leu Gln Gly
325 330 335
Gln Lys Ile Val Pro Ala Leu Gly Phe Ile Leu Ser Met Lys His Gly
340 345 350
Leu Gln Ile Thr Val Thr Lys Arg Cys Ser Ala
355 360

(2) INFORMATION FOR SEQ ID NO:762:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 360 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..360

(D) OTHER INFORMATION: / Ceres Seq. ID 1567899

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:762:

Met Thr Ser Lys Leu Lys Tyr Gly Leu Val Pro Leu Leu Asn His Phe
1 5 10 15
Ala Glu Glu Gly Thr Thr Leu Asp Leu Gln Ser Val Phe Gly Arg Phe
20 25 30
Thr Phe Asp Thr Ile Phe Ile Leu Ile Thr Gly Ser Asp Pro Arg Ser
35 40 45
Leu Ser Ile Glu Met Pro Glu Asp Glu Phe Ala Lys Ala Leu Asp Asp
50 55 60
Val Gly Glu Gly Ile Leu Tyr Arg His Phe Lys Pro Arg Phe Leu Trp
65 70 75 80
Lys Leu Gln Asn Trp Ile Gly Phe Gly Gln Glu Lys Lys Leu Thr Glu
85 90 95
Ala Asn Ala Thr Phe Asp Arg Val Cys Ala Lys Tyr Ile Ser Ala Lys
100 105 110
Arg Glu Glu Ile Lys Arg Ser Gln Gly Thr Ser Asn Gly Gly Ser Gln
115 120 125
Asp Leu Leu Thr Ser Phe Ile Lys Leu Asp Thr Thr Lys Tyr Lys Leu
130 135 140
Leu Asn Pro Ser Asp Asp Lys Phe Leu Arg Asp Asn Ile Leu Ala Phe
145 150 155 160
Ile Leu Ala Gly Arg Asp Thr Thr Ala Thr Ala Leu Ser Trp Phe Phe
165 170 175
Trp Leu Leu Ser Glu Asn Pro His Val Val Ala Lys Ile His Gln Glu
180 185 190
Ile Asn Ile Asn Thr Asp Leu Ser Arg Thr Gly Asn Ser Gln Glu Asn

195	200	205
Val Asp Lys Leu Val Tyr Leu His Gly Ala Leu Cys Glu Ala Met Arg		
210	215	220
Leu Tyr Pro Pro Val Ser Phe Gly Arg Lys Ser Pro Ile Lys Ser Asp		
225	230	235
Val Leu Pro Ser Gly His Lys Val Asp Ala Asn Ser Lys Ile Ile Ile		
245	250	255
Cys Leu Tyr Ala Leu Gly Arg Met Arg Ala Val Trp Gly Glu Asp Ala		
260	265	270
Ser Gln Phe Lys Pro Glu Arg Trp Ile Ser Glu Asn Gly Gly Ile Lys		
275	280	285
His Glu Pro Ser Phe Lys Phe Leu Ser Phe Asn Ala Gly Pro Arg Thr		
290	295	300
Cys Leu Gly Lys His Leu Ala Met Thr Gln Met Lys Ile Val Ala Val		
305	310	315
Glu Ile Leu Arg Asn Tyr Asp Ile Lys Val Leu Gln Gly Gln Lys Ile		
325	330	335
Val Pro Ala Leu Gly Phe Ile Leu Ser Met Lys His Gly Leu Gln Ile		
340	345	350
Thr Val Thr Lys Arg Cys Ser Ala		
355	360	

(2) INFORMATION FOR SEQ ID NO:763:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1104 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1104

(D) OTHER INFORMATION: / Ceres Seq. ID 1567904

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:763:

ggcttgctgc	agaagttggg	attcgttctt	ttataatttg	ccctgaaaac	gaaaacgaaa	60
ataaaaaagcg	gagagagaga	tggctagata	cgatcgagca	attactgtct	tctcccccca	120
cggtcacctc	tttcaagtgc	aatacgcctt	tgaagccgtc	cgcaagggta	acgcgcgcgt	180
cggtgtccgc	ggtagcgaca	ccgttgtcct	cgccgtcgag	aagaagtcca	cccccaagct	240
tcaggattct	agatcagcca	gaaaaattgt	gagccttgac	aatcacattg	ccttggcatg	300
cgcggggctc	aaggtgatg	cccagctctt	gattaacaaa	gcaaggatcg	agtgtaaaag	360
ccacaggctt	acaactgagg	accctgtcac	tggtgagtac	atcactcgct	acattgtctg	420
ccttcaacag	aagtataacc	aaagtgtgtg	tgtagacccc	ttcgggtctt	ctactcttat	480
cgttggtctt	gacccttact	ctcgccctcc	ttccctatat	cagactgac	cttctgggac	540
tttctctgct	tggaaagcta	atgctaccgc	cagaaactcc	aactctatta	gggaattccct	600
cgagaagaac	tacaaagaat	cctctggcca	agaaaactatt	aaactcgcta	tccgtgctct	660
gcttgaggtg	gttgagagtg	gcggaagaaa	cattgaggtt	gcgctaagta	cacgggagga	720
aactGgGctg	cgccagctag	aagaagctga	aattgatgca	atcgttgcca	agatcgaaag	780
tgaaggcgcg	cgacagaagc	gcacagaaga	gcctcccaaa	ggaaacttga	taaaaacaata	840
actgtttctg	tttctcaatc	tgaactttacc	ttcttcgtgt	ctttctgttc	tcaactcttg	900
tttgactcga	gccactcttt	tggcaaaaaga	agaacctgac	cccatcgttt	tgtttaacttg	960
aaaatgctcc	aaaaaaaaaac	tgaagaaaag	gtttaaaaat	cgcttgatct	tgatcaaac	1020
aaggataaat	ttctgtgtgc	tcatgtgtag	atagagaagt	gactctccat	tttctattta	1080
taagtaagca	gaacaattag	tggt				

(2) INFORMATION FOR SEQ ID NO:764:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 253 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..253

(D) OTHER INFORMATION: / Ceres Seq. ID 1567905

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:764:

```
Met Ala Arg Tyr Asp Arg Ala Ile Thr Val Phe Ser Pro Asp Gly His
1      5      10      15
Leu Phe Gln Val Glu Tyr Ala Leu Glu Ala Val Arg Lys Gly Asn Ala
20     25     30
Ala Val Gly Val Arg Gly Thr Asp Thr Val Val Leu Ala Val Glu Lys
35     40     45
Lys Ser Thr Pro Lys Leu Gln Asp Ser Arg Ser Ala Arg Lys Ile Val
50     55     60
Ser Leu Asp Asn His Ile Ala Leu Ala Cys Ala Gly Leu Lys Ala Asp
65     70     75     80
Ala Arg Val Leu Ile Asn Lys Ala Arg Ile Glu Cys Gln Ser His Arg
85     90     95
Leu Thr Leu Glu Asp Pro Val Thr Val Glu Tyr Ile Thr Arg Tyr Ile
100    105    110
Ala Gly Leu Gln Gln Lys Tyr Thr Gln Ser Gly Gly Val Arg Pro Phe
115    120    125
Gly Leu Ser Thr Leu Ile Val Gly Phe Asp Pro Tyr Ser Arg Leu Pro
130    135    140
Ser Leu Tyr Gln Thr Asp Pro Ser Gly Thr Phe Ser Ala Trp Lys Ala
145    150    155    160
Asn Ala Thr Gly Arg Asn Ser Asn Ser Ile Arg Glu Phe Leu Glu Lys
165    170    175
Asn Tyr Lys Glu Ser Ser Gly Gln Glu Thr Ile Lys Leu Ala Ile Arg
180    185    190
Ala Leu Leu Glu Val Val Glu Ser Gly Gly Lys Asn Ile Glu Val Ala
195    200    205
Val Met Thr Arg Glu Glu Thr Gly Leu Arg Gln Leu Glu Glu Ala Glu
210    215    220
Ile Asp Ala Ile Val Ala Lys Ile Glu Ala Glu Gly Arg Arg Ser
225    230    235    240
Ser Gln Glu Arg Pro Ser Lys Gly Asn Leu Ile Lys Gln
245    250
```

(2) INFORMATION FOR SEQ ID NO:765:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1956 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1956

(D) OTHER INFORMATION: / Ceres Seq. ID 1567929

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:765:

```
ctctcatttt Gctactcttc ttcaaaagca cactcaatat ttcgagatcc tctcgggcttg 60
ttcgtctctc gtgaacgac ccactctattg ttctctgctg gtctcagatt cgactcaactt 120
ggatattctc gatactgaag aagcctcctt ctctcttttc cgctcttccc gatgccgac 180
gataagatct caaagatgta tgctagttaa gagaaggagg aacgtgcgag gatggcatca 240
tttgttggtg caatggctat cagtgatctg gtttaagtota ctttagggcc aaagggcatg 300
gataaaatct tacaactctac tggtagaggt catgcggtca ctgttactaa cgatggtgct 360
actattctca agtcaacttca catagacaac cctgcagcta aagttcttgt tgacatctcg 420
aaagtccaag atgatgaggt tggatgatgga actactctgt ttgtttcttt ggccggcgag 480
cttctgaggg aagcagaaaa gctcttggtt tctaagattc accctatgac catcatagca 540
ggttacagaa tggctctcga atgtgctcgt aatgctttac tgaagagagt cattgataac 600
aaggacaagt cagagaagtt taggtcagac ttgttgaa ga ttgcgatgac tacttttatg 660
tccaaaattc tctcacagga caaggaacat ttgcagaaaa tggccgtgga tgcgtgtttc 720
aggctaaagg gaagcagaaa ctgggaagct attcagatca tcaaaaaaac tggagggtct 780
ctgaaggatt cgttttttga tgaagggttt attcttgaca agaaaatagg aattggcgag 840
```

cctaagcgca	tagaagaatgc	aaatatcttta	gtagctaata	ctgctatgga	taccgataaa	900
gtgaagattt	acgggtgcaag	tgctcogtgtg	gattccatga	ccaaggtgtgc	tgagattgaa	960
ggggctttaga	aggaaaaaaat	gaagacaaag	gtgaagaaga	tcataaggcca	cggaatacaac	1020
tgcttttgta	acagggcagtt	gatctacaat	ttccctgagg	aactctttgc	tgatgtcgtg	1080
atacttgcta	ttgagcatgc	tgacttttag	ggaatagagc	gtctttggtt	ggttactgtg	1140
ggtgaaattg	cttcgacctt	tgacaaccca	gagttctgta	agcttgggca	ttgcaagcct	1200
atagaaagaaa	tcattgattgg	tgaagacaag	ttgattcatt	tcctgtgttg	tgaatggggc	1260
caggcttggt	caattgtcct	aagaggggccc	agtcaccatg	tcctagatga	cggtgaaaga	1320
tcactccatg	atgccttatg	tgtactctct	caaacagtga	atgatactag	agttttgctt	1380
ggaggtggtt	ggccagagat	ggtgatggca	aaggaaagtag	atgagcttgc	aaggaaaact	1440
gctggcaaaa	aatctcatgc	caattgaagct	ttctcacgtg	ctctagtgtc	tataccgaca	1500
acaactcgctg	acaaacgctgg	tttagacagt	gccgaattgg	ttgctoaagt	ctgtgcagag	1560
caccacactg	aagggtgtgaa	cgctgggagtc	gacgtcatca	ctggagctgt	aggagatgat	1620
gaagagagag	gaattctatga	agcattcaaa	gtgaagcaag	cggttctgct	ttcagccaca	1680
gaagcatctg	agatgatatt	gcgagttggat	gaatcatta	catgtgctcc	taggaggaga	1740
gaagacagga	tgtgaaaaac	tcaacacaaa	acatgaagc	tggtggggagc	ctagagattc	1800
catgattgtg	ttttcgattt	ggatcagaat	acaaacttttc	taatatgttt	aatgttttgc	1860
tcctccttag	aactcatctt	tttgttttgt	ttccttttaa	tcctgttttg	agtttgaatt	1920
tagacttttg	aaaaaagtgt	tagctccaaa	gttttt			

(2) INFORMATION FOR SEQ ID NO:766:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 527 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..527

(D) OTHER INFORMATION: / Ceres Seq. ID 1567930

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:766:

Met	Pro	Ile	Asp	Lys	Ile	Phe	Lys	Asp	Asp	Ala	Ser	Glu	Glu	Lys	Gly
1			5					10						15	
Glu	Arg	Ala	Arg	Met	Ala	Ser	Phe	Val	Gly	Ala	Met	Ala	Ile	Ser	Asp
			20					25					30		
Leu	Val	Lys	Ser	Thr	Leu	Gly	Pro	Lys	Gly	Met	Asp	Lys	Ile	Leu	Gln
			35				40					45			
Ser	Thr	Gly	Arg	Gly	His	Ala	Val	Thr	Val	Thr	Asn	Asp	Gly	Ala	Thr
			50				55				60				
Ile	Leu	Lys	Ser	Leu	His	Ile	Asp	Asn	Pro	Ala	Ala	Lys	Val	Leu	Val
65					70				75					80	
Asp	Ile	Ser	Lys	Val	Gln	Asp	Asp	Glu	Val	Gly	Asp	Gly	Thr	Thr	Ser
				85				90					95		
Val	Val	Val	Leu	Ala	Gly	Glu	Leu	Leu	Arg	Glu	Ala	Glu	Lys	Leu	Val
			100					105					110		
Ala	Ser	Lys	Ile	His	Pro	Met	Thr	Ile	Ile	Ala	Gly	Tyr	Arg	Met	Ala
			115				120					125			
Ser	Glu	Cys	Ala	Arg	Asn	Ala	Leu	Leu	Lys	Arg	Val	Ile	Asp	Asn	Lys
			130			135				140					
Asp	Asn	Ala	Glu	Lys	Phe	Arg	Ser	Asp	Leu	Leu	Lys	Ile	Ala	Met	Thr
145				150					155					160	
Thr	Leu	Cys	Ser	Lys	Ile	Leu	Ser	Gln	Asp	Lys	Glu	His	Phe	Ala	Glu
			165					170					175		
Met	Ala	Val	Asp	Ala	Val	Phe	Arg	Leu	Lys	Gly	Ser	Thr	Asn	Leu	Glu
			180					185					190		
Ala	Ile	Gln	Ile	Ile	Lys	Lys	Pro	Gly	Gly	Ser	Leu	Lys	Asp	Ser	Phe
			195				200					205			
Leu	Asp	Glu	Gly	Phe	Ile	Leu	Asp	Lys	Lys	Ile	Gly	Ile	Gly	Gln	Pro
210						215				220					
Lys	Arg	Ile	Glu	Asn	Ala	Asn	Ile	Leu	Val	Ala	Asn	Thr	Ala	Met	Asp
225				230						235				240	

```

Thr Asp Lys Val Lys Ile Tyr Gly Ala Arg Val Arg Val Asp Ser Met
                245                250                255
Thr Lys Val Ala Glu Ile Glu Gly Ala Glu Lys Glu Lys Met Lys Asp
                260                265                270
Lys Val Lys Lys Lys Ile Ile Gly His Gly Ile Asn Cys Phe Val Asn Arg
                275                280                285
Gln Leu Ile Tyr Asn Phe Pro Glu Glu Leu Phe Ala Asp Ala Gly Ile
                290                295                300
Leu Ala Ile Glu His Ala Asp Phe Glu Gly Ile Glu Arg Leu Gly Leu
305                310                315                320
Val Thr Gly Gly Glu Ile Ala Ser Thr Phe Asp Asn Pro Glu Ser Val
                325                330                335
Lys Leu Gly His Cys Lys Leu Ile Glu Glu Ile Met Ile Gly Glu Asp
                340                345                350
Lys Leu Ile His Phe Ser Gly Cys Glu Met Gly Gln Ala Cys Ser Ile
                355                360                365
Val Leu Arg Gly Ala Ser His His Val Leu Asp Glu Ala Glu Arg Ser
370                375                380
Leu His Asp Ala Leu Cys Val Leu Ser Gln Thr Val Asn Asp Thr Arg
385                390                395                400
Val Leu Leu Gly Gly Trp Pro Glu Met Val Met Ala Lys Glu Val
                405                410                415
Asp Glu Leu Ala Arg Lys Thr Ala Gly Lys Lys Ser His Ala Ile Glu
                420                425                430
Ala Phe Ser Arg Ala Leu Val Ala Ile Pro Thr Thr Ile Ala Asp Asn
                435                440                445
Ala Gly Leu Asp Ser Ala Glu Leu Val Ala Gln Leu Arg Ala Glu His
450                455                460
His Thr Glu Gly Cys Asn Ala Gly Ile Asp Val Ile Thr Gly Ala Val
465                470                475                480
Gly Asp Met Glu Glu Arg Gly Ile Tyr Glu Ala Phe Lys Val Lys Gln
                485                490                495
Ala Val Leu Leu Ser Ala Thr Glu Ala Ser Glu Met Ile Leu Arg Val
500                505                510
Asp Glu Ile Ile Thr Cys Ala Pro Arg Arg Arg Glu Asp Arg Met
515                520                525

```

(2) INFORMATION FOR SEQ ID NO:767:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 507 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..507
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567931

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:767:

```

Met Ala Ser Phe Val Gly Ala Met Ala Ile Ser Asp Leu Val Lys Ser
1           5           10           15
Thr Leu Gly Pro Lys Gly Met Asp Lys Ile Leu Gln Ser Thr Gly Arg
                20                25                30
Gly His Ala Val Thr Val Thr Asn Asp Gly Ala Thr Ile Leu Lys Ser
                35                40                45
Leu His Ile Asp Asn Pro Ala Ala Lys Val Leu Val Asp Ile Ser Lys
50                55                60
Val Gln Asp Asp Glu Val Gly Asp Gly Thr Thr Ser Val Val Val Leu
65                70                75                80
Ala Gly Glu Leu Leu Arg Glu Ala Glu Lys Leu Val Ala Ser Lys Ile
                85                90                95
His Pro Met Thr Ile Ile Ala Gly Tyr Arg Met Ala Ser Glu Cys Ala

```

100	105	110
Arg Asn Ala Leu Leu Lys Arg Val Ile Asp Asn Lys Asp Asn Ala Glu		
115	120	125
Lys Phe Arg Ser Asp Leu Leu Lys Ile Ala Met Thr Thr Leu Cys Ser		
130	135	140
Lys Ile Leu Ser Gln Asp Lys Glu His Phe Ala Glu Met Ala Val Asp		
145	150	155
Ala Val Phe Arg Leu Lys Gly Ser Thr Asn Leu Glu Ala Ile Gln Ile		
165	170	175
Ile Lys Lys Pro Gly Gly Ser Leu Lys Asp Ser Phe Leu Asp Glu Gly		
180	185	190
Phe Ile Leu Asp Lys Lys Ile Gly Ile Gly Gln Pro Lys Arg Ile Glu		
195	200	205
Asn Ala Asn Ile Leu Val Ala Asn Thr Ala Met Asp Thr Asp Lys Val		
210	215	220
Lys Ile Tyr Gly Ala Arg Val Arg Val Asp Ser Met Thr Lys Val Ala		
225	230	235
Glu Ile Glu Gly Ala Glu Lys Glu Lys Met Lys Asp Lys Val Lys Lys		
245	250	255
Ile Ile Gly His Gly Ile Asn Cys Phe Val Asn Arg Gln Leu Ile Tyr		
260	265	270
Asn Phe Pro Glu Glu Leu Phe Ala Asp Ala Gly Ile Leu Ala Ile Glu		
275	280	285
His Ala Asp Phe Glu Gly Ile Glu Arg Leu Gly Leu Val Thr Gly Gly		
290	295	300
Glu Ile Ala Ser Thr Phe Asp Asn Pro Glu Ser Val Lys Leu Gly His		
305	310	315
Cys Lys Leu Ile Glu Glu Ile Met Ile Gly Glu Asp Lys Leu Ile His		
325	330	335
Phe Ser Gly Cys Glu Met Gly Gln Ala Cys Ser Ile Val Leu Arg Gly		
340	345	350
Ala Ser His His Val Leu Asp Glu Ala Glu Arg Ser Leu His Asp Ala		
355	360	365
Leu Cys Val Leu Ser Gln Thr Val Asn Asp Thr Arg Val Leu Leu Gly		
370	375	380
Gly Gly Trp Pro Glu Met Val Met Ala Lys Glu Val Asp Glu Leu Ala		
385	390	395
Arg Lys Thr Ala Gly Lys Lys Ser His Ala Ile Glu Ala Phe Ser Arg		
405	410	415
Ala Leu Val Ala Ile Pro Thr Thr Ile Ala Asp Asn Ala Gly Leu Asp		
420	425	430
Ser Ala Glu Leu Val Ala Gln Leu Arg Ala Glu His His Thr Glu Gly		
435	440	445
Cys Asn Ala Gly Ile Asp Val Ile Thr Gly Ala Val Gly Asp Met Glu		
450	455	460
Glu Arg Gly Ile Tyr Glu Ala Phe Lys Val Lys Gln Ala Val Leu Leu		
465	470	475
Ser Ala Thr Glu Ala Ser Glu Met Ile Leu Arg Val Asp Glu Ile Ile		
485	490	495
Thr Cys Ala Pro Arg Arg Arg Glu Asp Arg Met		
500	505	

- (2) INFORMATION FOR SEQ ID NO:768:
- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 500 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
- (A) NAME/KEY: peptide
- (B) LOCATION: 1..500

(D) OTHER INFORMATION: / Ceres Seq. ID 1567932
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:768:

Met	Ala	Ile	Ser	Asp	Leu	Val	Lys	Ser	Thr	Leu	Gly	Pro	Lys	Gly	Met
1			5						10					15	
Asp	Lys	Ile	Leu	Gln	Ser	Thr	Gly	Arg	Gly	His	Ala	Val	Thr	Val	Thr
			20					25					30		
Asn	Asp	Gly	Ala	Thr	Ile	Leu	Lys	Ser	Leu	His	Ile	Asp	Asn	Pro	Ala
			35					40					45		
Ala	Lys	Val	Leu	Val	Asp	Ile	Ser	Lys	Val	Gln	Asp	Asp	Glu	Val	Gly
			50					55				60			
Asp	Gly	Thr	Thr	Ser	Val	Val	Val	Leu	Ala	Gly	Glu	Leu	Leu	Arg	Glu
65					70					75				80	
Ala	Glu	Lys	Leu	Val	Ala	Ser	Lys	Ile	His	Pro	Met	Thr	Ile	Ile	Ala
				85					90					95	
Gly	Tyr	Arg	Met	Ala	Ser	Glu	Cys	Ala	Arg	Asn	Ala	Leu	Leu	Lys	Arg
			100					105					110		
Val	Ile	Asp	Asn	Lys	Asp	Asn	Ala	Glu	Lys	Phe	Arg	Ser	Asp	Leu	Leu
			115					120					125		
Lys	Ile	Ala	Met	Thr	Thr	Leu	Cys	Ser	Lys	Ile	Leu	Ser	Gln	Asp	Lys
			130					135				140			
Glu	His	Phe	Ala	Glu	Met	Ala	Val	Asp	Ala	Val	Phe	Arg	Leu	Lys	Gly
145					150						155				160
Ser	Thr	Asn	Leu	Glu	Ala	Ile	Gln	Ile	Ile	Lys	Lys	Pro	Gly	Gly	Ser
				165					170					175	
Leu	Lys	Asp	Ser	Phe	Leu	Asp	Glu	Gly	Phe	Ile	Leu	Asp	Lys	Lys	Ile
			180					185					190		
Gly	Ile	Gly	Gln	Pro	Lys	Arg	Ile	Glu	Asn	Ala	Asn	Ile	Leu	Val	Ala
			195					200				205			
Asn	Thr	Ala	Met	Asp	Thr	Asp	Lys	Val	Lys	Ile	Tyr	Gly	Ala	Arg	Val
			210					215				220			
Arg	Val	Asp	Ser	Met	Thr	Lys	Val	Ala	Glu	Ile	Glu	Gly	Ala	Glu	Lys
225					230					235					240
Glu	Lys	Met	Lys	Asp	Lys	Val	Lys	Lys	Ile	Ile	Gly	His	Gly	Ile	Asn
				245					250					255	
Cys	Phe	Val	Asn	Arg	Gln	Leu	Ile	Tyr	Asn	Phe	Pro	Glu	Glu	Leu	Phe
			260					265					270		
Ala	Asp	Ala	Gly	Ile	Leu	Ala	Ile	Glu	His	Ala	Asp	Phe	Glu	Gly	Ile
			275					280				285			
Glu	Arg	Leu	Gly	Leu	Val	Thr	Gly	Gly	Glu	Ile	Ala	Ser	Thr	Phe	Asp
			290				295				300				
Asn	Pro	Glu	Ser	Val	Lys	Leu	Gly	His	Cys	Lys	Leu	Ile	Glu	Glu	Ile
305					310					315					320
Met	Ile	Gly	Glu	Asp	Lys	Leu	Ile	His	Phe	Ser	Gly	Cys	Glu	Met	Gly
				325					330					335	
Gln	Ala	Cys	Ser	Ile	Val	Leu	Arg	Gly	Ala	Ser	His	His	Val	Leu	Asp
			340					345					350		
Glu	Ala	Glu	Arg	Ser	Leu	His	Asp	Ala	Leu	Cys	Val	Leu	Ser	Gln	Thr
			355				360					365			
Val	Asn	Asp	Thr	Arg	Val	Leu	Leu	Gly	Gly	Gly	Trp	Pro	Glu	Met	Val
			370				375					380			
Met	Ala	Lys	Glu	Val	Asp	Glu	Leu	Ala	Arg	Lys	Thr	Ala	Gly	Lys	Lys
385					390					395					400
Ser	His	Ala	Ile	Glu	Ala	Phe	Ser	Arg	Ala	Leu	Val	Ala	Ile	Pro	Thr
				405					410					415	
Thr	Ile	Ala	Asp	Asn	Ala	Gly	Leu	Asp	Ser	Ala	Glu	Leu	Val	Ala	Gln
			420					425					430		
Leu	Arg	Ala	Glu	His	His	Thr	Glu	Gly	Cys	Asn	Ala	Gly	Ile	Asp	Val
			435					440				445			
Ile	Thr	Gly	Ala	Val	Gly	Asp	Met	Glu	Glu	Arg	Gly	Ile	Tyr	Glu	Ala
			450				455					460			
Phe	Lys	Val	Lys	Gln	Ala	Val	Leu	Leu	Ser	Ala	Thr	Glu	Ala	Ser	Glu

465 470 475 480
Met Ile Leu Arg Val Asp Glu Ile Ile Thr Cys Ala Pro Arg Arg Arg
485 490 495
Glu Asp Arg Met
500

(2) INFORMATION FOR SEQ ID NO:769:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1504 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1504
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567933

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:769:

atcttcgctt	gcttctctct	caaaaggtga	aaaattagag	cgagagagat	agagagagat	60
ttcaaaacga	aaatccagag	aaagggctct	gccagtttag	ggcatccttg	tgggtgagag	120
agcgattgag	agatttcaaa	aggaggaaga	ggaagatcac	agtgtagagag	agatttagag	180
ggagagaaga	aagagagatt	ctttttgagt	gtgttagggg	ttcatttctc	ctcgagatct	240
acatttatct	cttctcatgg	aacggaagct	tgtgttttgg	ggaatcccgct	gggatattga	300
ttccgatggg	cttaaggatt	acatgtcaaa	atttgagagac	ttggaggatt	gtattgtcat	360
gaaggatcga	tcaatctggaa	gatctcgtgg	atttggtatg	gtcacttttg	cttcagccga	420
agatgcaagg	aatgctttga	aaggtgaaca	cttttttagg	aacaggatct	tggaagttaa	480
agtggtctaca	ccaaaggaag	agatgagaca	gcctgcacaaa	aaagtgcaga	ggatctctgt	540
tgctcgaact	cttctcatcag	tctctgaatc	agatttccga	agccattttg	agaggtatgg	600
ggaaataaca	gacttataca	tgctcaagga	ctacaactcg	aagcagaccc	gacgaatagg	660
gtttatcaca	ttctctagtg	ctgattcaag	ggaggatctg	atggaggaca	ctcatgatct	720
gggagggtaca	acagtttctg	ttgatcgggc	aacaccaaaa	gaggtgatgc	atccgcctag	780
gccaccgccca	gtggctagaa	tgtcgcgcc	accgctggct	attgcaggtg	gattttggag	840
tccaggtgtgt	tatggagctt	atgatgttta	catttctgca	gtacaagat	acgcagcgct	900
tggtgccctt	actttgtatg	ataatccgcg	cacgttttat	ggaagagggg	aaccaaccac	960
aaggggaata	ggaaacaaga	tctttgttgg	acggcttctc	caagaagcat	ccgttgatga	1020
tcttcgcgat	tattttggga	gattttggca	tattcaagat	gcttatattc	caaaggaccc	1080
aaagagaagt	ggacatagag	gttttggatt	tgttaccttt	gctgaaaatg	gtgttgaca	1140
tcgtgtagcc	cgaagatctc	atgaaatctg	tggaacaagag	gtagcaatag	attcacgaac	1200
gcctcttgat	gaagctggac	ctagcgcctg	cgcaagtctc	atgttaagtt	cttctcgctc	1260
tgaatttttt	gggtgctatg	gaggtcctat	gcgcgcattt	ggtcgaatgt	atggaggcat	1320
gagcttggag	gattggggag	atggaatgcc	aaacgcgaaga	ccatcaagac	cagaccggag	1380
gtaccggcca	tactaatgca	gcagaccaac	atttcattag	ctttggctgt	gtccttttat	1440
agaaacttca	ctttgtcaga	tctattttaa	ttgaagcttt	tgtttatgtt	ttaccctcgg	1500

(2) INFORMATION FOR SEQ ID NO:770:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 379 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..379
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567934

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:770:

Met	Glu	Arg	Lys	Leu	Val	Val	Leu	Gly	Ile	Pro	Trp	Asp	Ile	Asp	Ser
1				5				10					15		
Asp	Gly	Leu	Lys	Asp	Tyr	Met	Ser	Lys	Phe	Gly	Asp	Leu	Glu	Asp	Cys
			20					25				30			
Ile	Val	Met	Lys	Asp	Arg	Ser	Thr	Gly	Arg	Ser	Arg	Gly	Phe	Gly	Tyr
			35				40					45			

Val Thr Phe Ala Ser Ala Glu Asp Ala Lys Asn Ala Leu Lys Gly Glu
50 55 60
His Phe Leu Gly Asn Arg Ile Leu Glu Val Lys Val Ala Thr Pro Lys
65 70 75 80
Glu Glu Met Arg Gln Pro Ala Lys Lys Val Thr Arg Ile Phe Val Ala
85 90 95
Arg Ile Pro Ser Ser Val Ser Glu Ser Asp Phe Arg Ser His Phe Glu
100 105 110
Arg Tyr Gly Glu Ile Thr Asp Leu Tyr Met Pro Lys Asp Tyr Asn Ser
115 120 125
Lys Gln His Arg Arg Ile Gly Phe Ile Thr Phe Ser Ser Ala Asp Ser
130 135 140
Val Glu Asp Leu Met Glu Asp Thr His Asp Leu Gly Gly Thr Thr Val
145 150 155 160
Ala Val Asp Arg Ala Thr Pro Lys Glu Asp Asp His Pro Pro Arg Pro
165 170 175
Pro Pro Val Ala Arg Met Ser Arg Pro Pro Val Ala Ile Ala Gly Gly
180 185 190
Phe Gly Ala Pro Gly Gly Tyr Gly Ala Tyr Asp Ala Tyr Ile Ser Ala
195 200 205
Ala Thr Arg Tyr Ala Ala Leu Gly Ala Pro Thr Leu Tyr Asp Asn Pro
210 215 220
Ala Thr Phe Tyr Gly Arg Gly Glu Pro Thr Thr Arg Gly Ile Gly Asn
225 230 235 240
Lys Ile Phe Val Gly Arg Leu Pro Gln Glu Ala Ser Val Asp Asp Leu
245 250 255
Arg Asp Tyr Phe Gly Arg Phe Gly His Ile Gln Asp Ala Tyr Ile Pro
260 265 270
Lys Asp Pro Lys Arg Ser Gly His Arg Gly Phe Gly Phe Val Thr Phe
275 280 285
Ala Glu Asn Gly Val Ala Asp Arg Val Ala Arg Arg Ser His Glu Ile
290 295 300
Cys Gly Gln Glu Val Ala Ile Asp Ser Ala Thr Pro Leu Asp Glu Ala
305 310 315 320
Gly Pro Ser Ala Gly Ala Ser Ser Met Leu Ser Ser Ser Arg Pro Glu
325 330 335
Tyr Phe Gly Gly Tyr Gly Gly Pro Met Arg Ala Phe Gly Arg Met Tyr
340 345 350
Gly Gly Met Ser Leu Asp Asp Trp Gly Tyr Gly Met Pro Asn Ala Arg
355 360 365
Pro Ser Arg Pro Asp Arg Arg Tyr Arg Pro Tyr
370 375

(2) INFORMATION FOR SEQ ID NO:771:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 357 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..357
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567935

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:771:

Met Ser Lys Phe Gly Asp Leu Glu Asp Cys Ile Val Met Lys Asp Arg
1 5 10 15
Ser Thr Gly Arg Ser Arg Gly Phe Gly Tyr Val Thr Phe Ala Ser Ala
20 25 30
Glu Asp Ala Lys Asn Ala Leu Lys Gly Glu His Phe Leu Gly Asn Arg
35 40 45
Ile Leu Glu Val Lys Val Ala Thr Pro Lys Glu Glu Met Arg Gln Pro

50 55 60
Ala Lys Lys Val Thr Arg Ile Phe Val Ala Arg Ile Pro Ser Ser Val
65 70 75 80
Ser Glu Ser Asp Phe Arg Ser His Phe Glu Arg Tyr Gly Glu Ile Thr
85 90 95
Asp Leu Tyr Met Pro Lys Asp Tyr Asn Ser Lys Gln His Arg Arg Ile
100 105 110
Gly Phe Ile Thr Phe Ser Ser Ala Asp Ser Val Glu Asp Leu Met Glu
115 120 125
Asp Thr His Asp Leu Gly Gly Thr Thr Val Ala Val Asp Arg Ala Thr
130 135 140
Pro Lys Glu Asp Asp His Pro Pro Arg Pro Pro Val Ala Arg Met
145 150 155 160
Ser Arg Pro Pro Val Ala Ile Ala Gly Gly Phe Gly Ala Pro Gly Gly
165 170 175
Tyr Gly Ala Tyr Asp Ala Tyr Ile Ser Ala Ala Thr Arg Tyr Ala Ala
180 185 190
Leu Gly Ala Pro Thr Leu Tyr Asp Asn Pro Ala Thr Phe Tyr Gly Arg
195 200 205
Gly Glu Pro Thr Thr Arg Gly Ile Gly Asn Lys Ile Phe Val Gly Arg
210 215 220
Leu Pro Gln Glu Ala Ser Val Asp Asp Leu Arg Asp Tyr Phe Gly Arg
225 230 235 240
Phe Gly His Ile Gln Asp Ala Tyr Ile Pro Lys Asp Pro Lys Arg Ser
245 250 255
Gly His Arg Gly Phe Gly Phe Val Thr Phe Ala Glu Asn Gly Val Ala
260 265 270
Asp Arg Val Ala Arg Arg Ser His Glu Ile Cys Gly Gln Glu Val Ala
275 280 285
Ile Asp Ser Ala Thr Pro Leu Asp Glu Ala Gly Pro Ser Ala Gly Ala
290 295 300
Ser Ser Met Leu Ser Ser Ser Arg Pro Glu Tyr Phe Gly Gly Tyr Gly
305 310 315 320
Gly Pro Met Arg Ala Phe Gly Arg Met Tyr Gly Gly Met Ser Leu Asp
325 330 335
Asp Trp Gly Tyr Gly Met Pro Asn Ala Arg Pro Ser Arg Pro Asp Arg
340 345 350
Arg Tyr Arg Pro Tyr
355

(2) INFORMATION FOR SEQ ID NO:772:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 345 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..345

(D) OTHER INFORMATION: / Ceres Seq. ID 1567936

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:772:

Met Lys Asp Arg Ser Thr Gly Arg Ser Arg Gly Phe Gly Tyr Val Thr
1 5 10 15
Phe Ala Ser Ala Glu Asp Ala Lys Asn Ala Leu Lys Gly Glu His Phe
20 25 30
Leu Gly Asn Arg Ile Leu Glu Val Lys Val Ala Thr Pro Lys Glu Glu
35 40 45
Met Arg Gln Pro Ala Lys Lys Val Thr Arg Ile Phe Val Ala Arg Ile
50 55 60
Pro Ser Ser Val Ser Glu Ser Asp Phe Arg Ser His Phe Glu Arg Tyr
65 70 75 80

Gly Glu Ile Thr Asp Leu Tyr Met Pro Lys Asp Tyr Asn Ser Lys Gln
85 90 95
His Arg Arg Ile Gly Phe Ile Thr Phe Ser Ser Ala Asp Ser Val Glu
100 105 110
Asp Leu Met Glu Asp Thr His Asp Leu Gly Gly Thr Thr Val Ala Val
115 120 125
Asp Arg Ala Thr Pro Lys Glu Asp Asp His Pro Pro Arg Pro Pro Pro
130 135 140
Val Ala Arg Met Ser Arg Pro Pro Val Ala Ile Ala Gly Gly Phe Gly
145 150 155 160
Ala Pro Gly Gly Tyr Gly Ala Tyr Asp Ala Tyr Ile Ser Ala Ala Thr
165 170 175
Arg Tyr Ala Ala Leu Gly Ala Pro Thr Leu Tyr Asp Asn Pro Ala Thr
180 185 190
Phe Tyr Gly Arg Gly Glu Pro Thr Thr Arg Gly Ile Gly Asn Lys Ile
195 200 205
Phe Val Gly Arg Leu Pro Gln Glu Ala Ser Val Asp Asp Leu Arg Asp
210 215 220
Tyr Phe Gly Arg Phe Gly His Ile Gln Asp Ala Tyr Ile Pro Lys Asp
225 230 235 240
Pro Lys Arg Ser Gly His Arg Gly Phe Gly Phe Val Thr Phe Ala Glu
245 250 255
Asn Gly Val Ala Asp Arg Val Ala Arg Arg Ser His Glu Ile Cys Gly
260 265 270
Gln Glu Val Ala Ile Asp Ser Ala Thr Pro Leu Asp Glu Ala Gly Pro
275 280 285
Ser Ala Gly Ala Ser Ser Met Leu Ser Ser Ser Arg Pro Glu Tyr Phe
290 295 300
Gly Gly Tyr Gly Gly Pro Met Arg Ala Phe Gly Arg Met Tyr Gly Gly
305 310 315 320
Met Ser Leu Asp Asp Trp Gly Tyr Gly Met Pro Asn Ala Arg Pro Ser
325 330 335
Arg Pro Asp Arg Arg Tyr Arg Pro Tyr
340 345

(2) INFORMATION FOR SEQ ID NO:773:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1140 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1140

(D) OTHER INFORMATION: / Ceres Seq. ID 1567941

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:773:

attttttcttg	agagatccaa	aaaaagatc	agaaagaaga	agaagacgac	tccaaaaaWc	60
gatgccgtat	tacaccaaacg	acgacaatga	cgtcgacgat	ttcacggaat	acgatccgat	120
gccttatagt	ggaggtctacg	acatcacccgt	gacatacggc	cgttcaattc	caccgtccga	180
cgagacttgt	taccctctct	ctctctctct	cggcgacgccc	tttgatgatc	agcgacctaa	240
tttctctctc	aacaacgatt	cttctgctta	tgacgaccaa	gctcttaaaa	ccgagtcacg	300
tagctatgca	gcaccccgac	ccgttgatc	tggatctgat	tttgcccgga	aacctaatc	360
tggatattga	gggagaacgg	aggttgagta	tggccggaaa	actgaatcgg	agcatggatc	420
tggctatggt	gggagaattg	agagcgatta	cgtgaagcct	agctatggcg	gtcacgagga	480
tggatggtgac	gatggtcaca	aaaaacatag	tggtaaggat	tatgatgatg	gagatgagaa	540
gagtaagaag	aaggagaagg	agaagaagaa	ggataagaag	aatagcagta	ataactctga	600
agatgatgat	tttaagaaga	agaagaagaa	atagcagtat	aaggagcatt	atgatgatga	660
tgattatgat	gagaagaaga	agaagaagaa	agactataat	gatgatgatg	agaagaagaa	720
gaagaagcat	tataatgatg	atgatgatga	gaagaagaag	aagcattaca	atgatgatga	780
tgatgagaag	aagaagaaga	aggagatcat	tgatgatgat	gataagaaga	agaagaagca	840
ctatgataat	gatgatgatg	agaagaagaa	gaagaaggat	catcgtgatg	atgatgatga	900

gaagaagaag aagaagdata accaccacaa gggacatgac taaaaaaggt ttatgatttg	960
ggatttgcac ttttatgact aaataagtaa caacaactta agcacacttc tgctctctac	1020
gtttatgtca atgtgtgttt tgtttttgcg tctgtgtttt gctgctaact tcaatgagat	1080
cttcataagt catatgtaat atgttttagtg tacgtgtgttt ctagtgatgt cgtttggtct	1140

(2) INFORMATION FOR SEQ ID NO:774:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 210 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..210
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567942

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:774:

Phe	Phe	Leu	Arg	Asp	Pro	Lys	Lys	Val	Ser	Glu	Arg	Arg	Arg	Arg	Arg	Arg	1	5	10	15
Leu	Gln	Lys	Xaa	Met	Pro	Tyr	Tyr	Thr	Asn	Asp	Asp	Asn	Asp	Val	Asp	Asp	20	25	30	35
Asp	Phe	Thr	Glu	Tyr	Asp	Pro	Met	Pro	Tyr	Ser	Gly	Gly	Tyr	Asp	Ile		40	45	50	55
Thr	Val	Thr	Tyr	Gly	Arg	Ser	Ile	Pro	Pro	Ser	Asp	Glu	Thr	Cys	Tyr		60	65	70	75
Pro	Leu	Ser	Ser	Leu	Ser	Gly	Asp	Ala	Phe	Glu	Tyr	Gln	Arg	Pro	Asn		80	85	90	95
Phe	Ser	Ser	Asn	Asn	Asp	Ser	Ser	Ala	Tyr	Asp	Asp	Gln	Ala	Leu	Lys		100	105	110	115
Thr	Glu	Tyr	Ser	Ser	Tyr	Ala	Arg	Pro	Gly	Pro	Val	Gly	Ser	Gly	Ser		120	125	130	135
Asp	Phe	Gly	Arg	Lys	Pro	Asn	Ser	Gly	Tyr	Gly	Gly	Arg	Thr	Glu	Val		140	145	150	155
Glu	Tyr	Gly	Arg	Lys	Thr	Glu	Ser	Glu	His	Gly	Ser	Gly	Tyr	Gly	Gly		160	165	170	175
Arg	Ile	Glu	Ser	Asp	Tyr	Val	Lys	Pro	Ser	Tyr	Gly	Gly	His	Glu	Asp		180	185	190	195
Asp	Gly	Asp	Asp	Gly	His	Lys	Lys	His	Ser	Gly	Lys	Asp	Tyr	Asp	Asp		200	205	210	

(2) INFORMATION FOR SEQ ID NO:775:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 190 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..190
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567943

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:775:

Met	Pro	Tyr	Tyr	Thr	Asn	Asp	Asp	Asn	Asp	Val	Asp	Asp	Phe	Thr	Glu	1	5	10	15
Tyr	Asp	Pro	Met	Pro	Tyr	Ser	Gly	Gly	Tyr	Asp	Ile	Thr	Val	Thr	Tyr	20	25	30	

(2) INFORMATION FOR SEQ ID NO:776:

(A) LENGTH: 171 amino acids

(C) STRANDEDNESS:

(D) TOPOLOGY: lin

MOLECULE TYPE: peptid

(ix) FEATURE:

(A) NAME

(B) LOCATION: 1..171

(D) OTHER INFORMATION

SEQUENCE DESCRIPTION: SEQ ID NO:776:

(XI) SEQUENCE DESCRIPTION: SEQ ID NO: 73:
Pro Tyr Ser Gly Gly Tyr Asp Ile Thr Val T

(2) INFORMATION FOR SEQ ID NO:777:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1257 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..1257
(D) OTHER INFORMATION: / Ceres Seq. ID 1567945

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:777:

agtataaaga	cgacaaagta	aacaaaaaaa	aaaagagttc	tcttacaatt	ttcctaaatt	60
cttgattttg	agattttcact	ttttccgatt	tgaacaaatg	atgataaact	gcggtggagc	120
caaggcgggc	aaatcgctgt	taatggcggc	tggaccaagt	ttgttctcga	cggtccgtac	180
ggtttcgtct	cacgaggctt	tatcagcaag	ccatatattg	aagcctgggt	ttacatctgc	240
ttggatatgg	actagagctc	cgacgattgg	aggtatgaga	ttcgctagca	cgatcactct	300
gggagagaaa	actccgatga	aggaggagga	cgcgaaatcg	aagaaaaacg	agaacgaatc	360
caccggtgga	gacgcgcgcg	gaggtataaa	caaggagagt	aaaggaaatc	cgagctattg	420
gggtgttgaa	cctaataaga	ttactaaga	agatggttct	gaatggaagt	ggaactgttt	480
caggccatgg	gagacgtata	aagctgatat	agatagattc	gaagaaagcat	catgttccaa	540
cgaggtttct	tgatagaata	gcttattgga	ctgttaaatc	tttctgttgg	cctaccgatt	600
tgttctttcca	gaggagatat	ggatgtcgag	ctatgatgct	tgaacctgta	gcagcagcat	660
ctcgtaaggt	tggaggaatg	ttactacact	gcaaatcgct	tcgacgtttt	gagcaaaagt	720
gaggatggat	taaggctctt	cttgagggaag	cagagaatga	gagaatgcac	cttatgacat	780
tcctggaagt	cgcgaaacgc	aaatgggtacg	agagagcgct	cgtgatcact	gtgcaaggag	840
tcttcttcaa	cgcttatttc	cttggttact	taatctctcc	caagtgttgc	catcgatagg	900
ttgggtacct	tgaagaagaa	gcgatccatt	cttatactga	gtttctcaag	gaacttgaca	960
aaggtaacat	tgagaatggt	cctgctccgg	ctattgctat	tgattactgg	aggcttctcg	1020
ctgatgcgac	Acttctgat	gttctgatgg	ttgttctgtc	tgacgagcgt	catcacctgt	1080
atgtaaacca	ttttgcatct	gatattcact	accaaggctc	tgaactaaag	gaagctccag	1140
ctccaattgg	gtatcattga	ttcgattaaa	agaagagcgt	tttctcaagt	ttaaaacttt	1200
gttctaaaga	atttaagttc	tttgacttgt	atatacataa	tcacctctgc	ttaagct	

(2) INFORMATION FOR SEQ ID NO:778:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 175 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..175
(D) OTHER INFORMATION: / Ceres Seq. ID 1567946

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:778:

Met	Met	Leu	Glu	Thr	Val	Ala	Ala	Val	Pro	Gly	Met	Val	Gly	Gly	Met
1				5				10					15		
Leu	Leu	His	Cys	Lys	Ser	Leu	Arg	Arg	Glu	Gln	Ser	Gly	Gly	Trp	
				20				25				30			
Ile	Lys	Ala	Leu	Leu	Glu	Glu	Ala	Glu	Asn	Glu	Arg	Met	His	Leu	Met
				35				40				45			
Thr	Phe	Met	Glu	Val	Ala	Lys	Pro	Lys	Trp	Tyr	Glu	Arg	Ala	Leu	Val
				50				55				60			
Ile	Thr	Val	Gln	Gly	Val	Phe	Phe	Asn	Ala	Tyr	Phe	Leu	Gly	Tyr	Leu
65				70				75				80			
Ile	Ser	Pro	Lys	Phe	Ala	His	Arg	Met	Val	Gly	Tyr	Leu	Glu	Glu	Glu
				85				90				95			
Ala	Ile	His	Ser	Tyr	Thr	Glu	Phe	Leu	Lys	Glu	Leu	Asp	Lys	Gly	Asn
				100				105				110			
Ile	Glu	Asn	Val	Pro	Ala	Pro	Ala	Ile	Ala	Ile	Asp	Tyr	Trp	Arg	Leu
				115				120				125			
Pro	Ala	Asp	Ala	Thr	Leu	Arg	Asp	Val	Val	Met	Val	Val	Arg	Ala	Asp
				130				135				140			
Glu	Ala	His	His	Arg	Asp	Val	Asn	His	Phe	Ala	Ser	Asp	Ile	His	Tyr
145				150				155				160			
Gln	Gly	Arg	Glu	Leu	Lys	Glu	Ala	Pro	Ala	Pro	Ile	Gly	Tyr	His	
				165				170				175			

(2) INFORMATION FOR SEQ ID NO:779:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 174 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..174
 (D) OTHER INFORMATION: / Ceres Seq. ID 1567947
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:779:
Met Leu Glu Thr Val Ala Ala Val Pro Gly Met Val Gly Met Leu
1 5 10 15
Leu His Cys Lys Ser Leu Arg Arg Phe Glu Gln Ser Gly Trp Ile
 20 25 30
Lys Ala Leu Leu Glu Glu Ala Glu Asn Glu Arg Met His Leu Met Thr
 35 40 45
Phe Met Glu Val Ala Lys Pro Lys Trp Tyr Glu Arg Ala Leu Val Ile
50 55 60
Thr Val Gln Gly Val Phe Phe Asn Ala Tyr Phe Leu Gly Tyr Leu Ile
65 70 75 80
Ser Pro Lys Phe Ala His Arg Met Val Gly Tyr Leu Glu Glu Ala
 85 90 95
Ile His Ser Tyr Thr Glu Phe Leu Lys Glu Leu Asp Lys Gly Asn Ile
 100 105 110
Glu Asn Val Pro Ala Pro Ala Ile Ala Ile Asp Tyr Trp Arg Leu Pro
 115 120 125
Ala Asp Ala Thr Leu Arg Asp Val Val Met Val Val Arg Ala Asp Glu
130 135 140
Ala His His Arg Asp Val Asn His Phe Ala Ser Asp Ile His Tyr Gln
145 150 155 160
Gly Arg Glu Leu Lys Glu Ala Pro Ala Pro Ile Gly Tyr His
 165 170
(2) INFORMATION FOR SEQ ID NO:780:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 164 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..164
 (D) OTHER INFORMATION: / Ceres Seq. ID 1567948
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:780:
Met Val Gly Gly Met Leu Leu His Cys Lys Ser Leu Arg Arg Phe Glu
1 5 10 15
Gln Ser Gly Gly Trp Ile Lys Ala Leu Leu Glu Glu Ala Glu Asn Glu
 20 25 30
Arg Met His Leu Met Thr Phe Met Glu Val Ala Lys Pro Lys Trp Tyr
35 40 45
Glu Arg Ala Leu Val Ile Thr Val Gln Gly Val Phe Phe Asn Ala Tyr
50 55 60
Phe Leu Gly Tyr Leu Ile Ser Pro Lys Phe Ala His Arg Met Val Gly
65 70 75 80
Tyr Leu Glu Glu Glu Ala Ile His Ser Tyr Thr Glu Phe Leu Lys Glu
 85 90 95
Leu Asp Lys Gly Asn Ile Glu Asn Val Pro Ala Pro Ala Ile Ala Ile
 100 105 110
Asp Tyr Trp Arg Leu Pro Ala Asp Ala Thr Leu Arg Asp Val Val Met
115 120 125

Val Val Arg Ala Asp Glu Ala His His Arg Asp Val Asn His Phe Ala
130 135 140
Ser Asp Ile His Tyr Gln Gly Arg Glu Leu Lys Glu Ala Pro Ala Pro
145 150 155 160
Ile Gly Tyr His

(2) INFORMATION FOR SEQ ID NO:781:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1969 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1969

(D) OTHER INFORMATION: / Ceres Seq. ID 1567957

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:781:

aacagctggc catgctatgc atgtgttcat caatggccaa ttatctggat ctgcgtatgg 60
tagtttagac tctctaaac taacttttgc gaaaggtgtg aatctaaagag ctggtttcaa 120
caaaattgcg atactaagca tcgctgttgg tctccgaat ctgggtccac attttgagac 180
atggaatgct ggagtttttg gtccagtttc attgaatggt ctcaatggcg gacgaaaaga 240
tctatcatgg cagaaaatga ctataaaggt tggctctaaa ggagagtctc tgaagtcttc 300
ttcaactagt gggagctcac cggttgagtg ggcagaaggt gcatttgttg cacagaaaaca 360
accacttact tgggtacaaga cgactttctc tgcctccagct ggaattccgc cattggcgtgt 420
agacatggga agcatgggaa aaggtcaaat atggataaat gggcagagct tgggacgtca 480
ctggcctgca tataaagcag ttggttcttg cagcgagtggt tcttatactg gaacattcag 540
agaggacaag tgccttaagaa actgtggaga ggcttctcaa agatgggtacc atgtcccaag 600
gtcgttgctc aaacaaagtg gcaatctatt ggttgtcttt gaggagtggtg gaggagaccc 660
gaacggaaac tcgttgtgtc gaagagaagt ggacagtgtg tgtgcagata tctatgaatg 720
gccaatcaag ctggtgaact accaatgtca tgcttctgga aaagttaata aaccattgtca 780
tcccaaaagt catctgcaat gcgggGccgc gacaaaagat caccaccgtg aagtttgtca 840
gtttcgggac acctgaaggg acttgttgta gttaccgtca aggaagctgt catgcccatc 900
actcctatga cgctttcaac aaactatgtg ttgggcagaa ctggtgttct gtaactgtag 960
caccggagat gtttgttgga gatccgtgtc caaatgtgtg gaagaaactc gcggtggaag 1020
cggtttgtgc ttaaatgaaa gcagacgcag cagcaatcaa aagactgtaa aggtgggtac 1080
ttacgcattc ttacaggttt ctgatggtat tagtatgttt tatgaagaca acagaagaag 1140
ttggtatttt tctagctcct tattttatca cggtggaagt tgtacaaaag gacgcaaac 1200
gcggttcaac aatttcaga gttgtgatt atatgtaaat aagcttggtg aggttttgtt 1260
attgtaaccc aagaagaag atgaagaaga agaagcacat tgagactgga gaacttaagt 1320
ccatgtgtag attcttctc ttcttcttct ttgttcttag aaacacaca aacccccaa 1380
acttaaaaaa taactctaca gagatggctg ttggaatcct tgaggttagt ctgatcagtg 1440
gcaaaggtct caagcgtct ctgtttcttg gtaagataga gagatccaat 1500
acaaagggca aaccgcgcaa agcagcgttg ctaagaaga tggaggtaga aatccgcact 1560
ggaatgataa attgaaatgg agagcagagt ttctgtgctc cggcgccagc tacaaaactc 1620
tcgtcgaagt catggatcat gatactttct cctctgacga cctctatggc gaagccacgg 1680
tacatgtgaa agagctattg gaaatgggag tggagaaggg aacgcggcga ctaaggccaa 1740
ccaagtacaa cattgttgac tccgatctct cctttgttgg cgagctcttc attggagttt 1800
cttactctct ttgtcagag aggggaatgg atggagaaca gtttgaggga tggagacata 1860
gccaagttga ttagtttggg ttcttaaaac tgctgattt atcttctct tctatcttta 1920
gtgtcaacat catataagata ttcataagta caaaaaatta tttaaattg

(2) INFORMATION FOR SEQ ID NO:782:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 279 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..279

(D) OTHER INFORMATION: / Ceres Seq. ID 1567958

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:782:

Thr Ala Gly His Ala Met His Val Phe Ile Asn Gly Gln Leu Ser Gly
1 5 10 15
Ser Ala Tyr Gly Ser Leu Asp Ser Pro Lys Leu Thr Phe Arg Lys Gly
20 25 30
Val Asn Leu Arg Ala Gly Phe Asn Lys Ile Ala Ile Leu Ser Ile Ala
35 40 45
Val Gly Leu Pro Asn Val Gly Pro His Phe Glu Thr Trp Asn Ala Gly
50 55 60
Val Leu Gly Pro Val Ser Leu Asn Gly Leu Asn Gly Gly Arg Lys Asp
65 70 75 80
Leu Ser Trp Gln Lys Trp Thr Tyr Lys Val Gly Leu Lys Gly Glu Ser
85 90 95
Leu Ser Leu His Ser Leu Ser Gly Ser Ser Ser Val Glu Trp Ala Glu
100 105 110
Gly Ala Phe Val Ala Gln Lys Gln Pro Leu Thr Trp Tyr Lys Thr Thr
115 120 125
Phe Ser Ala Pro Ala Gly Asn Ser Pro Leu Ala Val Asp Met Gly Ser
130 135 140
Met Gly Lys Gly Gln Ile Trp Ile Asn Gly Gln Ser Leu Gly Arg His
145 150 155 160
Trp Pro Ala Tyr Lys Ala Val Gly Ser Cys Ser Glu Cys Ser Tyr Thr
165 170 175
Gly Thr Phe Arg Glu Asp Lys Cys Leu Arg Asn Cys Gly Glu Ala Ser
180 185 190
Gln Arg Trp Tyr His Val Pro Arg Ser Trp Leu Lys Pro Ser Gly Asn
195 200 205
Leu Leu Val Val Phe Glu Glu Trp Gly Gly Asp Pro Asn Gly Ile Ser
210 215 220
Leu Val Arg Arg Glu Val Asp Ser Val Cys Ala Asp Ile Tyr Glu Trp
225 230 235 240
Gln Ser Thr Leu Val Asn Tyr Gln Leu His Ala Ser Gly Lys Val Asn
245 250 255
Lys Pro Leu His Pro Lys Val His Leu Gln Cys Gly Ala Arg Thr Lys
260 265 270
Asp His His Arg Glu Val Cys
275

(2) INFORMATION FOR SEQ ID NO:783:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 274 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..274

(D) OTHER INFORMATION: / Ceres Seq. ID 1567959

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:783:

Met His Val Phe Ile Asn Gly Gln Leu Ser Gly Ser Ala Tyr Gly Ser
1 5 10 15
Leu Asp Ser Pro Lys Leu Thr Phe Arg Lys Gly Val Asn Leu Arg Ala
20 25 30
Gly Phe Asn Lys Ile Ala Ile Leu Ser Ile Ala Val Gly Leu Pro Asn
35 40 45
Val Gly Pro His Phe Glu Thr Trp Asn Ala Gly Val Leu Gly Pro Val
50 55 60
Ser Leu Asn Gly Leu Asn Gly Gly Arg Lys Asp Leu Ser Trp Gln Lys
65 70 75 80
Trp Thr Tyr Lys Val Gly Leu Lys Gly Glu Ser Leu Ser Leu His Ser

Met	Lys	Lys	Lys	Lys	His	Ile	Glu	Thr	Gly	Glu	Ser	Lys	Ser	Met	Cys
1				5					10					15	
Arg	Phe	Phe	Phe	Phe	Phe	Phe	Phe	Phe	Phe	Arg	Asn	Asn	Thr	Asn	Pro
			20					25					30		
Lys	Asn	Leu	Lys	Asn	Asn	Ser	Thr	Gly	Met	Ala	Val	Gly	Ile	Leu	Glu
		35					40					45			
Val	Ser	Leu	Ile	Ser	Gly	Lys	Gly	Leu	Lys	Arg	Ser	Asp	Phe	Leu	Gly
		50				55					60				
Lys	Ile	Asp	Pro	Tyr	Val	Glu	Ile	Gln	Tyr	Lys	Gly	Gln	Thr	Arg	Lys
65					70					75				80	
Ser	Ser	Val	Ala	Lys	Glu	Asp	Gly	Gly	Arg	Asn	Pro	Thr	Trp	Asn	Asp
			85						90					95	
Lys	Leu	Lys	Trp	Arg	Ala	Glu	Phe	Pro	Gly	Ser	Gly	Ala	Asp	Tyr	Lys
			100					105					110		
Leu	Ile	Val	Lys	Val	Met	Asp	His	Asp	Thr	Phe	Ser	Ser	Asp	Asp	Phe
		115						120					125		
Ile	Gly	Glu	Ala	Thr	Val	His	Val	Lys	Glu	Leu	Leu	Glu	Met	Gly	Val
		130				135					140				
Glu	Lys	Gly	Thr	Ala	Glu	Leu	Arg	Pro	Thr	Lys	Tyr	Asn	Ile	Val	Asp
145					150					155				160	
Ser	Asp	Leu	Ser	Phe	Val	Gly	Glu	Leu	Leu	Ile	Gly	Val	Ser	Tyr	Ser
				165					170					175	
Leu	Leu	Gln	Asp	Arg	Gly	Met	Asp	Gly	Glu	Gln	Phe	Gly	Gly	Trp	Lys
		180						185					190		

His Ser Gln Val Asp
195

(2) INFORMATION FOR SEQ ID NO:785:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1858 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1858
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567964

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:785:

ctctcttaaac	tgttttttaa	ctctccatct	ctaaaaagac	catcaacgct	cttctctttta	60
ttgcagcaga	aacagaaacc	agttcaataa	agcttttttg	taagaaaaat	tgaaggaaaa	120
agataattga	aaactcgtag	agagaaaagt	gcacagaatc	tgaattctcg	acactttttta	180
ccacgaataa	tgattctctt	ttgaaaaaca	tgactcaatg	ttttctttat	ctttttctctt	240
gaattgaggt	ttgtttgtac	ttaaaagtat	ctcctttatc	taccgttgac	tgattctact	300
cttttattct	caactttttc	ctgatttgct	cgtgtgttta	cttcaattcc	tcagtttctg	360
tgtgaaaagt	tgaagtttcat	gtgatcaaaa	ttggggcctt	actactttta	agagaatgag	420
tgacaaaagc	gaattttccg	caagaaagaa	ggatttggct	aatacgcgac	tggattttga	480
tcctccggag	aatccaatgt	tgggtctctt	tcogatgatg	gattcattca	gagaaactct	540
ttggcatgat	tgtggtttca	atgtccacac	agatgcagac	acttccctta	gaggttaata	600
taatatgtat	atcacctctt	aaatggggtg	gaatatggct	cagttccctg	cagattcagg	660
attcattgag	cgtgctgcga	agttttcttt	ttttggkatg	tggtgaaatg	atgatgaacc	720
aacacaacat	atctctttga	gttccagatt	caactggctt	gtttcttcaa	gatacacaga	780
ttcttagtgg	atccaaacta	gataatggct	ctcttactga	tgcattcaag	ttagtgaag	840
agagatcgat	taataatgta	tcagagattt	ctcaatctag	tggaggtaat	ggatcatgat	900
atgtctaaagt	tgggcaaaaca	tcttccaagg	gggtttagtag	taagaagagg	aaaagacttg	960
ggaagggatt	tgaagaagaa	gaagataaaa	agcaaaaagg	tggcgaagt	ccaacttcaa	1020
atgcgaacaa	gacaaacagt	gagaagcaac	cttctgatto	tttaaaagtg	gggtatatct	1080
acatgagggc	acgaagaggc	caggctacta	atagtcacag	tcttgctgaa	agtgaaagaa	1140
gagaaaaaat	cagtgaaagg	atgaagttct	tgcagaatct	tgtgccaggt	tgcgacaagg	1200
tgactggtaa	ggcagttatg	ctcgatgaaa	tcattaacta	tgtgcaatca	cttcaatgcc	1260
aaatcgagtt	tttatcgatg	aaactttcgg	ctgtgaatcc	tgtgctcgat	tttaacctgt	1320
aaagcctctc	tgcaaaagat	gctcttcaat	catctgcacc	gacatttccc	cacaacatgt	1380
cgatgcttta	tctctctgta	tcgtatctct	ctcaaacagg	attcatgcaa	ccgaacattt	1440
ctccaatggt	gctatttgat	ggaggattaa	aacggcagga	aacacatgga	tatgaaagt	1500
atcacacaaa	tctgttccac	aagaaccatg	aaacggcgac	tgcacctgat	catgaagata	1560
caacagctga	catgaaggtg	gagccgtaga	tgtttcttct	tcactttgtc	ctcagcttta	1620
gctgtcgata	tagtgccgcc	cggctcgagaa	ttttattaac	ttcgaacaga	agagtgaata	1680
cgaaacagag	gaggaacagc	attttgtctt	tgaataattg	acagctcccg	gagaaagagt	1740
cgagagtaag	aatcaacaat	gttgtgtaat	gaatagctac	tgtctgcttc	ttttgtagct	1800
attgtctgct	tcttttttgt	acataataat	ccatgcaagg	gaagaggaat	gttaattcc	

(2) INFORMATION FOR SEQ ID NO:786:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 347 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..347
- (D) OTHER INFORMATION: / Ceres Seq. ID 1567965

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:786:

Met	Met	Val	Val	Ser	Met	Ser	Thr	Gln	Met	Gln	Thr	Leu	Pro	Leu	Glu
1		5						10				15			
Val	Ile	Ile	Ile	Leu	Ile	Tyr	Leu	Leu	Lys	Trp	Val	Gly	Ile	Trp	Leu
		20						25				30			

Ser Ser Leu Gln Ile Gln Asp Ser Leu Ser Val Leu Gln Ser Phe Leu
35 40 45
Phe Leu Xaa Cys Gly Glu Met Met Met Asn Gln Gln Ser Ser Leu
50 55 60
Gly Val Pro Asp Ser Thr Gly Leu Phe Leu Gln Asp Thr Gln Ile Pro
65 70 75 80
Ser Gly Ser Lys Leu Asp Asn Gly Pro Leu Thr Asp Ala Ser Lys Leu
85 90 95
Val Lys Glu Arg Ser Ile Asn Asn Val Ser Glu Asp Ser Gln Ser Ser
100 105 110
Gly Gly Asn Gly His Asp Asp Ala Lys Cys Gly Gln Thr Ser Ser Lys
115 120 125
Gly Phe Ser Ser Lys Lys Arg Lys Arg Ile Gly Lys Asp Cys Glu Glu
130 135 140
Glu Glu Asp Lys Lys Gln Lys Asp Glu Gln Ser Pro Thr Ser Asn Ala
145 150 155 160
Asn Lys Thr Asn Ser Glu Lys Gln Pro Ser Asp Ser Leu Lys Asp Gly
165 170 175
Tyr Ile His Met Arg Ala Arg Arg Gly Gln Ala Thr Asn Ser His Ser
180 185 190
Leu Ala Glu Arg Val Arg Arg Glu Lys Ile Ser Glu Arg Met Lys Phe
195 200 205
Leu Gln Asp Leu Val Pro Gly Cys Asp Lys Val Thr Gly Lys Ala Val
210 215 220
Met Leu Asp Glu Ile Ile Asn Tyr Val Gln Ser Leu Gln Cys Gln Ile
225 230 235 240
Glu Phe Leu Ser Met Lys Leu Ser Ala Val Asn Pro Val Leu Asp Phe
245 250 255
Asn Leu Glu Ser Leu Leu Ala Lys Asp Ala Leu Gln Ser Ser Ala Pro
260 265 270
Thr Phe Pro His Asn Met Ser Met Leu Tyr Pro Pro Val Ser Tyr Leu
275 280 285
Ser Gln Thr Gly Phe Met Gln Pro Asn Ile Ser Ser Met Leu Leu Leu
290 295 300
Ser Gly Gly Leu Lys Arg Gln Glu Thr His Gly Tyr Glu Ser Asp His
305 310 315 320
His Asn Leu Val His Lys Asn His Glu Thr Gly Thr Ala Pro Asp His
325 330 335
Glu Asp Thr Thr Ala Asp Met Lys Val Glu Pro
340 345

(2) INFORMATION FOR SEQ ID NO:787:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 346 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..346

(D) OTHER INFORMATION: / Ceres Seq. ID 1567966

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:787:

Met Val Val Ser Met Ser Thr Gln Met Gln Thr Leu Pro Leu Glu Val
1 5 10 15
Ile Ile Ile Leu Ile Tyr Leu Leu Lys Trp Val Gly Ile Trp Leu Ser
20 25 30
Ser Leu Gln Ile Gln Asp Ser Leu Ser Val Leu Gln Ser Phe Leu Phe
35 40 45
Leu Xaa Cys Gly Glu Met Met Met Asn Gln Gln Gln Ser Ser Leu Gly
50 55 60
Val Pro Asp Ser Thr Gly Leu Phe Leu Gln Asp Thr Gln Ile Pro Ser

65				70				75				80
Gly	Ser	Lys	Leu	Asp	Asn	Gly	Pro	Leu	Thr	Asp	Ala	Ser
				85					90			Lys
												95
Lys	Glu	Arg	Ser	Ile	Asn	Asn	Val	Ser	Glu	Asp	Ser	Gln
			100					105				110
Gly	Asn	Gly	His	Asp	Asp	Ala	Lys	Cys	Gly	Gln	Thr	Ser
			115				120					125
Phe	Ser	Ser	Lys	Lys	Arg	Lys	Arg	Ile	Gly	Lys	Asp	Cys
							135				140	Glu
												145
Glu	Asp	Lys	Lys	Gln	Lys	Asp	Glu	Gln	Ser	Pro	Thr	Ser
					150					155		Asn
												160
Lys	Thr	Asn	Ser	Glu	Lys	Gln	Pro	Ser	Asp	Ser	Leu	Lys
				165					170			Asp
												175
Ile	His	Met	Arg	Ala	Arg	Arg	Gly	Gln	Ala	Thr	Asn	Ser
			180				185					His
												190
Ala	Glu	Arg	Val	Arg	Arg	Glu	Lys	Ile	Ser	Glu	Arg	Met
			195				200					Lys
												205
Gln	Asp	Leu	Val	Pro	Gly	Cys	Asp	Lys	Val	Thr	Gly	Lys
							215					Ala
												220
Leu	Asp	Glu	Ile	Ile	Asn	Tyr	Val	Gln	Ser	Leu	Gln	Cys
					230							Gln
												240
Phe	Leu	Ser	Met	Lys	Leu	Ser	Ala	Val	Asn	Pro	Val	Leu
				245					250			Asp
												255
Leu	Glu	Ser	Leu	Leu	Ala	Lys	Asp	Ala	Leu	Gln	Ser	Ser
				260								Ala
												270
Phe	Pro	His	Asn	Met	Ser	Met	Leu	Tyr	Pro	Pro	Val	Ser
												285
												Tyr
												290
Gln	Thr	Gly	Phe	Met	Gln	Pro	Asn	Ile	Ser	Ser	Met	Leu
					295							Leu
												300
Gly	Gly	Leu	Lys	Arg	Gln	Glu	Thr	His	Gly	Tyr	Glu	Ser
					310							Asp
												320
Asn	Leu	Val	His	Lys	Asn	His	Glu	Thr	Gly	Thr	Ala	Pro
				325					330			Asp
												335
Asp	Thr	Thr	Ala	Asp	Met	Lys	Val	Glu	Pro			
			340						345			

(2) INFORMATION FOR SEQ ID NO:788:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 342 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..342

(D) OTHER INFORMATION: / Ceres Seq. ID 1567967

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:788:

Met	Ser	Thr	Gln	Met	Gln	Thr	Leu	Pro	Leu	Glu	Val	Ile	Ile	Ile	Leu
1				5				10						15	
Ile	Tyr	Leu	Leu	Lys	Trp	Val	Gly	Ile	Trp	Leu	Ser	Ser	Leu	Gln	Ile
			20				25						30		
Gln	Asp	Ser	Leu	Ser	Val	Leu	Gln	Ser	Phe	Leu	Phe	Leu	Xaa	Cys	Gly
			35				40					45			
Glu	Met	Met	Met	Asn	Gln	Gln	Gln	Ser	Ser	Leu	Gly	Val	Pro	Asp	Ser
			50				55					60			
Thr	Gly	Leu	Phe	Leu	Gln	Asp	Thr	Gln	Ile	Pro	Ser	Gly	Ser	Lys	Leu
			65			70			75					80	
Asp	Asn	Gly	Pro	Leu	Thr	Asp	Ala	Ser	Lys	Leu	Val	Lys	Glu	Arg	Ser
				85				90						95	
Ile	Asn	Asn	Val	Ser	Glu	Asp	Ser	Gln	Ser	Ser	Gly	Gly	Asn	Gly	His
			100					105						110	

Asp Asp Ala Lys Cys Gly Gln Thr Ser Ser Lys Gly Phe Ser Ser Lys
115 120 125
Lys Arg Lys Arg Ile Gly Lys Asp Cys Glu Glu Glu Asp Lys Lys
130 135 140
Gln Lys Asp Glu Gln Ser Pro Thr Ser Asn Ala Asn Lys Thr Asn Ser
145 150 155 160
Glu Lys Gln Pro Ser Asp Ser Leu Lys Asp Gly Tyr Ile His Met Arg
165 170 175
Ala Arg Arg Gly Gln Ala Thr Asn Ser His Ser Leu Ala Glu Arg Val
180 185 190
Arg Arg Glu Lys Ile Ser Glu Arg Met Lys Phe Leu Gln Asp Leu Val
195 200 205
Pro Gly Cys Asp Lys Val Thr Gly Lys Ala Val Met Leu Asp Glu Ile
210 215 220
Ile Asn Tyr Val Gln Ser Leu Gln Cys Gln Ile Glu Phe Leu Ser Met
225 230 235 240
Lys Leu Ser Ala Val Asn Pro Val Leu Asp Phe Asn Leu Glu Ser Leu
245 250 255
Leu Ala Lys Asp Ala Leu Gln Ser Ser Ala Pro Thr Phe Pro His Asn
260 265 270
Met Ser Met Leu Tyr Pro Pro Val Ser Tyr Leu Ser Gln Thr Gly Phe
275 280 285
Met Gln Pro Asn Ile Ser Ser Met Leu Leu Leu Ser Gly Gly Leu Lys
290 295 300
Arg Gln Glu Thr His Gly Tyr Glu Ser Asp His His Asn Leu Val His
305 310 315 320
Lys Asn His Glu Thr Gly Thr Ala Pro Asp His Glu Asp Thr Thr Ala
325 330 335
Asp Met Lys Val Glu Pro
340

(2) INFORMATION FOR SEQ ID NO:789:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 522 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..522

(D) OTHER INFORMATION: / Ceres Seq. ID 1567975

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:789:

aaccctagct	tggtccacgc	tcagagcatt	ttggccattt	gggccactca	agttatcttg	60
atggggagctg	ttgaaggcta	cagagtcgca	ggaaatgggc	cattgggaga	ggccgaggac	120
ttgctttacc	ccggtggcag	cttcgaccca	ttgggtcttg	ctaccgaccc	agaggcttcc	180
gcggagttga	agggtgaagga	gctcaagaac	ggaagattgg	ctatgttctc	tatgtttgga	240
ttcttcgttc	aagccattgt	cactggtaag	ggaccgatag	agaaccttgc	tgaccatttg	300
gccgatccag	tcaacaacaa	cgcattgggc	ttcgcaacca	actttgttcc	cggaaagtga	360
gccaaagtgtt	atcagtttgt	attttgcttt	tccttcagtc	ttttgaattc	gagtgagaga	420
catgaggaga	aagagaaggt	tgGtatgtga	tggttttgaga	ctttcagatg	taaattkgca	480
agactttgta	tgattttgca	ttaatcaaac	tcatttttct	ct		

(2) INFORMATION FOR SEQ ID NO:790:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..119

(D) OTHER INFORMATION: / Ceres Seq. ID 1567976

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:790:

Asn	Pro	Ser	Leu	Val	His	Ala	Gln	Ser	Ile	Leu	Ala	Ile	Trp	Ala	Thr
1			5						10					15	
Gln	Val	Ile	Leu	Met	Gly	Ala	Val	Glu	Gly	Tyr	Arg	Val	Ala	Gly	Asn
			20					25					30		
Gly	Pro	Leu	Gly	Glu	Ala	Glu	Asp	Leu	Leu	Tyr	Pro	Gly	Gly	Ser	Phe
			35				40					45			
Asp	Pro	Leu	Gly	Leu	Ala	Thr	Asp	Pro	Glu	Ala	Phe	Ala	Glu	Leu	Lys
			50			55					60				
Val	Lys	Glu	Leu	Lys	Asn	Gly	Arg	Leu	Ala	Met	Phe	Ser	Met	Phe	Gly
65					70				75					80	
Phe	Phe	Val	Gln	Ala	Ile	Val	Thr	Gly	Lys	Gly	Pro	Ile	Glu	Asn	Leu
				85					90				95		
Ala	Asp	His	Leu	Ala	Asp	Pro	Val	Asn	Asn	Asn	Ala	Trp	Ala	Phe	Ala
			100				105						110		
Thr	Asn	Phe	Val	Pro	Gly	Lys									
			115												

(2) INFORMATION FOR SEQ ID NO:791:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 99 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..99

(D) OTHER INFORMATION: / Ceres Seq. ID 1567977

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:791:

Met	Gly	Ala	Val	Glu	Gly	Tyr	Arg	Val	Ala	Gly	Asn	Gly	Pro	Leu	Gly
1				5					10					15	
Glu	Ala	Glu	Asp	Leu	Leu	Tyr	Pro	Gly	Gly	Ser	Phe	Asp	Pro	Leu	Gly
			20					25					30		
Leu	Ala	Thr	Asp	Pro	Glu	Ala	Phe	Ala	Glu	Leu	Lys	Val	Lys	Glu	Leu
			35			40					45				
Lys	Asn	Gly	Arg	Leu	Ala	Met	Phe	Ser	Met	Phe	Gly	Phe	Phe	Val	Gln
			50			55					60				
Ala	Ile	Val	Thr	Gly	Lys	Gly	Pro	Ile	Glu	Asn	Leu	Ala	Asp	His	Leu
65				70				75					80		
Ala	Asp	Pro	Val	Asn	Asn	Asn	Ala	Trp	Ala	Phe	Ala	Thr	Asn	Phe	Val
			85				90						95		
Pro	Gly	Lys													

(2) INFORMATION FOR SEQ ID NO:792:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 852 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..852

(D) OTHER INFORMATION: / Ceres Seq. ID 1567993

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:792:

ctttggaggt	cagggaaaagg	aaaaatcacg	ttctacctcg	atcctgaggt	agattttaca	60
caggagaaat	ctgataactca	ggaaaattca	gggaaaagag	gagacgtatt	gttcctctcca	120
caaaagccct	atatggttct	gggatctttg	cgtaGcaat	tgttttatcc	tacctggagt	180
gcaactgtgg	aggagacgac	acctggtggc	agtaatatg	acggttcacc	acctctgctg	240
attagagagg	acggaaatga	aaagccgaca	acagatgatc	tgatgcggac	tctagagaag	300

gtttgtctttg gacatatagc ggatcgcttt ggtgggtcttg attcgataca cgagtggctcc 360
agtgttctct cacttgggtga gcagcagcgc cttgcctttg caccggttatt gctgtctcag 420
ccaaagctgg cgtctcttga tgaatccacc agtgcgttgg atgaagctaa tgaggcgcttc 480
ctgtaccagc aaatccagtc ggctggcatt acatatataa gcattggcca ccgccggact 540
ttaacgaaat tcataacaa gatettacaa atctcaacgg cagaccggaa gagcaatgaa 600
cgtaactggc gaataagagga cgtggatgcc caagattctt tgtacggtag attgaatcaa 660
aaggagggtgc caagtgggaag ctgatcaaaa cctgattgat tacataagag acagaagcag 720
caggtaaatc tgcaaacggg tgtcatgaaa catataagaa acatgttttg tgtccatttt 780
gtatataatc taccagactt gacgttgact gaagatgcaa gtaaatagag agattaatac 840
agatacgagt gc

(2) INFORMATION FOR SEQ ID NO:793:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 227 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..227

(D) OTHER INFORMATION: / Ceres Seq. ID 1567994

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:793:

Leu Trp Arg Ser Gly Lys Gly Lys Ile Thr Phe Tyr Leu Asp Pro Glu
1 5 10 15
Val Asp Phe Thr Gln Glu Lys Ser Asp Thr Gln Glu Asn Ser Gly Lys
20 25 30
Arg Gly Asp Val Leu Phe Leu Pro Gln Arg Pro Tyr Met Val Leu Gly
35 40 45
Ser Leu Arg Gln Gln Leu Leu Tyr Pro Thr Trp Ser Ala Thr Val Glu
50 55 60
Glu Thr Thr Pro Gly Gly Ser Asn Ile Asp Gly Ser Pro Pro Leu Leu
65 70 75 80
Ile Arg Glu Asp Gly Asn Glu Lys Pro Thr Thr Asp Asp Leu Met Arg
85 90 95
Thr Leu Glu Lys Val Cys Leu Gly His Ile Ala Asp Arg Phe Gly Gly
100 105 110
Leu Asp Ser Ile His Glu Trp Ser Ser Val Leu Ser Leu Gly Glu Gln
115 120 125
Gln Arg Leu Ala Phe Ala Arg Leu Leu Leu Ser Gln Pro Lys Leu Ala
130 135 140
Leu Leu Asp Glu Ser Thr Ser Ala Leu Asp Glu Ala Asn Glu Ala Phe
145 150 155 160
Leu Tyr Gln Gln Ile Gln Ser Ala Gly Ile Thr Tyr Ile Ser Ile Gly
165 170 175
His Arg Arg Thr Leu Thr Lys Phe His Asn Lys Ile Leu Gln Ile Ser
180 185 190
Thr Ala Asp Pro Lys Ser Asn Glu Arg Asn Trp Arg Ile Glu Asp Val
195 200 205
Asp Ala Gln Asp Ser Leu Tyr Gly Arg Leu Asn Gln Lys Glu Val Pro
210 215 220
Ser Gly Ser
225

(2) INFORMATION FOR SEQ ID NO:794:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 183 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..183

(D) OTHER INFORMATION: / Ceres Seq. ID 1567995

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:794:

Met Val Leu Gly Ser Leu Arg Gln Gln Leu Leu Tyr Pro Thr Trp Ser
1 5 10 15
Ala Thr Val Glu Glu Thr Thr Pro Gly Gly Ser Asn Ile Asp Gly Ser
20 25 30
Pro Pro Leu Leu Ile Arg Glu Asp Gly Asn Glu Lys Pro Thr Thr Asp
35 40 45
Asp Leu Met Arg Thr Leu Glu Lys Val Cys Leu Gly His Ile Ala Asp
50 55 60
Arg Phe Gly Gly Leu Asp Ser Ile His Glu Trp Ser Ser Val Leu Ser
65 70 75 80
Leu Gly Glu Gln Gln Arg Leu Ala Phe Ala Arg Leu Leu Ser Gln
85 90 95
Pro Lys Leu Ala Leu Leu Asp Glu Ser Thr Ser Ala Leu Asp Glu Ala
100 105 110
Asn Glu Ala Phe Leu Tyr Gln Gln Ile Gln Ser Ala Gly Ile Thr Tyr
115 120 125
Ile Ser Ile Gly His Arg Arg Thr Leu Thr Lys Phe His Asn Lys Ile
130 135 140
Leu Gln Ile Ser Thr Ala Asp Pro Lys Ser Asn Glu Arg Asn Trp Arg
145 150 155 160
Ile Glu Asp Val Asp Ala Gln Asp Ser Leu Tyr Gly Arg Leu Asn Gln
165 170 175
Lys Glu Val Pro Ser Gly Ser
180

(2) INFORMATION FOR SEQ ID NO:795:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 133 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..133

(D) OTHER INFORMATION: / Ceres Seq. ID 1567996

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:795:

Met Arg Thr Leu Glu Lys Val Cys Leu Gly His Ile Ala Asp Arg Phe
1 5 10 15
Gly Gly Leu Asp Ser Ile His Glu Trp Ser Ser Val Leu Ser Leu Gly
20 25 30
Glu Gln Gln Arg Leu Ala Phe Ala Arg Leu Leu Ser Gln Pro Lys
35 40 45
Leu Ala Leu Leu Asp Glu Ser Thr Ser Ala Leu Asp Glu Ala Asn Glu
50 55 60
Ala Phe Leu Tyr Gln Gln Ile Gln Ser Ala Gly Ile Thr Tyr Ile Ser
65 70 75 80
Ile Gly His Arg Arg Thr Leu Thr Lys Phe His Asn Lys Ile Leu Gln
85 90 95
Ile Ser Thr Ala Asp Pro Lys Ser Asn Glu Arg Asn Trp Arg Ile Glu
100 105 110
Asp Val Asp Ala Gln Asp Ser Leu Tyr Gly Arg Leu Asn Gln Lys Glu
115 120 125
Val Pro Ser Gly Ser
130

(2) INFORMATION FOR SEQ ID NO:796:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1336 base pairs

(B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..1336
(D) OTHER INFORMATION: / Ceres Seq. ID 1567997

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:796:

caacatattg	ccaagacc	ctttgattgc	ttggaaaatt	atattttgc	atggagcatt	60
tgaagctatt	cttcagctgc	tctgcctg	taaaagagtt	gaggggtccaa	tatctccagc	120
cggaaccga	ccagtttaca	aggccaatgc	tctgctgct	tactttgtga	cactagcaac	180
ctatcttgg	ctttgttgg	ttggaatctt	caaccctgca	attgtctatg	atcacttggg	240
tgaataattt	tccgcaactaa	tattcgggaag	cttcataattt	tgtgttttgt	tgtacataaa	300
agggcattgt	gcaccttcac	caagtgcactc	tgggttcattg	ggtaacctaa	taattgactt	360
ctattggggc	atggagttgt	accctcgaa	tggtaagagc	tttgacatca	aggtgtttac	420
taattgcaga	tccggaatga	tgtcttgggc	agttcttgca	gtccactgact	gcataaaaaca	480
gtatgaata	aatggcaaa	tatctgattc	aatgctgggt	aacaccatcc	tgatgtgtgt	540
gtatgtcaca	aaattctctc	gggtgggaagc	tgggtattgg	aacaccatgg	acattgcaca	600
tgaccgagct	ggattctata	tatgctgggg	ttgtctagtg	tgggtgcctt	ctgtctacac	660
tctctcaggg	atgtaccttg	tgaaccaccc	cgtcgaaactc	ggaactcagt	tggcaatata	720
cattctcgtt	gcaggaaatc	tgtgcattta	cataaactat	gactgtgata	gacaaaaggca	780
agagttcagg	aggacaaaac	ggaaatgttt	ggtttgggga	agagcccccgt	caagattgtt	840
ggcgctgat	actacaacat	ctgggtgaaac	taaaactagt	cttctcttaa	cgtctgtgat	900
tgggggattg	gctgcctcatt	tccattatgt	tccatgagac	tttaagtgtt	tctctcggac	960
Cgtaccggct	ctcttcgata	actctctggc	atactcttac	gtcatatttc	tcacctctct	1020
tctctttgat	cgagccaaga	gagacgatga	ccgatgccga	tcaaagtatg	ggaaaatttg	1080
gaagctgat	tgtgagaag	tcaaatcacg	gatcattccg	ggaattttat	gattgtaacg	1140
aagctgtgtg	tctctcattt	ctactattta	cgtaaatgac	aacgttggaa	tcatacaaa	1200
accgtgcaca	aacaaaattt	caaattgatg	cgtatagacat	tcttttgcgt	atttgtatgc	1260
tataggtttt	caaatctcta	gCtacgotta	tgtatttccc	tagattatca	aagttagcct	1320
gccgttttct	aatttt					

(2) INFORMATION FOR SEQ ID NO:797:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 376 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..376
(D) OTHER INFORMATION: / Ceres Seq. ID 1567998

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:797:

Asn	Ile	Trp	Pro	Arg	Pro	Thr	Leu	Ile	Ala	Trp	Lys	Ile	Ile	Phe	Cys
1				5					10					15	
Tyr	Gly	Ala	Phe	Glu	Ala	Ile	Leu	Gln	Leu	Leu	Pro	Gly	Lys	Arg	
				20				25				30			
Val	Glu	Gly	Pro	Ile	Ser	Pro	Ala	Gly	Asn	Arg	Pro	Val	Trp	Lys	Ala
				35			40				45				
Asn	Gly	Leu	Ala	Ala	Tyr	Phe	Val	Thr	Leu	Ala	Thr	Trp	Leu	Gly	Leu
				50			55				60				
Trp	Trp	Phe	Gly	Ile	Phe	Asn	Pro	Ala	Ile	Val	Tyr	Asp	His	Leu	Gly
				65			70			75				80	
Glu	Ile	Phe	Ser	Ala	Leu	Ile	Phe	Gly	Ser	Phe	Ile	Phe	Cys	Val	Leu
				85				90						95	
Leu	Tyr	Ile	Lys	Gly	His	Val	Ala	Pro	Ser	Ser	Ser	Asp	Ser	Gly	Ser
				100				105						110	
Cys	Gly	Asn	Leu	Ile	Ile	Asp	Phe	Tyr	Trp	Gly	Met	Glu	Leu	Tyr	Pro
				115			120					125			
Arg	Ile	Gly	Lys	Ser	Phe	Asp	Ile	Lys	Val	Phe	Thr	Asn	Cys	Arg	Phe
				130			135					140			

Gly Met Met Ser Trp Ala Val Leu Ala Val Thr Tyr Cys Ile Lys Gln
145 150 155 160
Tyr Glu Ile Asn Gly Lys Val Ser Asp Ser Met Leu Val Asn Thr Ile
165 170 175
Leu Met Leu Val Tyr Val Thr Lys Phe Phe Trp Trp Glu Ala Gly Tyr
180 185 190
Trp Asn Thr Met Asp Ile Ala His Asp Arg Ala Gly Phe Tyr Ile Cys
195 200 205
Trp Gly Cys Leu Val Trp Val Pro Ser Val Tyr Thr Ser Pro Gly Met
210 215 220
Tyr Leu Val Asn His Pro Val Glu Leu Gly Thr Gln Leu Ala Ile Tyr
225 230 235 240
Ile Leu Val Ala Gly Ile Leu Cys Ile Tyr Ile Asn Tyr Asp Cys Asp
245 250 255
Arg Gln Arg Gln Glu Phe Arg Arg Thr Asn Gly Lys Cys Leu Val Trp
260 265 270
Gly Arg Ala Pro Ser Lys Ile Val Ala Ser Tyr Thr Thr Thr Ser Gly
275 280 285
Glu Thr Lys Thr Ser Leu Leu Leu Thr Ser Gly Trp Trp Gly Leu Ala
290 295 300
Arg His Phe His Tyr Val Pro Glu Ile Leu Ser Ala Phe Phe Trp Thr
305 310 315 320
Val Pro Ala Leu Phe Asp Asn Phe Leu Ala Tyr Phe Tyr Val Ile Phe
325 330 335
Leu Thr Leu Leu Leu Phe Asp Arg Ala Lys Arg Asp Asp Arg Cys
340 345 350
Arg Ser Lys Tyr Gly Lys Tyr Trp Lys Leu Tyr Cys Glu Lys Val Lys
355 360 365
Tyr Arg Ile Ile Pro Gly Ile Tyr
370 375

(2) INFORMATION FOR SEQ ID NO:798:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 253 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..253
(D) OTHER INFORMATION: / Ceres Seq. ID 1567999
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:798:
Met Glu Leu Tyr Pro Arg Ile Gly Lys Ser Phe Asp Ile Lys Val Phe
1 5 10 15
Thr Asn Cys Arg Phe Gly Met Met Ser Trp Ala Val Leu Ala Val Thr
20 25 30
Tyr Cys Ile Lys Gln Tyr Glu Ile Asn Gly Lys Val Ser Asp Ser Met
35 40 45
Leu Val Asn Thr Ile Leu Met Leu Val Tyr Val Thr Lys Phe Phe Trp
50 55 60
Trp Glu Ala Gly Tyr Trp Asn Thr Met Asp Ile Ala His Asp Arg Ala
65 70 75 80
Gly Phe Tyr Ile Cys Trp Gly Cys Leu Val Trp Val Pro Ser Val Tyr
85 90 95
Thr Ser Pro Gly Met Tyr Leu Val Asn His Pro Val Glu Leu Gly Thr
100 105 110
Gln Leu Ala Ile Tyr Ile Leu Val Ala Gly Ile Leu Cys Ile Tyr Ile
115 120 125
Asn Tyr Asp Cys Asp Arg Gln Arg Gln Glu Phe Arg Arg Thr Asn Gly
130 135 140
Lys Cys Leu Val Trp Gly Arg Ala Pro Ser Lys Ile Val Ala Ser Tyr

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(2) INFORMATION FOR SEQ ID NO:799:
  (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 231 amino acids
      (B) TYPE: amino acid
      (C) STRANDEDNESS:
      (D) TOPOLOGY: linear
  (ii) MOLECULE TYPE: peptide
  (ix) FEATURE:
      (A) NAME/KEY: peptide
      (B) LOCATION: 1..231
      (D) OTHER INFORMATION: / Ceres Seq. ID 1568000
  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:799:
```

(2) INFORMATION FOR SEQ ID NO:800:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 564 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

[illegible]

65

70

(2) INFORMATION FOR SEQ ID NO:803:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1364 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1364

(D) OTHER INFORMATION: / Ceres Seq. ID 1568029

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:803:

ctataaatagg	aacaccatgg	aaaggaaaaag	agacacacac	aaataaagaa	aacgaaaaaca	60
ctttttact	tatatgtcag	ccatggctcc	gactttgcaa	ggccagtgga	tcaaggtggg	120
gcagaaagga	ggaacgggac	caggacctag	aagttcacac	ggcatagccg	cggtcggaga	180
caagctctac	agtttcggcg	gcgagttaac	accaaacaac	cacatcgaca	aagacctota	240
cgtctttgac	ttcaacactc	aaacttggtc	aatcgctcaa	cccaaggagg	acgccccaac	300
tgatctctgc	ttaggcgtgc	gcattggtgc	cgtagggaac	aagatctata	tctttggagg	360
ccgcgatgag	aaccgcaact	tcgaaaactt	tcgctcctac	gatacgggtg	catccgagtg	420
gaacattcctg	acgaagcttg	atgaggtggg	aggaccggag	gctcgtaact	tccattcgat	480
ggcttcggat	gaaaaccatg	tgatatgtat	cggtgggggtg	agcaaaaggcg	gtactatgaa	540
tactcccacg	cggttcagga	caatcgaggc	gtataacatt	gctggggaaa	tgggctcagc	600
taccggatcc	aggagataac	ttcgagaaaa	gaggaggagc	gggattcgct	gtggtacaag	660
ggaagatttt	gggtgtttat	gggttttgca	ccctcgattg	gcccggggcg	aaagatgact	720
atgagttctaa	tgctgtgcaa	ttctatgac	cggtctccaa	aaagtggacc	gaagttagaga	780
ctacaggagc	gaacaccttc	gcaaggagcg	tgtttgccca	tcggttagtg	ggaaagataa	840
taataaatat	tgcaagtgag	gtatggcctg	atctcaatgg	gcattatggt	ccgGggacgc	900
tgctcaaatg	gggatatgcc	ttggacaccg	agacactggt	gtgggaaaaa	ttgggagaaa	960
aaggtgcacc	agccatacac	cgaggtttga	ctgcctatac	tgctgccact	gtcgatggaa	1020
agaaatggcct	cctcatgcat	ggcggaagag	ttccgaccaa	cgagcggaac	gatgatctct	1080
acttctatgc	ggatcaattc	gcttaatgag	tgctcaagatt	gtgtgtgtgt	gtgtgtgtgt	1140
ttaatattta	ttactatcca	ataaggagcc	ctaattggtt	gctgtattat	tcaaaattat	1200
ctgtgtgtgg	gactcgtcga	gcttttttac	tctaattgag	cctactcatg	gtgtgtgtgag	1260
tggttctcca	agtatcattg	tccaataagg	agccaattta	tttatggctg	gctgttttat	1320
tcaaaattat	gtgtatgtgt	taataattaa	agattgaatt	atct		

(2) INFORMATION FOR SEQ ID NO:804:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 178 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..178

(D) OTHER INFORMATION: / Ceres Seq. ID 1568030

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:804:

Met	Ala	Pro	Thr	Leu	Gln	Gly	Gln	Trp	Ile	Lys	Val	Gly	Gln	Lys	Gly
1				5				10						15	
Gly	Thr	Gly	Pro	Gly	Pro	Arg	Ser	Ser	His	Gly	Ile	Ala	Ala	Val	Gly
				20				25						30	
Asp	Lys	Leu	Tyr	Ser	Phe	Gly	Gly	Glu	Leu	Thr	Pro	Asn	Lys	His	Ile
				35				40						45	
Asp	Lys	Asp	Leu	Tyr	Val	Phe	Asp	Phe	Asn	Thr	Gln	Thr	Trp	Ser	Ile
				50				55						60	
Ala	Gln	Pro	Lys	Gly	Asp	Ala	Pro	Thr	Val	Ser	Cys	Leu	Gly	Val	Arg
				70				75						80	
Met	Val	Ala	Val	Gly	Thr	Lys	Ile	Tyr	Ile	Phe	Gly	Gly	Arg	Asp	Glu
				85				90						95	
Asn	Arg	Asn	Phe	Glu	Asn	Phe	Arg	Ser	Tyr	Asp	Thr	Val	Thr	Ser	Glu

100 105 110
Trp Thr Phe Leu Thr Lys Leu Asp Glu Val Gly Gly Pro Glu Ala Arg
115 120 125
Thr Phe His Ser Met Ala Ser Asp Glu Asn His Val Tyr Val Phe Gly
130 135 140
Gly Val Ser Lys Gly Gly Thr Met Asn Thr Pro Thr Arg Phe Arg Thr
145 150 155 160
Ile Glu Ala Tyr Asn Ile Ala Gly Glu Met Gly Ser Ala Thr Gly Ser
165 170 175
Arg Arg

(2) INFORMATION FOR SEQ ID NO:805:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 98 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..98

(D) OTHER INFORMATION: / Ceres Seq. ID 1568031

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:805:

Met Val Ala Val Gly Thr Lys Ile Tyr Ile Phe Gly Gly Arg Asp Glu
1 5 10 15
Asn Arg Asn Phe Glu Asn Phe Arg Ser Tyr Asp Thr Val Thr Ser Glu
20 25 30
Trp Thr Phe Leu Thr Lys Leu Asp Glu Val Gly Gly Pro Glu Ala Arg
35 40 45
Thr Phe His Ser Met Ala Ser Asp Glu Asn His Val Tyr Val Phe Gly
50 55 60
Gly Val Ser Lys Gly Gly Thr Met Asn Thr Pro Thr Arg Phe Arg Thr
65 70 75 80
Ile Glu Ala Tyr Asn Ile Ala Gly Glu Met Gly Ser Ala Thr Gly Ser
85 90 95
Arg Arg

(2) INFORMATION FOR SEQ ID NO:806:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 95 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..95

(D) OTHER INFORMATION: / Ceres Seq. ID 1568032

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:806:

Met Gly Ile Met Val Pro Gly Arg Cys Pro Met Arg Asp Met Arg Trp
1 5 10 15
Thr Pro Arg His Trp Cys Gly Lys Ser Trp Glu Lys Lys Val His Gln
20 25 30
Pro Tyr His Glu Val Gly Leu Pro Ile Leu Leu Pro Leu Ser Met Glu
35 40 45
Arg Met Ala Ser Ser Cys Met Ala Glu Ser Phe Arg Pro Thr Ser Glu
50 55 60
Leu Met Ile Ser Thr Ser Met Arg Ser Ile Gln Leu Asn Ala Cys Gln
65 70 75 80
Asp Leu Cys Cys Val Cys Gly Ser Leu Ile Phe Ile Thr Ile Gln
85 90 95

(2) INFORMATION FOR SEQ ID NO:807:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1127 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1127

(D) OTHER INFORMATION: / Ceres Seq. ID 1568037

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:807:

aatcgaaaaa	acctcggtc	gatctcacat	ttataatctc	tcactctctc	tctttctctg	60
gtaaatcatc	aagtgtgaag	atgggtggctg	tgaggcgaa	gagaacacaa	cgctcaaac	120
ctagatccga	accacgcgaa	cacatgtcgg	atcatgattc	cgattccgat	tgggatacac	180
tctgcgaaga	atgcagttcc	ggtaaacac	cagcaaaagt	gcttctttgc	gacaaatgcg	240
ataaaagggt	Ctcatctttt	ctgtctcaga	ccgatcctcg	tttcagttcc	caaaaggctct	300
tggttctgcc	cttctgtgtc	caaacatcag	atccctaaat	ctttccctct	tattcagact	360
aaaattatag	atttcttcgc	gattaagcgg	tctccagatt	catctcaaat	ctcaagttct	420
tcagatagta	tgggaagaaa	acggaaaaag	actagcttgg	tgatgtcaaa	gaagaagaga	480
aggctttctc	catacaatcc	tagcaatgat	cctcaaagga	ggctagagca	aatggcgctct	540
ctggccaact	cgttgagagc	ttccaacacc	aagttcagca	atgagcttac	ttatgtatct	600
ggaaaggctc	caagatctgc	aaaccaagct	gcttttgaga	aaggaggcat	gcaggttcta	660
tctaaagaag	gcgtagagac	cttagccttg	tgaagaaaa	tgatggacct	cggtgaatgc	720
ccgcacacta	tggttcgtct	cgatccctat	gaagggttca	cagtagaggc	ggacagggtt	780
ataaaagact	ggacaattat	cacagagtat	gttgagatg	ttgattatct	gagcaataga	840
gaagatgact	atgatggaga	cagtatgatg	actctacttc	atgcctctga	tctctcgaga	900
tgtctcgtaa	tttgccctga	cagacgcagt	aacatcgccc	ggttcacag	tggtcatcac	960
aatcactcac	cagaaggagc	gaagaagcag	aacctgaagt	gtgtgaggtt	caacatcaac	1020
ggagaagcta	gggttcttct	cgtagcta	agagacatat	cgaaagggga	aagattgtat	1080
tatgattaca	acggatatga	acatgagtat	ccaactgaac	attttgt		

(2) INFORMATION FOR SEQ ID NO:808:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 324 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..324

(D) OTHER INFORMATION: / Ceres Seq. ID 1568038

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:808:

Met	Ile	Pro	Ile	Pro	Ile	Gly	Ile	Gln	Ser	Ala	Lys	Asn	Ala	Val	Pro
1				5				10						15	
Val	Asn	Asn	Gln	Gln	Ser	Cys	Phe	Phe	Ala	Thr	Asn	Ala	Ile	Lys	Xaa
				20				25						30	
Ser	His	Leu	Phe	Cys	Leu	Arg	Pro	Ile	Leu	Val	Ser	Val	Pro	Lys	Gly
		35					40				45				
Ser	Trp	Phe	Cys	Pro	Ser	Cys	Ser	Lys	His	Gln	Ile	Pro	Lys	Ser	Phe
		50				55				60					
Pro	Leu	Ile	Gln	Thr	Lys	Ile	Ile	Asp	Phe	Phe	Arg	Ile	Lys	Arg	Ser
				70				75						80	
Pro	Asp	Ser	Ser	Gln	Ile	Ser	Ser	Ser	Ser	Asp	Ser	Ile	Gly	Lys	Lys
				85				90						95	
Arg	Lys	Lys	Thr	Ser	Leu	Val	Met	Ser	Lys	Lys	Lys	Arg	Arg	Leu	Leu
				100			105							110	
Pro	Tyr	Asn	Pro	Ser	Asn	Asp	Pro	Gln	Arg	Arg	Leu	Glu	Gln	Met	Ala
				115			120							125	
Ser	Leu	Ala	Thr	Ala	Leu	Arg	Ala	Ser	Asn	Thr	Lys	Phe	Ser	Asn	Glu
				130			135							140	

Leu	Thr	Tyr	Val	Ser	Gly	Lys	Ala	Pro	Arg	Ser	Ala	Asn	Gln	Ala	Ala	
145					150					155					160	
Phe	Glu	Lys	Gly	Gly	Met	Gln	Val	Leu	Ser	Lys	Glu	Gly	Val	Glu	Thr	
				165					170						175	
Leu	Ala	Leu	Cys	Lys	Lys	Met	Met	Asp	Leu	Gly	Glu	Cys	Pro	Pro	Leu	
			180					185					190			
Met	Val	Val	Phe	Asp	Pro	Tyr	Glu	Gly	Phe	Thr	Val	Glu	Ala	Asp	Arg	
			195				200					205				
Phe	Ile	Lys	Asp	Trp	Thr	Ile	Ile	Thr	Glu	Tyr	Val	Gly	Asp	Val	Asp	
	210					215					220					
Tyr	Leu	Ser	Asn	Arg	Glu	Asp	Asp	Tyr	Asp	Gly	Asp	Ser	Met	Met	Thr	
225					230				235						240	
Leu	Leu	His	Ala	Ser	Asp	Pro	Ser	Arg	Cys	Leu	Val	Ile	Cys	Pro	Asp	
				245					250					255		
Arg	Arg	Ser	Asn	Ile	Ala	Arg	Phe	Ile	Ser	Gly	Ile	Asn	Asn	His	Ser	
			260				265							270		
Pro	Glu	Gly	Arg	Lys	Lys	Gln	Asn	Leu	Lys	Cys	Val	Arg	Phe	Asn	Ile	
			275				280					285				
Asn	Gly	Glu	Ala	Arg	Val	Leu	Leu	Val	Ala	Asn	Arg	Asp	Ile	Ser	Lys	
	290				295					300						
Gly	Glu	Arg	Leu	Tyr	Tyr	Asp	Tyr	Asn	Gly	Tyr	Glu	His	Glu	Tyr	Pro	
305					310				315						320	
Thr	Glu	His	Phe													

(2) INFORMATION FOR SEQ ID NO:809:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 221 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..221

(D) OTHER INFORMATION: / Ceres Seq. ID 1568039

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:809:

Met	Ser	Lys	Lys	Lys	Arg	Arg	Leu	Leu	Pro	Tyr	Asn	Pro	Ser	Asn	Asp	
1				5					10					15		
Pro	Gln	Arg	Arg	Leu	Glu	Gln	Met	Ala	Ser	Leu	Ala	Thr	Ala	Leu	Arg	
			20				25					30				
Ala	Ser	Asn	Thr	Lys	Phe	Ser	Asn	Glu	Leu	Thr	Tyr	Val	Ser	Gly	Lys	
	35					40					45					
Ala	Pro	Arg	Ser	Ala	Asn	Gln	Ala	Ala	Phe	Glu	Lys	Gly	Gly	Met	Gln	
	50				55					60						
Val	Leu	Ser	Lys	Glu	Gly	Val	Glu	Thr	Leu	Ala	Leu	Cys	Lys	Lys	Met	
65				70					75						80	
Met	Asp	Leu	Gly	Glu	Cys	Pro	Pro	Leu	Met	Val	Val	Phe	Asp	Pro	Tyr	
			85					90					95			
Glu	Gly	Phe	Thr	Val	Glu	Ala	Asp	Arg	Phe	Ile	Lys	Asp	Trp	Thr	Ile	
			100				105						110			
Ile	Thr	Glu	Tyr	Val	Gly	Asp	Val	Asp	Tyr	Leu	Ser	Asn	Arg	Glu	Asp	
	115					120						125				
Asp	Tyr	Asp	Gly	Asp	Ser	Met	Met	Thr	Leu	Leu	His	Ala	Ser	Asp	Pro	
	130					135					140					
Ser	Arg	Cys	Leu	Val	Ile	Cys	Pro	Asp	Arg	Arg	Ser	Asn	Ile	Ala	Arg	
145					150					155					160	
Phe	Ile	Ser	Gly	Ile	Asn	Asn	His	Ser	Pro	Glu	Gly	Arg	Lys	Lys	Gln	
			165					170						175		
Asn	Leu	Lys	Cys	Val	Arg	Phe	Asn	Ile	Asn	Gly	Glu	Ala	Arg	Val	Leu	
			180					185					190			
Leu	Val	Ala	Asn	Arg	Asp	Ile	Ser	Lys	Gly	Glu	Arg	Leu	Tyr	Tyr	Asp	

195 200 205
Tyr Asn Gly Tyr Glu His Glu Tyr Pro Thr Glu His Phe
210 215 220
(2) INFORMATION FOR SEQ ID NO:810:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 198 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..198
(D) OTHER INFORMATION: / Ceres Seq. ID 1568040
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:810:
Met Ala Ser Leu Ala Thr Ala Leu Arg Ala Ser Asn Thr Lys Phe Ser
1 5 10 15
Asn Glu Leu Thr Tyr Val Ser Gly Lys Ala Pro Arg Ser Ala Asn Gln
20 25 30
Ala Ala Phe Glu Lys Gly Gly Met Gln Val Leu Ser Lys Glu Gly Val
35 40 45
Glu Thr Leu Ala Leu Cys Lys Lys Met Met Asp Leu Gly Glu Cys Pro
50 55 60
Pro Leu Met Val Val Phe Asp Pro Tyr Glu Gly Phe Thr Val Glu Ala
65 70 75 80
Asp Arg Phe Ile Lys Asp Trp Thr Ile Ile Thr Glu Tyr Val Gly Asp
85 90 95
Val Asp Tyr Leu Ser Asn Arg Glu Asp Asp Tyr Asp Gly Asp Ser Met
100 105 110
Met Thr Leu Leu His Ala Ser Asp Pro Ser Arg Cys Leu Val Ile Cys
115 120 125
Pro Asp Arg Arg Ser Asn Ile Ala Arg Phe Ile Ser Gly Ile Asn Asn
130 135 140
His Ser Pro Glu Gly Arg Lys Lys Gln Asn Leu Lys Cys Val Arg Phe
145 150 155 160
Asn Ile Asn Gly Glu Ala Arg Val Leu Leu Val Ala Asn Arg Asp Ile
165 170 175
Ser Lys Gly Glu Arg Leu Tyr Tyr Asp Tyr Asn Gly Tyr Glu His Glu
180 185 190
Tyr Pro Thr Glu His Phe

195
(2) INFORMATION FOR SEQ ID NO:811:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1714 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..1714
(D) OTHER INFORMATION: / Ceres Seq. ID 1568045
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:811:
acactgttta tctgattcgt cttctctgat aatcaagagt agtagtgagg ttctctggaa 60
aatattcgat ttttaaaaga cttctgatgat gacattaaac tcactatctc cagctgaatc 120
caaagctatt tctttcttgg atacctccag gtccaatcca atccctaaac tctcaggctg 180
gtttagtgtt aggaggaggga atcaaggagg aggttttggg aaaggtgtta agtgttcagt 240
gaaagtgcag cagcaacaac aacctctctc agcatggcct gggagagctg tccctgaggc 300
gcctcgtcaa tcttgggatg gaccaaaacc catctctatc gttggatcta ctggttctat 360
tggaactcag acattggata ttgtggctga gaatcctgac aaattcagag ttgtgctct 420
agctgctggt tcgaatgtta ctctacttgc tgatcaggta aggagattta agcctgcatt 480

ggtgtgctgtt	agaaacagagt	cactgatttaa	tgagctttaa	gaggctttatg	ctgattttgga	540
ctataaaact	gagattattc	caggagagca	aggagtgtat	gagggttgccc	gacatccctga	600
agctgttaacc	gttgtttaccg	gaatagtagg	ttgtgcggga	ctaaagccta	cggttgtgc	660
aattgaagca	ggaaaggaca	ttgctcttgc	aaacaaagag	acattaatcg	caggtgtgtcc	720
ttctgtcgtt	ccgcttgcca	acaaacataa	tgtaaagatt	cttcggcgag	attcagaaca	780
ttctgccata	tttcagtgta	ttcaagggtt	gctctgaagg	gctctgcca	agataatctt	840
gactgcacat	gggtggagctt	ttagggtattg	gctctgcgaa	aagctaaagg	aagtttaaggt	900
agcggatgag	ttgaagcatt	caaaactggaa	catgggaaaag	aaaatcactg	tggactctgc	960
tacgcttttc	aacaagggtc	ttgaggtcat	tgaagcgcat	tattgttttg	gagctgagta	1020
tgacgatata	gattgtcatt	catccgcgaaa	gtatcataca	ttccatgatt	gaacacacagg	1080
attcatctgt	gcttgcctcaa	ttgggttggc	ctgatatgag	tttccagatt	ctctacacaca	1140
tgctatggcc	cgtatagatt	cctgtgtctg	aagtaacttg	gccaagactt	gaccttttgca	1200
aactcgtgtc	attgactttc	aagaaaccag	acaattgtgaa	atccccatcc	atggatctgt	1260
cttatctgtc	tggacgagct	ggaggcacaa	tgactggagt	tctcagcgcc	gccaatgaga	1320
aagctgttga	aatgttcaat	gatgaaaaga	taagctattt	ggatactctc	aaggtttgtgg	1380
aattaaacatg	cgataaacat	cgaaaacagat	ttgtaacatc	acgcgtctct	gaagagattg	1440
ttcactatga	cttctgggca	cgtgaatatg	ccgcgaatgt	cgagctttct	tctggtgcta	1500
ggccagttca	tgcataga	attggttgtt	ggaagaacat	aaggaaagctt	ctgagggaaat	1560
gttgaagaaa	gattagtgtg	gagaatgggg	tactacttaa	tagcgttttt	ggcaaggatt	1620
atggattgtg	tagctaattt	atctgtgato	cgaaacagcc	aaactgataa	tttgaaccca	1680
ttttaccaaa	taaaacggag	cttaattGtt	tcac			

(2) INFORMATION FOR SEQ ID NO:812:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 328 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..328

(D) OTHER INFORMATION: / Ceres Seq. ID 1568046

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:812:

Met	Met	Thr	Leu	Asn	Ser	Leu	Ser	Pro	Ala	Glu	Ser	Lys	Ala	Ile	Ser
1				5				10						15	
Phe	Leu	Asp	Thr	Ser	Arg	Phe	Asn	Pro	Ile	Pro	Lys	Leu	Ser	Gly	Gly
			20					25						30	
Phe	Ser	Leu	Arg	Arg	Arg	Asn	Gln	Gly	Arg	Gly	Phe	Gly	Lys	Gly	Val
			35				40					45			
Lys	Cys	Ser	Val	Lys	Val	Gln	Gln	Gln	Gln	Pro	Pro	Pro	Ala	Trp	
	50					55				60					
Pro	Gly	Arg	Ala	Val	Pro	Glu	Ala	Pro	Arg	Gln	Ser	Trp	Asp	Gly	Pro
65				70				75						80	
Lys	Pro	Ile	Ser	Ile	Val	Gly	Ser	Thr	Gly	Ser	Ile	Gly	Thr	Gln	Thr
			85					90						95	
Leu	Asp	Ile	Val	Ala	Glu	Asn	Pro	Asp	Lys	Phe	Arg	Val	Val	Ala	Leu
			100					105						110	
Ala	Ala	Gly	Ser	Asn	Val	Thr	Leu	Leu	Ala	Asp	Gln	Val	Arg	Arg	Phe
			115				120					125			
Lys	Pro	Ala	Leu	Val	Ala	Val	Arg	Asn	Glu	Ser	Leu	Ile	Asn	Glu	Leu
			130				135					140			
Lys	Glu	Ala	Leu	Ala	Asp	Leu	Asp	Tyr	Lys	Leu	Glu	Ile	Ile	Pro	Gly
145				150						155				160	
Glu	Gln	Gly	Val	Ile	Glu	Val	Ala	Arg	His	Pro	Glu	Ala	Val	Thr	Val
			165					170						175	
Val	Thr	Gly	Ile	Val	Gly	Cys	Ala	Gly	Leu	Lys	Pro	Thr	Val	Ala	Ala
			180					185						190	
Ile	Glu	Ala	Gly	Lys	Asp	Ile	Ala	Leu	Ala	Asn	Lys	Glu	Thr	Leu	Ile
			195					200						205	
Ala	Gly	Gly	Pro	Phe	Val	Leu	Pro	Leu	Ala	Asn	Lys	His	Asn	Val	Lys
	210						215							220	

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Ile Leu Pro Ala Asp Ser Glu His Ser Ala Ile Phe Gln Cys Ile Gln
225                      230                      235                      240
Gly Leu Pro Glu Gly Ala Leu Arg Lys Ile Ile Leu Thr Ala Ser Gly
                      245                      250                      255
Gly Ala Phe Arg Asp Trp Pro Val Glu Lys Leu Lys Glu Val Lys Val
                      260                      265                      270
Ala Asp Ala Leu Lys His Pro Asn Trp Asn Met Gly Lys Lys Ile Thr
                      275                      280                      285
Val Asp Ser Ala Thr Leu Phe Asn Lys Gly Leu Glu Val Ile Glu Ala
290                      295                      300
His Tyr Leu Phe Gly Ala Glu Tyr Asp Asp Ile Asp Cys His Ser Ser
305                      310                      315                      320
Ala Lys Tyr His Thr Phe His Asp
                      325

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(2) INFORMATION FOR SEQ ID NO:813:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 327 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..327

(D) OTHER INFORMATION: / Ceres Seq. ID 1568047

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:813:

```

Met Thr Leu Asn Ser Leu Ser Pro Ala Glu Ser Lys Ala Ile Ser Phe
1                      5                      10                      15
Leu Asp Thr Ser Arg Phe Asn Pro Ile Pro Lys Leu Ser Gly Gly Phe
20                      25                      30
Ser Leu Arg Arg Arg Asn Gln Gly Arg Gly Phe Gly Lys Gly Val Lys
35                      40                      45
Cys Ser Val Lys Val Gln Gln Gln Gln Pro Pro Pro Ala Trp Pro
50                      55                      60
Gly Arg Ala Val Pro Glu Ala Pro Arg Gln Ser Trp Asp Gly Pro Lys
65                      70                      75                      80
Pro Ile Ser Ile Val Gly Ser Thr Gly Ser Ile Gly Thr Gln Thr Leu
85                      90                      95
Asp Ile Val Ala Glu Asn Pro Asp Lys Phe Arg Val Val Ala Leu Ala
100                      105                      110
Ala Gly Ser Asn Val Thr Leu Leu Ala Asp Gln Val Arg Arg Phe Lys
115                      120                      125
Pro Ala Leu Val Ala Val Arg Asn Glu Ser Leu Ile Asn Glu Leu Lys
130                      135                      140
Glu Ala Leu Ala Asp Leu Asp Tyr Lys Leu Glu Ile Ile Pro Gly Glu
145                      150                      155                      160
Gln Gly Val Ile Glu Val Ala Arg His Pro Glu Ala Val Thr Val Val
165                      170                      175
Thr Gly Ile Val Gly Cys Ala Gly Leu Lys Pro Thr Val Ala Ala Ile
180                      185                      190
Glu Ala Gly Lys Asp Ile Ala Leu Ala Asn Lys Glu Thr Leu Ile Ala
195                      200                      205
Gly Gly Pro Phe Val Leu Pro Leu Ala Asn Lys His Asn Val Lys Ile
210                      215                      220
Leu Pro Ala Asp Ser Glu His Ser Ala Ile Phe Gln Cys Ile Gln Gly
225                      230                      235                      240
Leu Pro Glu Gly Ala Leu Arg Lys Ile Ile Leu Thr Ala Ser Gly Gly
245                      250                      255
Ala Phe Arg Asp Trp Pro Val Glu Lys Leu Lys Glu Val Lys Val Ala
260                      265                      270
Asp Ala Leu Lys His Pro Asn Trp Asn Met Gly Lys Lys Ile Thr Val

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	275		280		285	
Asp	Ser	Ala	Thr	Leu	Phe	Asn
	290		295		300	
Tyr	Leu	Phe	Gly	Ala	Glu	Tyr
	305		310		315	
Lys	Tyr	His	Thr	Phe	His	Asp
						325

(2) INFORMATION FOR SEQ ID NO:814:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1428 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1428
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568058

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:814:

ccccaccct	caaagatctc	tcaaaagaatg	gcttcgcg	ctgttgcac	gatggtctt	60
gaccctaaag	catcacgcgc	cttgatggat	ctatccaccg	cagacgaaga	agatctctat	120
ggccgcctca	aatcgcttga	acgacaacta	gagttaccgc	atatccaaga	agaatattgt	180
aaagacgagc	aaaagaattc	caaacgagag	ctgttacgag	cacaagaaga	ggtcaaacga	240
attcaatccg	tgccctttgt	gataggtcag	tctcatggag	tgatagatca	gaacaacggc	300
atcgctggat	ctactactgg	ctccaattac	taagtccaga	ttctcagcac	aatcaataga	360
gaactcttaa	agcctttctg	ttccgtcgct	cttcaccgtc	actccaacgc	ccttgttgat	420
gttttgcctc	cgaggagctg	ttctagcctc	tcccttctca	gccaatctga	gaagcctgac	480
gtctcctaca	atgatattgg	aggatgcgat	attcagaaaac	aggaaattcg	tgaggctgtt	540
gaattgcctc	ttaccaccca	cgagctttac	aaacagattg	gtattgaccc	acctcgtgga	600
gtcttgctct	atggacctcc	tggtacttga	aagacatagt	tggtcaaggc	tggtgccaat	660
cacacaaact	ctgccttcat	tagggttgtt	ggatccgagt	ttgtgcaaaa	gtatctcggc	720
gagggacctc	gtatggttgc	tgatgtcttc	cgctttgcca	aggaaaaatg	tccagctatc	780
atcttcattg	atgaggtaga	tgccatcgct	actgttaggt	ttgatgtcca	aacaggagcc	840
gatagggaag	ttcagcgat	tctcatggag	cttottaatc	agatggatgg	atttgaccag	900
accgtgaatg	tcaaggctcat	aatggcaaca	aacaggggag	acactctaga	tccgtctctc	960
ttacgtctcg	gaagacttga	tcgtaagatt	gagttccccc	ttcctgatag	acgtcctaaa	1020
aggcttggtt	tccagggtat	cacctccaaa	atgaacctta	gcgatgaggt	tgacttgga	1080
gactatgttt	caaggcctga	taaaattagc	gctgctgaga	tagcagcaat	ttgccaggaa	1140
gctggtatgc	atgcggtgcg	aaagaacaga	tatgtgatac	taacctaaag	tttcgagaag	1200
ggctaccgcg	caaatgttaa	gaagccagac	acggactttg	agttttacaa	gtgaagagaa	1260
agcagaagtg	gaaccagatt	atggctgttg	ttaaaattcc	agtggtgttt	gagaattatt	1320
aaggacatgg	aatcaaat	gcagtttaat	taagaactaa	gttgcatnct	cctaatttct	1380
gtaactcgag	ttcacatttg	tttttagtct	atcagctttt	tacagttc		

(2) INFORMATION FOR SEQ ID NO:815:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 205 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..205
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568059

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:815:

Met	Leu	Ala	Lys	Ala	Val	Ala	Asn	His	Thr	Thr	Ala	Ala	Phe	Ile	Arg
1			5				10						15		
Val	Val	Gly	Ser	Glu	Phe	Val	Gln	Lys	Tyr	Leu	Gly	Glu	Gly	Pro	Arg
			20				25						30		
Met	Val	Arg	Asp	Val	Phe	Arg	Leu	Ala	Lys	Glu	Asn	Ala	Pro	Ala	Ile
			35				40						45		

```

Ile Phe Ile Asp Glu Val Asp Ala Ile Ala Thr Ala Arg Phe Asp Ala
50                                     55                                     60
Gln Thr Gly Ala Asp Arg Glu Val Gln Arg Ile Leu Met Glu Leu Leu
65                                     70                                     75                                     80
Asn Gln Met Asp Gly Phe Asp Gln Thr Val Asn Val Lys Val Ile Met
85                                     90                                     95
Ala Thr Asn Arg Ala Asp Thr Leu Asp Pro Ala Leu Leu Arg Pro Gly
100                                    105                                    110
Arg Leu Asp Arg Lys Ile Glu Phe Pro Leu Pro Asp Arg Arg Gln Lys
115                                    120                                    125
Arg Leu Val Phe Gln Val Cys Thr Ser Lys Met Asn Leu Ser Asp Glu
130                                    135                                    140
Val Asp Leu Glu Asp Tyr Val Ser Arg Pro Asp Lys Ile Ser Ala Ala
145                                    150                                    155                                    160
Glu Ile Ala Ala Ile Cys Gln Glu Ala Gly Met His Ala Val Arg Lys
165                                    170                                    175
Asn Arg Tyr Val Ile Leu Pro Lys Asp Phe Glu Lys Gly Tyr Arg Ala
180                                    185                                    190
Asn Val Lys Lys Pro Asp Thr Asp Phe Glu Phe Tyr Lys
195                                    200                                    205

```

(2) INFORMATION FOR SEQ ID NO:816:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 173 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..173

(D) OTHER INFORMATION: / Ceres Seq. ID 1568060

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:816:

```

Met Val Arg Asp Val Phe Arg Leu Ala Lys Glu Asn Ala Pro Ala Ile
1      5      10      15
Ile Phe Ile Asp Glu Val Asp Ala Ile Ala Thr Ala Arg Phe Asp Ala
20      25      30
Gln Thr Gly Ala Asp Arg Glu Val Gln Arg Ile Leu Met Glu Leu Leu
35      40      45
Asn Gln Met Asp Gly Phe Asp Gln Thr Val Asn Val Lys Val Ile Met
50      55      60
Ala Thr Asn Arg Ala Asp Thr Leu Asp Pro Ala Leu Leu Arg Pro Gly
65      70      75      80
Arg Leu Asp Arg Lys Ile Glu Phe Pro Leu Pro Asp Arg Arg Gln Lys
85      90      95
Arg Leu Val Phe Gln Val Cys Thr Ser Lys Met Asn Leu Ser Asp Glu
100     105     110
Val Asp Leu Glu Asp Tyr Val Ser Arg Pro Asp Lys Ile Ser Ala Ala
115     120     125
Glu Ile Ala Ala Ile Cys Gln Glu Ala Gly Met His Ala Val Arg Lys
130     135     140
Asn Arg Tyr Val Ile Leu Pro Lys Asp Phe Glu Lys Gly Tyr Arg Ala
145     150     155     160
Asn Val Lys Lys Pro Asp Thr Asp Phe Glu Phe Tyr Lys
165     170

```

(2) INFORMATION FOR SEQ ID NO:817:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 129 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..129
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568061

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:817:

```
Met Glu Leu Leu Asn Gln Met Asp Gly Phe Asp Gln Thr Val Asn Val
1      5      10      15
Lys Val Ile Met Ala Thr Asn Arg Ala Asp Thr Leu Asp Pro Ala Leu
20      25      30
Leu Arg Pro Gly Arg Leu Asp Arg Lys Ile Glu Phe Pro Leu Pro Asp
35      40      45
Arg Arg Gln Lys Arg Leu Val Phe Gln Val Cys Thr Ser Lys Met Asn
50      55      60
Leu Ser Asp Glu Val Asp Leu Glu Asp Tyr Val Ser Arg Pro Asp Lys
65      70      75      80
Ile Ser Ala Ala Glu Ile Ala Ala Ile Cys Gln Glu Ala Gly Met His
85      90      95
Ala Val Arg Lys Asn Arg Tyr Val Ile Leu Pro Lys Asp Phe Glu Lys
100      105      110
Gly Tyr Arg Ala Asn Val Lys Lys Pro Asp Thr Asp Phe Glu Phe Tyr
115      120      125
Lys
```

(2) INFORMATION FOR SEQ ID NO:818:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 883 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..883
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568087

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:818:

```
aaaacaaaag aggaacttga gaattttatg cttgagacaa aatggcagaa gatactgacg      60
aggaagagtg cgactacttg tttaaaggcg tgttgatcgg agactcagcc gtcggaaaaat      120
caaacctcct gtctagattt tctaaagacg agttccgggt tgactctaaa ccaaccatcg      180
gagtagagtt tgcttacccg aatgttcacg tcggagataa aatcatcaag gctcagattt      240
gggacacccg cggccaagaa agatttcgag caatcacaag ttcgtactac cgtggagcat      300
taggggcatt actgattttc gacatcacta gacgaacaac ttctgacaac atcaagaaaat      360
gctcttttga gcttagagac ttgcaccaat ccgaaaacgt cgttgtcttc gtcggaaaaca      420
aatctgactc ccgacaatct agagaagtgt aagaagacga gggttaagact ctagcagaat      480
cagaaggctc ctactctctc gagacttcgg ctttagagaa tgttaacgtc gaagaagcgt      540
ttctagtgtg gatcggaagg atacatgagg ttgttactca gaggatagct tcggaaaaaca      600
aatccaacgg tgcctgcgac cctcacatta acggtaatgg gaacggtacg gtccctccgg      660
ttggtaaaga aattgtgaat atacacgaag tcaactgctac tcaaccccta ttaagctcat      720
cttccaactg ttgttttaag taaataatta atgtattttt ttogttttatt gttttggaat      780
actttgatga tgtttttatt tgccctgtgKA tctcgtgaaaa ttttgccctg gttgagtaca      840
tgaattttaa tcatacaat atatccaat aaatatgaaa atc
```

(2) INFORMATION FOR SEQ ID NO:819:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 233 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..233
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568088

[illegible]

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1246 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..1246
(D) OTHER INFORMATION: / Ceres Seq. ID 1568089

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:820:

aaagagattta	acgttaGttgt	ggtgagagag	tatgatccaa	agagagaactt	aacgagtgtgtg	60
gaagagcgttg	agggaaacgtg	tgaagtccgga	tctttattag	tggatctcat	gggtgaccctt	120
ctctgccggga	tcgcacaactc	tctctcttttc	caatgctgttg	tggcagagat	cggtaaatgag	180
atagctcgga	tgtacagag	agaactcaaaa	atggtgacac	tgtgtgttaaa	tgcatttacct	240
caaccccgaca	acgtttctgcc	ggaataataac	accaccaaac	tctgcctctg	ctccgcctgtg	300
agagttctcct	ctgttttacag	gaggtatggga	tttaggtctga	aactgtgttga	agaagattgaa	360
gagtggttttc	tacgaaacaga	cgcctgtttac	tctactacgtc	aaactgaaaa	cgacaacata	420
gcttgcgtcca	aaactcttacc	cgagaaaagt	ggttactcca	aattcgtcat	accaactttc	480
tttgttcatac	cgtgtcttcaa	ccacccagctc	actgtctctc	gaactgactaa	aatactcaaa	540
ctctgctcctc	ccgacgctga	gtcactcaac	cgcaaacgat	tctcaaccac	cgggtttttc	600
ctcttcggaca	tcaactcaat	ctctacccac	aaactctccc	tgcgcatac	ctcggctgtg	660
ccacgtggaga	gagacaaact	ttccgggtgc	ttacccgacc	agacccgggt	atgggcgctt	720
ataagttatt	ggaaacgttaa	agatgttttac	agactcaag	tcaaaaggac	tgcgcctctt	780
aaacgcattgt	tagctaaagtc	aacccgcgttc	ttcgacaggag	cgttctcgtt	tttgaaaatc	840
ccgtgtctgt	ccaactctttt	caagtctgtc	gcgatgcatt	ttatgaagtc	tatcgtgtgc	900
gagggcgca	gagcggcgga	gatgtcgtag	gcgcgtttgt	caacacgaca	tactaactgac	960
agaaaacacg	gttgtgcgct	cgtgtcgtgc	gaggtggcga	cgtgttgagc	gctcagagtt	1020
cgattctcac	tttgaagag	actctccqcc	gaggaatttgt	ggtgtttgaa	acgtctccga	1080

tatgacgatg acgcgctaga ctggaccaag tcaccacctg gattgtctat tttcgttgac 1140
cctagagaaa tataataatt tgtatagaat atattaagag gactctaaca attgcaacca 1200
aacacacaaa caaaaattac agaattaaat accaaatctc agtctc

(2) INFORMATION FOR SEQ ID NO:821:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 384 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..384
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568090

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:821:

Lys	Gly	Phe	Asn	Val	Val	Val	Val	Arg	Glu	Tyr	Asp	Pro	Lys	Arg	Asp
1			5						10					15	
Leu	Thr	Ser	Val	Glu	Glu	Leu	Glu	Ser	Cys	Glu	Val	Gly	Ser	Leu	
			20					25					30		
Leu	Val	Asp	Leu	Met	Gly	Asp	Pro	Leu	Ala	Arg	Ile	Arg	Gln	Ser	Pro
			35				40					45			
Ser	Phe	His	Met	Leu	Val	Ala	Glu	Ile	Gly	Asn	Glu	Ile	Val	Gly	Met
			50				55				60				
Ile	Arg	Gly	Thr	Ile	Lys	Met	Val	Thr	Arg	Gly	Val	Asn	Ala	Leu	Arg
			65				70				75			80	
Gln	Ala	Asp	Asp	Val	Ser	Pro	Glu	Ile	Asn	Thr	Thr	Lys	Leu	Ala	Phe
							85			90				95	
Val	Ser	Gly	Leu	Arg	Val	Ser	Pro	Phe	Tyr	Arg	Arg	Met	Gly	Ile	Gly
			100					105					110		
Leu	Lys	Leu	Val	Gln	Arg	Leu	Glu	Glu	Trp	Phe	Leu	Arg	Asn	Asp	Ala
			115				120					125			
Val	Tyr	Ser	Tyr	Val	Gln	Thr	Glu	Asn	Asp	Asn	Ile	Ala	Ser	Val	Lys
			130				135				140				
Leu	Phe	Thr	Glu	Lys	Ser	Gly	Tyr	Ser	Lys	Phe	Arg	Thr	Pro	Thr	Phe
			145				150				155			160	
Leu	Val	Asn	Pro	Val	Phe	Asn	His	Arg	Val	Thr	Val	Ser	Arg	Arg	Val
							165			170				175	
Lys	Ile	Ile	Lys	Leu	Ala	Pro	Ser	Asp	Ala	Glu	Ser	Leu	Tyr	Arg	Asn
			180					185					190		
Arg	Phe	Ser	Thr	Thr	Glu	Phe	Phe	Pro	Ser	Asp	Ile	Asn	Ser	Ile	Leu
			195				200					205			
Thr	Asn	Lys	Leu	Ser	Leu	Gly	Thr	Tyr	Leu	Ala	Val	Pro	Arg	Gly	Gly
			210				215				220				
Asp	Asn	Val	Ser	Gly	Ser	Leu	Pro	Asp	Gln	Thr	Gly	Ser	Trp	Ala	Val
							225				235			240	
Ile	Ser	Ile	Trp	Asn	Ser	Lys	Asp	Val	Tyr	Arg	Leu	Gln	Val	Lys	Gly
							245			250				255	
Ala	Ser	Arg	Leu	Lys	Arg	Met	Leu	Ala	Lys	Ser	Thr	Arg	Val	Phe	Asp
			260					265				270			
Gly	Ala	Phe	Pro	Phe	Leu	Lys	Ile	Pro	Ser	Phe	Pro	Asn	Leu	Phe	Lys
			275				280					285			
Ser	Phe	Ala	Met	His	Phe	Met	Tyr	Gly	Ile	Gly	Gly	Glu	Gly	Pro	Arg
			290				295				300				
Ala	Ala	Glu	Met	Val	Glu	Ala	Leu	Cys	Ser	His	Ala	His	Asn	Leu	Ala
							305				315			320	
Arg	Lys	Ser	Gly	Cys	Ala	Val	Val	Ala	Ala	Glu	Val	Ala	Ser	Cys	Glu
							325			330				335	
Pro	Leu	Arg	Val	Gly	Ile	Pro	His	Trp	Lys	Val	Leu	Ser	Pro	Glu	Asp
			340					345				350			
Leu	Trp	Cys	Leu	Lys	Arg	Leu	Arg	Tyr	Asp	Asp	Asp	Gly	Val	Asp	Trp
			355				360					365			

Thr Lys Ser Pro Pro Gly Leu Ser Ile Phe Val Asp Pro Arg Glu Ile
370 375 380

(2) INFORMATION FOR SEQ ID NO:822:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 348 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..348

(D) OTHER INFORMATION: / Ceres Seq. ID 1568091

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:822:

Met	Gly	Asp	Pro	Leu	Ala	Arg	Ile	Arg	Gln	Ser	Pro	Ser	Phe	His	Met
1				5					10					15	
Leu	Val	Ala	Glu	Ile	Gly	Asn	Glu	Ile	Val	Gly	Met	Ile	Arg	Gly	Thr
			20					25					30		
Ile	Lys	Met	Val	Thr	Arg	Gly	Val	Asn	Ala	Leu	Arg	Gln	Ala	Asp	Asp
			35				40					45			
Val	Ser	Pro	Glu	Ile	Asn	Thr	Thr	Lys	Leu	Ala	Phe	Val	Ser	Gly	Leu
			50			55					60				
Arg	Val	Ser	Pro	Phe	Tyr	Arg	Arg	Met	Gly	Ile	Gly	Leu	Lys	Leu	Val
			65		70				75					80	
Gln	Arg	Leu	Glu	Glu	Trp	Phe	Leu	Arg	Asn	Asp	Ala	Val	Tyr	Ser	Tyr
				85					90					95	
Val	Gln	Thr	Glu	Asn	Asp	Asn	Ile	Ala	Ser	Val	Lys	Leu	Phe	Thr	Glu
			100					105					110		
Lys	Ser	Gly	Tyr	Ser	Lys	Phe	Arg	Thr	Pro	Thr	Phe	Leu	Val	Asn	Pro
			115				120					125			
Val	Phe	Asn	His	Arg	Val	Thr	Val	Ser	Arg	Arg	Val	Lys	Ile	Ile	Lys
			130				135					140			
Leu	Ala	Pro	Ser	Asp	Ala	Glu	Ser	Leu	Tyr	Arg	Asn	Arg	Phe	Ser	Thr
			145			150				155					160
Thr	Glu	Phe	Phe	Pro	Ser	Asp	Ile	Asn	Ser	Ile	Leu	Thr	Asn	Lys	Leu
				165				170					175		
Ser	Leu	Gly	Thr	Tyr	Leu	Ala	Val	Pro	Arg	Gly	Gly	Asp	Asn	Val	Ser
			180				185					190			
Gly	Ser	Leu	Pro	Asp	Gln	Thr	Gly	Ser	Trp	Ala	Val	Ile	Ser	Ile	Trp
			195				200					205			
Asn	Ser	Lys	Asp	Val	Tyr	Arg	Leu	Gln	Val	Lys	Gly	Ala	Ser	Arg	Leu
			210			215					220				
Lys	Arg	Met	Leu	Ala	Lys	Ser	Thr	Arg	Val	Phe	Asp	Gly	Ala	Phe	Pro
			225			230				235				240	
Phe	Leu	Lys	Ile	Pro	Ser	Phe	Pro	Asn	Leu	Phe	Lys	Ser	Phe	Ala	Met
			245					250					255		
His	Phe	Met	Tyr	Gly	Ile	Gly	Gly	Glu	Gly	Pro	Arg	Ala	Ala	Glu	Met
			260				265						270		
Val	Glu	Ala	Leu	Cys	Ser	His	Ala	His	Asn	Leu	Ala	Arg	Lys	Ser	Gly
			275				280					285			
Cys	Ala	Val	Val	Ala	Ala	Glu	Val	Ala	Ser	Cys	Glu	Pro	Leu	Arg	Val
			290			295					300				
Gly	Ile	Pro	His	Trp	Lys	Val	Leu	Ser	Pro	Glu	Asp	Leu	Trp	Cys	Leu
			305			310				315				320	
Lys	Arg	Leu	Arg	Tyr	Asp	Asp	Asp	Gly	Val	Asp	Trp	Thr	Lys	Ser	Pro
			325					330					335		
Pro	Gly	Leu	Ser	Ile	Phe	Val	Asp	Pro	Arg	Glu	Ile				
			340				345								

(2) INFORMATION FOR SEQ ID NO:823:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 333 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..333
 (D) OTHER INFORMATION: / Ceres Seq. ID 1568092
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:823:

Met	Leu	Val	Ala	Glu	Ile	Gly	Asn	Glu	Ile	Val	Gly	Met	Ile	Arg	Gly	
1				5				10						15		
Thr	Ile	Lys	Met	Val	Thr	Arg	Gly	Val	Asn	Ala	Leu	Arg	Gln	Ala	Asp	
			20					25					30			
Asp	Val	Ser	Pro	Glu	Ile	Asn	Thr	Thr	Lys	Leu	Ala	Phe	Val	Ser	Gly	
			35				40					45				
Leu	Arg	Val	Ser	Pro	Phe	Tyr	Arg	Arg	Met	Gly	Ile	Gly	Leu	Lys	Leu	
	50					55				60						
Val	Gln	Arg	Leu	Glu	Glu	Trp	Phe	Leu	Arg	Asn	Asp	Ala	Val	Tyr	Ser	
65					70			75						80		
Tyr	Val	Gln	Thr	Glu	Asn	Asp	Asn	Ile	Ala	Ser	Val	Lys	Leu	Phe	Thr	
				85				90					95			
Glu	Lys	Ser	Gly	Tyr	Ser	Lys	Phe	Arg	Thr	Pro	Thr	Phe	Leu	Val	Asn	
			100					105					110			
Pro	Val	Phe	Asn	His	Arg	Val	Thr	Val	Ser	Arg	Arg	Val	Lys	Ile	Ile	
			115				120					125				
Lys	Leu	Ala	Pro	Ser	Asp	Ala	Glu	Ser	Leu	Tyr	Arg	Asn	Arg	Phe	Ser	
	130					135					140					
Thr	Thr	Glu	Phe	Phe	Pro	Ser	Asp	Ile	Asn	Ser	Ile	Leu	Thr	Asn	Lys	
145					150				155					160		
Leu	Ser	Leu	Gly	Thr	Tyr	Leu	Ala	Val	Pro	Arg	Gly	Gly	Asp	Asn	Val	
			165					170					175			
Ser	Gly	Ser	Leu	Pro	Asp	Gln	Thr	Gly	Ser	Trp	Ala	Val	Ile	Ser	Ile	
			180				185					190				
Trp	Asn	Ser	Lys	Asp	Val	Tyr	Arg	Leu	Gln	Val	Lys	Gly	Ala	Ser	Arg	
			195				200					205				
Leu	Lys	Arg	Met	Leu	Ala	Lys	Ser	Thr	Arg	Val	Phe	Asp	Gly	Ala	Phe	
	210					215					220					
Pro	Phe	Leu	Lys	Ile	Pro	Ser	Phe	Pro	Asn	Leu	Phe	Lys	Ser	Phe	Ala	
225					230				235					240		
Met	His	Phe	Met	Tyr	Gly	Ile	Gly	Gly	Glu	Gly	Pro	Arg	Ala	Ala	Glu	
			245						250				255			
Met	Val	Glu	Ala	Leu	Cys	Ser	His	Ala	His	Asn	Leu	Ala	Arg	Lys	Ser	
			260					265					270			
Gly	Cys	Ala	Val	Val	Ala	Ala	Glu	Val	Ala	Ser	Cys	Glu	Pro	Leu	Arg	
			275				280					285				
Val	Gly	Ile	Pro	His	Trp	Lys	Val	Leu	Ser	Pro	Glu	Asp	Leu	Trp	Cys	
	290					295					300					
Leu	Lys	Arg	Leu	Arg	Tyr	Asp	Asp	Gly	Val	Asp	Trp	Thr	Lys	Ser		
			310					315					320			
Pro	Pro	Gly	Leu	Ser	Ile	Phe	Val	Asp	Pro	Arg	Glu	Ile				
			325					330								

(2) INFORMATION FOR SEQ ID NO:824:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1183 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: DNA (genomic)
 (ix) FEATURE:

U.S. PAT. & TM. OFF. FILED

(A) NAME/KEY: -

(B) LOCATION: 1..1183

(D) OTHER INFORMATION: / Ceres Seq. ID 1568093

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:824:

acatcatctt	cattaatctg	atcaataaat	agggtaaatc	aaaagtcacg	aaaccaaacac	60
agttcaattt	tacgaaaact	ctcagaaatg	gagaagtagc	agaagctaga	gaaggtcggg	120
ctgaagaaaa	ctcgtctcga	gatggacgaa	gaaggtatct	caaccaatgc	tcttcgtgag	180
atctcgtctc	tccagatggt	atcaaacctg	atctatgttg	tccgattact	ctcgtcggaa	240
catgttctac	aaccatcaac	caaatctcaa	tctaccaaat	ccaatctcta	tctcgttttc	300
gagtatctcg	atactgatct	taagaaatct	atcgattcgt	ataggaaaag	acctaatctc	360
aagcctcttg	agcctttttt	gattcagaag	ttgatgtttc	agcctttgtt	aggtgttcgc	420
catgttcaat	gtcattggtg	gcttcacgtg	gatcttaaac	cgcagaatct	tctctcgttg	480
aaagataaag	agcttcttta	gattgctgat	ttgggtcttg	gtcgtgcttt	tactgttctc	540
cttaagctct	atacgcatag	gattgttact	ctttgtgata	gagctcctga	agttctctct	600
ggatctactc	attattcaac	tggtgttgac	atgtgtgtcg	ttggttgat	ctttgctgag	660
atggttcgga	ggcaagctct	tttccctggt	gattctgagt	ttcagcaatt	gcttcacatc	720
tgcaggttgc	taggaacacc	aactgagcag	caatggcctg	gtgtttccac	Attcgctgac	780
ttgcattgtt	accctaagtg	ggagcgcgaa	gacttaactc	ttgctgttcc	tctcttttca	840
cctcaaggag	ttgatcttct	cacgaaaatg	ctcaagtaca	atccagccga	aagaatttca	900
gcacaaaacg	cacttgatca	cccatatttt	gcacagcctg	acaagctctc	gttctgaagt	960
ctattgtctg	atctgtgtgc	atcgtcttgg	tgaattttaa	catttgatct	atctttgttt	1020
cgcagacatt	agtgctcttat	gtttggttta	gagatttgta	gtctttcaga	agaaactggt	1080
aaaagctgtg	ttctcaagtg	aattgtaaac	acaatggtgt	ggt		1140

(2) INFORMATION FOR SEQ ID NO:825:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 309 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..309

(D) OTHER INFORMATION: / Ceres Seq. ID 1568094

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:825:

Met	Glu	Lys	Tyr	Glu	Lys	Leu	Glu	Lys	Val	Gly	Glu	Gly	Thr	Tyr	Gly
1				5					10					15	
Lys	Val	Tyr	Lys	Ala	Met	Glu	Lys	Gly	Thr	Gly	Lys	Leu	Val	Ala	Leu
			20					25					30		
Lys	Lys	Thr	Arg	Leu	Glu	Met	Asp	Glu	Gly	Ile	Pro	Pro	Thr	Ala	
			35				40			45					
Leu	Arg	Glu	Ile	Ser	Leu	Leu	Gln	Met	Leu	Ser	Thr	Ser	Ile	Tyr	Val
			50				55			60					
Val	Arg	Leu	Leu	Cys	Val	Glu	His	Val	His	Gln	Pro	Ser	Thr	Lys	Ser
			65				70			75				80	
Gln	Ser	Thr	Lys	Ser	Asn	Leu	Tyr	Leu	Val	Phe	Glu	Tyr	Leu	Asp	Thr
			85					90						95	
Asp	Leu	Lys	Lys	Phe	Ile	Asp	Ser	Tyr	Arg	Lys	Gly	Pro	Asn	Pro	Lys
			100					105					110		
Pro	Leu	Glu	Pro	Phe	Leu	Ile	Gln	Lys	Leu	Met	Phe	Gln	Leu	Cys	Lys
			115				120					125			
Gly	Val	Ala	His	Cys	His	Ser	His	Gly	Val	Leu	His	Arg	Asp	Leu	Lys
			130				135					140			
Pro	Gln	Asn	Leu	Leu	Leu	Val	Lys	Asp	Lys	Glu	Leu	Leu	Lys	Ile	Ala
			145				150			155				160	
Asp	Leu	Gly	Leu	Gly	Arg	Ala	Phe	Thr	Val	Pro	Leu	Lys	Ser	Tyr	Thr
			165					170						175	
His	Glu	Ile	Val	Thr	Leu	Trp	Tyr	Arg	Ala	Pro	Glu	Val	Leu	Leu	Gly
			180					185					190		
Ser	Thr	His	Tyr	Ser	Thr	Gly	Val	Asp	Met	Trp	Ser	Val	Gly	Cys	Ile

(2) INFORMATION FOR SEO ID NO:826:

(A) LENGTH: 288 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: lin

MOLECULE TYPE: peptide

(1X) FEATURE:
(A) NAM

```
(A) NAME/KEY: peptide
(B) LOCATION: 1 388
```

(B) LOCATION: 1..288
(D) OTHER INFORMATION:

(B) OTHER INFORMATION: / Ceres Seq. ID 1568093
SEQUENCE DESCRIPTION: SEQ ID NO: 826:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:826:
Gla Iaa Gla Thr Gla Iaa Iaa Val Ala Iaa I

Met	Glu	Lys	Gly	Thr	Gly	Lys	Leu	Val	Ala	Leu	Lys	Lys	Thr	Alf	Leu
1				5					10					15	
Glu	Met	Asp	Glu	Glu	Gly	Ile	Pro	Pro	Thr	Ala	Leu	Arg	Glu	Ile	Ser
			20					25					30		
Leu	Leu	Gln	Met	Leu	Ser	Thr	Ser	Ile	Tyr	Val	Val	Arg	Leu	Leu	Cys
		35						40				45			
Val	Glu	His	Val	His	Gln	Pro	Ser	Thr	Lys	Ser	Gln	Ser	Thr	Lys	Ser
	50					55					60				
Asn	Leu	Tyr	Leu	Val	Phe	Glu	Tyr	Leu	Asp	Thr	Asp	Leu	Lys	Lys	Phe
					70					75					80
Ile	Asp	Ser	Tyr	Arg	Lys	Gly	Pro	Asn	Pro	Lys	Pro	Leu	Glu	Pro	Phe
				85					90					95	
Leu	Ile	Gln	Lys	Leu	Met	Phe	Gln	Leu	Cys	Lys	Gly	Val	Ala	His	Cys
			100					105					110		
His	Ser	His	Gly	Val	Leu	His	Arg	Asp	Leu	Lys	Pro	Gln	Asn	Leu	Leu
			115					120				125			
Leu	Val	Lys	Asp	Lys	Glu	Leu	Leu	Lys	Ile	Ala	Asp	Leu	Gln	Leu	Gly
	130					135					140				
Arg	Ala	Phe	Thr	Val	Pro	Leu	Lys	Ser	Tyr	Thr	His	Glu	Ile	Val	Thr
145					150					155					160
Leu	Trp	Tyr	Arg	Ala	Pro	Glu	Val	Leu	Leu	Gly	Ser	Thr	His	Tyr	Ser
			165						170					175	
Thr	Gly	Val	Asp	Met	Trp	Ser	Val	Gly	Cys	Ile	Phe	Ala	Glu	Met	Val
			180					185					190		
Arg	Arg	Gln	Ala	Leu	Phe	Pro	Gly	Asp	Ser	Glu	Phe	Gln	Gln	Leu	Leu
		195					200					205			
His	Ile	Phe	Arg	Leu	Leu	Gly	Thr	Pro	Thr	Glu	Gln	Gln	Trp	Pro	Gly
	210					215					220				
Val	Ser	Thr	Leu	Arg	Asp	Trp	His	Val	Tyr	Pro	Lys	Trp	Glu	Pro	Gln
225					230					235					240
Asp	Leu	Thr	Leu	Ala	Val	Pro	Ser	Leu	Ser	Pro	Gln	Gly	Val	Asp	Leu
			245						250				255		
Leu	Thr	Lys	Met	Leu	Lys	Tyr	Asn	Pro	Ala	Glu	Arg	Ile	Ser	Ala	Lys
			260					265					270		

Thr Ala Leu Asp His Pro Tyr Phe Asp Ser Leu Asp Lys Ser Gln Phe
275 280 285

(2) INFORMATION FOR SEQ ID NO:827:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 271 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..271
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568096

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:827:

```
Met Asp Glu Glu Gly Ile Pro Pro Thr Ala Leu Arg Glu Ile Ser Leu
1      5      10      15
Leu Gln Met Leu Ser Thr Ser Ile Tyr Val Val Arg Leu Leu Cys Val
20      25      30
Glu His Val His Gln Pro Ser Thr Lys Ser Gln Ser Thr Lys Ser Asn
35      40      45
Leu Tyr Leu Val Phe Glu Tyr Leu Asp Thr Asp Leu Lys Lys Phe Ile
50      55      60
Asp Ser Tyr Arg Lys Gly Pro Asn Pro Lys Pro Leu Glu Pro Phe Leu
65      70      75      80
Ile Gln Lys Leu Met Phe Gln Leu Cys Lys Gly Val Ala His Cys His
85      90      95
Ser His Gly Val Leu His Arg Asp Leu Lys Pro Gln Asn Leu Leu Leu
100      105      110
Val Lys Asp Lys Glu Leu Leu Lys Ile Ala Asp Leu Gly Leu Gly Arg
115      120      125
Ala Phe Thr Val Pro Leu Lys Ser Tyr Thr His Glu Ile Val Thr Leu
130      135      140
Trp Tyr Arg Ala Pro Glu Val Leu Leu Gly Ser Thr His Tyr Ser Thr
145      150      155      160
Gly Val Asp Met Trp Ser Val Gly Cys Ile Phe Ala Glu Met Val Arg
165      170      175
Arg Gln Ala Leu His Pro Gly Asp Ser Glu Phe Gln Gln Leu Leu His
180      185      190
Ile Phe Arg Leu Leu Gly Thr Pro Thr Glu Gln Gln Trp Pro Gly Val
195      200      205      210
Ser Thr Leu Arg Asp Trp His Val Tyr Pro Lys Trp Glu Pro Gln Asp
215      220      225
Leu Thr Leu Ala Val Pro Ser Leu Ser Pro Gln Gly Val Asp Leu Leu
230      235      240
Thr Lys Met Leu Lys Tyr Asn Pro Ala Glu Arg Ile Ser Ala Lys Thr
245      250      255
Ala Leu Asp His Pro Tyr Phe Asp Ser Leu Asp Lys Ser Gln Phe
260      265      270
```

(2) INFORMATION FOR SEQ ID NO:828:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1212 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1212
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568100

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:828:

ctgtctctct	tcagtgacac	aaacccaaa	aaaagtagtg	agaaacaaaa	tcgaggtaac	60
tactagatga	agacagtagc	gcaattaaat	attgcggttg	trgttgtagt	gcaggctctt	120
attggaatgt	tgagatcatc	ggaggctcaa	cttcaaatga	atttctacgc	gaagagctgt	180
ccaaacgcag	agaaaatcat	ttcagatcat	attcaaaaatc	atatccacaa	tggtcctctt	240
cttcagctc	ctctcatccg	aatgcacttc	catgattgct	tcggtagggg	atgtgacgga	300
tcggtgttga	taaatccaac	atctggtaac	gcagagagag	atgcaccacc	gaattctaac	360
cttagaggat	tcggtttctg	ggaaaaggatt	aaggctcttc	ttgaaaaagt	gtgtccttaag	420
actgtttctt	gcgcagatat	cattgctttg	actgctagag	acacagttgt	cgccaccgga	480
ggtccttcat	ggagtgttcc	aacgggaaga	agagacggtg	ggatctcaaa	tttgaaggag	540
gctacgaata	acttccacc	tccaacgagt	aatttccaga	ctttacgacg	acttttcaaa	600
aaccaaggcc	ttaattctcaa	ggaccttggt	ctgctctctg	gggctcacac	gactgtgtgc	660
tcacattggt	cttccatgaa	tactcgtctc	tacaactctc	cgactacagt	caaacaagat	720
ccatctctcg	atagccagta	cgcagcta	ctaaaggcta	acaaatgtaa	gagcctaacc	780
gcaaatagca	ccatcctgga	gatggatccc	ggtagtagca	gaagcttcga	tctcagttat	840
tataggctgt	tcttgaagag	gagagcgctg	ttccaatctg	attctgcctt	gacacagaac	900
tcagcgagct	tgaagggtgat	caacgacttg	gtcaaacggtt	ctgaaaaaga	gtttttcaaa	960
gcttttctga	agtcgaatrg	agaagatggg	gagagttaaw	gtgaCaGact	ggctcagctg	1020
gtgtgatcag	gacacgggtg	tctgtcgtcg	gaagttagta	agcttggtcg	gaatgtgggt	1080
tgttatggct	attgtgtgtt	tgtgtgactt	tcggaaaaaa	caaatgtgtg	taatttaatt	1140
ttgtgtttgt	tgtatttggt	tttatgcacc	caagaatgat	gtgttatggt	tcaattaata	1200
tgtgaatcat	tt					

(2) INFORMATION FOR SEQ ID NO:829:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 310 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..310

(D) OTHER INFORMATION: / Ceres Seq. ID 1568101

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:829:

Met	Lys	Thr	Met	Thr	Gln	Leu	Asn	Ile	Ala	Val	Xaa	Val	Val	Val	Thr
1					5				10					15	
Val	Leu	Ile	Gly	Met	Leu	Arg	Ser	Ser	Glu	Ala	Gln	Leu	Gln	Met	Asn
			20					25					30		
Phe	Tyr	Ala	Lys	Ser	Cys	Pro	Asn	Ala	Glu	Lys	Ile	Ile	Ser	Asp	His
		35					40					45			
Ile	Gln	Asn	His	Ile	His	Asn	Gly	Pro	Ser	Leu	Ala	Ala	Pro	Leu	Ile
		50				55					60				
Arg	Met	His	Phe	His	Asp	Cys	Phe	Val	Arg	Gly	Cys	Asp	Gly	Ser	Val
		65				70				75				80	
Leu	Ile	Asn	Ser	Thr	Ser	Gly	Asn	Ala	Glu	Arg	Asp	Ala	Pro	Pro	Asn
			85						90					95	
Leu	Thr	Leu	Arg	Gly	Phe	Gly	Phe	Val	Glu	Arg	Ile	Lys	Ala	Leu	Leu
			100					105					110		
Glu	Lys	Val	Cys	Pro	Lys	Thr	Val	Ser	Cys	Ala	Asp	Ile	Ile	Ala	Leu
		115					120					125			
Thr	Ala	Arg	Asp	Thr	Val	Val	Ala	Thr	Gly	Gly	Pro	Ser	Trp	Ser	Val
		130					135				140				
Pro	Thr	Gly	Arg	Arg	Asp	Gly	Arg	Ile	Ser	Asn	Leu	Lys	Glu	Ala	Thr
		145				150				155					160
Asn	Asn	Ile	Pro	Pro	Pro	Thr	Ser	Asn	Phe	Thr	Thr	Leu	Arg	Arg	Leu
			165					170					175		
Phe	Lys	Asn	Gln	Gly	Leu	Asn	Leu	Lys	Asp	Leu	Val	Leu	Leu	Ser	Gly
		180						185					190		
Ala	His	Thr	Ile	Gly	Val	Ser	His	Cys	Ser	Ser	Met	Asn	Thr	Arg	Leu
		195					200					205			
Tyr	Asn	Phe	Ser	Thr	Thr	Val	Lys	Gln	Asp	Pro	Ser	Leu	Asp	Ser	Gln

210	215	220
Tyr Ala Ala Asn Leu Lys	Ala Asn Lys Cys	Lys Ser Leu Asn Asp Asn
225	230	235
Ser Thr Ile Leu Glu Met	Asp Pro Gly Ser	Ser Arg Ser Phe Asp Leu
245	250	255
Ser Tyr Tyr Arg Leu Val	Leu Lys Arg Arg	Gly Leu Phe Gln Ser Asp
260	265	270
Ser Ala Leu Thr Thr Asn	Ser Ala Thr Leu Lys Val	Ile Asn Asp Leu
275	280	285
Val Asn Gly Ser Glu Lys	Lys Phe Phe Lys Ala	Phe Ala Lys Ser Met
290	295	300
Xaa Glu Asp Gly Glu Ser		
305	310	

(2) INFORMATION FOR SEQ ID NO:830:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 307 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..307

(D) OTHER INFORMATION: / Ceres Seq. ID 1568102

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:830:

Met Thr Gln Leu Asn Ile Ala Val Xaa Val Val Val Thr Val Leu Ile	
1	5 10 15
Gly Met Leu Arg Ser Ser Glu Ala Gln Leu Gln Met Asn Phe Tyr Ala	
	20 25 30
Lys Ser Cys Pro Asn Ala Glu Lys Ile Ile Ser Asp His Ile Gln Asn	
	35 40 45
His Ile His Asn Gly Pro Ser Leu Ala Ala Pro Leu Ile Arg Met His	
	50 55 60
Phe His Asp Cys Phe Val Arg Gly Cys Asp Gly Ser Val Leu Ile Asn	
	65 70 75
Ser Thr Ser Gly Asn Ala Glu Arg Asp Ala Pro Pro Asn Leu Thr Leu	
	85 90 95
Arg Gly Phe Gly Phe Val Glu Arg Ile Lys Ala Leu Leu Glu Lys Val	
	100 105 110
Cys Pro Lys Thr Val Ser Cys Ala Asp Ile Ile Ala Leu Thr Ala Arg	
	115 120 125
Asp Thr Val Val Ala Thr Gly Gly Pro Ser Trp Ser Val Pro Thr Gly	
	130 135 140
Arg Arg Asp Gly Arg Ile Ser Asn Leu Lys Glu Ala Thr Asn Asn Ile	
	145 150 155
Pro Pro Pro Thr Ser Asn Phe Thr Thr Leu Arg Arg Leu Phe Lys Asn	
	165 170 175
Gln Gly Leu Asn Leu Lys Asp Leu Val Leu Leu Ser Gly Ala His Thr	
	180 185 190
Ile Gly Val Ser His Cys Ser Ser Met Asn Thr Arg Leu Tyr Asn Phe	
	195 200 205
Ser Thr Thr Val Lys Gln Asp Pro Ser Leu Asp Ser Gln Tyr Ala Ala	
	210 215 220
Asn Leu Lys Ala Asn Lys Cys Lys Ser Leu Asn Asp Asn Ser Thr Ile	
	225 230 235
Leu Glu Met Asp Pro Gly Ser Ser Arg Ser Phe Asp Leu Ser Tyr Tyr	
	245 250 255
Arg Leu Val Leu Lys Arg Arg Gly Leu Phe Gln Ser Asp Ser Ala Leu	
	260 265 270
Thr Thr Asn Ser Ala Thr Leu Lys Val Ile Asn Asp Leu Val Asn Gly	
	275 280 285

Ser Glu Lys Lys Phe Phe Lys Ala Phe Ala Lys Ser Met Xaa Glu Asp
290 295 300
Gly Glu Ser
305

(2) INFORMATION FOR SEQ ID NO:831:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 290 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..290

(D) OTHER INFORMATION: / Ceres Seq. ID 1568103

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:831:

Met Leu Arg Ser Ser Glu Ala Gln Leu Gln Met Asn Phe Tyr Ala Lys
1 5 10 15
Ser Cys Pro Asn Ala Glu Lys Ile Ile Ser Asp His Ile Gln Asn His
20 25 30
Ile His Asn Gly Pro Ser Leu Ala Ala Pro Leu Ile Arg Met His Phe
35 40 45
His Asp Cys Phe Val Arg Gly Cys Asp Gly Ser Val Leu Ile Asn Ser
50 55 60
Thr Ser Gly Asn Ala Glu Arg Asp Ala Pro Pro Asn Leu Thr Leu Arg
65 70 75 80
Gly Phe Gly Phe Val Glu Arg Ile Lys Ala Leu Leu Glu Lys Val Cys
85 90 95
Pro Lys Thr Val Ser Cys Ala Asp Ile Ile Ala Leu Thr Ala Arg Asp
100 105 110
Thr Val Val Ala Thr Gly Gly Pro Ser Trp Ser Val Pro Thr Gly Arg
115 120 125
Arg Asp Gly Arg Ile Ser Asn Leu Lys Glu Ala Thr Asn Asn Ile Pro
130 135 140
Pro Pro Thr Ser Asn Phe Thr Thr Leu Arg Arg Leu Phe Lys Asn Gln
145 150 155 160
Gly Leu Asn Leu Lys Asp Leu Val Leu Leu Ser Gly Ala His Thr Ile
165 170 175
Gly Val Ser His Cys Ser Ser Met Asn Thr Arg Leu Tyr Asn Phe Ser
180 185 190
Thr Thr Val Lys Gln Asp Pro Ser Leu Asp Ser Gln Tyr Ala Ala Asn
195 200 205
Leu Lys Ala Asn Lys Cys Lys Ser Leu Asn Asp Asn Ser Thr Ile Leu
210 215 220
Glu Met Asp Pro Gly Ser Ser Arg Ser Phe Asp Leu Ser Tyr Tyr Arg
225 230 235 240
Leu Val Leu Lys Arg Arg Gly Leu Phe Gln Ser Asp Ser Ala Leu Thr
245 250 255
Thr Asn Ser Ala Thr Leu Lys Val Ile Asn Asp Leu Val Asn Gly Ser
260 265 270
Glu Lys Lys Phe Phe Lys Ala Phe Ala Lys Ser Met Xaa Glu Asp Gly
275 280 285
Glu Ser
290

(2) INFORMATION FOR SEQ ID NO:832:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1734 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(D) OTHER INFORMATION: / Ceres Seq. ID 1568104

(2) INFORMATION FOR SEQ ID NO:833:

(ii) MOLECULE TYPE: peptide

(D) OTHER INFORMATION: / Ceres Seq. ID 1568105

Ser	Met	Ala	Leu	5	Asp	Ala	Phe	Phe	Phe	Ile	Val	Ser	Leu	Phe	Leu	Leu
1										10					15	
Phe	Pro	Ser	Pro	20	Ser	Ala	Ser	Glu	Ser	Thr	Thr	Gln	Phe	Cys	Ser	Ala
									25					30		
Gly	Arg	Glu	Asn	Gly	Val		Gly	Ser	Cys	Gly	Val	Ser	Ser	Thr	Arg	Ile
		35					40						45			
Leu	Ile	Lys	Gly	Gly	Thr	Val	Val	Asn	Ala	His	His	Gln	Glu	Glu	Leu	Ala
		50					55				60					
Asp	Val	Tyr	Val	Glu	Asn	Gly	Ile	Ile	Val	Ala	Val	Gln	Pro	Asn	Ile	
65					70					75					80	
Lys	Val	Gly	Asp	Glu	Val	Thr	Val	Leu	Asp	Ala	Thr	Gly	Lys	Phe	Val	
				85					90					95		
Met	Pro	Gly	Gly	Ile	Asp	Pro	His	Thr	His	Leu	Ala	Met	Glu	Phe	Met	
			100					105					110			
Gly	Thr	Glu	Thr	Ile	Asp	Asp	Phe	Phe	Ser	Gly	Gln	Ala	Ala	Ala	Leu	

115	120	125
Ala Gly Gly Thr Thr Met His Ile Asp Phe Val Ile Pro Val Asn Gly		
130	135	140
Asn Leu Val Ala Gly Phe Glu Ala Tyr Glu Asn Lys Ser Arg Glu Ser		
145	150	155
Cys Met Asp Tyr Gly Phe His Met Ala Ile Thr Lys Trp Asp Glu Gly		
165	170	175
Val Ser Arg Asp Met Glu Met Leu Val Lys Glu Lys Gly Ile Asn Ser		
180	185	190
Phe Lys Phe Phe Leu Ala Tyr Lys Gly Ser Leu Met Val Thr Asp Asp		
195	200	205
Leu Leu Leu Glu Gly Leu Lys Arg Cys Lys Ser Leu Gly Ala Leu Ala		
210	215	220
Met Val His Ala Glu Asn Gly Asp Ala Val Phe Glu Gly Gln Lys Arg		
225	230	235
Met Ile Xaa Leu Gly Ile Tyr Arg Ser Arg Gly Ser Cys Ser Phe Gln		
245	250	255
Gly Leu Leu Cys Ser Arg Glu Arg Pro Leu Leu Glu Gln Phe Val Trp		
260	265	270
Leu Val Leu Leu Thr Arg Leu Ser Met Leu Phe Met		
275	280	

(2) INFORMATION FOR SEQ ID NO:834:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 283 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..283
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568106

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:834:

Met Ala Leu Asp Ala Phe Phe Phe Ile Val Ser Leu Phe Leu Phe	1	5	10	15
Pro Ser Pro Ser Ala Ser Glu Ser Thr Thr Gln Phe Cys Ser Ala Gly	20	25	30	
Arg Glu Asn Gly Val Gly Ser Cys Gly Val Ser Ser Thr Arg Ile Leu	35	40	45	
Ile Lys Gly Gly Thr Val Val Asn Ala His His Gln Glu Leu Ala Asp	50	55	60	
Val Tyr Val Glu Asn Gly Ile Ile Val Ala Val Gln Pro Asn Ile Lys	65	70	75	80
Val Gly Asp Glu Val Thr Val Leu Asp Ala Thr Gly Lys Phe Val Met	85	90	95	
Pro Gly Gly Ile Asp Pro His Thr His Leu Ala Met Glu Phe Met Gly	100	105	110	
Thr Glu Thr Ile Asp Asp Phe Phe Ser Gly Gln Ala Ala Ala Leu Ala	115	120	125	
Gly Gly Thr Thr Met His Ile Asp Phe Val Ile Pro Val Asn Gly Asn	130	135	140	
Leu Val Ala Gly Phe Glu Ala Tyr Glu Asn Lys Ser Arg Glu Ser Cys	145	150	155	160
Met Asp Tyr Gly Phe His Met Ala Ile Thr Lys Trp Asp Glu Gly Val	165	170	175	
Ser Arg Asp Met Glu Met Leu Val Lys Glu Lys Gly Ile Asn Ser Phe	180	185	190	
Lys Phe Phe Leu Ala Tyr Lys Gly Ser Leu Met Val Thr Asp Asp Leu	195	200	205	
Leu Leu Glu Gly Leu Lys Arg Cys Lys Ser Leu Gly Ala Leu Ala Met	210	215	220	

Val His Ala Glu Asn Gly Asp Ala Val Phe Glu Gly Gln Lys Arg Met
225 230 235 240
Ile Xaa Leu Gly Ile Tyr Arg Ser Arg Gly Ser Cys Ser Phe Gln Gly
245 250 255
Leu Leu Cys Ser Arg Glu Arg Pro Leu Leu Glu Gln Phe Val Trp Leu
260 265 270
Val Leu Leu Thr Arg Leu Ser Met Leu Phe Met
275 280

(2) INFORMATION FOR SEQ ID NO:835:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 281 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..281

(D) OTHER INFORMATION: / Ceres Seq. ID 1568107

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:835:

Met Leu Phe Ser Arg Pro Pro Val Leu Glu Gly Glu Ala Thr Ala Arg
1 5 10 15
Ala Ile Arg Leu Ala Arg Phe Ile Asn Thr Pro Leu Tyr Val Val His
20 25 30
Val Met Ser Val Asp Ala Met Asp Glu Ile Ala Lys Ala Arg Lys Ser
35 40 45
Gly Gln Lys Val Ile Gly Glu Pro Val Val Ser Gly Leu Ile Leu Asp
50 55 60
Asp His Trp Leu Trp Asp Pro Asp Phe Thr Ile Ala Ser Lys Tyr Val
65 70 75 80
Met Ser Pro Pro Ile Arg Pro Val Gly His Gly Lys Ala Leu Gln Asp
85 90 95
Ala Leu Ser Thr Gly Ile Leu Gln Leu Val Gly Thr Asp His Cys Thr
100 105 110
Phe Asn Ser Thr Gln Lys Ala Leu Gly Leu Asp Asp Phe Arg Lys Ile
115 120 125
Pro Asn Gly Val Asn Gly Leu Glu Glu Arg Met His Leu Ile Trp Asp
130 135 140
Thr Met Val Glu Ser Gly Gln Leu Ser Ala Thr Asp Tyr Val Arg Ile
145 150 155 160
Thr Ser Thr Glu Cys Ala Arg Ile Phe Asn Ile Tyr Pro Arg Lys Gly
165 170 175
Ala Ile Leu Ala Gly Ser Asp Ala Asp Ile Ile Ile Leu Asn Pro Asn
180 185 190
Ser Ser Tyr Glu Ile Ser Ser Lys Ser His His Ser Arg Ser Asp Thr
195 200 205
Asn Val Tyr Glu Gly Arg Arg Gly Lys Gly Lys Val Glu Val Thr Ile
210 215 220
Ala Gly Gly Arg Ile Val Trp Glu Asn Glu Glu Leu Lys Val Val Pro
225 230 235 240
Arg Ser Gly Lys Tyr Ile Glu Met Pro Pro Phe Ser Tyr Leu Phe Asp
245 250 255
Gly Ile Glu Lys Ser Asp Ala Asn Tyr Leu Ser Ser Leu Arg Ala Pro
260 265 270
Val Lys Arg Val Arg Thr Glu Ala Thr
275 280

(2) INFORMATION FOR SEQ ID NO:836:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 659 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single

(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..659

(D) OTHER INFORMATION: / Ceres Seq. ID 1568124

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:836:

ctctttttct	tcattcttca	tctctctcc	cacaaaagag	gacaaaaaac	caaataacga	60
gaagtcocat	ttctctttgt	tgtcttaggt	gttaccttca	tcaaccaaac	gcaatggcga	120
acgcggcgtc	ggggatggcg	gtggaggacg	agtgttaagct	gaagtttttg	gagctaaaag	180
cgaaagaaaa	ctatagggtc	ataatattca	ggatagatgg	acaacaagtg	gtggtagaaa	240
agctgggaag	cccccaagag	aactacgacg	atttcaccaa	ttacctaccg	ccaaaatgaat	300
gcgcgtacgc	cgtttatgac	ttcgacttca	ccactgctga	gaatatccag	aagagcaaga	360
tctttctcat	agcatggtca	ccggattcat	ctagagtaag	gatgaagatg	gtgtatgcga	420
gtctaaagga	caggttccaag	agggaaattgg	atgggtattca	gggtggagtta	caagccactg	480
acccgagcga	gatgagttct	gacatcatca	aaagtgcgaac	ttcttagatc	tccttgcctt	540
tcataattata	tatccataat	cattgtcatt	caaacatttt	cctcatctta	tgttaactttc	600
gatcttggtt	tcattcattc	ttgttcttga	ctgttttttt	ctatGtttat	ttacatttt	

(2) INFORMATION FOR SEQ ID NO:837:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 174 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..174

(D) OTHER INFORMATION: / Ceres Seq. ID 1568125

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:837:

Leu	Phe	Leu	His	Ser	Ser	Ser	Leu	Leu	Pro	Gln	Lys	Arg	Thr	Lys	Asn
1			5						10					15	
Gln	Ile	Thr	Arg	Ser	Pro	Ile	Ser	Leu	Cys	Cys	Leu	Arg	Cys	Tyr	Leu
			20					25						30	
His	Gln	Pro	Asn	Ala	Met	Ala	Asn	Ala	Ala	Ser	Gly	Met	Ala	Val	Glu
			35				40					45			
Asp	Glu	Cys	Lys	Leu	Lys	Phe	Leu	Glu	Leu	Lys	Ala	Lys	Arg	Asn	Tyr
			50			55					60				
Arg	Phe	Ile	Ile	Phe	Arg	Ile	Asp	Gly	Gln	Gln	Val	Val	Val	Glu	Lys
			65		70			75						80	
Leu	Gly	Ser	Pro	Gln	Glu	Asn	Tyr	Asp	Asp	Phe	Thr	Asn	Tyr	Leu	Pro
			85					90					95		
Pro	Asn	Glu	Cys	Arg	Tyr	Ala	Val	Tyr	Asp	Phe	Asp	Phe	Thr	Thr	Ala
			100					105					110		
Glu	Asn	Ile	Gln	Lys	Ser	Lys	Ile	Phe	Phe	Ile	Ala	Trp	Ser	Pro	Asp
			115				120					125			
Ser	Ser	Arg	Val	Arg	Met	Lys	Met	Val	Tyr	Ala	Ser	Ser	Lys	Asp	Arg
			130			135					140				
Phe	Lys	Arg	Glu	Leu	Asp	Gly	Ile	Gln	Val	Glu	Leu	Gln	Ala	Thr	Asp
			145		150					155					160
Pro	Ser	Glu	Met	Ser	Leu	Asp	Ile	Ile	Lys	Ser	Arg	Thr	Leu		
			165						170						

(2) INFORMATION FOR SEQ ID NO:838:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 137 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..137

(D) OTHER INFORMATION: / Ceres Seq. ID 1568126

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:838:

```
Met Ala Asn Ala Ala Ser Gly Met Ala Val Glu Asp Glu Cys Lys Leu
1      5      10
Lys Phe Leu Glu Leu Lys Ala Lys Arg Asn Tyr Arg Phe Ile Ile Phe
20     25     30
Arg Ile Asp Gly Gln Gln Val Val Val Glu Lys Leu Gly Ser Pro Gln
35     40     45
Glu Asn Tyr Asp Asp Phe Thr Asn Tyr Leu Pro Pro Asn Glu Cys Arg
50     55     60
Tyr Ala Val Tyr Asp Phe Asp Phe Thr Thr Ala Glu Asn Ile Gln Lys
65     70     75     80
Ser Lys Ile Phe Phe Ile Ala Trp Ser Pro Asp Ser Ser Arg Val Arg
85     90     95
Met Lys Met Val Tyr Ala Ser Ser Lys Asp Arg Phe Lys Arg Glu Leu
100    105    110
Asp Gly Ile Gln Val Glu Leu Gln Ala Thr Asp Pro Ser Glu Met Ser
115    120    125
Leu Asp Ile Ile Lys Ser Arg Thr Leu
130    135
```

(2) INFORMATION FOR SEQ ID NO:839:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 130 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..130

(D) OTHER INFORMATION: / Ceres Seq. ID 1568127

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:839:

```
Met Ala Val Glu Asp Glu Cys Lys Leu Lys Phe Leu Glu Leu Lys Ala
1      5      10
Lys Arg Asn Tyr Arg Phe Ile Ile Phe Arg Ile Asp Gly Gln Gln Val
20     25     30
Val Val Glu Lys Leu Gly Ser Pro Gln Glu Asn Tyr Asp Asp Phe Thr
35     40     45
Asn Tyr Leu Pro Pro Asn Glu Cys Arg Tyr Ala Val Tyr Asp Phe Asp
50     55     60
Phe Thr Thr Ala Glu Asn Ile Gln Lys Ser Lys Ile Phe Phe Ile Ala
65     70     75     80
Trp Ser Pro Asp Ser Ser Arg Val Arg Met Lys Met Val Tyr Ala Ser
85     90     95
Ser Lys Asp Arg Phe Lys Arg Glu Leu Asp Gly Ile Gln Val Glu Leu
100    105    110
Gln Ala Thr Asp Pro Ser Glu Met Ser Leu Asp Ile Ile Lys Ser Arg
115    120    125
Thr Leu
130
```

(2) INFORMATION FOR SEQ ID NO:840:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1320 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1320

(D) OTHER INFORMATION: / Ceres Seq. ID 1568128

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:840:

ataagcggtt	tcattatt	cttcttcac	gattcttgat	tttgcaagaa	gacaattcaa	60
gaaagcgatt	tagaagacgg	aggagttctt	accggagatc	ttatacttat	ggatggaatg	120
tacaatttcc	attcgggccg	tgattattca	gataagtcgg	ttctgatgat	gtcacccggg	180
agtctcatgt	ttccttcoga	tlaccaagct	ttgctatgtt	cctccgcccg	tgaaaatcgt	240
gtctctgatg	ttttcggatc	cgacgagcta	ctctcagtag	cctgtctccg	tttgtcgtcg	300
gaggcggttt	cgatcgctcc	ggagatccga	agaaatgatg	ataacgtttc	tctaactgtc	360
atcacaagcta	aaatcgcttg	tcattccttcg	tatcctcgct	tacttcaagc	ttacatcgat	420
tgccaaaaga	aacaggtcgg	agcaccaccg	gagatagcgt	gtttactaga	ggagattcaa	480
cgggagagtg	atgtttataa	gcaagaggtt	gttccttctt	cttgctttgg	agctgatcct	540
gagcttgatg	aattttatga	aacgtactgc	gatatattag	tgaaatacaa	atcgcatcta	600
gcaagaccgt	ttgacgaggg	aacgtgtttc	ttgaacaaga	ttgagatgca	gtacaggaa	660
ctatgtactc	gtgtcgagtc	tgccaggggg	gtttctgagg	atggtgtaat	atcatctgac	720
gaggaaactga	gtggaggtga	tcattgaggtg	gcagagggatg	ggagacaaag	atgtggaagac	780
cgggacctca	aaagataggtt	Gctacgcata	tttggaagcc	gtattagtag	tttaaaagct	840
gagttctcaa	agaagaagaa	gaaaggaaag	ttacctagag	aagcaagaca	agctcttctc	900
gatttgtgta	atctccatta	taagtggcct	taccctactg	aaggagataa	gatagcatta	960
gctgatgcga	cggggttaga	ccagaaacaa	atcaacaatt	ggtttataaa	ccaaaggaaa	1020
cgctattgga	agccatcaga	gaatatgcct	tttgctatga	tgtagtattc	tagtggatca	1080
ttctttaccg	aggaatgaat	ttatttaccg	tatttattta	acgttactta	aaaagatgga	1140
tgatataatt	tgcccttgct	tgccgacaa	caaaagaaaa	aagaaagaaa	agagtgaaag	1200
atgggacgca	caatgaatta	tgaattattc	actcactcac	atgtagtaga	aggaacaagg	1260
gaacaagtca	aaatgctttg	taactattat	tatcggtgaa	taaaaataac	ttcttttgct	1320

(2) INFORMATION FOR SEQ ID NO:841:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 329 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..329

(D) OTHER INFORMATION: / Ceres Seq. ID 1568129

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:841:

Met	Asp	Gly	Met	Tyr	Asn	Phe	His	Ser	Ala	Gly	Asp	Tyr	Ser	Asp	Lys
1		5						10					15		
Ser	Val	Leu	Met	Met	Ser	Pro	Glu	Ser	Leu	Met	Phe	Pro	Ser	Asp	Tyr
		20						25					30		
Gln	Ala	Leu	Leu	Cys	Ser	Ser	Ala	Gly	Glu	Asn	Arg	Val	Ser	Asp	Val
		35						40					45		
Phe	Gly	Ser	Asp	Glu	Leu	Leu	Ser	Val	Ala	Val	Ser	Ala	Leu	Ser	Ser
		50						55					60		
Glu	Ala	Ala	Ser	Ile	Ala	Pro	Glu	Ile	Arg	Arg	Asn	Asp	Asp	Asn	Val
		65						70					75		
Ser	Leu	Thr	Val	Ile	Lys	Ala	Lys	Ile	Ala	Cys	His	Pro	Ser	Tyr	Pro
		85						90					95		
Arg	Leu	Leu	Gln	Ala	Tyr	Ile	Asp	Cys	Gln	Lys	Lys	Gln	Val	Gly	Ala
		100						105					110		
Pro	Pro	Glu	Ile	Ala	Cys	Leu	Leu	Glu	Glu	Ile	Gln	Arg	Glu	Ser	Asp
		115						120					125		
Val	Tyr	Lys	Gln	Glu	Val	Val	Pro	Ser	Ser	Cys	Phe	Gly	Ala	Asp	Pro
		130						135					140		
Glu	Leu	Asp	Glu	Phe	Met	Glu	Thr	Tyr	Cys	Asp	Ile	Leu	Val	Lys	Tyr
		145						150					155		
Lys	Ser	Asp	Leu	Ala	Arg	Pro	Phe	Asp	Glu	Ala	Thr	Cys	Phe	Leu	Asn
		165						170					175		
Lys	Ile	Glu	Met	Gln	Leu	Arg	Asn	Leu	Cys	Thr	Gly	Val	Glu	Ser	Ala
		180						185					190		

1	Met	Met	Ser	Pro	5	Glu	Ser	Leu	Met	Phe	Pro	Ser	Asp	Tyr	Gln	Ala	Leu
1	Leu	Cys	Ser	Ser	20	Ala	Gly	Glu	Asn	Arg	Val	Ser	Asp	Val	Phe	Gly	Ser
Asp	Glu	Leu	Leu	Ser	Val	Ala	Val	Ser	Ala	25	Ser	Leu	Ser	Ser	Glu	Ala	Ala
Ser	Ile	Ala	Pro	Glu	Ile	Arg	Arg	Asn	Asp	Asp	Asn	Val	Ser	Leu	Thr		
Val	Ile	Lys	Ala	Lys	Ile	Ala	Cys	His	Pro	Ser	Tyr	Pro	Arg	Leu	Leu		
65	Gln	Ala	Tyr	Ile	Asp	Cys	Gln	Lys	Lys	Gln	Val	Gly	Ala	Pro	Pro	Glu	
Ile	Ala	Cys	Leu	Leu	Glu	Glu	Ile	Gln	Arg	Glu	Ser	Asp	Val	Tyr	Lys		
Gln	Glu	Val	Val	Pro	Ser	Ser	Cys	Phe	Gly	Ala	Asp	Pro	Glu	Leu	Asp		
Glu	Phe	Met	Glu	Thr	Tyr	Cys	Asp	Ile	Leu	Val	Lys	Tyr	Lys	Ser	Asp		
Leu	Ala	Arg	Pro	Phe	Asp	Glu	Ala	Thr	Cys	Phe	Leu	Asn	Lys	Ile	Glu		
145	Met	Gln	Leu	Arg	Asn	Leu	Cys	Thr	Gly	Val	Glu	Ser	Ala	Arg	Gly	Val	
Ser	Glu	Asp	Gly	Val	Ile	Ser	Ser	Asp	Glu	Glu	Leu	Ser	Gly	Gly	Asp		
His	Glu	Val	Ala	Glu	Asp	Gly	Arg	Gln	Arg	Cys	Glu	Asp	Arg	Asp	Leu		
Lys	Asp	Arg	Leu	Leu	Arg	Lys	Phe	Gly	Ser	Arg	Ile	Ser	Thr	Leu	Lys		
Leu	Glu	Phe	Ser	Lys	Lys	Lys	Lys	Lys	Gly	Lys	Leu	Pro	Arg	Glu	Ala		
225	Arg	Gln	Ala	Leu	Leu	Asp	Trp	Trp	Asn	Leu	His	Tyr	Lys	Trp	Pro	Tyr	
Pro	Thr	Glu	Gly	Asp	Lys	Ile	Ala	Leu	Ala	Asp	Ala	Thr	Gly	Leu	Asp		
Gln	Lys	Gln	Ile	Asn	Asn	Trp	Phe	Ile	Asn	Gln	Arg	Lys	Arg	His	Trp		
Lys	Pro	Ser	Glu	Asn	Met	Pro	Phe	Ala	Met	Met	Asp	Asp	Ser	Ser	Gly		

Ser Phe Phe Thr Glu Glu
305 310

(2) INFORMATION FOR SEQ ID NO:844:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1312 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1312
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568152

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:844:

tctctatggt	gtagttcttg	tacagttggc	tctcttttca	agaatcgctcg	cggttgacct	60
ccgtgcctct	ccgatcaact	tccattctct	ttaaagtacg	agagattcat	caaggaacag	120
ctcattaaag	ccatggcctc	gaaagaggtt	tctttttcct	tctgttgtga	ttgtcattgt	180
tggtggaatc	gtggcggttt	cttatcagtc	caagttgaaa	ccacctccgc	cgaagctatg	240
tggtctctcc	gaaggtccac	cgatcacagc	gccgcggata	aagcttcaag	atggggaggta	300
tttggcttcc	aaagagcatg	gaattccaag	agagaaagct	aaccgcaaaa	tcgtcttcat	360
ccatggatcc	gattgttgtg	gacacgatgc	cgttttcgcc	actctgcttt	ctccggattt	420
agtagaggaa	ctaggtgtat	atatgttttc	attcgacaga	ccggctattt	gtgagagtga	480
tcgcgaccca	agtctgtacc	cgcgaaagct	ggtttcggat	attgaagagc	tagctgatca	540
gttgagtcta	ggatcgaaat	tttatgtgct	cggtgtactc	atggggaggac	aagcagcatg	600
gggatgtctt	aaatacattc	ctcataggtt	agccggagta	acactagtgt	ctccagtgtt	660
taactattat	tgggaagata	tacctttgaa	cgttttccact	gaaggtttta	actttcaaca	720
aaagagagat	caattggcag	ttcgtgttgc	tcactatact	ctctgggtta	ttctatttgtg	780
gaacacacaa	aaatGgttcc	ctggttcgag	tattgcaaac	cgagatcaca	gtctcttgcc	840
acagccggat	aaagatatca	tttcaagctt	gtgtttcttc	aggaaaccac	attgggcaga	900
ggtaaggcag	caaggaatac	atgagagtat	taaccgtgac	atgatcgttg	gttttgggaa	960
ctgggaattt	gatcctttag	acctcgagaa	tccgtttttg	aataaggaag	gtctctgtgc	1020
tttgggcaca	ggagatgagg	acatgtttag	acctgcgaag	ctgcagcgtt	acctttgtca	1080
tcagcttcca	tgggttcact	atcatgaggt	tccgagaagt	ggccactctt	tcacatcac	1140
taaaggtgta	gttgatgaca	ttgtaaaagt	gctcttaacc	tccggtgtaa	gagcatctag	1200
agttgtattt	tgatcattgt	tagcttccaa	aaactctgaa	aaaaatcccc	aaaaataata	1260
cggtacacaa	agagttatgt	actagtata	tttgacagca	tcgtagttaa	tt	

(2) INFORMATION FOR SEQ ID NO:845:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 372 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..372
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568153

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:845:

Met	Thr	Arg	Asp	Ser	Ser	Arg	Asn	Ser	Ser	Leu	Lys	Pro	Trp	Pro	Arg
1			5				10				15				
Lys	Ser	Phe	Leu	Phe	Pro	Ser	Val	Val	Ile	Val	Ile	Val	Gly	Ile	Ile
			20				25						30		
Val	Ala	Phe	Thr	Tyr	Gln	Ser	Lys	Leu	Lys	Pro	Pro	Pro	Pro	Lys	Leu
			35				40					45			
Cys	Gly	Ser	Ser	Gly	Gly	Pro	Pro	Ile	Thr	Ala	Pro	Arg	Ile	Lys	Leu
			50				55					60			
Gln	Asp	Gly	Arg	Tyr	Leu	Ala	Tyr	Lys	Glu	His	Gly	Leu	Pro	Arg	Glu
			65				70				75				80
Lys	Ala	Asn	Arg	Lys	Ile	Val	Phe	Ile	His	Gly	Ser	Asp	Cys	Cys	Arg
			85				90					95			
His	Asp	Ala	Val	Phe	Ala	Thr	Leu	Leu	Ser	Pro	Asp	Leu	Val	Glu	Glu

Met	Val	Ser	Phe	Asp	Arg	Pro	Gly	Tyr	Cys	Glu	Ser	Asp	Pro	His	Pro
1			5						10					15	
Ser	Arg	Thr	Pro	Arg	Ser	Leu	Val	Ser	Asp	Ile	Glu	Glu	Leu	Ala	Asp
			20					25					30		
Gln	Leu	Ser	Leu	Gly	Ser	Lys	Phe	Tyr	Val	Leu	Gly	Tyr	Ser	Met	Gly
		35					40					45			
Gly	Gln	Ala	Ala	Trp	Gly	Cys	Leu	Lys	Tyr	Ile	Pro	His	Arg	Leu	Ala
	50					55					60				
Gly	Val	Thr	Leu	Val	Ala	Pro	Val	Val	Asn	Tyr	Tyr	Trp	Lys	Asn	Leu
65				70					75					80	
Pro	Leu	Asn	Val	Ser	Thr	Glu	Gly	Phe	Asn	Phe	Gln	Gln	Lys	Arg	Asp
			85						90					95	
Gln	Leu	Ala	Val	Arg	Val	Ala	His	Tyr	Thr	Pro	Trp	Leu	Ile	Tyr	Trp
			100					105					110		

Trp	Asn	Thr	Gln	Lys	Trp	Phe	Pro	Gly	Ser	Ser	Ile	Ala	Asn	Arg	Asp	
	115						120					125				
His	Ser	Leu	Leu	Ala	Gln	Pro	Asp	Lys	Asp	Ile	Ile	Ser	Lys	Leu	Gly	
	130					135					140					
Ser	Ser	Arg	Lys	Pro	His	Trp	Ala	Glu	Val	Arg	Gln	Gln	Gly	Ile	His	
	145				150					155					160	
Glu	Ser	Ile	Asn	Arg	Asp	Met	Ile	Val	Gly	Phe	Gly	Asn	Trp	Glu	Phe	
			165						170					175		
Asp	Pro	Leu	Asp	Leu	Glu	Asn	Pro	Phe	Leu	Asn	Lys	Glu	Gly	Ser	Val	
			180					185					190			
His	Leu	Trp	Gln	Gly	Asp	Glu	Asp	Met	Leu	Val	Pro	Ala	Lys	Leu	Gln	
		195					200					205				
Arg	Tyr	Leu	Ala	His	Gln	Leu	Pro	Trp	Val	His	Tyr	His	Glu	Val	Pro	
	210					215					220					
Arg	Ser	Gly	His	Phe	Phe	His	Tyr	Thr	Lys	Gly	Val	Val	Asp	Asp	Ile	
	225				230					235					240	
Val	Lys	Ser	Leu	Leu	Thr	Ser	Gly	Val	Arg	Ala	Ser	Arg	Val	Cys	Ile	
			245					250						255		

(2) INFORMATION FOR SEQ ID NO:847:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 210 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..210

(D) OTHER INFORMATION: / Ceres Seq. ID 1568155

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:847:

Met	Gly	Gly	Gln	Ala	Ala	Trp	Gly	Cys	Leu	Lys	Tyr	Ile	Pro	His	Arg	
1			5					10					15			
Leu	Ala	Gly	Val	Thr	Leu	Val	Ala	Pro	Val	Val	Asn	Tyr	Tyr	Trp	Lys	
			20					25					30			
Asn	Leu	Pro	Leu	Asn	Val	Ser	Thr	Glu	Gly	Phe	Asn	Phe	Gln	Gln	Lys	
			35				40					45				
Arg	Asp	Gln	Leu	Ala	Val	Arg	Val	Ala	His	Tyr	Thr	Pro	Trp	Leu	Ile	
	50					55					60					
Tyr	Trp	Trp	Asn	Thr	Gln	Lys	Trp	Phe	Pro	Gly	Ser	Ser	Ile	Ala	Asn	
	65				70				75					80		
Arg	Asp	His	Ser	Leu	Ala	Gln	Pro	Asp	Lys	Asp	Ile	Ile	Ser	Lys		
			85					90					95			
Leu	Gly	Ser	Ser	Arg	Lys	Pro	His	Trp	Ala	Glu	Val	Arg	Gln	Gln	Gly	
			100					105					110			
Ile	His	Glu	Ser	Ile	Asn	Arg	Asp	Met	Ile	Val	Gly	Phe	Gly	Asn	Trp	
	115						120					125				
Glu	Phe	Asp	Pro	Leu	Asp	Leu	Glu	Asn	Pro	Phe	Leu	Asn	Lys	Glu	Gly	
	130					135						140				
Ser	Val	His	Leu	Trp	Gln	Gly	Asp	Glu	Asp	Met	Leu	Val	Pro	Ala	Lys	
	145				150					155					160	
Leu	Gln	Arg	Tyr	Leu	Ala	His	Gln	Leu	Pro	Trp	Val	His	Tyr	His	Glu	
			165						170					175		
Val	Pro	Arg	Ser	Gly	His	Phe	Phe	His	Tyr	Thr	Lys	Gly	Val	Val	Asp	
			180					185					190			
Asp	Ile	Val	Lys	Ser	Leu	Leu	Thr	Ser	Gly	Val	Arg	Ala	Ser	Arg	Val	
		195					200					205				
Cys	Ile															
	210															

(2) INFORMATION FOR SEQ ID NO:848:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1261 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1261

(D) OTHER INFORMATION: / Ceres Seq. ID 1568160

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:848:

```
gaaaaacaaa ttaggggtttt taatttcocag attgttttgt ttatttgaat aaatctccgc      60
aagtttcaat taggttgcaa aaatcgaga aMattttctt cgattccaaa aaatgggaa      120
aaattttgtt ettcacttcc gcttctgagg ttgtgggagg acaatcatca tcacgatcag      180
gtaaaagaa aagtgatgaa gggatgatca agtatggttt tagtctagt aaaggaaaaa      240
ctaaccatcc aatggaagat tatcatgttg ctaactttat caacatccaa gaccatgaat      300
tgggtctttt tgctatttat gatggtoata tgggtgatag tgcctctgct tacttgaga      360
aacgtctctt ctccaatctc cttaaggagg gagagtgttg ggttgatcct cgaaggtcta      420
ttgcaaaagc ttatgagaag acggaagcga ttctatcgaa tagttctgac ttgggtcggtg      480
gtggtttctac tgctgtgact gctatattga ttaatgggag aaagtgttgg atagctaagt      540
ttggtgattc acgaagctgtt ctttctaatg gtggcgctat aacgcagatg agtacagatc      600
atgagcctcg tactgaaaagg tcgagtattg aagatagagg tggatttcta tccaatctac      660
caggtgatgt tctctgggtg aatggtcact tagctgtgtc tcgtgctttt ggagataaagg      720
gacttaagac acacttgagt tcagagcctg acalaaaaa agctactgta gatagccaga      780
cagatgttct tctcttggtc agtgatggca tctggaaggt gatgacaaat gaagagccaa      840
tggagatagc gagaagagtg aagagatccac agaaaagcggc aaaggaatca acagctgaag      900
cattgagaag agagagatcaa gacgacatat cttgtgtcgt ggtccgattc agatgacaaa      960
ctctctgaaa ggatacttacc ggggagatgg gttccttata taataatttc aatcaaaagt      1020
tcatcaggac aaaaaagctt gttttcaact gattcgactc tgatgatctt gggtcggttt      1080
aggacctgtc taagtttcaa tttgtgatta gctgcttctt gctatagett atgtgcgttc      1140
gttgtgtaaa ttgtgtgttt taaagacgat aagaaaaatga acaaaaaagg agtggggaat      1200
ggagtttgtt ggtgggtgat ggggggtttt gttattataa ttggttgatt tgtatatYt      1260
t
```

(2) INFORMATION FOR SEQ ID NO:849:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 280 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..280

(D) OTHER INFORMATION: / Ceres Seq. ID 1568161

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:849:

```
Met Gly Lys Phe Cys Cys Phe Thr Ser Ala Ser Glu Val Val Gly Gly
1 5 10 15
Gln Ser Ser Ser Arg Ser Gly Lys Gly Arg Ser Asp Glu Gly Met Ile
20 25 30
Lys Tyr Gly Phe Ser Leu Val Lys Gly Lys Ala Asn His Pro Met Glu
35 40 45
Asp Tyr His Val Ala Asn Phe Ile Asn Ile Gln Asp His Glu Leu Gly
50 55 60
Leu Phe Ala Ile Tyr Asp Gly His Met Gly Asp Ser Val Pro Ala Tyr
65 70 75 80
Leu Gln Lys Arg Leu Phe Ser Asn Ile Leu Lys Glu Gly Glu Phe Trp
85 90 95
Val Asp Pro Arg Arg Ser Ile Ala Lys Ala Tyr Glu Lys Thr Glu Ala
100 105 110
Ile Leu Ser Asn Ser Ser Asp Leu Gly Arg Gly Gly Ser Thr Ala Val
115 120 125
```

Thr Ala Ile Leu Ile Asn Gly Arg Lys Leu Trp Ile Ala Asn Val Gly
130 135 140
Asp Ser Arg Ala Val Leu Ser His Gly Gly Ala Ile Thr Gln Met Ser
145 150 155 160
Thr Asp His Glu Pro Arg Thr Glu Arg Ser Ser Ile Glu Asp Arg Gly
165 170 175
Gly Phe Val Ser Asn Leu Pro Gly Asp Val Pro Arg Val Asn Gly Gln
180 185 190
Leu Ala Val Ser Arg Ala Phe Gly Asp Lys Gly Leu Lys Thr His Leu
195 200 205
Ser Ser Glu Pro Asp Ile Lys Glu Ala Thr Val Asp Ser Gln Thr Asp
210 215 220
Val Leu Leu Leu Ala Ser Asp Gly Ile Trp Lys Val Met Thr Asn Glu
225 230 235 240
Glu Ala Met Glu Ile Ala Arg Arg Val Lys Asp Pro Gln Lys Ala Ala
245 250 255
Lys Glu Leu Thr Ala Glu Ala Leu Arg Arg Glu Ser Lys Asp Ile
260 265 270
Ser Cys Val Val Val Arg Phe Arg
275 280

(2) INFORMATION FOR SEQ ID NO:850:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 250 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..250

(D) OTHER INFORMATION: / Ceres Seq. ID 1568162

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:850:

Met Ile Lys Tyr Gly Phe Ser Leu Val Lys Gly Lys Ala Asn His Pro
1 5 10 15
Met Glu Asp Tyr His Val Ala Asn Phe Ile Asn Ile Gln Asp His Glu
20 25 30
Leu Gly Leu Phe Ala Ile Tyr Asp Gly His Met Gly Asp Ser Val Pro
35 40 45
Ala Tyr Leu Gln Lys Arg Leu Phe Ser Asn Ile Leu Lys Glu Gly Glu
50 55 60
Phe Trp Val Asp Pro Arg Arg Ser Ile Ala Lys Ala Tyr Glu Lys Thr
65 70 75 80
Glu Ala Ile Leu Ser Asn Ser Ser Asp Leu Gly Arg Gly Ser Thr
85 90 95
Ala Val Thr Ala Ile Leu Ile Asn Gly Arg Lys Leu Trp Ile Ala Asn
100 105 110
Val Gly Asp Ser Arg Ala Val Leu Ser His Gly Gly Ala Ile Thr Gln
115 120 125
Met Ser Thr Asp His Glu Pro Arg Thr Glu Arg Ser Ser Ile Glu Asp
130 135 140
Arg Gly Gly Phe Val Ser Asn Leu Pro Gly Asp Val Pro Arg Val Asn
145 150 155 160
Gly Gln Leu Ala Val Ser Arg Ala Phe Gly Asp Lys Gly Leu Lys Thr
165 170 175
His Leu Ser Ser Glu Pro Asp Ile Lys Glu Ala Thr Val Asp Ser Gln
180 185 190
Thr Asp Val Leu Leu Leu Ala Ser Asp Gly Ile Trp Lys Val Met Thr
195 200 205
Asn Glu Glu Ala Met Glu Ile Ala Arg Arg Val Lys Asp Pro Gln Lys
210 215 220
Ala Ala Lys Glu Leu Thr Ala Glu Ala Leu Arg Arg Glu Ser Lys Asp

(2) INFORMATION FOR SEO ID NO:851:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 234 amino ac

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: \lim

MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1 234

(D) OTHER INFORMATION: / Ceres Seq. ID 1568163

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:851:

[illegible]

(2) INFORMATION FOR SEO ID NO:852:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1128 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1128

(D) OTHER INFORMATION: / Ceres Seq. ID 1568176

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:852:

acacatacaa	gactctctc	acagaacgat	ttagatttaa	tccggaaaaa	gttcagtcag	60
tgacataaat	gttcgaatcg	aacatgggtc	tccaaacact	atctctctct	tctcctccaa	120
tccaccgtct	ctatcttcac	catcttcaga	tctctccctc	tcttcgggtca	cccagcaaga	180
ttctctctca	gatacatgga	aagactcttg	ccatctgac	ttctctgtac	cttcattttg	240

cagaaatttc	tgctagaggt	ttaccggcgt	tgaacaaagc	ttccttgaag	aagctaccaa	300
tcaaaggatc	tacottttctg	ctggggcgaga	gcttgttgat	ggttttctgct	caccacagct	360
tggcagcagc	agcagaaatc	ataaagcctt	aaccgattta	cgAagttgga	gagttatttg	420
aacttagtat	tcagctttct	tacttgctgt	tactactggg	gttgcttggg	gttggtactt	480
tctatgtgat	cogtcaagta	ctgttacgca	gagaactaga	cctctccgct	aaagaattgc	540
aggagcaagt	aaggagcgga	gatgcaaagt	caacagagct	ctttgagctt	ggcgagctga	600
tgttgaggaa	gtttttatcct	gcagccaaca	agtttttgca	acaagctatc	cagaaatggg	660
acgggtgatga	tcaagatcct	gctcaggtct	ataacgctct	tgagtgagtg	tatgtacgag	720
aggataaact	tgacaaagga	attgctcagt	ttgaaatggc	ggtagaagctg	caaccggggt	780
atgtaacagc	ttggaacaac	cttggggatg	cttatgagaa	gaagaaggag	ttgcctttgg	840
cattgaatgc	gtttgaagaa	gtttttgtgt	ttgatccaaa	caataagggtg	gctcgccoty	900
ggcgagatgc	gttgaaggat	cgctggaagc	tttataaagg	gtttgtggct	gttaagctca	960
agaaacgggtg	acggctcaaa	caagatgcaa	actctgaacc	aagaacgggt	ggctctcttc	1020
ccctctgtgt	atttttttgg	tttggttaata	tgtatggaga	ttttgtgtta	atatgaaaat	1080
gaaaactttgt	tgttttttgt	aaccaataaa	atcagatggt	taaaactt		

(2) INFORMATION FOR SEQ ID NO:853:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 322 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..322

(D) OTHER INFORMATION: / Ceres Seq. ID 1568177

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:853:

Thr	Tyr	Lys	Thr	Leu	Leu	Thr	Glu	Arg	Phe	Arg	Phe	Asn	Arg	Glu	Lys
1			5					10						15	
Val	Gln	Ser	Val	Thr	Leu	Met	Phe	Glu	Ser	Asn	Met	Val	Leu	Gln	Thr
			20					25					30		
Leu	Ser	Ser	Ser	Pro	Pro	Ile	His	Arg	Leu	Tyr	Leu	His	His	Ser	
			35				40					45			
Gln	Ile	Leu	Pro	Ser	Ser	Gly	Ser	Pro	Ser	Lys	Ile	Ser	Leu	Gln	Ile
			50			55					60				
His	Gly	Arg	Thr	Leu	Ala	Ile	Arg	Ser	Phe	His	Asp	Tyr	Val	Phe	Ala
			65			70				75				80	
Glu	Ile	Ser	Ala	Arg	Gly	Leu	Pro	Ala	Leu	Asn	Lys	Ala	Ser	Leu	Lys
			85						90				95		
Lys	Leu	Pro	Ile	Lys	Gly	Ser	Thr	Phe	Leu	Leu	Gly	Gln	Ser	Leu	Leu
			100				105					110			
Met	Val	Ser	Ala	His	Pro	Gln	Leu	Ala	Ala	Ala	Ala	Glu	Ile	Ile	Lys
			115			120						125			
Pro	Glu	Pro	Ile	Tyr	Glu	Val	Gly	Glu	Leu	Phe	Glu	Leu	Ser	Ile	Gln
			130			135					140				
Leu	Ser	Tyr	Leu	Leu	Leu	Leu	Gly	Leu	Leu	Gly	Val	Gly	Thr	Phe	
			145			150				155				160	
Tyr	Val	Ile	Arg	Gln	Val	Leu	Val	Arg	Arg	Glu	Leu	Asp	Leu	Ser	Ala
			165						170					175	
Lys	Glu	Leu	Gln	Glu	Gln	Val	Arg	Ser	Gly	Asp	Ala	Ser	Ala	Thr	Glu
			180				185					190			
Leu	Phe	Glu	Leu	Gly	Ala	Val	Met	Leu	Arg	Lys	Phe	Tyr	Pro	Ala	Ala
			195			200					205				
Asn	Lys	Phe	Leu	Gln	Gln	Ala	Ile	Gln	Lys	Trp	Asp	Gly	Asp	Asp	Gln
			210			215					220				
Asp	Leu	Ala	Gln	Val	Tyr	Asn	Ala	Leu	Gly	Val	Ser	Tyr	Val	Arg	Glu
			225			230				235				240	
Asp	Lys	Leu	Asp	Lys	Gly	Ile	Ala	Gln	Phe	Glu	Met	Ala	Val	Lys	Leu
			245						250					255	
Gln	Pro	Gly	Tyr	Val	Thr	Ala	Trp	Asn	Asn	Leu	Gly	Asp	Ala	Tyr	Glu
			260					265						270	

Lys Lys Lys Glu Leu Pro Leu Ala Leu Asn Ala Phe Glu Glu Val Leu
275 280 285
Leu Phe Asp Pro Asn Asn Lys Val Ala Arg Pro Xaa Arg Asp Ala Leu
290 295 300
Lys Asp Arg Val Lys Leu Tyr Lys Gly Val Val Ala Val Lys Ser Lys
305 310 315 320
Lys Arg

(2) INFORMATION FOR SEQ ID NO:854:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 300 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..300

(D) OTHER INFORMATION: / Ceres Seq. ID 1568178

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:854:

Met Phe Glu Ser Asn Met Val Leu Gln Thr Leu Ser Ser Ser Ser Pro
1 5 10 15
Pro Ile His Arg Leu Tyr Leu His His Ser Gln Ile Leu Pro Ser Ser
20 25 30
Gly Ser Pro Ser Lys Ile Ser Leu Gln Ile His Gly Arg Thr Leu Ala
35 40 45
Ile Arg Ser Phe His Asp Tyr Val Phe Ala Glu Ile Ser Ala Arg Gly
50 55 60
Leu Pro Ala Leu Asn Lys Ala Ser Leu Lys Lys Leu Pro Ile Lys Gly
65 70 75 80
Ser Thr Phe Leu Leu Gly Gln Ser Leu Leu Met Val Ser Ala His Pro
85 90 95
Gln Leu Ala Ala Ala Ala Glu Ile Ile Lys Pro Glu Pro Ile Tyr Glu
100 105 110
Val Gly Glu Leu Phe Glu Leu Ser Ile Gln Leu Ser Tyr Leu Leu Leu
115 120 125
Leu Leu Gly Leu Leu Gly Val Gly Thr Phe Tyr Val Ile Arg Gln Val
130 135 140
Leu Val Arg Arg Glu Leu Asp Leu Ser Ala Lys Glu Leu Gln Glu Gln
145 150 155 160
Val Arg Ser Gly Asp Ala Ser Ala Thr Glu Leu Phe Glu Leu Gly Ala
165 170 175
Val Met Leu Arg Lys Phe Tyr Pro Ala Ala Asn Lys Phe Leu Gln Gln
180 185 190
Ala Ile Gln Lys Trp Asp Gly Asp Asp Gln Asp Leu Ala Gln Val Tyr
195 200 205
Asn Ala Leu Gly Val Ser Tyr Val Arg Glu Asp Lys Leu Asp Lys Gly
210 215 220
Ile Ala Gln Phe Glu Met Ala Val Lys Leu Gln Pro Gly Tyr Val Thr
225 230 235 240
Ala Trp Asn Asn Leu Gly Asp Ala Tyr Glu Lys Lys Lys Glu Leu Pro
245 250 255
Leu Ala Leu Asn Ala Phe Glu Glu Val Leu Leu Phe Asp Pro Asn Asn
260 265 270
Lys Val Ala Arg Pro Xaa Arg Asp Ala Leu Lys Asp Arg Val Lys Leu
275 280 285
Tyr Lys Gly Val Val Ala Val Lys Ser Lys Lys Arg
290 295 300

(2) INFORMATION FOR SEQ ID NO:855:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 295 amino acids

- (B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..295
 (D) OTHER INFORMATION: / Ceres Seq. ID 1568179
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:855:

Met	Val	Leu	Gln	Thr	Leu	Ser	Ser	Ser	Ser	Pro	Pro	Ile	His	Arg	Leu
1			5						10					15	
Tyr	Leu	His	His	Ser	Gln	Ile	Leu	Pro	Ser	Ser	Gly	Ser	Pro	Ser	Lys
			20				25						30		
Ile	Ser	Leu	Gln	Ile	His	Gly	Arg	Thr	Leu	Ala	Ile	Arg	Ser	Phe	His
			35				40					45			
Asp	Tyr	Val	Phe	Ala	Glu	Ile	Ser	Ala	Arg	Gly	Leu	Pro	Ala	Leu	Asn
	50					55				60					
Lys	Ala	Ser	Leu	Lys	Lys	Leu	Pro	Ile	Lys	Gly	Ser	Thr	Phe	Leu	Leu
65					70				75					80	
Gly	Gln	Ser	Leu	Leu	Met	Val	Ser	Ala	His	Pro	Gln	Leu	Ala	Ala	Ala
				85					90					95	
Ala	Glu	Ile	Ile	Lys	Pro	Glu	Pro	Ile	Tyr	Glu	Val	Gly	Glu	Leu	Phe
			100					105					110		
Glu	Leu	Ser	Ile	Gln	Leu	Ser	Tyr	Leu	Leu	Leu	Leu	Gly	Leu	Leu	
			115				120					125			
Gly	Val	Gly	Thr	Phe	Tyr	Val	Ile	Arg	Gln	Val	Leu	Val	Arg	Arg	Glu
	130					135					140				
Leu	Asp	Leu	Ser	Ala	Lys	Glu	Leu	Gln	Glu	Gln	Val	Arg	Ser	Gly	Asp
	145				150				155					160	
Ala	Ser	Ala	Thr	Glu	Leu	Phe	Glu	Leu	Gly	Ala	Val	Met	Leu	Arg	Lys
			165					170					175		
Phe	Tyr	Pro	Ala	Ala	Asn	Lys	Phe	Leu	Gln	Gln	Ala	Ile	Gln	Lys	Trp
			180				185						190		
Asp	Gly	Asp	Asp	Gln	Asp	Leu	Ala	Gln	Val	Tyr	Asn	Ala	Leu	Gly	Val
	195					200					205				
Ser	Tyr	Val	Arg	Glu	Asp	Lys	Leu	Asp	Lys	Gly	Ile	Ala	Gln	Phe	Glu
	210					215					220				
Met	Ala	Val	Lys	Leu	Gln	Pro	Gly	Tyr	Val	Thr	Ala	Trp	Asn	Asn	Leu
225					230					235				240	
Gly	Asp	Ala	Tyr	Glu	Lys	Lys	Lys	Glu	Leu	Pro	Leu	Ala	Leu	Asn	Ala
			245					250					255		
Phe	Glu	Glu	Val	Leu	Leu	Phe	Asp	Pro	Asn	Asn	Lys	Val	Ala	Arg	Pro
			260				265						270		
Xaa	Arg	Asp	Ala	Leu	Lys	Asp	Arg	Val	Lys	Leu	Tyr	Lys	Gly	Val	Val
		275					280						285		
Ala	Val	Lys	Ser	Lys	Lys	Arg									
	290				295										

(2) INFORMATION FOR SEQ ID NO:856:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1525 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
 (A) NAME/KEY: -
 (B) LOCATION: 1..1525
 (D) OTHER INFORMATION: / Ceres Seq. ID 1568180

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:856:

gaatgctgct	tacctcatgt	gatgctcgta	tcattcccag	ggcaaggctca	cataagccct	60
ctctcttcgtc	toggaaagat	catgctctct	aaaggcttaa	togtcacctt	tgtaaccaca	120

gaggaacccat tgggcaagaa gatgcgtcaa gccacaata ttcaagacgg tgtgctcaaa 180
ccggctcgggc taggttttct ccggttccag tcttccgagg atggatttgt ctacaagaaga 240
gactttgatt tgttacaata atcacttgaa gtttccggaa aacgagagat caagaattctt 300
gtcaagaana atgagaagca accagtgaga tgtctcataa ataagtccct tgttccatgg 360
gtttgtgaca tagccgagga gcttcaaatc ccatcagctg tttctttgggt ccagtccttgt 420
gcttgcctcg ccgcttatta ctattaccac caccagttag ttaagtcttc gaccgaiaacc 480
gagccggaaa taaccggtga cgtcccttcc aagccattaa aattgaagca tgacgagSat 540
ccctagcttt cttcacccct cctctccgct gtctctcata ggaggtacca ttttagagca 600
gatcaagcga cttcacaagc ctttctctgt tctcatcgaa acttttcaag aacttgaaaa 660
agataccatt gaccacatgt cccagctctg cctccaagtc aacttcaacc ccatcggtcc 720
gctttttact atggctaaaa ccataaggtc tgacatcaag ggagacatct ccaagccaga 780
tagtgactgc atagagtgag ttcaactcga agaaccatcc tccgtttgtt acatctcttt 840
tgggactttg gctttcttga agcaaaacca gatcgacgag attgctcaeg gcattctcaa 900
ctccgggttg tctgtcttat ggggttttgc tctctcccta gaaggcttag ccatagaacc 960
acatgtcttg cctctagagc ttgaagagaa agggaaagatt gtggaaatgt gtcaacaaga 1020
gaaAGYtttg gctcatcctg ccggttgcttg cttcttaagt cactgtggat ggaactcaac 1080
catggaggct ttaacttcag gacttccctg tatttgttcc ccgagtgagg gagatcaggt 1140
gacaaatgag ggtgacctga ttgtgttttt caagacagga ttgagactca gccgtggagg 1200
ttctgatgag aggattgttc caaggaggga ggttgctgag cgaactgttg agggcaccgt 1260
tgagagaagc gcggtggagc tgagagaaaa ccgtcggagg tggaaggagg agggcgagtc 1320
tgccgtggct tacggtggaa catcggaagc gaattttcaa gatttgtgtt acaagtttgtt 1380
tgatgtcaag acaatgacaa acattataaa tgtctgttaa gtctgaata tcatattgat 1440
acttgttatt accgatttat gatttttaat tgtttaatat gtactaaatt gtatgcatcg 1500
atataaagtg aacaatttta tgttg

(2) INFORMATION FOR SEQ ID NO:857:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 296 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..296

(D) OTHER INFORMATION: / Ceres Seq. ID 1568181

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:857:

Met	Thr	Xaa	Ile	Pro	Ser	Phe	Leu	His	Pro	Ser	Pro	Leu	Ser	Ser
1				5				10					15	
Ile	Gly	Gly	Thr	Ile	Leu	Glu	Gln	Ile	Lys	Arg	Leu	His	Lys	Pro
			20					25					30	Phe
Ser	Val	Leu	Ile	Glu	Thr	Phe	Gln	Glu	Leu	Glu	Lys	Asp	Thr	Ile
			35				40					45		Asp
His	Met	Ser	Gln	Leu	Cys	Pro	Gln	Val	Asn	Phe	Asn	Pro	Ile	Gly
			50				55					60		Pro
Leu	Phe	Thr	Met	Ala	Lys	Thr	Ile	Arg	Ser	Asp	Ile	Lys	Gly	Asp
			65				70					75		Ile
Ser	Lys	Pro	Asp	Ser	Asp	Cys	Ile	Glu	Trp	Leu	His	Ser	Arg	Glu
			85					90					95	Pro
Ser	Ser	Val	Val	Tyr	Ile	Ser	Phe	Gly	Thr	Leu	Ala	Phe	Leu	Lys
			100					105					110	Gln
Asn	Gln	Ile	Asp	Glu	Ile	Ala	His	Gly	Ile	Leu	Asn	Ser	Gly	Leu
			115				120					125		Ser
Cys	Leu	Trp	Val	Leu	Arg	Pro	Pro	Leu	Glu	Gly	Leu	Ala	Ile	Glu
			130				135					140		Pro
His	Val	Leu	Pro	Leu	Glu	Leu	Glu	Glu	Lys	Gly	Lys	Ile	Val	Glu
			145				150				155			Trp
Cys	Gln	Gln	Glu	Lys	Xaa	Leu	Ala	His	Pro	Ala	Val	Ala	Cys	Phe
			165					170				175		Leu
Ser	His	Cys	Gly	Trp	Asn	Ser	Thr	Met	Glu	Ala	Leu	Thr	Ser	Gly
			180					185				190		Val
Pro	Val	Ile	Cys	Phe	Pro	Gln	Trp	Gly	Asp	Gln	Val	Thr	Asn	Ala
														Val

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	195		200		205
Tyr	Leu	Ile	Gly	Val	Phe
210					Lys
Ser	Asp	Glu	Arg	Ile	Val
225					Pro
Glu	Ala	Thr	Val	Gly	Glu
					230
Arg	Trp	Lys	Glu	Ala	Glu
					245
Glu	Arg	Asn	Phe	Gln	Glu
					260
Met	Thr	Asn	Ile	Asn	Asn
					275
					290
					295

(2) INFORMATION FOR SEQ ID NO:858:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 247 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..247
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568182

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:858:

Met	Ser	Gln	Leu	Cys	Pro	Gln	Val	Asn	Phe	Asn	Pro	Ile	Gly	Pro	Leu
1				5							10			15	
Phe	Thr	Met	Ala	Lys	Thr	Ile	Arg	Ser	Asp	Ile	Lys	Gly	Asp	Ile	Ser
			20					25					30		
Lys	Pro	Asp	Ser	Asp	Cys	Ile	Glu	Trp	Leu	His	Ser	Arg	Glu	Pro	Ser
			35				40					45			
Ser	Val	Val	Tyr	Ile	Ser	Phe	Gly	Thr	Leu	Ala	Phe	Leu	Lys	Gln	Asn
			50			55					60				
Gln	Ile	Asp	Glu	Ile	Ala	His	Gly	Ile	Leu	Asn	Ser	Gly	Leu	Ser	Cys
65				70					75					80	
Leu	Trp	Val	Leu	Arg	Pro	Pro	Leu	Glu	Gly	Leu	Ala	Ile	Glu	Pro	His
			85						90				95		
Val	Leu	Pro	Leu	Glu	Leu	Glu	Glu	Lys	Gly	Lys	Ile	Val	Glu	Trp	Cys
			100					105					110		
Gln	Gln	Glu	Lys	Xaa	Leu	Ala	His	Pro	Ala	Val	Ala	Cys	Phe	Leu	Ser
			115				120					125			
His	Cys	Gly	Trp	Asn	Ser	Thr	Met	Glu	Ala	Leu	Thr	Ser	Gly	Val	Pro
130						135					140				
Val	Ile	Cys	Phe	Pro	Gln	Trp	Gly	Asp	Gln	Val	Thr	Asn	Ala	Val	Tyr
145					150				155						160
Leu	Ile	Gly	Val	Phe	Lys	Thr	Gly	Leu	Arg	Leu	Ser	Arg	Gly	Ala	Ser
			165						170					175	
Asp	Glu	Arg	Ile	Val	Pro	Arg	Glu	Glu	Val	Ala	Glu	Arg	Leu	Leu	Glu
			180					185					190		
Ala	Thr	Val	Gly	Glu	Lys	Ala	Val	Glu	Leu	Arg	Glu	Asn	Ala	Arg	Arg
			195				200					205			
Trp	Lys	Glu	Glu	Ala	Glu	Ser	Ala	Val	Ala	Tyr	Gly	Gly	Thr	Ser	Glu
210						215					220				
Arg	Asn	Phe	Gln	Glu	Phe	Val	Asp	Lys	Leu	Val	Asp	Val	Lys	Thr	Met
225				230					235						240
Thr	Asn	Ile	Asn	Asn	Val	Val									
				245											

(2) INFORMATION FOR SEQ ID NO:859:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 229 amino acids
- (B) TYPE: amino acid

(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..229
 (D) OTHER INFORMATION: / Ceres Seq. ID 1568183
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:859:
Met Ala Lys Thr Ile Arg Ser Asp Ile Lys Gly Asp Ile Ser Lys Pro
1 5 10 15
Asp Ser Asp Cys Ile Glu Trp Leu His Ser Arg Glu Pro Ser Ser Val
 20 25 30
Val Tyr Ile Ser Phe Gly Thr Leu Ala Phe Leu Lys Gln Asn Gln Ile
 35 40 45
Asp Glu Ile Ala His Gly Ile Leu Asn Ser Gly Leu Ser Cys Leu Trp
 50 55 60
Val Leu Arg Pro Pro Leu Glu Gly Leu Ala Ile Glu Pro His Val Leu
 65 70 75 80
Pro Leu Glu Leu Glu Glu Lys Gly Lys Ile Val Glu Trp Cys Gln Gln
 85 90 95
Glu Lys Xaa Leu Ala His Pro Ala Val Ala Cys Phe Leu Ser His Cys
 100 105 110
Gly Trp Asn Ser Thr Met Glu Ala Leu Thr Ser Gly Val Pro Val Ile
 115 120 125
Cys Phe Pro Gln Trp Gly Asp Gln Val Thr Asn Ala Val Tyr Leu Ile
 130 135 140
Gly Val Phe Lys Thr Gly Leu Arg Leu Ser Arg Gly Ala Ser Asp Glu
 145 150 155 160
Arg Ile Val Pro Arg Glu Glu Val Ala Glu Arg Leu Leu Glu Ala Thr
 165 170 175
Val Gly Glu Lys Ala Val Glu Leu Arg Glu Asn Ala Arg Arg Trp Lys
 180 185 190
Glu Glu Ala Glu Ser Ala Val Ala Tyr Gly Gly Thr Ser Glu Arg Asn
 195 200 205
Phe Gln Glu Phe Val Asp Lys Leu Val Asp Val Lys Thr Met Thr Asn
 210 215 220
Ile Asn Asn Val Val
225

(2) INFORMATION FOR SEQ ID NO:860:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1295 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..1295
(D) OTHER INFORMATION: / Ceres Seq. ID 1568184
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:860:

aaaacaaaaa aacacagcct ttgtttcgtt tctctgcgat ttcttcgatt ttctctttct 60
tcgttttgat ttccagattt gtttaactcg gtcgttgccg tgacttcaaa ttctctaaaa 120
gagagagaga gagagagagg agatagtcca gaaaatctgt cagacttggg atctttctcg 180
gcaatgcgac gctttgtcgc cgcgaaatcc ctctcccgag aggatacaac ctttttgtca 240
ttctctttct ctctcggtgac gcggtttctc aaggctcttc ctctccggtc agatccaaga 300
gatgtccgct aattctcatc ctccctaatt caaaaacgct ctctgtaalg cagcgcgcgg 360
tgccgcgcgc ggggtttgttg cggctacggt ttgtgtctct ctgtgatgta taataacgag 420
gttttcaggt catgggctgc ctaagctcgg tgatgcaaac atcaaaagta gtctaatgtt 480
tggcagctct gagcagatct tcaagagaga agggatgcgt ggcctatacc gcggtctctc 540
ccctactgtc atggctcttc tctccaattg gccattttt ttacaaatgt atgaccagct 600
caagagcttt ctttgttcaa atgatcacia actcagcggtt ggagctaacg tattgtcgtc 660

ttcgggagct	ggagctgc	ctaccattgc	cacaaatcct	ctttgggtgc	tcaagactag	720
acttcagaca	caaggaaatga	gagtggtgat	agtgccatag	aaaagcacat	tttctgcttt	780
aaggagaata	gcttatgagg	agggaaattcg	cggtattgtac	agtggtcttg	tcctcgactg	840
agctggtatc	agtcgatgtg	ccattcagtt	tccacacatg	gagatgatca	aagtgtactt	900
ggccaaagaa	ggtgataaat	cagtcgataa	cctcaatgct	cggtgatgtg	cagttgcctc	960
ttcgattgca	aagatatattg	catccacatt	aacttaccgc	cacgaggtag	tacgagctag	1020
gcttcaagag	caagggcacc	acagtgagaa	acgttactca	ggagtaagag	attgcatcaa	1080
gaaagtgttt	gagaaagatg	ggttccttgg	ttttacaga	ggCtgcgcga	cgaacttact	1140
gagacaaact	cctgcagcag	ttataacttt	cactagcttc	gaaatggtgc	atcgtttctt	1200
cgctcactat	ataccttctg	agcaaaagctc	tatactttaa	atccggtttt	ttttttttga	1260
tgatgatgac	gattaaaaag	tatttttaca	caggt			

(2) INFORMATION FOR SEQ ID NO:861:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 312 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..312
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568185

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:861:

Met	Ser	Ala	Asn	Ser	His	Pro	Pro	Asn	Ser	Lys	Asn	Val	Leu	Cys	Asn
1			5						10					15	
Ala	Ala	Ala	Gly	Ala	Ala	Ala	Gly	Val	Ala	Ala	Thr	Phe	Val	Cys	
			20					25				30			
Pro	Leu	Asp	Val	Ile	Lys	Thr	Arg	Phe	Gln	Val	His	Gly	Leu	Pro	Lys
		35					40				45				
Leu	Gly	Asp	Ala	Asn	Ile	Lys	Gly	Ser	Leu	Ile	Val	Gly	Ser	Leu	Glu
		50				55					60				
Gln	Ile	Phe	Lys	Arg	Glu	Gly	Met	Arg	Gly	Leu	Tyr	Arg	Gly	Leu	Ser
		65			70				75					80	
Pro	Thr	Val	Met	Ala	Leu	Leu	Ser	Asn	Trp	Ala	Ile	Tyr	Phe	Thr	Met
			85					90						95	
Tyr	Asp	Gln	Leu	Lys	Ser	Phe	Leu	Cys	Ser	Asn	Asp	His	Lys	Leu	Ser
			100					105					110		
Val	Gly	Ala	Asn	Val	Leu	Ala	Ala	Ser	Gly	Ala	Gly	Ala	Ala	Thr	Thr
			115				120					125			
Ile	Ala	Thr	Asn	Pro	Leu	Trp	Val	Val	Lys	Thr	Arg	Leu	Gln	Thr	Gln
			130			135					140				
Gly	Met	Arg	Val	Gly	Ile	Val	Pro	Tyr	Lys	Ser	Thr	Phe	Ser	Ala	Leu
		145			150					155				160	
Arg	Arg	Ile	Ala	Tyr	Glu	Glu	Gly	Ile	Arg	Gly	Leu	Tyr	Ser	Gly	Leu
			165					170						175	
Val	Pro	Ala	Leu	Ala	Gly	Ile	Ser	His	Val	Ala	Ile	Gln	Phe	Pro	Thr
			180				185						190		
Tyr	Glu	Met	Ile	Lys	Val	Tyr	Leu	Ala	Lys	Lys	Gly	Asp	Lys	Ser	Val
		195					200					205			
Asp	Asn	Leu	Asn	Ala	Arg	Asp	Val	Ala	Val	Ala	Ser	Ser	Ile	Ala	Lys
		210			215					220					
Ile	Phe	Ala	Ser	Thr	Leu	Thr	Tyr	Pro	His	Glu	Val	Val	Arg	Ala	Arg
			225		230				235					240	
Leu	Gln	Glu	Gln	Gly	His	His	Ser	Glu	Lys	Arg	Tyr	Ser	Gly	Val	Arg
			245					250						255	
Asp	Cys	Ile	Lys	Lys	Val	Phe	Glu	Lys	Asp	Gly	Phe	Pro	Gly	Phe	Tyr
			260				265						270		
Arg	Gly	Cys	Ala	Thr	Asn	Leu	Leu	Arg	Thr	Thr	Pro	Ala	Ala	Val	Ile
		275				280						285			
Thr	Phe	Thr	Ser	Phe	Glu	Met	Val	His	Arg	Phe	Leu	Val	Thr	His	Ile
		290				295					300				

Pro Ser Glu Gln Ser Ser Ile Leu
305 310

(2) INFORMATION FOR SEQ ID NO:862:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 241 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..241
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568186

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:862:

Met	Arg	Gly	Leu	Tyr	Arg	Gly	Leu	Ser	Pro	Thr	Val	Met	Ala	Leu	Leu
1			5						10					15	
Ser	Asn	Trp	Ala	Ile	Tyr	Phe	Thr	Met	Tyr	Asp	Gln	Leu	Lys	Ser	Phe
		20						25					30		
Leu	Cys	Ser	Asn	Asp	His	Lys	Leu	Ser	Val	Gly	Ala	Asn	Val	Leu	Ala
		35					40					45			
Ala	Ser	Gly	Ala	Gly	Ala	Ala	Thr	Thr	Ile	Ala	Thr	Asn	Pro	Leu	Trp
	50					55					60				
Val	Val	Lys	Thr	Arg	Leu	Gln	Thr	Gln	Gly	Met	Arg	Val	Gly	Ile	Val
	65				70				75					80	
Pro	Tyr	Lys	Ser	Thr	Phe	Ser	Ala	Leu	Arg	Arg	Ile	Ala	Tyr	Glu	Glu
			85						90					95	
Gly	Ile	Arg	Gly	Leu	Tyr	Ser	Gly	Leu	Val	Pro	Ala	Leu	Ala	Gly	Ile
			100					105					110		
Ser	His	Val	Ala	Ile	Gln	Phe	Pro	Thr	Tyr	Glu	Met	Ile	Lys	Val	Tyr
		115					120					125			
Leu	Ala	Lys	Lys	Gly	Asp	Lys	Ser	Val	Asp	Asn	Leu	Asn	Ala	Arg	Asp
	130					135					140				
Val	Ala	Val	Ala	Ser	Ser	Ile	Ala	Lys	Ile	Phe	Ala	Ser	Thr	Leu	Thr
	145				150					155				160	
Tyr	Pro	His	Glu	Val	Val	Arg	Ala	Arg	Leu	Gln	Glu	Gln	Gly	His	His
			165						170					175	
Ser	Glu	Lys	Arg	Tyr	Ser	Gly	Val	Arg	Asp	Cys	Ile	Lys	Lys	Val	Phe
			180				185						190		
Glu	Lys	Asp	Gly	Phe	Pro	Gly	Phe	Tyr	Arg	Gly	Cys	Ala	Thr	Asn	Leu
		195				200					205				
Leu	Arg	Thr	Thr	Pro	Ala	Ala	Val	Ile	Thr	Phe	Thr	Ser	Phe	Glu	Met
	210					215					220				
Val	His	Arg	Phe	Leu	Val	Thr	His	Ile	Pro	Ser	Glu	Gln	Ser	Ser	Ile
	225				230					235					240
Leu															

(2) INFORMATION FOR SEQ ID NO:863:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 229 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..229
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568187

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:863:

Met	Ala	Leu	Leu	Ser	Asn	Trp	Ala	Ile	Tyr	Phe	Thr	Met	Tyr	Asp	Gln
1			5						10					15	
Leu	Lys	Ser	Phe	Leu	Cys	Ser	Asn	Asp	His	Lys	Leu	Ser	Val	Gly	Ala

20	25	30
Asn Val Leu Ala Ala Ser Gly Ala Gly Ala Ala Thr Thr Ile Ala Thr		
35	40	45
Asn Pro Leu Trp Val Val Lys Thr Arg Leu Gln Thr Gln Gly Met Arg		
50	55	60
Val Gly Ile Val Pro Tyr Lys Ser Thr Phe Ser Ala Leu Arg Arg Ile		
65	70	75
Ala Tyr Glu Glu Gly Ile Arg Gly Leu Tyr Ser Gly Leu Val Pro Ala		
85	90	95
Leu Ala Gly Ile Ser His Val Ala Ile Gln Phe Pro Thr Tyr Glu Met		
100	105	110
Ile Lys Val Tyr Leu Ala Lys Lys Gly Asp Lys Ser Val Asp Asn Leu		
115	120	125
Asn Ala Arg Asp Val Ala Val Ala Ser Ser Ile Ala Lys Ile Phe Ala		
130	135	140
Ser Thr Leu Thr Tyr Pro His Glu Val Val Arg Ala Arg Leu Gln Glu		
145	150	155
Gln Gly His His Ser Glu Lys Arg Tyr Ser Gly Val Arg Asp Cys Ile		
165	170	175
Lys Lys Val Phe Glu Lys Asp Gly Phe Pro Gly Phe Tyr Arg Gly Cys		
180	185	190
Ala Thr Asn Leu Leu Arg Thr Thr Pro Ala Ala Val Ile Thr Phe Thr		
195	200	205
Ser Phe Glu Met Val His Arg Phe Leu Val Thr His Ile Pro Ser Glu		
210	215	220
Gln Ser Ser Ile Leu		
225		

(2) INFORMATION FOR SEQ ID NO:864:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1302 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1302
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568188

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:864:

aagatttggg	tatttattga	accgagtggt	ttctttcgtt	gactcgccca	ccatggaagc	60
tgaagatacc	caagatatca	tcactgcgtg	agcttgaatc	tcgcgccttg	caactgcaat	120
tgggtctcac	aggcttggga	tcagaagcat	agtgctggaa	tcttctgagc	agctgagagc	180
aacagagattt	gcactttcat	tatatattta	tgcttggaa	gccatggaag	ctctcggtat	240
ttctcagcat	attcgcagtc	tcggtgatcg	cttccaagga	tgggtgtcca	gaccatttc	300
tgccaggagat	cctcctaaga	aaatgttatt	tccagaatct	gaagaatatg	aggttcgatg	360
catacagagg	aagctcttgt	tagacgctct	agcgggagaa	ttgcctcaag	ggaccatcac	420
gttctcatct	aagcttggtc	acatcgaaat	gtccggacac	tacaagatgg	ttcatctctc	480
cgacgggact	atacttaaaa	ccaagggttt	ggttaggggt	gatggagtga	agtcagtgtg	540
tggttaagtgc	ctagagcttca	agaatccgtg	taaaacttcc	cgtgtagcaa	tcgcgggagt	600
cgctcatttc	cagacagggcc	acgaattagg	gagaagggtc	tttcagtttt	attgccaacg	660
gtttcgttcc	gggtttcatct	catgtgacca	aaacactgtc	tactggttcc	taacccacac	720
ctctactgat	ttagataaga	aaaatcatca	gaagatcaaa	cagtttgtgc	tgaccaagat	780
caaaagacttg	cctgacaaca	tcaagagtat	cctggagacc	actgatcttg	atagtttgtt	840
gatgaatcca	ctcatgtatc	gacctccctg	ggaaacttct	tgggcaaaaa	gtgcaaaa	900
caacgtatgt	gttcgacggg	atgcacttca	cccgaatgac	cctgatattg	gacaagggtg	960
ttgctcggcg	atggagagac	gagttatctc	cgctcgttgt	ctcgggtga	caatgaaagc	1020
taagaatatg	aaaggtgaaa	cagaagatga	gaacgagagt	tataggcgga	ttgagagatg	1080
tttgaagaag	tatgcaggat	cgaggaaaat	gagaagcatt	gactcttata	ctacatcata	1140
tacagtaggt	ttcatacagc	agagcagagg	caagtggagt	acctttttat	gagacacagt	1200
catgtcctct	ttcctttctt	ggttgcKgtA	gYtgaaaaag	tctcatttca	actgtggaag	1260
acttagccat	gaatgattct	caatgagcaa	gcacaatggt	ag		

(2) INFORMATION FOR SEQ ID NO:865:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 409 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..409

(D) OTHER INFORMATION: / Ceres Seq. ID 1568189

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:865:

Lys Phe Gly Tyr Leu Leu Asn Arg Val Val Ser Phe Val Asp Ser Pro
1 5 10 15
Thr Met Glu Ala Glu Ser Thr Gln Asp Ile Ile Val Gly Ala Gly
20 25 30
Ile Ser Gly Leu Ala Thr Ala Leu Gly Leu His Arg Leu Gly Ile Arg
35 40 45
Ser Ile Val Leu Glu Ser Ser Glu Gln Leu Arg Ala Thr Gly Phe Ala
50 55 60
Leu Ser Leu Tyr Phe Asn Ala Trp Lys Ala Met Glu Ala Leu Gly Ile
65 70 75 80
Ser Gln His Ile Arg Ser Leu Gly Asp Arg Phe Gln Gly Trp Val Val
85 90 95
Arg Pro Ile Ser Ala Gly Asp Pro Pro Lys Glu Met Leu Phe Pro Glu
100 105 110
Ser Glu Glu Tyr Glu Val Arg Cys Ile Gln Arg Lys Leu Leu Asp
115 120 125
Ala Leu Ala Gly Glu Leu Pro Gln Gly Thr Ile Arg Phe Ser Ser Lys
130 135 140
Leu Val His Ile Glu Leu Ser Gly His Tyr Lys Met Val His Leu Ser
145 150 155 160
Asp Gly Thr Ile Leu Lys Thr Lys Val Leu Val Gly Cys Asp Gly Val
165 170 175
Lys Ser Val Val Gly Lys Trp Leu Gly Phe Lys Asn Pro Val Lys Thr
180 185 190
Ser Arg Val Ala Ile Arg Gly Ile Ala His Phe Gln Thr Gly His Glu
195 200 205
Leu Gly Arg Arg Phe Phe Gln Phe Tyr Gly Asn Gly Val Arg Ser Gly
210 215 220
Phe Ile Ser Cys Asp Gln Asn Thr Val Tyr Trp Phe Leu Thr His Thr
225 230 235 240
Ser Thr Asp Leu Asp Lys Lys Asn His Gln Lys Ile Lys Gln Phe Val
245 250 255
Leu Thr Lys Ile Lys Asp Leu Pro Asp Asn Ile Lys Ser Ile Leu Glu
260 265 270
Thr Thr Asp Leu Asp Ser Leu Val Met Asn Pro Leu Met Tyr Arg Pro
275 280 285
Pro Trp Glu Leu Leu Trp Ala Asn Ile Ala Lys Asp Asn Val Cys Val
290 295 300
Ala Gly Asp Ala Leu His Pro Met Thr Pro Asp Ile Gly Gln Gly Gly
305 310 315 320
Cys Ser Ala Met Glu Asp Gly Val Ile Leu Ala Arg Cys Leu Gly Glu
325 330 335
Ala Met Lys Ala Lys Asn Met Lys Gly Glu Thr Glu Asp Glu Asn Glu
340 345 350
Ser Tyr Arg Arg Ile Glu Asp Gly Leu Lys Lys Tyr Ala Gly Ser Arg
355 360 365
Lys Trp Arg Ser Ile Asp Leu Ile Thr Thr Ser Tyr Thr Val Gly Phe
370 375 380
Ile Gln Gln Ser Arg Gly Lys Trp Met Thr Leu Phe Arg Asp Lys Phe


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885                               390                               395                               400
Met Ser Ser Phe Leu Ser Trp Leu Xaa
      405
(2) INFORMATION FOR SEQ ID NO:866:
(i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 392 amino acids
    (B) TYPE: amino acid
    (C) STRANDEDNESS:
    (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
    (A) NAME/KEY: peptide
    (B) LOCATION: 1..392
    (D) OTHER INFORMATION: / Ceres Seq. ID I568I90
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:866:
Met Glu Ala Glu Ser Thr Gln Asp Ile Ile Val Gly Ala Gly Ile
1          5          10          15
Ser Gly Leu Ala Thr Ala Leu Gly Leu His Arg Leu Gly Ile Arg Ser
      20          25
Ile Val Leu Glu Ser Ser Glu Gln Leu Arg Ala Thr Gly Phe Ala Leu
      30          35
Ser Leu Tyr Phe Asn Ala Trp Lys Ala Met Glu Ala Leu Gly Ile Ser
      40          45
Gln His Ile Arg Ser Leu Gly Asp Arg Phe Gln Gly Trp Val Val Arg
      50          55          60          65          70          75          80
Pro Ile Ser Ala Gly Asp Pro Pro Lys Glu Met Leu Phe Pro Glu Ser
      85          90          95
Glu Glu Tyr Glu Val Arg Cys Ile Gln Arg Lys Leu Leu Leu Asp Ala
      100          105          110
Leu Ala Gly Glu Leu Pro Gln Gly Thr Ile Arg Phe Ser Ser Lys Leu
      115          120          125
Val His Ile Glu Leu Ser Gly His Tyr Lys Met Val His Leu Ser Asp
      130          135          140
Gly Thr Ile Leu Lys Thr Lys Val Leu Val Gly Cys Asp Gly Val Lys
      145          150          155          160
Ser Val Val Gly Lys Trp Leu Gly Phe Lys Asn Pro Val Lys Thr Ser
      165          170          175          180
Arg Val Ala Ile Arg Gly Ile Ala His Phe Gln Thr Gly His Glu Leu
      185          190          195
Gly Arg Arg Phe Phe Gln Phe Tyr Gly Asn Gly Val Arg Ser Gly Phe
      200          205
Ile Ser Cys Asp Gln Asn Thr Val Tyr Trp Phe Leu Thr His Thr Ser
      210          215          220
Thr Asp Leu Asp Lys Lys Asn His Gln Lys Ile Lys Gln Phe Val Leu
      225          230          235          240
Thr Lys Ile Lys Asp Leu Pro Asp Asn Ile Lys Ser Ile Leu Glu Thr
      245          250          255          260
Thr Asp Leu Asp Ser Leu Val Met Asn Pro Leu Met Tyr Arg Pro Pro
      265          270          275
Trp Glu Leu Leu Trp Ala Asn Ile Ala Lys Asp Asn Val Cys Val Ala
      280          285          290
Gly Asp Ala Leu His Pro Met Thr Pro Asp Ile Gly Gln Gly Gly Cys
      295          300          305
Ser Ala Met Glu Asp Gly Val Ile Leu Ala Arg Cys Leu Gly Glu Ala
      310          315          320
Met Lys Ala Lys Asn Met Lys Gly Glu Thr Glu Asp Glu Asn Glu Ser
      325          330          335
Tyr Arg Arg Ile Glu Asp Gly Leu Lys Lys Tyr Ala Gly Ser Arg Lys
      340          345          350          355
Trp Arg Ser Ile Asp Leu Ile Thr Thr Ser Tyr Thr Val Gly Phe Ile
      360          365

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Gln Gln Ser Arg Gly Lys Trp Met Thr Leu Phe Arg Asp Lys Phe Met
370 375 380
Ser Ser Phe Leu Ser Trp Leu Xaa
385 390

(2) INFORMATION FOR SEQ ID NO:867:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 335 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..335

(D) OTHER INFORMATION: / Ceres Seq. ID 1568191

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:867:

Met	Glu	Ala	Leu	Gly	Ile	Ser	Gln	His	Ile	Arg	Ser	Leu	Gly	Asp	Arg
1				5					10					15	
Phe	Gln	Gly	Trp	Val	Val	Arg	Pro	Ile	Ser	Ala	Gly	Asp	Pro	Pro	Lys
			20					25				30			
Glu	Met	Leu	Phe	Pro	Glu	Ser	Glu	Glu	Tyr	Glu	Val	Arg	Cys	Ile	Gln
		35					40					45			
Arg	Lys	Leu	Leu	Leu	Asp	Ala	Leu	Ala	Gly	Glu	Leu	Pro	Gln	Gly	Thr
		50				55					60				
Ile	Arg	Phe	Ser	Ser	Lys	Leu	Val	His	Ile	Glu	Leu	Ser	Gly	His	Tyr
65					70				75					80	
Lys	Met	Val	His	Leu	Ser	Asp	Gly	Thr	Ile	Leu	Lys	Thr	Lys	Val	Leu
			85						90					95	
Val	Gly	Cys	Asp	Gly	Val	Lys	Ser	Val	Val	Gly	Lys	Trp	Leu	Gly	Phe
			100					105					110		
Lys	Asn	Pro	Val	Lys	Thr	Ser	Arg	Val	Ala	Ile	Arg	Gly	Ile	Ala	His
			115				120					125			
Phe	Gln	Thr	Gly	His	Glu	Leu	Gly	Arg	Arg	Phe	Phe	Gln	Phe	Tyr	Gly
		130				135						140			
Asn	Gly	Val	Arg	Ser	Gly	Phe	Ile	Ser	Cys	Asp	Gln	Asn	Thr	Val	Tyr
145					150				155					160	
Trp	Phe	Leu	Thr	His	Thr	Ser	Thr	Asp	Leu	Asp	Lys	Lys	Asn	His	Gln
			165					170						175	
Lys	Ile	Lys	Gln	Phe	Val	Leu	Thr	Lys	Ile	Lys	Asp	Leu	Pro	Asn	Asn
			180					185					190		
Ile	Lys	Ser	Ile	Leu	Glu	Thr	Thr	Asp	Leu	Asp	Ser	Leu	Val	Met	Asn
			195				200					205			
Pro	Leu	Met	Tyr	Arg	Pro	Pro	Trp	Glu	Leu	Leu	Trp	Ala	Asn	Ile	Ala
			210			215					220				
Lys	Asp	Asn	Val	Cys	Val	Ala	Gly	Asp	Ala	Leu	His	Pro	Met	Thr	Pro
225					230				235					240	
Asp	Ile	Gly	Gln	Gly	Gly	Cys	Ser	Ala	Met	Glu	Asp	Gly	Val	Ile	Leu
			245						250					255	
Ala	Arg	Cys	Leu	Gly	Glu	Ala	Met	Lys	Ala	Lys	Asn	Met	Lys	Gly	Glu
			260				265						270		
Thr	Glu	Asp	Glu	Asn	Glu	Ser	Tyr	Arg	Arg	Ile	Glu	Asp	Gly	Leu	Lys
			275				280					285			
Lys	Tyr	Ala	Gly	Ser	Arg	Lys	Trp	Arg	Ser	Ile	Asp	Leu	Ile	Thr	Thr
			290			295					300				
Ser	Tyr	Thr	Val	Gly	Phe	Ile	Gln	Gln	Ser	Arg	Gly	Lys	Trp	Met	Thr
305					310					315				320	
Leu	Phe	Arg	Asp	Lys	Phe	Met	Ser	Ser	Phe	Leu	Ser	Trp	Leu	Xaa	
			325						330					335	

(2) INFORMATION FOR SEQ ID NO:868:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1364 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:

(A) NAME/KEY: -
(B) LOCATION: 1..1364
(D) OTHER INFORMATION: / Ceres Seq. ID 1568192

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:868:

cwywyactct	ctctttctcc	ttagcttctc	cttcaagggt	tttttgaaaa	gctgcaaaatt	60
tccatagcca	tggacactgc	taaatggcct	caggagtttg	ttgtgaagcc	aatgaacgag	120
atcgtgacaa	acacatgcct	aaaacaacag	tcgaatccct	cttctcctgc	tactctctgt	180
gaaaggaagg	caagaccgga	gaaagaccag	gctttgaact	gtccaagatg	caactcotta	240
aacaccaagt	tctgttacta	caacaactac	agcctgacgc	agcccaggta	ctttgtataa	300
gactgcagga	ggatattggc	cgcaGgtggt	tccttcagga	acatcccctg	cgggtggcgc	360
gtccgcaaga	acaaagagat	ttcttccaat	tcctcttctc	cttcaaccct	ttcgtctctt	420
ctttcaaga	aaactctttt	tgccaacaac	aacaacgcct	cgctctctct	tcctcatctt	480
aaacctaa	tttgtgaagc	agccgctact	aaagtccaag	acttgacggt	ttctcaaggg	540
tttggaagc	ccacagaggt	taaagatctc	aaactggcgt	tttctcaagg	gtttgggata	600
ggtcaccatc	atcacagatg	tatcccagag	tttgtgcaag	tagtaccacg	cagcagtagt	660
aagaacaacc	cactgttctc	aaacttctcg	gctttggagc	ttttagggat	ctctagttcc	720
tctgcttctc	ctaactcaag	ccctgtcttc	atgtcttctc	caaatgtcca	tgattcatcg	780
gtctacacag	catcggggtt	tggtctgagt	taccacaggt	ttcaagagtt	catgagacga	840
gctttgggat	tctctcttga	tggtggggat	cctctacgtc	aagaagaggg	gtccagtggt	900
actaataagt	gaagggcggt	gctgccattt	gagagcctcc	tcaaacctcc	agtttcatca	960
tcaagaccac	atagtgtggg	gaatgggcaat	ctgaagagag	ttaatgatga	gcgtagtgat	1020
catgaacatc	agaaagaaga	aggagaagct	gaccaatctg	ttgggttttg	gagtggtgat	1080
ttaagtgcgt	gtgcttctgc	tgctgcatct	ggtggtgggt	catggcaata	attatagatca	1140
tggaaccatc	ccatgagagt	ttttagaaca	aatgattaca	tttttcatcc	atgttttaaa	1200
aagatgagag	gggttaactat	ataatctggg	tacttactat	ttttagtctc	ttccttgggt	1260
ttccttctcc	ttttctaaaa	attattatta	actttgttgg	gttgggggat	gatactgtat	1320
gtatttagac	tctcttttaa	atcaatctca	gttgtagtt	acct		

(2) INFORMATION FOR SEQ ID NO:869:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 353 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1..353
(D) OTHER INFORMATION: / Ceres Seq. ID 1568193

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:869:

Met	Asp	Thr	Ala	Lys	Trp	Pro	Gln	Glu	Phe	Val	Val	Lys	Pro	Met	Asn
1				5				10						15	
Glu	Ile	Val	Thr	Asn	Thr	Cys	Leu	Lys	Gln	Gln	Ser	Asn	Pro	Pro	Ser
			20					25					30		
Pro	Ala	Thr	Pro	Val	Glu	Arg	Lys	Ala	Arg	Pro	Glu	Lys	Asp	Gln	Ala
			35				40					45			
Leu	Asn	Cys	Pro	Arg	Cys	Asn	Ser	Leu	Asn	Thr	Lys	Phe	Cys	Tyr	Tyr
			50				55				60				
Asn	Asn	Tyr	Ser	Leu	Thr	Gln	Pro	Arg	Tyr	Phe	Cys	Lys	Asp	Cys	Arg
65				70				75						80	
Arg	Tyr	Trp	Thr	Ala	Gly	Gly	Ser	Leu	Arg	Asn	Ile	Pro	Val	Gly	Gly
			85				90						95		
Gly	Val	Arg	Lys	Asn	Lys	Arg	Ser	Ser	Ser	Asn	Ser	Ser	Ser	Ser	Ser
			100				105					110			
Pro	Ser	Ser	Ser	Ser	Ser	Lys	Lys	Pro	Leu	Phe	Ala	Asn	Asn	Asn	
			115				120					125			
Thr	Pro	Thr	Pro	Pro	Leu	Pro	His	Leu	Asn	Pro	Lys	Ile	Gly	Glu	Ala

130	135	140
Ala Ala Thr Lys Val Gln Asp Leu Thr Phe Ser Gln Gly Phe Gly Asn		
145	150	155
Ala His Glu Val Lys Asp Leu Asn Leu Ala Phe Ser Gln Gly Phe Gly		
	165	170
Ile Gly His His His His Ser Ser Ile Pro Glu Phe Leu Gln Val Val		
	180	185
Pro Ser Ser Ser Met Lys Asn Asn Pro Leu Val Ser Thr Ser Ser Ala		
	195	200
Leu Glu Leu Leu Gly Ile Ser Ser Ser Ser Ala Ser Asn Ser Arg		
	210	215
Pro Ala Phe Met Ser Tyr Pro Asn Val His Asp Ser Ser Val Tyr Thr		
225	230	235
Ala Ser Gly Phe Gly Leu Ser Tyr Pro Gln Phe Gln Glu Phe Met Arg		
	245	250
Pro Ala Leu Gly Phe Ser Leu Asp Gly Gly Asp Pro Leu Arg Gln Glu		
	260	265
Glu Gly Ser Ser Gly Thr Asn Asn Gly Arg Pro Leu Leu Pro Phe Glu		
	275	280
Ser Leu Leu Lys Leu Pro Val Ser Ser Ser Ser Thr Asn Ser Gly Gly		
	290	295
Asn Gly Asn Leu Lys Glu Ile Asn Asp Glu Arg Ser Asp His Glu His		
305	310	315
Glu Lys Glu Glu Gly Glu Ala Asp Gln Ser Val Gly Phe Trp Ser Gly		
	325	330
Met Leu Ser Ala Gly Ala Ser Ala Ala Ala Ser Gly Gly Gly Ser Trp		
	340	345
		350
Gln		

(2) INFORMATION FOR SEQ ID NO:870:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 339 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..339

(D) OTHER INFORMATION: / Ceres Seq. ID 1568194

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:870:

Met	Asn	Glu	Ile	Val	Thr	Asn	Thr	Cys	Leu	Lys	Gln	Gln	Ser	Asn	Pro
1		5						10					15		
Pro	Ser	Pro	Ala	Thr	Pro	Val	Glu	Arg	Lys	Ala	Arg	Pro	Glu	Lys	Asp
		20						25					30		
Gln	Ala	Leu	Asn	Cys	Pro	Arg	Cys	Asn	Ser	Leu	Asn	Thr	Lys	Phe	Cys
		35					40					45			
Tyr	Tyr	Asn	Asn	Tyr	Ser	Leu	Thr	Gln	Pro	Arg	Tyr	Phe	Cys	Lys	Asp
	50				55					60					
Cys	Arg	Arg	Tyr	Trp	Thr	Ala	Gly	Gly	Ser	Leu	Arg	Asn	Ile	Pro	Val
	65				70				75				80		
Gly	Gly	Gly	Val	Arg	Lys	Asn	Lys	Arg	Ser	Ser	Ser	Asn	Ser	Ser	Ser
		85						90				95			
Ser	Ser	Pro	Ser	Ser	Ser	Ser	Ser	Lys	Lys	Pro	Leu	Phe	Ala	Asn	
	100					105						110			
Asn	Asn	Thr	Pro	Thr	Pro	Pro	Leu	Pro	His	Leu	Asn	Pro	Lys	Ile	Gly
	115					120						125			
Glu	Ala	Ala	Ala	Thr	Lys	Val	Gln	Asp	Leu	Thr	Phe	Ser	Gln	Gly	Phe
	130					135					140				
Gly	Asn	Ala	His	Glu	Val	Lys	Asp	Leu	Asn	Leu	Ala	Phe	Ser	Gln	Gly
145				150					155						160

Phe Gly Ile Gly His His His His Ser Ser Ile Pro Glu Phe Leu Gln
165 170 175
Val Val Pro Ser Ser Ser Met Lys Asn Asn Pro Leu Val Ser Thr Ser
180 185 190
Ser Ala Leu Glu Leu Leu Gly Ile Ser Ser Ser Ser Ala Ser Ser Asn
195 200 205
Ser Arg Pro Ala Phe Met Ser Tyr Pro Asn Val His Asp Ser Ser Val
210 215 220
Tyr Thr Ala Ser Gly Phe Gly Leu Ser Tyr Pro Gln Phe Gln Glu Phe
225 230 235 240
Met Arg Pro Ala Leu Gly Phe Ser Leu Asp Gly Gly Asp Pro Leu Arg
245 250 255
Gln Glu Glu Gly Ser Ser Gly Thr Asn Asn Gly Arg Pro Leu Leu Pro
260 265 270
Phe Glu Ser Leu Leu Lys Leu Pro Val Ser Ser Ser Ser Thr Asn Ser
275 280 285
Gly Gly Asn Gly Asn Leu Lys Glu Ile Asn Asp Glu Arg Ser Asp His
290 295 300
Glu His Glu Lys Glu Glu Gly Glu Ala Asp Gln Ser Val Gly Phe Trp
305 310 315 320
Ser Gly Met Leu Ser Ala Gly Ala Ser Ala Ala Ser Gly Gly Gly
325 330 335
Ser Trp Gln

(2) INFORMATION FOR SEQ ID NO:871:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1398 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1398
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568199

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:871:

atctaacttt	tccagataat	atattcaaaa	ttttacagag	aggaagaaga	agttcccgc	60
acttgtaga	gactataaaa	ctatcagatc	tctctctctc	gctctcttca	gatcacaaa	120
ttttcgtttt	taggggtctc	tcctcgatct	cggtttgtga	tcttcttttt	catcaatggc	180
gtctagtgtat	aaacaaacaa	gcccaaagcc	tccaccttca	ccgtctctctc	tccgttaattc	240
caagttttgtt	cagtcacaata	tgagaatttt	gatctcagga	ggagctggat	tcatgtgctc	300
tcacctgtgt	gataagctga	tgaaaaacga	aaagaatgag	gtgattgttg	ctgataaacta	360
tttcacgggt	tcaaaggaga	atctcaagaa	gtggattgtg	catccgagat	ttgaGgctta	420
tcctgcatga	tgctcacagag	Ccacttctga	tcgaggttga	tcagatttca	catcttgcat	480
gtctcgtctc	tccatgtctc	tacaagtaca	accctgtgaa	gacaatcaag	accaatgtca	540
ttggcacact	gaacatgcta	ggctcttgca	agcgtgttgg	agcaaggatt	ttgttaacct	600
caacctcaga	ggatatatga	gatctctctt	tccatcccca	gcccgagagc	tattggggag	660
atgtcaaccc	aattgggtgt	aggagctgtt	atgatgaagg	caagcgtgtt	gctgagacct	720
tgatgtttga	ctaccacagg	cagcatggaa	ttgaaatccg	cattgcccga	attcttaacaa	780
cttatgtgtcc	acgcatgaac	attgatgatg	gacgtgtttg	aaagcaactc	attgctcaag	840
cactcogtgg	tgaggcattg	actgttcaga	aaccagggac	acagactcgc	agttctgtgt	900
atgtatctga	catgtttgat	ggacttatgc	gcctaatgga	aggagatgac	actggctcca	960
tcaacatcgg	taaccacagg	gagttttaca	tggtggagtt	ggctgagaca	gtgaaagagc	1020
tgattaaccc	gagcatagag	ataaagatgg	ttgagaacac	accggatgat	ccaagacaga	1080
ggaagccatg	acatcacaaa	ggctaTaaga	agttttggga	tgggaaccac	aggtgaagct	1140
tcgtgaagcg	ctgcccctta	tggaagaaga	cttcaggcta	aggtcctggag	tccaagagaa	1200
ctaaaactcc	atcacccgat	atcacacgca	aacgtgaatg	ctactacata	cccagttcta	1260
cacttttcat	attctcttgt	gcaagtgtgt	tgtttccata	aatatgtttc	tactttccac	1320
agtcagaaat	tattctgata	gaaaaataaa	gattatgaac	gaatgctttt	tatatattag	1380
gaagataaaa	attacttt					

(2) INFORMATION FOR SEQ ID NO:872:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 178 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..178
 (D) OTHER INFORMATION: / Ceres Seq. ID 1568200
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:872:
Met Leu Gly Leu Ala Lys Arg Val Gly Ala Arg Ile Leu Leu Thr Ser
1 5 10 15
Thr Ser Glu Val Tyr Gly Asp Pro Leu Ile His Pro Gln Pro Glu Ser
 20 25 30
Tyr Trp Gly Asn Val Asn Pro Ile Gly Val Arg Ser Cys Tyr Asp Glu
 35 40 45
Gly Lys Arg Val Ala Glu Thr Leu Met Phe Asp Tyr His Arg Gln His
50 55 60
Gly Ile Glu Ile Arg Ile Ala Arg Ile Phe Asn Thr Tyr Gly Pro Arg
65 70 75 80
Met Asn Ile Asp Asp Gly Arg Val Val Ser Asn Phe Ile Ala Gln Ala
 85 90 95
Leu Arg Gly Glu Ala Leu Thr Val Gln Lys Pro Gly Thr Gln Thr Arg
 100 105 110
Ser Phe Cys Tyr Val Ser Asp Met Val Asp Gly Leu Met Arg Leu Met
 115 120 125
Glu Gly Asp Asp Thr Gly Pro Ile Asn Ile Gly Asn Pro Gly Glu Phe
130 135 140
Thr Met Val Glu Leu Ala Glu Thr Val Lys Glu Leu Ile Asn Pro Ser
145 150 155 160
Ile Glu Ile Lys Met Val Glu Asn Thr Pro Asp Asp Pro Arg Gln Arg
 165 170 175
Lys Pro

(2) INFORMATION FOR SEQ ID NO:873:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 122 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..122
 (D) OTHER INFORMATION: / Ceres Seq. ID 1568201
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:873:
Met Phe Asp Tyr His Arg Gln His Gly Ile Glu Ile Arg Ile Ala Arg
1 5 10 15
Ile Phe Asn Thr Tyr Gly Pro Arg Met Asn Ile Asp Asp Gly Arg Val
 20 25 30
Val Ser Asn Phe Ile Ala Gln Ala Leu Arg Gly Glu Ala Leu Thr Val
 35 40 45
Gln Lys Pro Gly Thr Gln Thr Arg Ser Phe Cys Tyr Val Ser Asp Met
50 55 60
Val Asp Gly Leu Met Arg Leu Met Glu Gly Asp Asp Thr Gly Pro Ile
65 70 75 80
Asn Ile Gly Asn Pro Gly Glu Phe Thr Met Val Glu Leu Ala Glu Thr
 85 90 95
Val Lys Glu Leu Ile Asn Pro Ser Ile Glu Ile Lys Met Val Glu Asn
 100 105 110

Thr Pro Asp Asp Pro Arg Gln Arg Lys Pro
115 120

(2) INFORMATION FOR SEQ ID NO:874:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 98 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..98
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568202

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:874:

```
Met Asn Ile Asp Asp Gly Arg Val Val Ser Asn Phe Ile Ala Gln Ala
1      5      10      15
Leu Arg Gly Glu Ala Leu Thr Val Gln Lys Pro Gly Thr Gln Thr Arg
20      25      30
Ser Phe Cys Tyr Val Ser Asp Met Val Asp Gly Leu Met Arg Leu Met
35      40      45
Glu Gly Asp Asp Thr Gly Pro Ile Asn Ile Gly Asn Pro Gly Glu Phe
50      55      60
Thr Met Val Glu Leu Ala Glu Thr Val Lys Glu Leu Ile Asn Pro Ser
65      70      75      80
Ile Glu Ile Lys Met Val Glu Asn Thr Pro Asp Asp Pro Arg Gln Arg
85      90      95
Lys Pro
```

(2) INFORMATION FOR SEQ ID NO:875:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2350 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..2350
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568213

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:875:

```
tccaatcccc tttttttttt cgtttcgtcg tttgttcgtt ttctctatcg ctctcgttca 60
tctacgcgaat ctctctcact aggtacagtt ttaaatgggt aagaagaagt cagacgagag 120
tgctgctacc acaaaagtga agccaagtgg gaaaagatgct tcgaaagatt ctaaaaaaga 180
gaaattgtca gtctcggcta tgcttgacgg catggatcag aaagatgata aaccgaagaa 240
gggctcatca tctagaacca aggtcgtctc gaaatctaca tcttacactg atggcataga 300
tcttctctct tctgatgaag aagacgacgg tgaatctgat gaggaaagaga gacagaagga 360
agctaggagg aagctgaaga gtgaacaaag gcaccttgag atatctgtga ctgataaagga 420
acaaaagaag cgagaggcga aagaaaagatt agctcttcag gctgcagagt cggcaaaagag 480
ggaggctatg aaggacgac atgatgcatt cactgtttgt attggaagca agacctcagt 540
gcttgaagg gacgacatgg ctgatgcaaa tgttaaggat attaccatag aatctttttc 600
tgtatctgct cgaggtaaag agcttttgaa gaatgcttct gtcaggattt cacatggtaa 660
aaggtagtgg ttgatcgggc caaacggaat gggaaagtct acactgttaa agcttttagc 720
ttggaggaag attccagtcg caaagaatat tgatgttctt cttgttgagc aagaggtggg 780
tggtgatgaa aagagtgtct tgaatgcagt tgtctctgcc aatgaagaag tggttaaagt 840
acgtgaagag gctgaagctc tgcagaagtc gtctcttgga gctgatggag aaaaatttga 900
tggtgaggat gatgatgata ctggagaaaa gcttgctgaa ctgtatgaca ggctgcagat 960
tttaggtcca gatgctgctg aagcacaggg atccaaaatt cttgcggggg taggtttcac 1020
aaaaAgatat gcaagtgcgt gcgactcagt ccttcagtgg tggctggagg atgcgaatat 1080
cattagctag agctctcttc ttgcacaacta cccttttgct gttagatgaa ccactaaccc 1140
atcttgacct gagagctgtt ctatgggttag aggagatttt gtgtcgtcgg aagaagacac 1200
tagttgttgt ttcacatgac cgggacttcc tcaacacagt ctgcacggag ataatacatc 1260
```

tccatgacca	gaatctccac	ttctaccgtg	gtaatttcga	tggtttttgaa	agcgatatg	1320
acgacgcgtcg	caaggagatg	aacaaaaaat	ttgatgtcta	cgacaaacag	atgaaagcag	1380
cgaagaggacg	tggaaccggg	ggctcaacagg	agaaggtaaa	ggacagggcc	aagtttactg	1440
ctgcaaaaaga	agcatcccaag	agtaagtcaa	agggcagaac	agtggaatgaa	gaaggcccaag	1500
caccagaagc	tccaaggaag	tggagagatt	acagtgtggt	gttccacttc	ccagaaccac	1560
ctgagctcac	tctctctctt	ctgcagttaa	ttgaggttag	cttcagctat	cccaacaggc	1620
cagattttcag	actctcgaa	gttgatgtag	gtatcgatat	ggggacacgg	gttgcgatag	1680
ttgggccttaa	cggagcagga	aagtccactc	tattaaatct	tcttgcggga	gattttagttc	1740
caacagaggg	tgaatatgaga	agaagccaga	agctgaggat	tggcaggtat	tctcagcatt	1800
ttgttgacct	tttaacaagt	ggggaaacac	cggttcagta	tctccttcgt	cttcattcctg	1860
accaagaggg	atttagcaag	caagaggcag	tgcgcgcgaa	gctaggcaag	tttgggctac	1920
caagtacaaa	tcaacttatc	ccaattgcga	aattgtctag	aggacaaaag	gctagggttg	1980
tgttcacctc	gatctcaatg	tcaaaaccac	acattttgct	cctggacagag	ctacaaaatc	2040
acttagacat	gcagagtata	gatgccttgg	cggatgcact	agatgagttc	acaggtggag	2100
ttgtgttgg	gagtcacgag	tgcgagacta	tatcacgtgt	atgtgcggaa	gaggagaaga	2160
gtcaaatgtt	ggttgtagaa	gacggaacag	tgaatttctt	cccaggcaca	tttgaagagt	2220
acaaagaaga	tctccaaaga	gaatatcaaa	cagaagttag	ttagtgaaat	ttgtttgtta	2280
gctcttaagg	taaactcaaa	ctcctttatg	ttttataaca	aactcaaaaa	gttttggaca	2340
attttatttt						

(2) INFORMATION FOR SEQ ID NO:876:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 331 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..331

(D) OTHER INFORMATION: / Ceres Seq. ID 1568214

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:876:

Met	Gly	Lys	Lys	Lys	Ser	Asp	Glu	Ser	Ala	Ala	Thr	Thr	Lys	Val	Lys
1				5						10				15	
Pro	Ser	Gly	Lys	Asp	Ala	Ser	Lys	Asp	Ser	Lys	Lys	Glu	Lys	Leu	Ser
				20						25				30	
Val	Ser	Ala	Met	Leu	Ala	Gly	Met	Asp	Gln	Lys	Asp	Asp	Lys	Pro	Lys
			35				40					45			
Lys	Gly	Ser	Ser	Ser	Arg	Thr	Lys	Ala	Ala	Pro	Lys	Ser	Thr	Ser	Tyr
			50				55					60			
Thr	Asp	Gly	Ile	Asp	Leu	Pro	Pro	Ser	Asp	Glu	Glu	Asp	Asp	Gly	Glu
65					70					75				80	
Ser	Asp	Glu	Glu	Glu	Arg	Gln	Lys	Glu	Ala	Arg	Arg	Lys	Leu	Lys	Ser
					85					90				95	
Glu	Gln	Arg	His	Leu	Glu	Ile	Ser	Val	Thr	Asp	Lys	Glu	Gln	Lys	Lys
			100						105					110	
Arg	Glu	Ala	Lys	Glu	Arg	Leu	Ala	Leu	Gln	Ala	Ala	Glu	Ser	Ala	Lys
			115				120					125			
Arg	Glu	Ala	Met	Lys	Asp	Asp	His	Asp	Ala	Phe	Thr	Val	Val	Ile	Gly
			130				135				140				
Ser	Lys	Thr	Ser	Val	Leu	Glu	Gly	Asp	Asp	Met	Ala	Asp	Ala	Asn	Val
145					150					155				160	
Lys	Asp	Ile	Thr	Ile	Glu	Ser	Phe	Ser	Val	Ser	Ala	Arg	Gly	Lys	Glu
			165						170					175	
Leu	Leu	Lys	Asn	Ala	Ser	Val	Arg	Ile	Ser	His	Gly	Lys	Arg	Tyr	Gly
			180						185				190		
Leu	Ile	Gly	Pro	Asn	Gly	Met	Gly	Lys	Ser	Thr	Leu	Glu	Lys	Leu	Leu
			195				200					205			
Ala	Trp	Arg	Lys	Ile	Pro	Val	Pro	Lys	Asn	Ile	Asp	Val	Leu	Leu	Val
			210				215					220			
Glu	Gln	Glu	Val	Val	Gly	Asp	Glu	Lys	Ser	Ala	Leu	Asn	Ala	Val	Val
225					230					235				240	

Ser Ala Asn Glu Glu Leu Val Lys Leu Arg Glu Glu Ala Glu Ala Leu
245 250 255
Gln Lys Ser Ser Ser Gly Ala Asp Gly Glu Asn Val Asp Gly Glu Asp
260 265 270
Asp Asp Asp Thr Gly Glu Lys Leu Ala Glu Leu Tyr Asp Arg Leu Gln
275 280 285
Ile Leu Gly Ser Asp Ala Ala Glu Ala Gln Ala Ser Lys Ile Leu Ala
290 295 300
Gly Leu Gly Phe Thr Lys Arg Tyr Ala Ser Cys Asp Ser Val Leu
305 310 315 320
Gln Trp Trp Leu Glu Asp Ala Asn Ile Ile Ser
325 330

(2) INFORMATION FOR SEQ ID NO:877:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 412 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..412
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568215

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:877:

Met Gln Val Arg Ala Thr Gln Ser Phe Ser Gly Gly Trp Arg Met Arg
1 5 10 15
Ile Ser Leu Ala Arg Ala Leu Phe Val Gln Pro Thr Leu Leu Leu Leu
20 25 30
Asp Glu Pro Thr Asn His Leu Asp Leu Arg Ala Val Leu Trp Leu Glu
35 40 45
Glu Tyr Leu Cys Arg Trp Lys Lys Thr Leu Val Val Val Ser His Asp
50 55 60
Arg Asp Phe Leu Asn Thr Val Cys Thr Glu Ile Ile His Leu His Asp
65 70 75 80
Gln Asn Leu His Phe Tyr Arg Gly Asn Phe Asp Gly Phe Glu Ser Gly
85 90 95
Tyr Glu Gln Arg Arg Lys Glu Met Asn Lys Lys Phe Asp Val Tyr Asp
100 105 110
Lys Gln Met Lys Ala Ala Lys Arg Thr Gly Asn Arg Gly Gln Gln Glu
115 120 125
Lys Val Lys Asp Arg Ala Lys Phe Thr Ala Ala Lys Glu Ala Ser Lys
130 135 140
Ser Lys Ser Lys Gly Lys Thr Val Asp Glu Glu Gly Pro Ala Pro Glu
145 150 155 160
Ala Pro Arg Lys Trp Arg Asp Tyr Ser Val Val Phe His Phe Pro Glu
165 170 175
Pro Thr Glu Leu Thr Pro Pro Leu Leu Gln Leu Ile Glu Val Ser Phe
180 185 190
Ser Tyr Pro Asn Arg Pro Asp Phe Arg Leu Ser Asn Val Asp Val Gly
195 200 205
Ile Asp Met Gly Thr Arg Val Ala Ile Val Gly Pro Asn Gly Ala Gly
210 215 220
Lys Ser Thr Leu Leu Asn Leu Leu Ala Gly Asp Leu Val Pro Thr Glu
225 230 235 240
Gly Glu Met Arg Arg Ser Gln Lys Leu Arg Ile Gly Arg Tyr Ser Gln
245 250 255
His Phe Val Asp Leu Leu Thr Met Gly Glu Thr Pro Val Gln Tyr Leu
260 265 270
Leu Arg Leu His Pro Asp Gln Glu Gly Phe Ser Lys Gln Glu Ala Val
275 280 285
Arg Ala Lys Leu Gly Lys Phe Gly Leu Pro Ser His Asn His Leu Ser

290	295	300
Pro Ile Ala Lys Leu Ser Arg Gly Gln Lys Ala Arg Val Val Phe Thr		
305	310	315
Ser Ile Ser Met Ser Lys Pro His Ile Leu Leu Leu Asp Glu Pro Thr		
	325	330
Asn His Leu Asp Met Gln Ser Ile Asp Ala Leu Ala Asp Ala Leu Asp		
	340	345
Glu Phe Thr Gly Gly Val Val Leu Val Ser His Asp Ser Arg Leu Ile		
	355	360
Ser Arg Val Cys Ala Glu Glu Glu Lys Ser Gln Ile Trp Val Val Glu		
	370	375
Asp Gly Thr Val Asn Phe Phe Pro Gly Thr Phe Glu Glu Tyr Lys Glu		
385	390	395
Asp Leu Gln Arg Glu Ile Lys Ala Glu Val Asp Glu		
	405	410

(2) INFORMATION FOR SEQ ID NO:878:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 398 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..398

(D) OTHER INFORMATION: / Ceres Seq. ID 1568216

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:878:

Met Arg Ile Ser Leu Ala Arg Ala Leu Phe Val Gln Pro Thr Leu Leu	
1	5
Leu Leu Asp Glu Pro Thr Asn His Leu Asp Leu Arg Ala Val Leu Trp	
	20
Leu Glu Glu Tyr Leu Cys Arg Trp Lys Lys Thr Leu Val Val Val Ser	
	35
His Asp Arg Asp Phe Leu Asn Thr Val Cys Thr Glu Ile Ile His Leu	
	50
His Asp Gln Asn Leu His Phe Tyr Arg Gly Asn Phe Asp Gly Phe Glu	
	65
Ser Gly Tyr Glu Gln Arg Arg Lys Glu Met Asn Lys Lys Phe Asp Val	
	85
Tyr Asp Lys Gln Met Lys Ala Ala Lys Arg Thr Gly Asn Arg Gly Gln	
	100
Gln Glu Lys Val Lys Asp Arg Ala Lys Phe Thr Ala Ala Lys Glu Ala	
	115
Ser Lys Ser Lys Ser Lys Gly Lys Thr Val Asp Glu Glu Gly Pro Ala	
	130
Pro Glu Ala Pro Arg Lys Trp Arg Asp Tyr Ser Val Val Phe His Phe	
	145
Pro Glu Pro Thr Glu Leu Thr Pro Pro Leu Leu Gln Leu Ile Glu Val	
	165
Ser Phe Ser Tyr Pro Asn Arg Pro Asp Phe Arg Leu Ser Asn Val Asp	
	180
Val Gly Ile Asp Met Gly Thr Arg Val Ala Ile Val Gly Pro Asn Gly	
	195
Ala Gly Lys Ser Thr Leu Leu Asn Leu Leu Ala Gly Asp Leu Val Pro	
	210
Thr Glu Gly Glu Met Arg Arg Ser Gln Lys Leu Arg Ile Gly Arg Tyr	
	225
Ser Gln His Phe Val Asp Leu Leu Thr Met Gly Glu Thr Pro Val Gln	
	245
Tyr Leu Leu Arg Leu His Pro Asp Gln Glu Gly Phe Ser Lys Gln Glu	
	260

Ala Val Arg Ala Lys Leu Gly Lys Phe Gly Leu Pro Ser His Asn His
275 280 285
Leu Ser Pro Ile Ala Lys Leu Ser Arg Gly Gln Lys Ala Arg Val Val
290 295 300
Phe Thr Ser Ile Ser Met Ser Lys Pro His Ile Leu Leu Leu Asp Glu
305 310 315 320
Pro Thr Asn His Leu Asp Met Gln Ser Ile Asp Ala Leu Ala Asp Ala
325 330 335
Leu Asp Glu Phe Thr Gly Gly Val Val Leu Val Ser His Asp Ser Arg
340 345 350
Leu Ile Ser Arg Val Cys Ala Glu Glu Glu Lys Ser Gln Ile Trp Val
355 360 365
Val Glu Asp Gly Thr Val Asn Phe Phe Pro Gly Thr Phe Glu Glu Tyr
370 375 380
Lys Glu Asp Leu Gln Arg Glu Ile Lys Ala Glu Val Asp Glu
385 390 395

(2) INFORMATION FOR SEQ ID NO:879:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 919 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..919
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568217

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:879:

aaaagaaga	aaaaaatgcc	ttcttttgc	tttgatctc	atcaccattt	ggcgaatcct	60
acagactgc	cqccgtactc	cgtcgaaatt	agcatcgacg	gtgactcttc	cgacttggat	120
ttctttgtc	aggtcgattt	agagtcggcg	ggtgtaccgg	cgccggagaa	acagctacat	180
tccggtgta	agaagaggag	aactaggagg	agaagaggga	ggaagaagaa	gaagaagaag	240
aaaggtgaa	gagattgcag	gatctgcat	cttcctttag	agactaacaa	agaagctgaa	300
gatgaagtg	aagaagaaga	agatgattct	gatgatgatg	aagatgaaga	agatgaagaa	360
gaagaagaag	aagaagaaga	atattatggt	ttgcctttgc	aattaggttg	ctcttgtaaa	420
ggtgatttg	gtgtgtctca	tagtaagtg	gctgagactt	ggtttaagat	caaaggaaac	480
atgacatgt	agatatgcgg	cgcaatggct	ctaaAcgtgg	ctgggtaaca	atctaaNtcc	540
ggagagcact	gcttctacac	attcacaagc	agctgcggga	caatctctaa	ctcagacaga	600
gccacagaga	atctggcatg	gtcgccctgt	tatgaacttc	ttacttgctg	ctatggtctt	660
cgctcttct	gtttcttggc	tttttcaact	caaaagtcctc	aagtgaagac	ttttccattc	720
ctctctctct	ctctcttctg	cccccccgca	cgagctcact	cttctcctgt	tcttgagccg	780
cttgcaatcg	ctgaatcaat	ccctcctgtt	gcttgattat	tcacacgttt	tgtagctgta	840
aaaaattgg	agtgctttaga	ttgttgtaac	ttgtgagatt	tacattttgt	ataatatigt	900
ctctctgctc	ggctctctgt					

(2) INFORMATION FOR SEQ ID NO:880:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 271 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..271
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568218

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:880:

Lys Arg Lys Lys Lys Met Pro Ser Phe Ala Phe Gly Ser His His His	
1 5 10	15
Leu Ala Asn Pro Thr Asp Ser Pro Pro Tyr Ser Val Glu Ile Ser Ile	
20 25 30	
Asp Gly Asp Ser Ser Asp Leu Asp Ser Leu Ser Gln Val Asp Leu Glu	

Ser	35			Pro	40			Leu	45			Lys
	Gly	Val			Ala	Pro	Glu		Ser	Gly	Gly	
Lys	Arg	Arg	Thr	Arg	Arg	Arg	Lys	Arg	Lys	Lys	Lys	Lys
65					70				75			80
Lys	Gly	Gly	Arg	Asp	Cys	Arg	Ile	Cys	His	Leu	Pro	Leu
				85					90			95
Lys	Glu	Ala	Glu	Asp	Glu	Asp	Glu	Glu	Glu	Asp	Asp	Ser
			100					105				110
Asp	Glu	Asp	Glu	Glu	Asp	Glu	Glu	Glu	Glu	Glu	Glu	Glu
		115					120			125		Tyr
Tyr	Gly	Leu	Pro	Leu	Gln	Leu	Gly	Cys	Ser	Cys	Lys	Gly
	130					135				140		Asn
Val	Ala	His	Ser	Lys	Cys	Ala	Glu	Thr	Trp	Phe	Lys	Ile
145					150					155		Lys
Met	Thr	Cys	Glu	Ile	Cys	Gly	Ala	Met	Ala	Leu	Asn	Val
				165				170				175
Gln	Ser	Xaa	Ser	Gly	Glu	His	Cys	Phe	Tyr	Thr	Phe	Thr
		180						185				190
Gly	Thr	Ile	Ser	Asn	Ser	Asp	Arg	Ala	Thr	Arg	Asn	Leu
		195				200					205	Ala
Pro	Cys	Tyr	Glu	Leu	Leu	Thr	Cys	Cys	Tyr	Gly	Leu	Arg
		210				215					220	Leu
Phe	Leu	Ala	Phe	Ser	Leu	Gln	Ser	Pro	Gln	Val	Lys	Arg
225					230					235		Phe
Leu	Ser	Leu	Ser	Leu	Phe	Arg	Pro	Pro	Ala	Arg	Ala	His
				245					250			255
Val	Leu	Glu	Pro	Leu	Ala	Ile	Ala	Glu	Ser	Ile	Pro	Pro
			260					265				270

(2) INFORMATION FOR SEQ ID NO:881:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 266 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..266
(D) OTHER INFORMATION: / Ceres Seq. ID 1568219

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:881:

Met	Pro	Ser	Phe	Ala	Phe	Gly	Ser	His	His	His	Leu	Ala	Asn	Pro	Thr
1			5						10					15	
Asp	Ser	Pro	Pro	Tyr	Ser	Val	Glu	Ile	Ser	Ile	Asp	Gly	Asp	Ser	Ser
			20					25					30		
Asp	Leu	Asp	Ser	Leu	Ser	Gln	Val	Asp	Leu	Glu	Ser	Gly	Gly	Val	Pro
		35					40					45			
Ala	Pro	Glu	Lys	Gln	Leu	His	Ser	Gly	Gly	Lys	Lys	Arg	Arg	Thr	Arg
	50					55					60				
Arg	Arg	Gly	Arg	Arg	Lys	Lys	Lys	Lys	Lys	Lys	Gly	Gly	Arg	Asp	
65				70					75					80	
Cys	Arg	Ile	Cys	His	Leu	Pro	Leu	Glu	Thr	Asn	Lys	Glu	Ala	Glu	Asp
			85					90						95	
Glu	Asp	Glu	Glu	Glu	Glu	Asp	Asp	Ser	Asp	Asp	Asp	Glu	Asp	Glu	Glu
		100					105					110			
Asp	Glu	Glu	Glu	Glu	Glu	Glu	Glu	Glu	Glu	Tyr	Tyr	Gly	Leu	Pro	Leu
		115					120					125			
Gln	Leu	Gly	Cys	Ser	Cys	Lys	Gly	Asp	Leu	Gly	Val	Ala	His	Ser	Lys
	130					135				140					
Cys	Ala	Glu	Thr	Trp	Phe	Lys	Ile	Lys	Gly	Asn	Met	Thr	Cys	Glu	Ile
145					150					155				160	

Cys Gly Ala Met Ala Leu Asn Val Ala Gly Glu Gln Ser Xaa Ser Gly
165 170 175
Glu His Cys Phe Tyr Thr Phe Thr Ser Ser Cys Gly Thr Ile Ser Asn
180 185 190
Ser Asp Arg Ala Thr Arg Asn Leu Ala Trp Ser Pro Cys Tyr Glu Leu
195 200 205
Leu Thr Cys Cys Tyr Gly Leu Arg Leu Arg Cys Phe Leu Ala Phe Ser
210 215 220
Leu Gln Ser Pro Gln Val Lys Arg Phe Pro Ser Leu Ser Leu Ser Leu
225 230 235 240
Phe Arg Pro Pro Ala Arg Ala His Ser Ser Pro Val Leu Glu Pro Leu
245 250 255
Ala Ile Ala Glu Ser Ile Pro Pro Val Ala
260 265

(2) INFORMATION FOR SEQ ID NO:882:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1475 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1475
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568230

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:882:

aaaatagaga	cctttcttta	acacagagaa	agagcctgag	agacaagtga	gaaacgcaac	60
aacaacaccg	aaagagagag	tcacaattcg	aaagagaaaa	agaatcaaat	tcctttcttc	120
tccttttttt	attttcaatt	attactttaa	tcttctttcc	cgctctctat	ttcttctctt	180
cttttagatc	aatacccggt	tagcttttct	cccatacgtc	tctccgttta	cgaccagtat	240
acagaggctg	gagctgggga	agaaaaggat	tgctatgga	gggagacgtc	ggaatagggt	300
tggtatgcca	gaataactatg	gatgggaagg	cgagtaattg	aaatggttta	gagaagactg	360
taccttcttg	ttgccttaag	gctatggcat	gtttactctga	ggaatgatct	aaagtgtcat	420
ccactgttgt	ttctgggtgg	ttttcggaac	ctcaccctcg	ctctgggaaa	aaaggcggca	480
aagcagtccta	tttcaacaac	ccatgtggc	caggagaagc	acactcactg	aaagtggaga	540
aagtctctgt	caaagacaag	tcggattttc	aggaagtctc	agtgttctcg	tcagccaagt	600
acggaaagggt	gcttgttcta	gatgggtatc	tacagctgac	cgaaaaagat	gaatgtgcac	660
atcaggagat	gatagcccat	ctgcttttat	gctctatata	ttccccataa	aatgttcttg	720
ttgttggtgg	aggtgatggg	gtgtgttctc	gagagatttc	tcgccatagt	tcgtttgagg	780
ttattgatat	ctgtgagata	gacaagatgg	ttatagatgt	gtctaagaag	ttcttccccg	840
agtttagcgt	tggttttgac	gatctctgtg	ttcaacttca	catgttgtag	gctgtgagtg	900
tcctccgtga	atccccgtga	gggaagtatg	atgccatcat	tgattgattc	tcagatcccc	960
taggtctctg	ctttgcgctt	gttgagaagc	ctttcttcga	gacactggct	agagcgttga	1020
agcctggggg	agttctttgt	aacatggcag	aaagtatgtg	gctccatact	catcttattg	1080
aaatatatgt	ctccattttg	cgtaaaacal	tcaaaagtgt	tcactatgcg	tgagcagcgc	1140
tcocacacata	tcacaagcgc	gtgatgtggt	tgctcttttg	ctctactgaa	ggaccagctg	1200
ttgacttcaa	gaacccaact	aacctatttg	agaaactaga	cggtgcgatg	accocataaa	1260
gagaaatgaa	gttctataac	cttgatatgc	acagagcccg	attgtcttgg	cccaatttcc	1320
tcggcgagaga	agtatgttca	cttctgggtt	cttgacttct	gtttggctct	accatatccc	1380
tcatatcaaa	cttttagaaa	ctttgaaga	ggaataataa	atcattgaag	gctttgtatc	1440
tcataagttta	ctcttttata	aaaagactta	tatttt			

(2) INFORMATION FOR SEQ ID NO:883:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 359 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..359

(D) OTHER INFORMATION: / Ceres Seq. ID 1568231

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:883:

Met	Glu	Gly	Asp	Val	Gly	Ile	Gly	Leu	Val	Cys	Gln	Asn	Thr	Met	Asp
1				5				10						15	
Gly	Lys	Ala	Ser	Asn	Gly	Asn	Gly	Leu	Glu	Lys	Thr	Val	Pro	Ser	Cys
				20				25						30	
Cys	Leu	Lys	Ala	Met	Ala	Cys	Leu	Pro	Glu	Asp	Asp	Ala	Lys	Cys	His
				35				40						45	
Ser	Thr	Val	Val	Ser	Gly	Trp	Phe	Ser	Glu	Pro	His	Pro	Arg	Ser	Gly
				50				55						60	
Lys	Lys	Gly	Gly	Lys	Ala	Val	Tyr	Phe	Asn	Asn	Pro	Met	Trp	Pro	Gly
65					70				75					80	
Glu	Ala	His	Ser	Leu	Lys	Val	Glu	Lys	Val	Leu	Phe	Lys	Asp	Lys	Ser
				85					90					95	
Asp	Phe	Gln	Glu	Val	Leu	Val	Phe	Glu	Ser	Ala	Thr	Tyr	Gly	Lys	Val
				100				105						110	
Leu	Val	Leu	Asp	Gly	Ile	Val	Gln	Leu	Thr	Glu	Lys	Asp	Glu	Cys	Ala
				115				120						125	
Tyr	Gln	Glu	Met	Ile	Ala	His	Leu	Pro	Leu	Cys	Ser	Ile	Ser	Ser	Pro
				130				135						140	
Lys	Asn	Val	Leu	Val	Val	Gly	Gly	Asp	Gly	Gly	Val	Leu	Arg	Glu	
145					150				155					160	
Ile	Ser	Arg	His	Ser	Ser	Val	Glu	Val	Ile	Asp	Ile	Cys	Glu	Ile	Asp
				165					170					175	
Lys	Met	Val	Ile	Asp	Val	Ser	Lys	Lys	Phe	Phe	Pro	Glu	Leu	Ala	Val
				180				185						190	
Gly	Phe	Asp	Asp	Pro	Arg	Val	Gln	Leu	His	Ile	Gly	Asp	Ala	Ala	Glu
				195				200						205	
Phe	Leu	Arg	Lys	Ser	Pro	Glu	Gly	Lys	Tyr	Asp	Ala	Ile	Ile	Val	Asp
				210				215							
Ser	Ser	Asp	Pro	Val	Gly	Pro	Ala	Leu	Ala	Leu	Val	Glu	Lys	Pro	Phe
225					230				235					240	
Phe	Glu	Thr	Leu	Ala	Arg	Ala	Leu	Lys	Pro	Gly	Gly	Val	Leu	Cys	Asn
				245					250					255	
Met	Ala	Glu	Ser	Met	Trp	Leu	His	Thr	His	Leu	Ile	Glu	Asp	Met	Ile
				260				265						270	
Ser	Ile	Cys	Arg	Gln	Thr	Phe	Lys	Ser	Val	His	Tyr	Ala	Trp	Ser	Ser
				275				280						285	
Val	Pro	Thr	Tyr	Pro	Ser	Gly	Val	Ile	Gly	Phe	Val	Leu	Cys	Ser	Thr
				290				295						300	
Glu	Gly	Pro	Ala	Val	Asp	Phe	Lys	Asn	Pro	Ile	Asn	Pro	Ile	Glu	Lys
305					310				315					320	
Leu	Asp	Gly	Ala	Met	Thr	His	Lys	Arg	Glu	Leu	Lys	Phe	Tyr	Asn	Ser
				325					330					335	
Asp	Met	His	Arg	Ala	Ala	Phe	Ala	Leu	Pro	Thr	Phe	Leu	Arg	Arg	Glu
				340				345						350	
Val	Ala	Ser	Leu	Leu	Ala	Ser									
				355											

(2) INFORMATION FOR SEQ ID NO:884:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 345 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..345

(D) OTHER INFORMATION: / Ceres Seq. ID 1568232

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:884:

Met Asp Gly Lys Ala Ser Asn Gly Asn Gly Leu Glu Lys Thr Val Pro

```

1           5           10           15
Ser Cys Cys Leu Lys Ala Met Ala Cys Leu Pro Glu Asp Asp Ala Lys
20           25           30
Cys His Ser Thr Val Val Ser Gly Trp Phe Ser Glu Pro His Pro Arg
35           40           45
Ser Gly Lys Lys Gly Gly Lys Ala Val Tyr Phe Asn Asn Pro Met Trp
50           55           60
Pro Gly Glu Ala His Ser Leu Lys Val Glu Lys Val Leu Phe Lys Asp
65           70           75
Lys Ser Asp Phe Gln Glu Val Leu Val Phe Glu Ser Ala Thr Tyr Gly
85           90           95
Lys Val Leu Val Leu Asp Gly Ile Val Gln Leu Thr Glu Lys Asp Glu
100          105          110
Cys Ala Tyr Gln Glu Met Ile Ala His Leu Pro Leu Cys Ser Ile Ser
115          120          125
Ser Pro Lys Asn Val Leu Val Val Gly Gly Gly Asp Gly Gly Val Leu
130          135          140
Arg Glu Ile Ser Arg His Ser Ser Val Glu Val Ile Asp Ile Cys Glu
145          150          155
Ile Asp Lys Met Val Ile Asp Val Ser Lys Lys Phe Phe Pro Glu Leu
165          170          175
Ala Val Gly Phe Asp Asp Pro Arg Val Gln Leu His Ile Gly Asp Ala
180          185          190
Ala Glu Phe Leu Arg Lys Ser Pro Glu Gly Lys Tyr Asp Ala Ile Ile
195          200          205
Val Asp Ser Ser Asp Pro Val Gly Pro Ala Leu Ala Leu Val Glu Lys
210          215          220
Pro Phe Phe Glu Thr Leu Ala Arg Ala Leu Lys Pro Gly Gly Val Leu
225          230          235
Cys Asn Met Ala Glu Ser Met Trp Leu His Thr His Leu Ile Glu Asp
245          250          255
Met Ile Ser Ile Cys Arg Gln Thr Phe Lys Ser Val His Tyr Ala Trp
260          265          270
Ser Ser Val Pro Thr Tyr Pro Ser Gly Val Ile Gly Phe Val Leu Cys
275          280          285
Ser Thr Glu Gly Pro Ala Val Asp Phe Lys Asn Pro Ile Asn Pro Ile
290          295          300
Glu Lys Leu Asp Gly Ala Met Thr His Lys Arg Glu Leu Lys Phe Tyr
305          310          315
Asn Ser Asp Met His Arg Ala Ala Phe Ala Leu Pro Thr Phe Leu Arg
325          330          335
Arg Glu Val Ala Ser Leu Leu Ala Ser
340          345

```

(2) INFORMATION FOR SEQ ID NO:885:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 323 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..323

(D) OTHER INFORMATION: / Ceres Seq. ID 1568233

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:885:

```

Met Ala Cys Leu Pro Glu Asp Asp Ala Lys Cys His Ser Thr Val Val
1           5           10           15
Ser Gly Trp Phe Ser Glu Pro His Pro Arg Ser Gly Lys Lys Gly Gly
20           25           30
Lys Ala Val Tyr Phe Asn Asn Pro Met Trp Pro Gly Glu Ala His Ser
35           40           45

```

Leu Lys Val Glu Lys Val Leu Phe Lys Asp Lys Ser Asp Phe Gln Glu
50 55 60
Val Leu Val Phe Glu Ser Ala Thr Tyr Gly Lys Val Leu Val Leu Asp
65 70 75 80
Gly Ile Val Gln Leu Thr Glu Lys Asp Glu Cys Ala Tyr Gln Glu Met
85 90 95
Ile Ala His Leu Pro Leu Cys Ser Ile Ser Ser Pro Lys Asn Val Leu
100 105 110
Val Val Gly Gly Gly Asp Gly Gly Val Leu Arg Glu Ile Ser Arg His
115 120 125
Ser Ser Val Glu Val Ile Asp Ile Cys Glu Ile Asp Lys Met Val Ile
130 135 140
Asp Val Ser Lys Lys Phe Phe Pro Glu Leu Ala Val Gly Phe Asp Asp
145 150 155 160
Pro Arg Val Gln Leu His Ile Gly Asp Ala Ala Glu Phe Leu Arg Lys
165 170 175
Ser Pro Glu Gly Lys Tyr Asp Ala Ile Ile Val Asp Ser Ser Asp Pro
180 185 190
Val Gly Pro Ala Leu Ala Leu Val Glu Lys Pro Phe Phe Glu Thr Leu
195 200 205
Ala Arg Ala Leu Lys Pro Gly Gly Val Leu Cys Asn Met Ala Glu Ser
210 215 220
Met Trp Leu His Thr His Leu Ile Glu Asp Met Ile Ser Ile Cys Arg
225 230 235 240
Gln Thr Phe Lys Ser Val His Tyr Ala Trp Ser Ser Val Pro Thr Tyr
245 250 255
Pro Ser Gly Val Ile Gly Phe Val Leu Cys Ser Thr Glu Gly Pro Ala
260 265 270
Val Asp Phe Lys Asn Pro Ile Asn Pro Ile Glu Lys Leu Asp Gly Ala
275 280 285
Met Thr His Lys Arg Glu Leu Lys Phe Tyr Asn Ser Asp Met His Arg
290 295 300
Ala Ala Phe Ala Leu Pro Thr Phe Leu Arg Arg Glu Val Ala Ser Leu
305 310 315 320
Leu Ala Ser

(2) INFORMATION FOR SEQ ID NO:886:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 439 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..439
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568234

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:886:

cacaaattca	gaagaaCaag	aacagagaaa	acagaggaag	aggtgagatg	gaggaaacttg	60
tagggcttct	gagaatccga	gtgaagagag	ggatcaatct	tgctcagcga	gacactctaa	120
gcagcgaccc	ttttgttgtc	ataaccatgg	gatcacagaa	gctgaagact	cgtgttgtgg	180
aaaataactg	caaccctgag	tggaacgagg	aattaacctt	tgcgttaaga	catcccgatg	240
aacctgtgaa	tcctgatagt	tatgataaag	atacattcac	atcgcacgac	aagatgggag	300
atgcaaagat	agatatataa	ccatttctgg	aggttoacaa	aatgggtttg	caagaacttc	360
cagatggaac	agagatcaag	agagttgtga	taactttgat	ggatagtgtt	ctgaaatcac	420
tccttttgtt	ttggagccc					

(2) INFORMATION FOR SEQ ID NO:887:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 145 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:

(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..145
 (D) OTHER INFORMATION: / Ceres Seq. ID 1568235
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:887:
Gln Ile Gln Lys Asn Lys Asn Arg Glu Asn Arg Gly Arg Gly Glu Met
1 5 10 15
Glu Glu Leu Val Gly Leu Leu Arg Ile Arg Val Lys Arg Gly Ile Asn
 20 25 30
Leu Ala Gln Arg Asp Thr Leu Ser Ser Asp Pro Phe Val Val Ile Thr
 35 40 45
Met Gly Ser Gln Lys Leu Lys Thr Arg Val Val Glu Asn Asn Cys Asn
 50 55 60
Pro Glu Trp Asn Glu Glu Leu Thr Leu Ala Leu Arg His Pro Asp Gly
65 70 75 80
Pro Val Asn Leu Ile Val Tyr Asp Lys Asp Thr Phe Thr Ser His Asp
 85 90 95
Lys Met Gly Asp Ala Lys Ile Asp Ile Lys Pro Phe Leu Glu Val His
 100 105 110
Lys Met Gly Leu Gln Glu Leu Pro Asp Gly Thr Glu Ile Lys Arg Val
 115 120 125
Val Ile Thr Leu Met Asp Ser Val Leu Lys Ser Leu Phe Leu Val Trp
130 135 140
Ser
145
(2) INFORMATION FOR SEQ ID NO:888:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 130 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..130
 (D) OTHER INFORMATION: / Ceres Seq. ID 1568236
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:888:
Met Glu Glu Leu Val Gly Leu Leu Arg Ile Arg Val Lys Arg Gly Ile
1 5 10 15
Asn Leu Ala Gln Arg Asp Thr Leu Ser Ser Asp Pro Phe Val Val Ile
 20 25 30
Thr Met Gly Ser Gln Lys Leu Lys Thr Arg Val Val Glu Asn Asn Cys
 35 40 45
Asn Pro Glu Trp Asn Glu Glu Leu Thr Leu Ala Leu Arg His Pro Asp
 50 55 60
Glu Pro Val Asn Leu Ile Val Tyr Asp Lys Asp Thr Phe Thr Ser His
65 70 75 80
Asp Lys Met Gly Asp Ala Lys Ile Asp Ile Lys Pro Phe Leu Glu Val
 85 90 95
His Lys Met Gly Leu Gln Glu Leu Pro Asp Gly Thr Glu Ile Lys Arg
 100 105 110
Val Val Ile Thr Leu Met Asp Ser Val Leu Lys Ser Leu Phe Leu Val
115 120 125
Trp Ser
130
(2) INFORMATION FOR SEQ ID NO:889:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 97 amino acids
 (B) TYPE: amino acid

(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..97
(D) OTHER INFORMATION: / Ceres Seq. ID 1568237
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:889:
Met Gly Ser Gln Lys Leu Lys Thr Arg Val Glu Asn Asn Cys Asn
1 5 10 15
Pro Glu Trp Asn Glu Glu Leu Thr Leu Ala Leu Arg His Pro Asp Glu
20 25 30
Pro Val Asn Leu Ile Val Tyr Asp Lys Asp Thr Phe Thr Ser His Asp
35 40 45
Lys Met Gly Asp Ala Lys Ile Asp Ile Lys Pro Phe Leu Glu Val His
50 55 60
Lys Met Gly Leu Gln Glu Leu Pro Asp Gly Thr Glu Ile Lys Arg Val
65 70 75 80
Val Ile Thr Leu Met Asp Ser Val Leu Lys Ser Leu Phe Leu Val Trp
85 90 95
Ser

(2) INFORMATION FOR SEQ ID NO:890:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 602 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..602
(D) OTHER INFORMATION: / Ceres Seq. ID 1568263

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:890:

aacaagagcg tccttttgatt ggttttggat tttgtgtgt tcctctcaaa atgacaaaaac 60
tatggacttc tctctctgct ctctattccc tcgctggacc cgtggtgatg ctgctctatc 120
cgtttatatgc gtccgtgata gcaatagaga gcccatcaaa agtagatgac gagcaatggc 180
ttgcttatgtg gattctctat tctttcctta ctctatcaga actcctcctt caatctctcc 240
tagagtggat accgatatgg tacacggcga aGctagtgtt tgtggcatgg ttggttttac 300
cacaaatttag agggagctgct tttatataca acaaagtcgt gaggggaacag ttcaagaagt 360
acggcatcct caaacctaag gtagagcatc aggcgtgagtg agtcaaaaag aggaggggagc 420
acaagagggc ttcaactgttg gggctccag tttctaactc ctttttgctt thctattttt 480
gtcttataac tcttttgata tacggaaaaa tggggtagtt ctattattga gccctctgctt 540
gaatgtatgt gaagaagacct tttattcgac gttaaaatat tatattagag attataaaatt 600
tt

(2) INFORMATION FOR SEQ ID NO:891:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 132 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..132
(D) OTHER INFORMATION: / Ceres Seq. ID 1568264

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:891:

Gln Glu Arg Pro Leu Ile Gly Phe Gly Phe Cys Cys Val Pro Leu Lys
1 5 10 15
Met Thr Lys Leu Trp Thr Ser Leu Ser Ala Leu His Ser Leu Ala Gly
20 25 30

Pro Val Val Met Leu Leu Tyr Pro Leu Tyr Ala Ser Val Ile Ala Ile
35 40 45
Glu Ser Pro Ser Lys Val Asp Asp Glu Gln Trp Leu Ala Tyr Trp Ile
50 55 60
Leu Tyr Ser Phe Leu Thr Leu Ser Glu Leu Ile Leu Gln Ser Leu Leu
65 70 75 80
Glu Trp Ile Pro Ile Trp Tyr Thr Ala Lys Leu Val Phe Val Ala Trp
85 90 95
Leu Val Leu Pro Gln Phe Arg Gly Ala Ala Phe Ile Tyr Asn Lys Val
100 105 110
Val Arg Glu Gln Phe Lys Lys Tyr Gly Ile Leu Lys Pro Lys Val Glu
115 120 125
His Gln Ala Glu
130

(2) INFORMATION FOR SEQ ID NO:892:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 116 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..116

(D) OTHER INFORMATION: / Ceres Seq. ID 1568265

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:892:

Met Thr Lys Leu Trp Thr Ser Leu Ser Ala Leu His Ser Leu Ala Gly
1 5 10 15
Pro Val Val Met Leu Leu Tyr Pro Leu Tyr Ala Ser Val Ile Ala Ile
20 25 30
Glu Ser Pro Ser Lys Val Asp Asp Glu Gln Trp Leu Ala Tyr Trp Ile
35 40 45
Leu Tyr Ser Phe Leu Thr Leu Ser Glu Leu Ile Leu Gln Ser Leu Leu
50 55 60
Glu Trp Ile Pro Ile Trp Tyr Thr Ala Lys Leu Val Phe Val Ala Trp
65 70 75 80
Leu Val Leu Pro Gln Phe Arg Gly Ala Ala Phe Ile Tyr Asn Lys Val
85 90 95
Val Arg Glu Gln Phe Lys Lys Tyr Gly Ile Leu Lys Pro Lys Val Glu
100 105 110
His Gln Ala Glu
115

(2) INFORMATION FOR SEQ ID NO:893:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 97 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..97

(D) OTHER INFORMATION: / Ceres Seq. ID 1568266

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:893:

Met Leu Leu Tyr Pro Leu Tyr Ala Ser Val Ile Ala Ile Glu Ser Pro
1 5 10 15
Ser Lys Val Asp Asp Glu Gln Trp Leu Ala Tyr Trp Ile Leu Tyr Ser
20 25 30
Phe Leu Thr Leu Ser Glu Leu Ile Leu Gln Ser Leu Leu Glu Trp Ile
35 40 45
Pro Ile Trp Tyr Thr Ala Lys Leu Val Phe Val Ala Trp Leu Val Leu

50	55	60	
Pro Gln Phe Arg Gly	Ala Ala Phe Ile Tyr Asn Lys Val Val Arg Glu		
65	70	75	80
Gln Phe Lys Lys Tyr	Gly Ile Leu Lys Pro Lys Val Glu His Gln Ala		
	85	90	95

Glu

(2) INFORMATION FOR SEQ ID NO:894:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1969 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1969
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568267

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:894:

aaaggctttt	aatattttat	catcttcagg	cttattcgat	ttctcttcaga	tttgaaatgg	60
tgctgtctcaa	ggctctctctc	gtctctactt	cgctatttga	tgccagaaaa	ccaggaaactt	120
ctggactccg	taagaagggtg	aaagtgttta	agcaaccaaa	ttaccttgaa	aattttgtcc	180
aggcaacggt	caatgctctt	actacagaga	aagttaaagg	tgcgacactt	gtgtttctctg	240
gtgatgggtcg	ttattattca	gagcaagcta	ttcagattat	agtaaaagatg	gcagcagcta	300
atgggtgttag	acgtgtgtgg	gttgggtcaaa	acagtcctgct	atcaactcct	gcagtatcag	360
ctattatttcg	tgaaaagata	ggggctgatg	gatctaaagc	cacaggagca	tttatcttaa	420
cagcaagctca	taactcctggt	ggcccaactg	aggatttcgg	aattaaagac	aatatggaaa	480
atgggtggacc	agctcctgaa	tcaatcactg	ataagattta	cgagaacaca	aagacaactca	540
aggagtacc	aatagcggaa	gatctacc	gggttgatat	ttctactatt	ggtataacca	600
gctttgaagg	acctgaagga	aagtttgacg	togaagtgtt	tgattctgca	gatgatacag	660
ttaaactaat	gaagtcaatc	ttcgactttg	aatccatcaa	gaaatttgcta	ttctatccaa	720
aattttacttt	ctgctatgat	cgattgcatg	gagtggtctg	agcatatgca	catgcgactc	780
ttgtcgaaga	actaggtgca	ccagaaaagt	cggtgttgaa	ctgtgtacc	aaggaggact	840
ttggaggggg	ccaccgggat	cccaatctta	cctatgctaa	ggagctcggt	gcacgcactg	900
gattgagtaa	aactgatgat	gctgggtggc	agcctccaga	ggttggtggc	gctgtgatg	960
gtgatgcaga	ccgaaacatg	atcctcggtt	aaaggttttt	cgtaactcct	tcggattcac	1020
ttgtcttaat	tgctgcaaat	gctgttgggg	ccataccata	cttcagctct	ggttttaaag	1080
gtgtgtctag	gagcatgccg	acctcagctg	cacttgatgt	cggttgcaaaa	aacttggggt	1140
tgaagttctt	tgaggttcca	acaggctgga	aattctttgg	caatctaagt	gatgctggga	1200
gtgtctctgt	atgcggagaa	gaagagtttg	gaaccgggtc	ggatcatatc	cgtagaagag	1260
atgggtactcg	ggcaggttctt	ctttggctat	caatactggc	tcacaagaac	agggaacc	1320
ttgatgggaa	tgcaaaactg	gtgacgggtg	aagacattgt	ccgccagcac	tggtgtacat	1380
atggccgtca	ctattacatc	cgatacgact	atgagaacgt	acgcgaact	tcagataaag	1440
aaactcatggg	acttttgggt	aagttgcaat	cttcacttcc	cgaagtcaac	aagattataa	1500
agggaattcca	tcagagaggt	gcaaatgttg	caagcccgaga	tgagttcgag	tacaagatc	1560
cagtagatgg	ctctgtttcca	aagcaccaag	ggatccgata	cttattcgag	gatgatacac	1620
gacttgtgtt	ccgtctctctg	ggaaactggc	cagaaggagc	aacaataaag	ctatacattg	1680
aacaatacga	gaaggagacc	tcaaaagatg	gcgcagatgc	tcaggatgct	cttgggtccc	1740
tggtgtgatg	tgcaattaaag	ctgtcgaaaa	tgcaagagtt	caccggcgca	tcataccaaa	1800
ctgtattacc	ataagacacg	tttcagaaga	cgctgtctcc	aataactact	tcattccaac	1860
ttcatttctt	atgaatttgg	gttttgcgtt	tttctgttta	ctgttatctc	tacacaagta	1920
tacttcaakA	catataatct	taattgaaata	tacattaggt	tgccaattg		

(2) INFORMATION FOR SEQ ID NO:895:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 417 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide

(B) LOCATION: 1..417

(D) OTHER INFORMATION: / Ceres Seq. ID 1568268

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:895:

```

Arg Leu Leu Ile Phe Tyr His Leu Gln Ala Tyr Ser Ile Phe Phe Arg
1      5      10      15
Phe Glu Met Val Ser Phe Lys Val Ser Leu Val Ser Thr Ser Pro Ile
20      25      30
Asp Gly Gln Lys Pro Gly Thr Ser Gly Leu Arg Lys Lys Val Lys Val
35      40      45
Phe Lys Gln Pro Asn Tyr Leu Glu Asn Phe Val Gln Ala Thr Phe Asn
50      55      60
Ala Leu Thr Thr Glu Lys Val Lys Gly Ala Thr Leu Val Val Ser Gly
65      70      75      80
Asp Gly Arg Tyr Tyr Ser Glu Gln Ala Ile Gln Ile Ile Val Lys Met
85      90      95
Ala Ala Ala Asn Gly Val Arg Arg Val Trp Val Gly Gln Asn Ser Leu
100     105     110
Leu Ser Thr Pro Ala Val Ser Ala Ile Ile Arg Glu Arg Val Gly Ala
115     120     125
Asp Gly Ser Lys Ala Thr Gly Ala Phe Ile Leu Thr Ala Ser His Asn
130     135     140
Pro Gly Gly Pro Thr Glu Asp Phe Gly Ile Lys Tyr Asn Met Glu Asn
145     150     155     160
Gly Gly Pro Ala Pro Glu Ser Ile Thr Asp Lys Ile Tyr Glu Asn Thr
165     170     175
Lys Thr Ile Lys Glu Tyr Pro Ile Ala Glu Asp Leu Pro Arg Val Asp
180     185     190
Ile Ser Thr Ile Gly Ile Thr Ser Phe Glu Gly Pro Glu Gly Lys Phe
195     200     205
Asp Val Glu Val Phe Asp Ser Ala Asp Asp Tyr Val Lys Leu Met Lys
210     215     220
Ser Ile Phe Asp Phe Glu Ser Ile Lys Lys Leu Leu Ser Tyr Pro Lys
225     230     235     240
Phe Thr Phe Cys Tyr Asp Ala Leu His Gly Val Ala Gly Ala Tyr Ala
245     250     255
His Arg Ile Phe Val Glu Glu Leu Gly Ala Pro Glu Ser Ser Leu Leu
260     265     270
Asn Cys Val Pro Lys Glu Asp Phe Gly Gly Gly His Pro Asp Pro Asn
275     280     285
Leu Thr Tyr Ala Lys Glu Leu Val Ala Arg Met Gly Leu Ser Lys Thr
290     295     300
Asp Asp Ala Gly Gly Glu Pro Pro Glu Phe Gly Ala Ala Ala Asp Gly
305     310     315     320
Asp Ala Asp Arg Asn Met Ile Leu Gly Lys Arg Phe Phe Val Thr Pro
325     330     335
Ser Asp Ser Val Ala Ile Ile Ala Ala Asn Ala Val Gly Ala Ile Pro
340     345     350
Tyr Phe Ser Ser Gly Leu Lys Gly Val Ala Arg Ser Met Pro Thr Ser
355     360     365
Ala Ala Leu Asp Val Val Ala Lys Asn Leu Gly Leu Lys Phe Phe Glu
370     375     380
Val Pro Thr Gly Trp Lys Phe Phe Gly Asn Leu Met Asp Ala Gly Met
385     390     395     400
Cys Ser Val Cys Gly Glu Glu Ser Phe Gly Thr Gly Ser Asp His Ile
405     410     415

```

Arg

(2) INFORMATION FOR SEQ ID NO:896:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 399 amino acids

(B) TYPE: amino acid

- (C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..399
(D) OTHER INFORMATION: / Ceres Seq. ID 1568269
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:896:

Met	Val	Ser	Phe	Lys	Val	Ser	Leu	Val	Ser	Thr	Ser	Pro	Ile	Asp	Gly
1				5					10					15	
Gln	Lys	Pro	Gly	Thr	Ser	Gly	Leu	Arg	Lys	Lys	Val	Lys	Val	Phe	Lys
			20					25					30		
Gln	Pro	Asn	Tyr	Leu	Glu	Asn	Phe	Val	Gln	Ala	Thr	Phe	Asn	Ala	Leu
			35				40					45			
Thr	Thr	Glu	Lys	Val	Lys	Gly	Ala	Thr	Leu	Val	Val	Ser	Gly	Asp	Gly
			50			55					60				
Arg	Tyr	Tyr	Ser	Glu	Gln	Ala	Ile	Gln	Ile	Ile	Val	Lys	Met	Ala	Ala
				70						75				80	
Ala	Asn	Gly	Val	Arg	Arg	Val	Trp	Val	Gly	Gln	Asn	Ser	Leu	Leu	Ser
				85					90				95		
Thr	Pro	Ala	Val	Ser	Ala	Ile	Ile	Arg	Glu	Arg	Val	Gly	Ala	Asp	Gly
			100					105					110		
Ser	Lys	Ala	Thr	Gly	Ala	Phe	Ile	Leu	Thr	Ala	Ser	His	Asn	Pro	Gly
			115					120				125			
Gly	Pro	Thr	Glu	Asp	Phe	Gly	Ile	Lys	Tyr	Asn	Met	Glu	Asn	Gly	Gly
			130			135						140			
Pro	Ala	Pro	Glu	Ser	Ile	Thr	Asp	Lys	Ile	Tyr	Glu	Asn	Thr	Lys	Thr
			145		150					155				160	
Ile	Lys	Glu	Tyr	Pro	Ile	Ala	Glu	Asp	Leu	Pro	Arg	Val	Asp	Ile	Ser
				165					170					175	
Thr	Ile	Gly	Ile	Thr	Ser	Phe	Glu	Gly	Pro	Glu	Gly	Lys	Phe	Asp	Val
			180					185					190		
Glu	Val	Phe	Asp	Ser	Ala	Asp	Asp	Tyr	Val	Lys	Leu	Met	Lys	Ser	Ile
			195				200					205			
Phe	Asp	Phe	Glu	Ser	Ile	Lys	Lys	Leu	Leu	Ser	Tyr	Pro	Lys	Phe	Thr
			210			215						220			
Phe	Cys	Tyr	Asp	Ala	Leu	His	Gly	Val	Ala	Gly	Ala	Tyr	Ala	His	Arg
				230					235					240	
Ile	Phe	Val	Glu	Glu	Leu	Gly	Ala	Pro	Glu	Ser	Ser	Leu	Leu	Asn	Cys
				245					250					255	
Val	Pro	Lys	Glu	Asp	Phe	Gly	Gly	Gly	His	Pro	Asp	Pro	Asn	Leu	Thr
			260					265					270		
Tyr	Ala	Lys	Glu	Leu	Val	Ala	Arg	Met	Gly	Leu	Ser	Lys	Thr	Asp	Asp
			275				280					285			
Ala	Gly	Gly	Glu	Pro	Pro	Glu	Phe	Gly	Ala	Ala	Ala	Asp	Gly	Asp	Ala
			290			295						300			
Asp	Arg	Asn	Met	Ile	Leu	Gly	Lys	Arg	Phe	Phe	Val	Thr	Pro	Ser	Asp
			305		310				315					320	
Ser	Val	Ala	Ile	Ile	Ala	Ala	Asn	Ala	Val	Gly	Ala	Ile	Pro	Tyr	Phe
				325					330					335	
Ser	Ser	Gly	Leu	Lys	Gly	Val	Ala	Arg	Ser	Met	Pro	Thr	Ser	Ala	Ala
			340				345						350		
Leu	Asp	Val	Val	Ala	Lys	Asn	Leu	Gly	Leu	Lys	Phe	Phe	Glu	Val	Pro
			355				360					365			
Thr	Gly	Trp	Lys	Phe	Phe	Gly	Asn	Leu	Met	Asp	Ala	Gly	Met	Cys	Ser
			370			375						380			
Val	Cys	Gly	Glu	Glu	Ser	Phe	Gly	Thr	Gly	Ser	Asp	His	Ile	Arg	
			385		390					395					

- (2) INFORMATION FOR SEQ ID NO:897:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 322 amino acids

(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..322
(D) OTHER INFORMATION: / Ceres Seq. ID 1568270
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:897:

Met	Ala	Ala	Ala	Asn	Gly	Val	Arg	Arg	Val	Trp	Val	Gly	Gln	Asn	Ser
1				5					10					15	
Leu	Leu	Ser	Thr	Pro	Ala	Val	Ser	Ala	Ile	Ile	Arg	Glu	Arg	Val	Gly
			20					25					30		
Ala	Asp	Gly	Gly	Ser	Lys	Ala	Thr	Gly	Ala	Phe	Ile	Leu	Thr	Ala	Ser
			35					40					45		His
Asn	Pro	Gly	Gly	Pro	Thr	Glu	Asp	Phe	Gly	Ile	Lys	Tyr	Asn	Met	Glu
			50			55					60				
Asn	Gly	Gly	Pro	Ala	Pro	Glu	Ser	Ile	Thr	Asp	Lys	Ile	Tyr	Glu	Asn
65					70				75					80	
Thr	Lys	Thr	Ile	Lys	Glu	Tyr	Pro	Ile	Ala	Glu	Asp	Leu	Pro	Arg	Val
			85						90				95		
Asp	Ile	Ser	Thr	Ile	Gly	Ile	Thr	Ser	Phe	Glu	Gly	Pro	Glu	Gly	Lys
			100					105					110		
Phe	Asp	Val	Glu	Val	Phe	Asp	Ser	Ala	Asp	Asp	Tyr	Val	Lys	Leu	Met
			115					120				125			
Lys	Ser	Ile	Phe	Asp	Phe	Glu	Ser	Ile	Lys	Lys	Leu	Leu	Ser	Tyr	Pro
			130			135						140			
Lys	Phe	Thr	Phe	Cys	Tyr	Asp	Ala	Leu	His	Gly	Val	Ala	Gly	Ala	Tyr
145				150					155					160	
Ala	His	Arg	Ile	Phe	Val	Glu	Glu	Leu	Gly	Ala	Pro	Glu	Ser	Ser	Leu
			165					170						175	
Leu	Asn	Cys	Val	Pro	Lys	Glu	Asp	Phe	Gly	Gly	Gly	His	Pro	Asp	Pro
			180					185					190		
Asn	Leu	Thr	Tyr	Ala	Lys	Glu	Leu	Val	Ala	Arg	Met	Gly	Leu	Ser	Lys
			195				200					205			
Thr	Asp	Asp	Ala	Gly	Gly	Glu	Pro	Pro	Glu	Phe	Gly	Ala	Ala	Ala	Asp
			210			215					220				
Gly	Asp	Ala	Asp	Arg	Asn	Met	Ile	Leu	Gly	Lys	Arg	Phe	Phe	Val	Thr
225				230						235				240	
Pro	Ser	Asp	Ser	Val	Ala	Ile	Ile	Ala	Ala	Asn	Ala	Val	Gly	Ala	Ile
			245						250					255	
Pro	Tyr	Phe	Ser	Ser	Gly	Leu	Lys	Gly	Val	Ala	Arg	Ser	Met	Pro	Thr
			260					265					270		
Ser	Ala	Ala	Leu	Asp	Val	Val	Ala	Lys	Asn	Leu	Gly	Leu	Lys	Phe	Phe
			275					280					285		
Glu	Val	Pro	Thr	Gly	Trp	Lys	Phe	Phe	Gly	Asn	Leu	Met	Asp	Ala	Gly
			290			295					300				
Met	Cys	Ser	Val	Cys	Gly	Glu	Glu	Ser	Phe	Gly	Thr	Gly	Ser	Asp	His
305					310					315				320	
Ile	Arg														

- (2) INFORMATION FOR SEQ ID NO:898:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1445 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..1445

(D) OTHER INFORMATION: / Ceres Seq. ID 1568286

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:898:

gcacaaaccac	cgccgtatata	ccacggccgt	cttatcaccg	gcaacaaccg	taggtttttg	60
ttttccgtcg	cgatggaggt	ggataagaag	gacgagagag	aggctgaatc	ttcggagcaa	120
gtgggtgaatc	catgggaagt	gtccgccaaa	gacggcgga	agatcgatta	cgacaagctt	180
attgacaaat	ttggatgtca	aaggcttgac	gagtcactga	ttgatctgtg	tcagagactg	240
acttctcgtc	aaccacacgt	gttccctccg	cgtagtgtct	tcttcgccca	Cggggatttc	300
aatgagattt	tggagcgtta	tgagagagga	gacaagtctt	atctctacac	tggaagagga	360
cttctcatcag	aagcattgca	tttggggcat	ttgattccct	tcatgtttac	caaataactg	420
caagaagctt	tcaaggttcc	ccttggtata	cagctcacgg	atgatgaaaa	aagatatatg	480
aagaacttat	cggtggagga	aagtcaaaag	cttgccagag	aaaatgcgaa	agatatattt	540
gctgtgggat	tcgatgtaac	aaagaccttc	attttctcgg	acttcgacta	gttgccgggt	600
gctttctata	aaaatatggt	gaaggttggc	aagtcggtta	cacttaataa	ggctatggga	660
atctttggct	tttccgggtg	agatcctatc	gcgaaactca	gtttccctcc	tgtgcaggga	720
gttccatctt	ttcctagctc	attccacat	ttgttccctg	gcaaggacaa	tctccgctgc	780
ttgattccct	gtgctattgt	ccaggatcct	tattttagaa	tgactcgtga	tgtcgcacc	840
cggttgaggc	atagcaagcc	cgccctgatt	gagtcacat	tttttccctg	gttgccaggga	900
gagaatggaa	aaatgtctgc	tagtgatcca	aattctgcta	tctatgtgac	tgattccgca	960
aaggacatta	aaaacaagat	aaacagatat	cggttttagt	gtgggcaaga	ctccattgag	1020
aagcacccag	aacttggagc	aaatctcgag	gttgacatac	ccgtcaagta	tctgagtttc	1080
ttcctcgaag	acgattctga	actagaacac	attaaaaagg	aatatggaga	aggaagaatg	1140
ctaaccaggag	aagtaaaagaa	gagacttacg	gaagtgttga	cagaatattg	ggagaaacac	1200
cgcaggggctc	gagctgctgt	tactgatgag	atggttgatg	cgctcatggc	ggtgagacct	1260
ctcccaagca	agttcgaaata	gaaaaagtca	gaaacccctt	ttggctctct	agcaacttca	1320
caTcYactcc	gtttgatttg	gatcagacga	tctttgggtg	tctattgata	gatttgatcc	1380
ttgaaattga	accatacttg	ttagtgtacaa	tttcatatt	tacatttatt	tatgaatcac	1440
attct						

(2) INFORMATION FOR SEQ ID NO:899:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 426 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..426
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568287

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:899:

Ala	Lys	Pro	Pro	Pro	Tyr	Ile	His	Gly	Arg	Leu	Ile	Thr	Gly	Asn	Asn
1				5				10					15		
Arg	Arg	Phe	Leu	Phe	Ser	Val	Ala	Met	Glu	Val	Asp	Lys	Lys	Asp	Glu
			20					25					30		
Arg	Glu	Ala	Glu	Ser	Ser	Glu	Gln	Val	Val	Asn	Pro	Trp	Glu	Val	Ser
			35					40				45			
Ala	Lys	Asp	Gly	Gly	Lys	Ile	Asp	Tyr	Asp	Lys	Leu	Ile	Asp	Lys	Phe
			50					55				60			
Gly	Cys	Gln	Arg	Leu	Asp	Glu	Ser	Leu	Ile	Asp	Arg	Val	Gln	Arg	Leu
			70					75					80		
Thr	Ser	Arg	Gln	Pro	His	Val	Phe	Leu	Arg	Arg	Ser	Val	Phe	Phe	Ala
			85					90					95		
His	Arg	Asp	Phe	Asn	Glu	Ile	Leu	Asp	Ala	Tyr	Glu	Arg	Gly	Asp	Lys
			100					105					110		
Phe	Tyr	Leu	Tyr	Thr	Gly	Arg	Gly	Pro	Ser	Ser	Glu	Ala	Leu	His	Leu
			115					120				125			
Gly	His	Leu	Ile	Pro	Phe	Met	Phe	Thr	Lys	Tyr	Leu	Gln	Glu	Ala	Phe
			130					135				140			
Lys	Val	Pro	Leu	Val	Ile	Gln	Leu	Thr	Asp	Asp	Glu	Lys	Ser	Ile	Trp
			145					150				155			160
Lys	Asn	Leu	Ser	Val	Glu	Glu	Ser	Gln	Arg	Leu	Ala	Arg	Glu	Asn	Ala
			165					170						175	

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Lys Asp Ile Ile Ala Cys Gly Phe Asp Val Thr Lys Thr Phe Ile Phe
180 185 190
Ser Asp Phe Asp Tyr Val Gly Gly Ala Phe Tyr Lys Asn Met Val Lys
195 200 205
Val Gly Lys Cys Val Thr Leu Asn Lys Ala Met Gly Ile Phe Gly Phe
210 215 220
Ser Gly Glu Asp Pro Ile Ala Lys Leu Ser Phe Pro Pro Val Gln Ala
225 230 235 240
Val Pro Ser Phe Pro Ser Ser Phe Pro His Leu Phe Pro Gly Lys Asp
245 250 255
Asn Leu Arg Cys Leu Ile Pro Cys Ala Ile Asp Gln Asp Pro Tyr Phe
260 265 270
Arg Met Thr Arg Asp Val Ala Pro Arg Leu Gly Tyr Ser Lys Pro Ala
275 280 285
Leu Ile Glu Ser Thr Phe Phe Pro Ala Leu Gln Gly Glu Asn Gly Lys
290 295 300
Met Ser Ala Ser Asp Pro Asn Ser Ala Ile Tyr Val Thr Asp Ser Ala
305 310 315 320
Lys Asp Ile Lys Asn Lys Ile Asn Arg Tyr Ala Phe Ser Gly Gly Gln
325 330 335
Asp Ser Ile Glu Lys His Arg Glu Leu Gly Ala Asn Leu Glu Val Asp
340 345 350
Ile Pro Val Lys Tyr Leu Ser Phe Phe Leu Glu Asp Asp Ser Glu Leu
355 360 365
Glu His Ile Lys Lys Glu Tyr Gly Glu Gly Arg Met Leu Thr Gly Glu
370 375 380
Val Lys Lys Arg Leu Thr Glu Val Leu Thr Glu Ile Val Glu Lys His
385 390 395 400
Arg Arg Ala Arg Ala Ala Val Thr Asp Glu Met Val Asp Ala Phe Met
405 410 415
Ala Val Arg Pro Leu Pro Ser Lys Phe Glu
420 425

(2) INFORMATION FOR SEQ ID NO:900:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 402 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..402
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568288

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:900:

Met Glu Val Asp Lys Lys Asp Glu Arg Glu Ala Glu Ser Ser Glu Gln
1 5 10 15
Val Val Asn Pro Trp Glu Val Ser Ala Lys Asp Gly Gly Lys Ile Asp
20 25 30
Tyr Asp Lys Leu Ile Asp Lys Phe Gly Cys Gln Arg Leu Asp Glu Ser
35 40 45
Leu Ile Asp Arg Val Gln Arg Leu Thr Ser Arg Gln Pro His Val Phe
50 55 60
Leu Arg Arg Ser Val Phe Phe Ala His Arg Asp Phe Asn Glu Ile Leu
65 70 75 80
Asp Ala Tyr Glu Arg Gly Asp Lys Phe Tyr Leu Tyr Thr Gly Arg Gly
85 90 95
Pro Ser Ser Glu Ala Leu His Leu Gly His Leu Ile Pro Phe Met Phe
100 105 110
Thr Lys Tyr Leu Gln Glu Ala Phe Lys Val Pro Leu Val Ile Gln Leu
115 120 125
Thr Asp Asp Glu Lys Ser Ile Trp Lys Asn Leu Ser Val Glu Glu Ser

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(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 292 amino acids

(C) STRANDEDNESS:

MOLECULE TYPE: peptid

(A) NAME/KEY: peptid

(D) OTHER INFORMATION

SEQUENCE DESCRIPTION: SEQ ID NO:901:
 Ser Lys Tyr Leu Gln Glu Ala Phe Lys Val Pro Leu

5 10

Trp Met Ser Ser Gly Ile Ser Ile Trp Lys A

Gln Leu Thr Asp Asp Glu Lys Ser Ile Trp Lys Asn Leu Ser Val Glu

20 25 30

Glu Ser Gln Arg Leu Ala Arg Glu Asn Ala Lys Asp Ile Ile Ala Cys

35 40 45

Gly Phe Asp Val Thr Lys Thr Phe Ile Phe Ser Asp Phe Asp Tyr Val

50 55 60

Gly Gly Ala Phe Tyr Lys Asn Met Val Lys Val Gly Lys Cys Val Thr

65 70 75 80

Leu Asn Lys Ala Met Gly Ile Phe Gly Phe Ser Gly Glu Asp Pro Ile

85 90 95

Ala Lys Leu Ser Phe Pro Pro Val Gln Ala Val Pro Ser Phe Pro Ser

100	105	110
-----	-----	-----

```

Ser Phe Pro His Leu Phe Pro Gly Lys Asp Asn Leu Arg Cys Leu Ile
    115                120                125
Pro Cys Ala Ile Asp Gln Asp Pro Tyr Phe Arg Met Thr Arg Asp Val
    130                135                140
Ala Pro Arg Leu Gly Tyr Ser Lys Pro Ala Leu Ile Glu Ser Thr Phe
    145                150                155                160
Phe Pro Ala Leu Gln Gly Glu Asn Gly Lys Met Ser Ala Ser Asp Pro
    165                170                175
Asn Ser Ala Ile Tyr Val Thr Asp Ser Ala Lys Asp Ile Lys Asn Lys
    180                185                190
Ile Asn Arg Tyr Ala Phe Ser Gly Gly Gln Asp Ser Ile Glu Lys His
    195                200                205
Arg Glu Leu Gly Ala Asn Leu Glu Val Asp Ile Pro Val Lys Tyr Leu
    210                215                220
Ser Phe Phe Leu Glu Asp Asp Ser Glu Leu Glu His Ile Lys Lys Glu
    225                230                235                240
Tyr Gly Glu Gly Arg Met Leu Thr Gly Glu Val Lys Lys Arg Leu Thr
    245                250                255
Glu Val Leu Thr Glu Ile Val Glu Lys His Arg Arg Ala Arg Ala Ala
    260                265                270
Val Thr Asp Glu Met Val Asp Ala Phe Met Ala Val Arg Pro Leu Pro
    275                280                285
Ser Lys Phe Glu
    290

```

(2) INFORMATION FOR SEQ ID NO:902:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 904 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..904
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568300

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:902:

```

ctttttttcg agaaaaacgA agttttctga gctaaactag atcagctatg ggcagccggtg    60
gtgctgcggc ggatttggaa gatgttcaga cggtggatct catgtcggag ctctcccgcc    120
gcctcaagtg ttctcagaag ccgcacaaac gcctcatctt cattggacat ccagggtcag    180
gaaaagggtac tcaatctcca gtagtgaagg atgagtattg cttgtgtcac ttatccactg    240
gagacatggt aagagctgct gtgtcttcta agacccctct tgggtgtaag gctaaagaag    300
ctatggaaaa aggagagctc gtctctgatg atttggttgt tgggtataatt gatgaagcca    360
tgaaacagcc aaaaatgcac aaaggattta tcttgatGg gttccccagg actgttactc    420
aggcagagaa cgtctgatgag atgcttaaga ggcgaggaaac tgaaaattgac aaagtcttca    480
actttgtcat tgatgacgca atcttggagg aaagaataac cgggcatgag atccaccat    540
cgagtggcag gagttaccac accaaatttg ctctcccaa aaccctgga gttgatgata    600
ttactggaga gcctctgac caacgtaaag atgataacgc tgatgttcta aagtcgagggc    660
tttcagcttt ccacagtcac actcaaccgg tgattgatta ctacgcaaag agggccgttc    720
tcacaaacat ccaggccgag aaggctcccc aagaagttac atcagaggtt aaaaagagcat    780
tgtcatgac aaagactcct caagcaaatc atctcctctg gttagaatcc attcttttcc    840
ttactacaag agagagacac atctatataa tccactcatc tgcggaatga cagttttttc    900
tttt

```

(2) INFORMATION FOR SEQ ID NO:903:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 246 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide

(B) LOCATION: 1..246

(D) OTHER INFORMATION: / Ceres Seq. ID 1568301

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:903:

```
Met Ala Thr Gly Gly Ala Ala Ala Asp Leu Glu Asp Val Gln Thr Val
1      5      10
Asp Leu Met Ser Glu Leu Leu Arg Arg Leu Lys Cys Ser Gln Lys Pro
20      25      30
Asp Lys Arg Leu Ile Phe Ile Gly Pro Pro Gly Ser Gly Lys Gly Thr
35      40      45
Gln Ser Pro Val Val Lys Asp Glu Tyr Cys Leu Cys His Leu Ser Thr
50      55      60
Gly Asp Met Leu Arg Ala Ala Val Ala Ser Lys Thr Pro Leu Gly Val
65      70      75      80
Lys Ala Lys Glu Ala Met Glu Lys Gly Glu Leu Val Ser Asp Asp Leu
85      90      95
Val Val Gly Ile Ile Asp Glu Ala Met Asn Lys Pro Lys Cys Gln Lys
100      105      110
Gly Phe Ile Leu Asp Gly Phe Pro Arg Thr Val Thr Gln Ala Glu Lys
115      120      125
Leu Asp Glu Met Leu Lys Arg Arg Gly Thr Glu Ile Asp Lys Val Leu
130      135      140
Asn Phe Ala Ile Asp Asp Ala Ile Leu Glu Glu Arg Ile Thr Gly Arg
145      150      155      160
Trp Ile His Pro Ser Ser Gly Arg Ser Tyr His Thr Lys Phe Ala Pro
165      170      175
Pro Lys Thr Pro Gly Val Asp Asp Ile Thr Gly Glu Pro Leu Ile Gln
180      185      190
Arg Lys Asp Asp Asn Ala Asp Val Leu Lys Ser Arg Leu Ala Ala Phe
195      200      205
His Ser Gln Thr Gln Pro Val Ile Asp Tyr Tyr Ala Lys Lys Ala Val
210      215      220
Leu Thr Asn Ile Gln Ala Glu Lys Ala Pro Gln Glu Val Thr Ser Glu
225      230      235      240
Val Lys Lys Ala Leu Ser
245
```

(2) INFORMATION FOR SEQ ID NO:904:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 228 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..228

(D) OTHER INFORMATION: / Ceres Seq. ID 1568302

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:904:

```
Met Ser Glu Leu Leu Arg Arg Leu Lys Cys Ser Gln Lys Pro Asp Lys
1      5      10      15
Arg Leu Ile Phe Ile Gly Pro Pro Gly Ser Gly Lys Gly Thr Gln Ser
20      25      30
Pro Val Val Lys Asp Glu Tyr Cys Leu Cys His Leu Ser Thr Gly Asp
35      40      45
Met Leu Arg Ala Ala Val Ala Ser Lys Thr Pro Leu Gly Val Lys Ala
50      55      60
Lys Glu Ala Met Glu Lys Gly Glu Leu Val Ser Asp Asp Leu Val Val
65      70      75      80
Gly Ile Ile Asp Glu Ala Met Asn Lys Pro Lys Cys Gln Lys Gly Phe
85      90      95
Ile Leu Asp Gly Phe Pro Arg Thr Val Thr Gln Ala Glu Lys Leu Asp
100      105      110
```

Glu Met Leu Lys Arg Arg Gly Thr Glu Ile Asp Lys Val Leu Asn Phe
115 120 125
Ala Ile Asp Asp Ala Ile Leu Glu Glu Arg Ile Thr Gly Arg Trp Ile
130 135 140
His Pro Ser Ser Gly Arg Ser Tyr His Thr Lys Phe Ala Pro Pro Lys
145 150 155 160
Thr Pro Gly Val Asp Asp Ile Thr Gly Glu Pro Leu Ile Gln Arg Lys
165 170 175
Asp Asp Asn Ala Asp Val Leu Lys Ser Arg Leu Ala Ala Phe His Ser
180 185 190
Gln Thr Gln Pro Val Ile Asp Tyr Tyr Ala Lys Lys Ala Val Leu Thr
195 200 205
Asn Ile Gln Ala Glu Lys Ala Pro Gln Glu Val Thr Ser Glu Val Lys
210 215 220
Lys Ala Leu Ser
225

(2) INFORMATION FOR SEQ ID NO:905:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 180 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..180
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568303

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:905:

Met Leu Arg Ala Ala Val Ala Ser Lys Thr Pro Leu Gly Val Lys Ala
1 5 10 15
Lys Glu Ala Met Glu Lys Gly Glu Leu Val Ser Asp Asp Leu Val Val
20 25 30
Gly Ile Ile Asp Glu Ala Met Asn Lys Pro Lys Cys Gln Lys Gly Phe
35 40 45
Ile Leu Asp Gly Phe Pro Arg Thr Val Thr Gln Ala Glu Lys Leu Asp
50 55 60
Glu Met Leu Lys Arg Arg Gly Thr Glu Ile Asp Lys Val Leu Asn Phe
65 70 75 80
Ala Ile Asp Asp Ala Ile Leu Glu Glu Arg Ile Thr Gly Arg Trp Ile
85 90 95
His Pro Ser Ser Gly Arg Ser Tyr His Thr Lys Phe Ala Pro Pro Lys
100 105 110
Thr Pro Gly Val Asp Asp Ile Thr Gly Glu Pro Leu Ile Gln Arg Lys
115 120 125
Asp Asp Asn Ala Asp Val Leu Lys Ser Arg Leu Ala Ala Phe His Ser
130 135 140
Gln Thr Gln Pro Val Ile Asp Tyr Tyr Ala Lys Lys Ala Val Leu Thr
145 150 155 160
Asn Ile Gln Ala Glu Lys Ala Pro Gln Glu Val Thr Ser Glu Val Lys
165 170 175
Lys Ala Leu Ser
180

(2) INFORMATION FOR SEQ ID NO:906:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1303 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -

(B) LOCATION: 1..1303

(D) OTHER INFORMATION: / Ceres Seq. ID 1568304

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:906:

aaagctcaga	tatctgaata	actcgtcttc	gtgcctctct	ctctctaaaa	gccatctct	60
ttctctctct	ctctctccat	tgaagaagaa	acctacottc	gtaattattc	ctcaattacg	120
atacatggtg	atgtttaaagg	gtcaacccaaa	aaatogaatc	ttgatcgatt	cottcattgc	180
ttgtggcatt	tagtgccacc	ccaatctctc	cccaagacgg	agattagaac	cctaaatcga	240
ttgtggcatt	catgggagag	acaaaaggtt	gagtttttca	ggttgagtga	ttttggggat	300
tgttatgatg	aatggagcgc	ttatggagct	agcgtttcta	ttcatgttac	caacggagaa	360
ttctttgttc	aatactatgt	tccttatctc	ttcgccatcc	agattttcac	cttctattcc	420
ttcttgatcc	gcttaagggg	agagctctga	gatgggggat	gtgagggtag	agatccggtt	480
agcgattcag	gtacggatga	gagtgctctc	gagggaagac	ttgagaacaa	caacgctttg	540
catccaagtg	atcgttttgg	ttatctttat	ctccaatact	ttgagagatc	agctccttat	600
accagagttc	ctctgatgga	taagatcaat	gaattggctc	aaagataccc	gggattgatg	660
tcgtttgaga	gcgttgatct	ttctccagct	agttggatgt	cagtagcatg	gtacccgatt	720
taccatatac	caatgggaag	aaccattaaa	gacttatcca	cgtgtttctc	cacttatcac	780
actctttctc	cttcttttca	agatatggaa	ccgggaagaaa	atgggtgggga	caaggagaga	840
gtgcggaggg	aagggggaaga	tataactctg	ctcccatctt	ggatgggtac	ttacaagatg	900
caaggcgatg	tttggctttc	gcaggaccac	gatgatcaag	agagattggc	ttcgtctttac	960
agtggttcgg	attcttgctc	taaacagctc	aggggtccaac	atcatgactt	caactacttc	1020
tgcaatatgt	caatgaactca	tcgtggctaa	acctcggttg	gatgacacca	tgatgtttgc	1080
ttgtttcttc	atatatagtc	taattcttgc	tttgtcttgc	aaccgcttgc	gttttgtaaa	1140
acgcatagga	gcgattcgct	ttgcagtggt	ttggttagaa	tagcgttttc	agttctctaa	1200
ccattgagag	agtatatgtc	gtatatagag	ttttgttgct	tggtgaaaca	gagtacaatt	1260
gtgtgtgctt	gtaaaaaaca	gagtgattgt	ttcttataag	ttg		

(2) INFORMATION FOR SEQ ID NO:907:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 308 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..308

(D) OTHER INFORMATION: / Ceres Seq. ID 1568305

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:907:

Met	Val	Asn	Val	Lys	Gly	Ser	Thr	Lys	Lys	Ser	Asn	Leu	Asp	Arg	Phe
1		5		10		15		20		25		30		35	
Leu	His	Cys	Ile	Thr	Pro	Leu	Val	Pro	Pro	Gln	Ser	Leu	Pro	Lys	Thr
		20		25		30		35		40		45		50	
Glu	Ile	Arg	Thr	Leu	Asn	Arg	Leu	Trp	His	Pro	Trp	Glu	Arg	Gln	Lys
		35		40		45		50		55		60		65	
Val	Glu	Phe	Phe	Arg	Leu	Ser	Asp	Leu	Trp	Asp	Cys	Tyr	Asp	Glu	Trp
		50		55		60		65		70		75		80	
Ser	Ala	Tyr	Gly	Ala	Ser	Val	Pro	Ile	His	Val	Thr	Asn	Gly	Glu	Ser
		65		70		75		80		85		90		95	
Leu	Val	Gln	Tyr	Tyr	Val	Pro	Tyr	Leu	Ser	Ala	Ile	Gln	Ile	Phe	Thr
		85		90		95		100		105		110		115	
Ser	His	Ser	Ser	Leu	Ile	Arg	Leu	Arg	Glu	Ser	Glu	Asp	Gly	Gly	Glu
		100		105		110		115		120		125		130	
Cys	Glu	Gly	Arg	Asp	Pro	Phe	Ser	Asp	Ser	Gly	Ser	Asp	Glu	Ser	Val
		115		120		125		130		135		140		145	
Ser	Glu	Gly	Leu	Glu	Asn	Asn	Thr	Leu	Leu	His	Pro	Ser	Asp	Arg	
		130		135		140		145		150		155		160	
Leu	Gly	Tyr	Leu	Tyr	Leu	Gln	Tyr	Phe	Glu	Arg	Ser	Ala	Pro	Tyr	Thr
		145		150		155		160		165		170		175	
Arg	Val	Pro	Leu	Met	Asp	Lys	Ile	Asn	Glu	Leu	Ala	Gln	Arg	Tyr	Pro
		165		170		175		180		185		190		195	
Gly	Leu	Met	Ser	Leu	Arg	Ser	Val	Asp	Leu	Ser	Pro	Ala	Ser	Trp	Met
		180		185		190		195		200		205		210	

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Ser Val Ala Trp Tyr Pro Ile Tyr His Ile Pro Met Gly Arg Thr Ile
195 200 205
Lys Asp Leu Ser Thr Cys Phe Leu Thr Tyr His Thr Leu Ser Ser Ser
210 215 220
Phe Gln Asp Met Glu Pro Glu Glu Asn Gly Gly Asp Lys Glu Arg Val
225 230 235 240
Arg Arg Glu Gly Glu Asp Ile Thr Leu Leu Pro Phe Gly Met Ala Thr
245 250 255
Tyr Lys Met Gln Gly Asp Val Trp Leu Ser Gln Asp His Asp Asp Gln
260 265 270
Glu Arg Leu Ala Ser Leu Tyr Ser Val Ala Asp Ser Trp Leu Lys Gln
275 280 285
Leu Arg Val Gln His His Asp Phe Asn Tyr Phe Cys Asn Met Ser Met
290 295 300
Thr His Arg Gly

(2) INFORMATION FOR SEQ ID NO:908:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1963 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1963
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568309

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:908:

atttaattggc	aaagccggaa	aatgacgtca	tcttaaccga	gaaacaaaca	tggagcacat	60
gggaagagct	tctctcgcgc	tgccgcgtac	accgtcacgg	taccgaatca	tggaaactctg	120
tttccgcgtga	aatccagaaa	ctgagtcoca	acctctgttc	cctcacgcgc	tcgcgttgcc	180
gccacaagta	ctctgacctc	aaaagccggt	tcactcaaga	gctggccgta	ccggaatccg	240
tcgctcgcat	ctcaaacgct	ccttggttag	aggagttaag	gaagctccgc	gtcgaatgagc	300
tcgcgtcgca	agttgaacag	tacgatttat	ccatctcaac	gttgcatcgc	aaggtggaagc	360
aaattggaaga	agagagagag	atgagtttca	ttaaaccgga	cacggaaaac	gagaatttag	420
atctagagag	gaagaaagag	cgtagCGatG	tccggtgaac	cagtcocaaa	ccgcgcgggt	480
cagctaattga	acgaaaccat	ttctccagat	cccaaagaaa	tcggatcgga	aaacacggag	540
agggaggagg	aaatggccgc	aagcgcgcgc	ggagaatcga	agcttgccgc	agaggattct	600
tgtagaggaa	gctgtgaaag	tgtggagaag	gaactgacga	cgaactcgga	gagagttgaa	660
ccggtgagtg	tgaccagagt	gatagagtcg	gaggacggag	cgaagtcgtg	agaggagatt	720
actagtatg	tgacagagtc	gcgagcttgc	ccaagaaagg	gaacgtcgga	gccggataag	780
gaagatcaat	ctccgacgag	cgccaaagat	ttcacccgtg	aatcacagcc	gttgattagt	840
tttgcgaga	tcttctctgc	tcatccctgt	ggttcccaat	tttcgcccgc	actcgaaagt	900
caggaaacaa	ttgagtgatc	tacaataatt	agagagcacg	tagattttga	gataattcgc	960
aagcgagtcg	aaggaggctt	gtacaaaagt	tggaggatca	actctttctg	tgatttgcgt	1020
ctacttgtga	ataatgcaag	agtggtttat	cagagaagat	cttcagaggt	taaattttgt	1080
gagcagcttc	accaactcgt	caagaaacag	atgactacta	ctctcaaggg	acttagtaat	1140
agagatgaga	tctcaatctc	accaccacaa	gaagaagtgt	ttgcaatccc	ttcatcaaa	1200
ctctgtttct	ctaaaccaa	aattgtctgt	cctaattatg	tagcttctgc	gaaacgtagt	1260
gccttggctg	ctaaaccttt	gctattattg	cctcctggac	cagataaaaa	ggccaaagaa	1320
acagatcatg	ttgtggacta	tgatgagaag	cgggtttcac	acaaggtatg	tgaagcctct	1380
gggaagacgc	atgatgactc	tctgattgtg	aagataataa	ctagaggaag	aacctcctcg	1440
acgggaaaag	tagctaacag	gaacgtcaag	aaccgtgact	ccagtttgaa	tgttgatgat	1500
agcaaaagata	aggttaagaa	aactgatgaa	gagaagaaag	gtggctcgaa	aaagaaaggg	1560
gtgcgaggtt	ttctcaggag	aatgaaaagt	ggactcttcg	atgacacatt	gaagcgtagc	1620
ttctgtctgc	attcttctac	tacgggaaaa	ggaggaggag	cggaaacagag	gaagaataac	1680
agcaacaaag	ctgataataa	gaaaacacgc	ataccaagga	taagacaaga	aaataagaaa	1740
gcaagctctg	tgaagagaag	caataatggt	cgaaactcag	aaagagaagc	tgctccatct	1800
tactctattc	tagcaaaagc	aagcagagaa	gctggtgaaa	aagaggagcg	gtctttctat	1860
tcaccacgat	tgaagaaacg	tgcaaggagg	tgatgtagtt	gttgactaac	ttatataact	1920
taacttgaga	tgaaaatcag	aaactaataa	attccaaaga	gtc		

(2) INFORMATION FOR SEQ ID NO:909:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 481 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..481

(D) OTHER INFORMATION: / Ceres Seq. ID 1568310

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:909:

Met	Ser	Gly	Glu	Pro	Val	Pro	Asn	Pro	Pro	Val	Gln	Leu	Met	Asn	Glu	
1			5					10						15		
Thr	Ile	Ser	Pro	Asp	Pro	Lys	Glu	Ile	Gly	Ser	Glu	Asn	Thr	Glu	Arg	
			20					25					30			
Glu	Glu	Glu	Met	Ala	Gly	Ser	Gly	Gly	Gly	Glu	Ser	Lys	Leu	Ala	Gly	
			35				40					45				
Glu	Asp	Ser	Cys	Arg	Gly	Ser	Cys	Glu	Ser	Val	Glu	Lys	Glu	Leu	Thr	
			50			55				60						
Thr	Asn	Ser	Glu	Arg	Val	Glu	Pro	Val	Ser	Val	Thr	Glu	Leu	Ile	Glu	
65				70					75					80		
Ser	Glu	Asp	Gly	Ala	Ser	Arg	Gly	Glu	Glu	Ile	Thr	Ser	Asp	Val	Gln	
			85					90						95		
Ser	Ser	Ala	Ser	Leu	Pro	Arg	Lys	Gly	Thr	Ser	Glu	Pro	Asp	Lys	Glu	
			100				105						110			
Asp	Gln	Ser	Pro	Thr	Ser	Ala	Lys	Asp	Phe	Thr	Val	Glu	Ser	Gln	Pro	
			115				120						125			
Leu	Ile	Ser	Phe	Val	Glu	Ile	Leu	Leu	Ser	His	Pro	Cys	Gly	Ser	His	
			130			135					140					
Phe	Ser	Arg	Arg	Leu	Glu	Arg	Gln	Glu	Thr	Ile	Glu	Tyr	Gly	Thr	Ile	
145				150					155						160	
Ile	Arg	Glu	His	Val	Asp	Phe	Glu	Ile	Ile	Arg	Lys	Arg	Val	Glu	Gly	
			165					170						175		
Gly	Leu	Tyr	Lys	Ser	Trp	Arg	Ile	Asn	Phe	Phe	Arg	Asp	Leu	Leu	Leu	
			180				185						190			
Leu	Val	Asn	Asn	Ala	Arg	Val	Phe	Tyr	His	Arg	Gly	Ser	Ser	Glu	Phe	
			195				200					205				
Lys	Phe	Ala	Glu	Gln	Leu	His	Gln	Leu	Val	Lys	Lys	Gln	Met	Thr	Thr	
			210			215						220				
Thr	Leu	Lys	Gly	Leu	Ser	Asn	Arg	Asp	Glu	Ile	Ser	Ile	Ser	Pro	Pro	
225				230					235					240		
Lys	Glu	Glu	Val	Val	Ala	Ile	Pro	Ser	Ser	Lys	Pro	Val	Ser	Ser	Lys	
			245						250					255		
Pro	Arg	Met	Ser	Val	Pro	Asn	Ile	Val	Ala	Cys	Arg	Lys	Arg	Ser	Ala	
			260				265							270		
Leu	Ala	Ala	Lys	Pro	Leu	Leu	Leu	Leu	Pro	Pro	Gly	Pro	Asp	Lys	Lys	
			275				280					285				
Ala	Lys	Lys	Thr	Asp	His	Val	Val	Asp	Tyr	Asp	Glu	Lys	Pro	Val	Ser	
			290			295					300					
Asp	Lys	Asp	Gly	Glu	Ala	Ser	Gly	Lys	Asp	Asp	Asp	Asp	Ser	Leu	Ile	
305				310					315					320		
Val	Lys	Ile	Ile	Thr	Arg	Gly	Arg	Thr	Ser	Ser	Thr	Gly	Lys	Val	Ala	
			325						330					335		
Asn	Arg	Asn	Val	Lys	Asn	Arg	Asp	Ser	Ser	Leu	Asn	Val	Asp	Asp	Ser	
			340				345							350		
Lys	Asp	Lys	Val	Lys	Lys	Thr	Asp	Glu	Glu	Lys	Lys	Gly	Gly	Ser	Lys	
			355				360					365				
Lys	Lys	Gly	Ala	Ala	Ser	Phe	Leu	Arg	Arg	Met	Lys	Val	Gly	Ser	Ser	
			370			375						380				
Asp	Asp	Thr	Leu	Lys	Arg	Ser	Ser	Ala	Ala	Asp	Ser	Ser	Thr	Thr	Gly	

385		390		395		400
Lys Gly Gly Gly Ala Glu Gln Arg Lys Asn Asn Ser Asn Lys Ala Asp		405		410		415
Asn Lys Lys Thr Pro Ile Pro Arg Ile Arg Gln Thr Asn Lys Lys Ala		420		425		430
Ser Pro Val Lys Arg Ser Asn Asn Gly Arg Asn Ser Glu Arg Glu Ala		435		440		445
Ala Pro Ser Tyr Pro Ile Leu Ala Lys Arg Ser Arg Glu Ala Gly Glu		450		455		460
Lys Glu Glu Ala Ser Ser Tyr Ser Pro Arg Leu Lys Lys Arg Ala Arg		465		470		475
Arg						480

(2) INFORMATION FOR SEQ ID NO:910:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 468 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..468

(D) OTHER INFORMATION: / Ceres Seq. ID 1568311

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:910:

Met Asn Glu Thr Ile Ser Pro Asp Pro Lys Glu Ile Gly Ser Glu Asn	
1 5 10 15	
Thr Glu Arg Glu Glu Met Ala Gly Ser Gly Gly Glu Ser Lys	
20 25 30	
Leu Ala Gly Glu Asp Ser Cys Arg Gly Ser Cys Glu Ser Val Glu Lys	
35 40 45	
Glu Leu Thr Thr Asn Ser Glu Arg Val Glu Pro Val Ser Val Thr Glu	
50 55 60	
Leu Ile Glu Ser Glu Asp Gly Ala Ser Arg Gly Glu Glu Ile Thr Ser	
65 70 75	
Asp Val Gln Ser Ser Ala Ser Leu Pro Arg Lys Gly Thr Ser Glu Pro	
85 90 95	
Asp Lys Glu Asp Gln Ser Pro Thr Ser Ala Lys Asp Phe Thr Val Glu	
100 105 110	
Ser Gln Pro Leu Ile Ser Phe Val Glu Ile Leu Leu Ser His Pro Cys	
115 120 125	
Gly Ser His Phe Ser Arg Arg Leu Glu Arg Gln Glu Thr Ile Glu Tyr	
130 135 140	
Gly Thr Ile Ile Arg Glu His Val Asp Phe Glu Ile Ile Arg Lys Arg	
145 150 155	
Val Glu Gly Gly Leu Tyr Lys Ser Trp Arg Ile Asn Phe Phe Arg Asp	
165 170 175	
Leu Leu Leu Leu Val Asn Asn Ala Arg Val Phe Tyr His Arg Gly Ser	
180 185 190	
Ser Glu Phe Lys Phe Ala Glu Gln Leu His Gln Leu Val Lys Lys Gln	
195 200 205	
Met Thr Thr Thr Leu Lys Gly Leu Ser Asn Arg Asp Glu Ile Ser Ile	
210 215 220	
Ser Pro Pro Lys Glu Glu Val Val Ala Ile Pro Ser Ser Lys Pro Val	
225 230 235	
Ser Ser Lys Pro Arg Met Ser Val Pro Asn Ile Val Ala Cys Arg Lys	
245 250 255	
Arg Ser Ala Leu Ala Ala Lys Pro Leu Leu Leu Leu Pro Gly Pro	
260 265 270	
Asp Lys Lys Ala Lys Lys Thr Asp His Val Val Asp Tyr Asp Glu Lys	
275 280 285	

Pro Val Ser Asp Lys Asp Gly Glu Ala Ser Gly Lys Asp Asp Asp Asp
290 295 300
Ser Leu Ile Val Lys Ile Ile Thr Arg Gly Arg Thr Ser Ser Thr Gly
305 310 315 320
Lys Val Ala Asn Arg Asn Val Lys Asn Arg Asp Ser Ser Leu Asn Val
325 330 335
Asp Asp Ser Lys Asp Lys Val Lys Lys Thr Asp Glu Glu Lys Lys Gly
340 345 350
Gly Ser Lys Lys Lys Gly Ala Ala Ser Phe Leu Arg Arg Met Lys Val
355 360 365
Gly Ser Ser Asp Asp Thr Leu Lys Arg Ser Ser Ala Ala Asp Ser Ser
370 375 380
Thr Thr Gly Lys Gly Gly Gly Ala Glu Gln Arg Lys Asn Asn Ser Asn
385 390 395 400
Lys Ala Asp Asn Lys Lys Thr Pro Ile Pro Arg Ile Arg Gln Thr Asn
405 410 415
Lys Lys Ala Ser Pro Val Lys Arg Ser Asn Asn Gly Arg Asn Ser Glu
420 425 430
Arg Glu Ala Ala Pro Ser Tyr Pro Ile Leu Ala Lys Arg Ser Arg Glu
435 440 445
Ala Gly Glu Lys Glu Glu Ala Ser Tyr Ser Pro Arg Leu Lys Lys
450 455 460
Arg Ala Arg Arg
465

(2) INFORMATION FOR SEQ ID NO:911:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 446 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..446

(D) OTHER INFORMATION: / Ceres Seq. ID 1568312

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:911:

Met Ala Gly Ser Gly Gly Gly Glu Ser Lys Leu Ala Gly Glu Asp Ser
1 5 10 15
Cys Arg Gly Ser Cys Glu Ser Val Glu Lys Glu Leu Thr Thr Asn Ser
20 25 30
Glu Arg Val Glu Pro Val Ser Val Thr Glu Leu Ile Glu Ser Glu Asp
35 40 45
Gly Ala Ser Arg Gly Glu Glu Ile Thr Ser Asp Val Gln Ser Ser Ala
50 55 60
Ser Leu Pro Arg Lys Gly Thr Ser Glu Pro Asp Lys Glu Asp Gln Ser
65 70 75 80
Pro Thr Ser Ala Lys Asp Phe Thr Val Glu Ser Gln Pro Leu Ile Ser
85 90 95
Phe Val Glu Ile Leu Leu Ser His Pro Cys Gly Ser His Phe Ser Arg
100 105 110
Arg Leu Glu Arg Gln Glu Thr Ile Glu Tyr Gly Thr Ile Ile Arg Glu
115 120 125
His Val Asp Phe Glu Ile Ile Arg Lys Arg Val Glu Gly Gly Leu Tyr
130 135 140
Lys Ser Trp Arg Ile Asn Phe Phe Arg Asp Leu Leu Leu Val Asn
145 150 155 160
Asn Ala Arg Val Phe Tyr His Arg Gly Ser Ser Glu Phe Lys Phe Ala
165 170 175
Glu Gln Leu His Gln Leu Val Lys Lys Gln Met Thr Thr Thr Leu Lys
180 185 190
Gly Leu Ser Asn Arg Asp Glu Ile Ser Ile Ser Pro Pro Lys Glu Glu

195	200	205
Val Val Ala Ile Pro Ser Ser Lys Pro Val Ser Ser Lys Pro Arg Met		
210	215	220
Ser Val Pro Asn Ile Val Ala Cys Arg Lys Arg Ser Ala Leu Ala Ala		
225	230	235
Lys Pro Leu Leu Leu Leu Pro Pro Gly Pro Asp Lys Lys Ala Lys Lys		
245	250	255
Thr Asp His Val Val Asp Tyr Asp Glu Lys Pro Val Ser Asp Lys Asp		
260	265	270
Gly Glu Ala Ser Gly Lys Asp Asp Asp Ser Leu Ile Val Lys Ile		
275	280	285
Ile Thr Arg Gly Arg Thr Ser Ser Thr Gly Lys Val Ala Asn Arg Asn		
290	295	300
Val Lys Asn Arg Asp Ser Ser Leu Asn Val Asp Ser Lys Asp Lys		
305	310	315
Val Lys Lys Thr Asp Glu Glu Lys Lys Gly Ser Lys Lys Lys Gly		
325	330	335
Ala Ala Ser Phe Leu Arg Arg Met Lys Val Gly Ser Ser Asp Asp Thr		
340	345	350
Leu Lys Arg Ser Ser Ala Ala Asp Ser Ser Thr Thr Gly Lys Gly Gly		
355	360	365
Gly Ala Glu Gln Arg Lys Asn Asn Ser Asn Lys Ala Asp Asn Lys Lys		
370	375	380
Thr Pro Ile Pro Arg Ile Arg Gln Thr Asn Lys Lys Ala Ser Pro Val		
385	390	395
Lys Arg Ser Asn Asn Gly Arg Asn Ser Glu Arg Glu Ala Ala Pro Ser		
405	410	415
Tyr Pro Ile Leu Ala Lys Arg Ser Arg Glu Ala Gly Glu Lys Glu Glu		
420	425	430
Ala Ser Ser Tyr Ser Pro Arg Leu Lys Lys Arg Ala Arg Arg		
435	440	445

(2) INFORMATION FOR SEQ ID NO:912:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 635 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..635
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568313

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:912:

ttacagtcoc	atgattcgtg	cttggTttga	tcctcaccat	catcaccaat	ccatctccac	60
cgacgatctc	aaccaccacc	atcaccttcc	tcacccggtt	caccaatcag	caatccocgg	120
aatcggtattc	gocctcagggt	aattatcttc	gggttttcgc	ataccagcac	ggtttcaggg	180
ccaagaagag	gagcagcacg	acggtctcac	tcacaagcgc	tcctctgctt	ctctctatttc	240
tcgccattga	caatcgaaac	taatcctcta	agtttcaggg	ctgtctagc	ttccatgcac	300
attgaagctt	gacttagatt	gtccggaaca	gggaagggtg	ttctcggttg	tgtagtcaat	360
ggcctgaatc	tagaanaacg	aaggaaatga	agaaagaaca	acagtttcag	gttctttcttc	420
ttctttcttc	aatattcttaa	cttgcgcgat	tgtaattttt	catattttca	ccagtttagac	480
caacgtttctt	ctgtagctca	attatggtta	gattocaagg	ttctgtcttg	ttgtgttatg	540
tttgtAacctt	tgatatcatca	tcattCotatt	gttactgctc	cctgtttotta	ttgtgttaact	600
ccgtggatgt	tctaataaag	ctgaaacctt	tctctc			

(2) INFORMATION FOR SEQ ID NO:913:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 82 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..82

(D) OTHER INFORMATION: / Ceres Seq. ID 1568314

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:913:

Tyr	Ser	Pro	Met	Ile	Arg	Ala	Trp	Phe	Asp	Pro	His	His	His	Gln
1			5						10				15	
Ser	Ile	Ser	Thr	Asp	Asp	Leu	Asn	His	His	His	Leu	Pro	Pro	Pro
			20					25				30		
Val	His	Gln	Ser	Ala	Ile	Pro	Gly	Ile	Gly	Phe	Ala	Ser	Gly	Leu
		35					40				45			
Ser	Ser	Gly	Phe	Arg	Ile	Pro	Ala	Arg	Phe	Gln	Gly	Gln	Glu	Glu
		50			55				60					
Gln	His	Asp	Gly	Leu	Thr	His	Lys	Pro	Ser	Ser	Ala	Ser	Ile	Ser
65				70					75				80	
Arg	His													

(2) INFORMATION FOR SEQ ID NO:914:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 79 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..79

(D) OTHER INFORMATION: / Ceres Seq. ID 1568315

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:914:

Met	Ile	Arg	Ala	Trp	Phe	Asp	Pro	His	His	His	Gln	Ser	Ile	Ser
1			5						10				15	
Thr	Asp	Asp	Leu	Asn	His	His	His	His	Leu	Pro	Pro	Pro	Val	Gln
			20					25				30		
Ser	Ala	Ile	Pro	Gly	Ile	Gly	Phe	Ala	Ser	Gly	Glu	Leu	Ser	Gly
		35					40				45			
Phe	Arg	Ile	Pro	Ala	Arg	Phe	Gln	Gly	Gln	Glu	Glu	Gln	His	Asp
		50			55					60				
Gly	Leu	Thr	His	Lys	Pro	Ser	Ser	Ala	Ser	Ser	Ile	Ser	Arg	His
65				70					75					

(2) INFORMATION FOR SEQ ID NO:915:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 44 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..44

(D) OTHER INFORMATION: / Ceres Seq. ID 1568316

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:915:

Met	Val	Arg	Phe	Gln	Gly	Phe	Val	Leu	Leu	Cys	Tyr	Val	Cys	Asn	Phe
1			5						10					15	
Val	Ser	Ser	Ser	Ser	Tyr	Cys	Tyr	Cys	Ser	Leu	Phe	Leu	Leu	Cys	Asn
			20				25					30			
Ser	Val	Asp	Val	Leu	Ile	Lys	Ser	Glu	Thr	Phe	Ser				
		35				40									

(2) INFORMATION FOR SEQ ID NO:916:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 407 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..407
(D) OTHER INFORMATION: / Ceres Seq. ID 1568321
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:916:
tttggggttg gttgagatga tgaagggaag agagagagtg tgggaggaga tggttaagga 60
gaatcaattg caagagaaga agcttgagga agttgggttg tgggtggttg ctgatgttat 120
actttggaggg attgcgactg tggcttgggt tttcttttac actttcttcg cggagacgca 180
agggaggatg cttgaggata tggatgagct tttcagtggt ttcaggtgga gagattccaa 240
gagtaagcct aagggttaacc ccgagaagac ggtaccgaat cccgaggttg agattggatc 300
aaacaagcag tggaaaggaag gagacacaca aagttcgtag gaaatttttg catgatgtga 360
atttgtatgg tatgGtgggt ttaatgataa aacgaacaaa ttagcgt

(2) INFORMATION FOR SEQ ID NO:917:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 112 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..112
(D) OTHER INFORMATION: / Ceres Seq. ID 1568322
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:917:
Leu Gly Leu Val Glu Met Met Lys Gly Lys Glu Arg Val Trp Glu Glu
1 5 10 15
Met Val Lys Glu Asn Gln Leu Gln Glu Lys Lys Leu Glu Glu Val Gly
20 25 30
Val Trp Trp Phe Ala Asp Val Ile Leu Gly Gly Ile Ala Thr Val Ala
35 40 45
Trp Val Phe Phe Tyr Thr Phe Leu Pro Glu Thr Gln Gly Arg Met Leu
50 55 60
Glu Asp Met Asp Glu Leu Phe Ser Gly Phe Arg Trp Arg Asp Ser Lys
65 70 75 80
Ser Lys Pro Lys Gly Asn Pro Glu Lys Thr Val Pro Asn Pro Glu Val
85 90 95
Glu Ile Gly Ser Asn Lys Gln Trp Lys Glu Gly Asp Thr Gln Ser Ser
100 105 110

(2) INFORMATION FOR SEQ ID NO:918:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 107 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..107
(D) OTHER INFORMATION: / Ceres Seq. ID 1568323
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:918:
Met Met Lys Gly Lys Glu Arg Val Trp Glu Glu Met Val Lys Glu Asn
1 5 10 15
Gln Leu Gln Glu Lys Lys Leu Glu Glu Val Gly Val Trp Trp Phe Ala
20 25 30
Asp Val Ile Leu Gly Gly Ile Ala Thr Val Ala Trp Val Phe Phe Tyr
35 40 45

Thr Phe Leu Pro Glu Thr Gln Gly Arg Met Leu Glu Asp Met Asp Glu
50 55 60
Leu Phe Ser Gly Phe Arg Trp Arg Asp Ser Lys Ser Lys Pro Lys Gly
65 70 75 80
Asn Pro Glu Lys Thr Val Pro Asn Pro Glu Val Glu Ile Gly Ser Asn
85 90 95
Lys Gln Trp Lys Glu Gly Asp Thr Gln Ser Ser
100 105

(2) INFORMATION FOR SEQ ID NO:919:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 106 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..106

(D) OTHER INFORMATION: / Ceres Seq. ID 1568324

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:919:

Met Lys Gly Lys Glu Arg Val Trp Glu Glu Met Val Lys Glu Asn Gln
1 5 10 15
Leu Gln Glu Lys Lys Leu Glu Glu Val Gly Val Trp Trp Phe Ala Asp
20 25 30
Val Ile Leu Gly Gly Ile Ala Thr Val Ala Trp Val Phe Phe Tyr Thr
35 40 45
Phe Leu Pro Glu Thr Gln Gly Arg Met Leu Glu Asp Met Asp Glu Leu
50 55 60
Phe Ser Gly Phe Arg Trp Arg Asp Ser Lys Ser Lys Pro Lys Gly Asn
65 70 75 80
Pro Glu Lys Thr Val Pro Asn Pro Glu Val Glu Ile Gly Ser Asn Lys
85 90 95
Gln Trp Lys Glu Gly Asp Thr Gln Ser Ser
100 105

(2) INFORMATION FOR SEQ ID NO:920:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 821 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..821

(D) OTHER INFORMATION: / Ceres Seq. ID 1568333

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:920:

aaaaaaaggga gaaagcttga aacgcgcgctt cttcttcttc tctgtcgttc tctctgtaaa 60
tcgcttcttc aatcatctct gtggatttgt ctcattctat aacttgggtga agaagatggt 120
gacggaagag gagctcaaaa gattgtacag aatccagaag acgttgtatgc agatgttaag 180
ggatcggtga tattttatcg cggattctga acttacgatg actaaacaac agtttattag 240
gaaacatggt gataacatga aaagagagga tcttgttact ctaagagcta agcgaataga 300
taatagtgat cagctctata tattcttccc tgatgaggcg aaagtgtggtg tgaagacgat 360
gaaaatgtac acgaacacga tgaatcaga gaattgtgttc agagctattt tggttgtgcA 420
acagaaacttg accccgcttg ctcgaaacttg cattagttag atctcttcta aGgtttcatc 480
tggaagtctt ccaGggaggg ggaatgcta gtgaacata aagaacatgt tcttgttctc 540
gagcatcaag ttcttaccac tgaagagaag aaaactttac tggagagata cacagtgaag 600
gagacacagc ttccaagatg caaagtgact gatccaatgc caagataact tggactaaaa 660
cgtggggcaag tcgtgaagat cattcgtccg agtgaacagg ctggtcgcta tgttaacctat 720
cgttatgttg tataagccaa agcaaaaggc tttgtgggat tgtaatgcga attgaacgct 780
gagagtgtgt aaacataaga gtaatgcttt tgtactaaac c

(2) INFORMATION FOR SEQ ID NO:921:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 169 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..169
(D) OTHER INFORMATION: / Ceres Seq. ID 1568334
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:921:

Lys	Lys	Gly	Glu	Ser	Leu	Lys	Arg	Arg	Phe	Phe	Phe	Ser	Val	Val
1				5					10				15	
Leu	Ser	Val	Asn	Arg	Phe	Phe	Asn	His	Leu	Cys	Gly	Phe	Val	Ile
			20				25					30		
His	Asn	Leu	Val	Lys	Lys	Met	Leu	Thr	Glu	Glu	Glu	Leu	Lys	Arg
			35			40					45			
Tyr	Arg	Ile	Gln	Lys	Thr	Leu	Met	Gln	Met	Leu	Arg	Asp	Arg	Gly
	50				55					60				Tyr
Phe	Ile	Ala	Asp	Ser	Glu	Leu	Thr	Met	Thr	Lys	Gln	Gln	Phe	Ile
65				70					75				80	Arg
Lys	His	Gly	Asp	Asn	Met	Lys	Arg	Glu	Asp	Leu	Val	Thr	Leu	Lys
			85						90				95	Ala
Lys	Arg	Asn	Asp	Asn	Ser	Asp	Gln	Leu	Tyr	Ile	Phe	Phe	Pro	Asp
			100					105					110	Glu
Ala	Lys	Val	Gly	Val	Lys	Thr	Met	Lys	Met	Tyr	Thr	Asn	Arg	Met
			115			120					125			Lys
Ser	Glu	Asn	Val	Phe	Arg	Ala	Ile	Leu	Val	Val	Gln	Gln	Asn	Leu
	130					135					140			Thr
Pro	Phe	Ala	Arg	Thr	Cys	Ile	Ser	Glu	Ile	Ser	Ser	Lys	Val	Ser
145				150					155					Ser
Gly	Ser	Phe	Pro	Gly	Arg	Arg	Lys	Cys						
				165										

(2) INFORMATION FOR SEQ ID NO:922:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 131 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..131
(D) OTHER INFORMATION: / Ceres Seq. ID 1568335
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:922:

Met	Leu	Thr	Glu	Glu	Leu	Lys	Arg	Leu	Tyr	Arg	Ile	Gln	Lys	Thr
1					5				10				15	
Leu	Met	Gln	Met	Leu	Arg	Asp	Arg	Gly	Tyr	Phe	Ile	Ala	Asp	Ser
			20				25					30		Glu
Leu	Thr	Met	Thr	Lys	Gln	Gln	Phe	Ile	Arg	Lys	His	Gly	Asp	Asn
			35			40					45			Met
Lys	Arg	Glu	Asp	Leu	Val	Thr	Leu	Lys	Ala	Lys	Arg	Asn	Asp	Asn
	50					55				60				Ser
Asp	Gln	Leu	Tyr	Ile	Phe	Phe	Pro	Asp	Glu	Ala	Lys	Val	Gly	Val
65				70					75				80	Lys
Thr	Met	Lys	Met	Tyr	Thr	Asn	Arg	Met	Lys	Ser	Glu	Asn	Val	Phe
			85					90					95	Arg
Ala	Ile	Leu	Val	Val	Gln	Gln	Asn	Leu	Thr	Pro	Phe	Ala	Arg	Thr
			100				105					110		Cys
Ile	Ser	Glu	Ile	Ser	Ser	Lys	Val	Ser	Ser	Gly	Ser	Phe	Pro	Gly
		115					120					125		Arg

Arg Lys Cys
130

(2) INFORMATION FOR SEQ ID NO:923:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 114 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..114
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568336

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:923:

Met	Gln	Met	Leu	Arg	Asp	Arg	Gly	Tyr	Phe	Ile	Ala	Asp	Ser	Glu	Leu
1			5					10					15		
Thr	Met	Thr	Lys	Gln	Gln	Phe	Ile	Arg	Lys	His	Gly	Asp	Asn	Met	Lys
			20					25					30		
Arg	Glu	Asp	Leu	Val	Thr	Leu	Lys	Ala	Lys	Arg	Asn	Asp	Asn	Ser	Asp
			35				40					45			
Gln	Leu	Tyr	Ile	Phe	Phe	Pro	Asp	Glu	Ala	Lys	Val	Gly	Val	Lys	Thr
			50			55					60				
Met	Lys	Met	Tyr	Thr	Asn	Arg	Met	Lys	Ser	Glu	Asn	Val	Phe	Arg	Ala
					70					75				80	
Ile	Leu	Val	Val	Gln	Gln	Asn	Leu	Thr	Pro	Phe	Ala	Arg	Thr	Cys	Ile
				85				90						95	
Ser	Glu	Ile	Ser	Ser	Lys	Val	Ser	Ser	Gly	Ser	Phe	Pro	Gly	Arg	Arg
			100				105						110		

Lys Cys

(2) INFORMATION FOR SEQ ID NO:924:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1264 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1264
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568357

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:924:

aatggattac	ttttcttcca	cacatatata	acttaactct	ctctttttct	cttttgcctt	60
aaccctccca	aagaaaagat	aagagccttt	taaaagtttt	ttttttacct	ttcttctcatg	120
gacttgtctg	tacttgcata	gcttaagtgg	ctgcaacagc	aacaaaatgt	ttcaactgag	180
tttcttcaga	tacttggctc	agatggggaga	gaagagctca	aaagagtga	gagttacttg	240
ggaaaAcaac	aatgatgagc	tgacagattt	cagacatttt	ccogaattcg	gaccggatta	300
tgatactact	gatggctgca	tttctaggac	aagttagcttc	catatggagc	cagtgaagaa	360
taatggacac	agcagagcca	ttaccttgca	gaacaagaga	aaaccagagg	gtaagacaga	420
aaagagagag	aagaagaaga	tcaaaagcaga	ggatgaaaca	gagccaaagca	tgaaggggaa	480
atcaaacatc	agtaacRoag	agacatcttc	agaaattcag	aaaccagatt	acattcatgt	540
tagggctaga	cgagggtgaag	ccacogacag	acatagctta	gcagagaggg	caagaagaga	600
aaagataagc	aagaagatga	aatgtctaca	agatatgttt	cctggatgca	acaaagttac	660
tggaataagc	ggatgtctgt	atgagatcat	caactatgtc	caatctctcg	accaacaagt	720
cgaattcttg	tcgatgaaac	ttctgtctat	aaatccagaa	cttgagtgtc	atatcgatga	780
ttatcccgca	aaacagtttc	aggcttactt	cacaggtctc	ccagaagggt	actcgaagca	840
gtcaatcatg	gcggattttc	ggcttttttc	attacatcag	caaggatctt	tagattactc	900
agtcataaac	tcagaccaca	ccacatctct	cggcgctaaa	gatcatatcat	catcaagctg	960
ggaaactcac	tcacagtgtc	tttacaacag	cttgagaacc	gattcttttt	ccaaattttt	1020
cagcctcaag	taaaaaaatt	agggatagcc	tcattaaaaa	aatcgcggtt	ttttgtgttt	1080
gtcttatcca	tttatctatc	tatctgaa	tttgaaccag	aaagacagag	gaaaccaatc	1140

caaagatctt tctcaatcta ttatcttcat acaaatatag tgattttacat atattccagg 1200
ggatatgtat atgtgtagaa gaaagagaaa aaactcttgt ggcatagca attccttttt 1260
ttgt

(2) INFORMATION FOR SEQ ID NO:925:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 276 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..276

(D) OTHER INFORMATION: / Ceres Seq. ID 1568358

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:925:

Met	Gly	Glu	Lys	Ser	Ser	Lys	Glu	Leu	Arg	Val	Thr	Trp	Glu	Asn	Asn
1			5				10						15		
Asn	Asp	Glu	Leu	Gln	Ser	Phe	Arg	His	Phe	Pro	Glu	Phe	Gly	Pro	Asp
			20				25						30		
Tyr	Asp	Thr	Thr	Asp	Gly	Cys	Ile	Ser	Arg	Thr	Ser	Ser	Phe	His	Met
			35				40						45		
Glu	Pro	Val	Lys	Asn	Asn	Gly	His	Ser	Arg	Ala	Ile	Thr	Leu	Gln	Asn
			50				55						60		
Lys	Arg	Lys	Pro	Glu	Gly	Lys	Thr	Glu	Lys	Arg	Glu	Lys	Lys	Lys	Ile
							70						75		80
Lys	Ala	Glu	Asp	Glu	Thr	Glu	Pro	Ser	Met	Lys	Gly	Lys	Ser	Asn	Met
							85						90		95
Ser	Asn	Xaa	Glu	Thr	Ser	Ser	Glu	Ile	Gln	Lys	Pro	Asp	Tyr	Ile	His
							100						105		110
Val	Arg	Ala	Arg	Arg	Gly	Glu	Ala	Thr	Asp	Arg	His	Ser	Leu	Ala	Glu
							115						120		125
Arg	Ala	Arg	Arg	Glu	Lys	Ile	Ser	Lys	Lys	Met	Lys	Cys	Leu	Gln	Asp
							130						135		140
Ile	Val	Pro	Gly	Cys	Asn	Lys	Val	Thr	Gly	Lys	Ala	Gly	Met	Leu	Asp
							145						150		155
Glu	Ile	Ile	Asn	Tyr	Val	Gln	Ser	Leu	Gln	Gln	Val	Glu	Phe	Leu	
							160						165		170
Ser	Met	Lys	Leu	Ser	Val	Ile	Asn	Pro	Glu	Leu	Glu	Cys	His	Ile	Asp
							175						180		185
Asp	Leu	Ser	Ala	Lys	Gln	Phe	Gln	Ala	Tyr	Phe	Thr	Gly	Pro	Pro	Glu
							190						195		200
Gly	Asp	Ser	Lys	Gln	Ser	Ile	Met	Ala	Asp	Phe	Arg	Ser	Phe	Pro	Leu
							205						210		215
His	Gln	Gln	Gly	Ser	Leu	Asp	Tyr	Ser	Val	Ile	Asn	Ser	Asp	His	Thr
							220						225		230
Thr	Ser	Leu	Gly	Ala	Lys	Asp	His	Thr	Ser	Ser	Ser	Trp	Glu	Thr	His
							235						240		245
Ser	Gln	Cys	Leu	Tyr	Asn	Ser	Leu	Arg	Thr	Asp	Ser	Ile	Ser	Asn	Phe
							250						255		260
Phe	Ser	Leu	Lys												265
															270
															275

(2) INFORMATION FOR SEQ ID NO:926:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 229 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..229

(D) OTHER INFORMATION: / Ceres Seq. ID 1568359

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:926:

Met Glu Pro Val Lys Asn Asn Gly His Ser Arg Ala Ile Thr Leu Gln
1 5 10 15
Asn Lys Arg Lys Pro Glu Gly Lys Thr Glu Lys Arg Glu Lys Lys
20 25 30
Ile Lys Ala Glu Asp Glu Thr Glu Pro Ser Met Lys Gly Lys Ser Asn
35 40 45
Met Ser Asn Xaa Glu Thr Ser Ser Glu Ile Gln Lys Pro Asp Tyr Ile
50 55 60
His Val Arg Ala Arg Arg Gly Glu Ala Thr Asp Arg His Ser Leu Ala
65 70 75 80
Glu Arg Ala Arg Arg Glu Lys Ile Ser Lys Lys Met Lys Cys Leu Gln
85 90 95
Asp Ile Val Pro Gly Cys Asn Lys Val Thr Gly Lys Ala Gly Met Leu
100 105 110
Asp Glu Ile Ile Asn Tyr Val Gln Ser Leu Gln Gln Gln Val Glu Phe
115 120 125
Leu Ser Met Lys Leu Ser Val Ile Asn Pro Glu Leu Glu Cys His Ile
130 135 140
Asp Asp Leu Ser Ala Lys Gln Phe Gln Ala Tyr Phe Thr Gly Pro Pro
145 150 155 160
Glu Gly Asp Ser Lys Gln Ser Ile Met Ala Asp Phe Arg Ser Phe Pro
165 170 175
Leu His Gln Gln Gly Ser Leu Asp Tyr Ser Val Ile Asn Ser Asp His
180 185 190
Thr Thr Ser Leu Gly Ala Lys Asp His Thr Ser Ser Ser Trp Glu Thr
195 200 205
His Ser Gln Cys Leu Tyr Asn Ser Leu Arg Thr Asp Ser Ile Ser Asn
210 215 220
Phe Phe Ser Leu Lys
225

(2) INFORMATION FOR SEQ ID NO:927:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 187 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..187

(D) OTHER INFORMATION: / Ceres Seq. ID 1568360

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:927:

Met Lys Gly Lys Ser Asn Met Ser Asn Xaa Glu Thr Ser Ser Glu Ile
1 5 10 15
Gln Lys Pro Asp Tyr Ile His Val Arg Ala Arg Arg Gly Glu Ala Thr
20 25 30
Asp Arg His Ser Leu Ala Glu Arg Ala Arg Arg Glu Lys Ile Ser Lys
35 40 45
Lys Met Lys Cys Leu Gln Asp Ile Val Pro Gly Cys Asn Lys Val Thr
50 55 60
Gly Lys Ala Gly Met Leu Asp Glu Ile Ile Asn Tyr Val Gln Ser Leu
65 70 75 80
Gln Gln Gln Val Glu Phe Leu Ser Met Lys Leu Ser Val Ile Asn Pro
85 90 95
Glu Leu Glu Cys His Ile Asp Asp Leu Ser Ala Lys Gln Phe Gln Ala
100 105 110
Tyr Phe Thr Gly Pro Pro Glu Gly Asp Ser Lys Gln Ser Ile Met Ala
115 120 125
Asp Phe Arg Ser Phe Pro Leu His Gln Gln Gly Ser Leu Asp Tyr Ser

130 135 140
Val Ile Asn Ser Asp His Thr Thr Ser Leu Gly Ala Lys Asp His Thr
145 150 155 160
Ser Ser Ser Trp Glu Thr His Ser Gln Cys Leu Tyr Asn Ser Leu Arg
165 170 175
Thr Asp Ser Ile Ser Asn Phe Phe Ser Leu Lys
180 185

(2) INFORMATION FOR SEQ ID NO:928:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1273 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..1273
(D) OTHER INFORMATION: / Ceres Seq. ID 1568365

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:928:

accacacac	aaagattcca	ttacaaataa	acaattttca	tatatatcta	taacaaaaaa	60
aaacaatggc	gacctcaagc	atgaagagca	ttccaatggc	gatcccaagt	ttctccatgt	120
gtcacaaagt	cgagctccct	aaagaaggca	aaactcgcga	cgctcccgaa	gccgaagaag	180
atgaaggggt	aagctgcgag	ttccaagaga	tgttggattc	ttcttctaag	gagagaggt	240
ggagaactcg	ttactcttac	ctattccaag	gggttttggt	ccaagccaaa	gagattcaag	300
ccatcatgtc	tttccaaaaa	catttccaat	ccctcgaaaa	cgacgtcggt	ctcgcaccaa	360
tacctaaatc	cggtacaacc	tggctaaaag	ctttaacttt	caccatcctt	aaccgtcaac	420
ggtttgatcc	ggttgcctcg	agtaccaaac	accctctttt	cacttccaac	cctcatgacc	480
ttgtaccttt	cttcgagtac	aagctttacg	ccaacggaga	tgttcccgat	ctctcgggtc	540
tagccagtcg	aagaacgttc	gcaaccactc	taccgttcgg	ttccttaaa	gaaacgatcg	600
agaaaaccgg	tgtgaaggtc	gtgtactttg	gccggaaccc	gtttgacaca	ttcatcttt	660
cgtggcatta	caccaacaac	atcaaatccg	agtcagtgag	cccagttctg	ctagaccaag	720
cttttgatct	gtatttgcgg	ggagtgatcg	ggtttggccc	gttttgggaa	cacatgtttg	780
gatactggag	agagagcttg	aagagaccag	agaaaagtct	ctttttaagg	tacgaggatc	840
tcaaaagcga	catcgagacc	aacttgaaga	ggcttgcaac	ttctttagag	cttctcttca	900
ccgaagaaga	ggaacgaaag	ggagttgtga	aGgctatcgc	cgagctgtgt	agcttcgaga	960
atctgaagaa	gttgagggtg	aacaagtcaa	acaagtgcgt	caagaacttt	gagaatcgat	1020
ctctgttttc	gaaaggagaa	gtgagtgatt	gggttaacta	tttgtcaact	tcacaagtgg	1080
aaagattgtc	agccttagtg	gatgacaagt	taggtggatc	tggtctcact	ttcaggttga	1140
gctaaatata	agggccacgt	cccccatctt	tactcttggt	ctgaggggct	actatatacg	1200
ttaaagctaa	ttaaggcagt	tgtattgttg	ttacagatag	acatcgaagc	aacgtaacgt	1260
ccataattaa	gtc					

(2) INFORMATION FOR SEQ ID NO:929:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 359 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..359
(D) OTHER INFORMATION: / Ceres Seq. ID 1568366

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:929:

Met	Ala	Thr	Ser	Ser	Met	Lys	Ser	Ile	Pro	Met	Ala	Ile	Pro	Ser	Phe
1					5			10						15	
Ser	Met	Cys	His	Lys	Leu	Glu	Leu	Leu	Lys	Glu	Gly	Lys	Thr	Arg	Asp
			20					25					30		
Val	Pro	Lys	Ala	Glu	Glu	Asp	Glu	Gly	Leu	Ser	Cys	Glu	Phe	Gln	Glu
			35				40					45			
Met	Leu	Asp	Ser	Leu	Pro	Lys	Glu	Arg	Gly	Trp	Arg	Thr	Arg	Tyr	Leu
	50					55						60			

Tyr Leu Phe Gln Gly Phe Trp Cys Gln Ala Lys Glu Ile Gln Ala Ile
65 70 75 80
Met Ser Phe Gln Lys His Phe Gln Ser Leu Glu Asn Asp Val Val Leu
85 90 95
Ala Thr Ile Pro Lys Ser Gly Thr Thr Trp Leu Lys Ala Leu Thr Phe
100 105 110
Thr Ile Leu Asn Arg His Arg Phe Asp Pro Val Ala Ser Ser Thr Asn
115 120 125
His Pro Leu Phe Thr Ser Asn Pro His Asp Leu Val Pro Phe Phe Glu
130 135 140
Tyr Lys Leu Tyr Ala Asn Gly Asp Val Pro Asp Leu Ser Gly Leu Ala
145 150 155 160
Ser Pro Arg Thr Phe Ala Thr His Leu Pro Phe Gly Ser Leu Lys Glu
165 170 175
Thr Ile Glu Lys Pro Gly Val Lys Val Val Tyr Leu Cys Arg Asn Pro
180 185 190
Phe Asp Thr Phe Ile Ser Ser Trp His Tyr Thr Asn Asn Ile Lys Ser
195 200 205
Glu Ser Val Ser Pro Val Leu Leu Asp Gln Ala Phe Asp Leu Tyr Cys
210 215 220
Arg Gly Val Ile Gly Phe Gly Pro Phe Trp Glu His Met Leu Gly Tyr
225 230 235 240
Trp Arg Glu Ser Leu Lys Arg Pro Glu Lys Val Phe Phe Leu Arg Tyr
245 250 255
Glu Asp Leu Lys Asp Asp Ile Glu Thr Asn Leu Lys Arg Leu Ala Thr
260 265 270
Phe Leu Glu Leu Pro Phe Thr Glu Glu Glu Arg Lys Gly Val Val
275 280 285
Lys Ala Ile Ala Glu Leu Cys Ser Phe Glu Asn Leu Lys Lys Leu Glu
290 295 300
Val Asn Lys Ser Asn Lys Ser Ile Lys Asn Phe Glu Asn Arg Phe Leu
305 310 315 320
Phe Arg Lys Gly Glu Val Ser Asp Trp Val Asn Tyr Leu Ser Pro Ser
325 330 335
Gln Val Glu Arg Leu Ser Ala Leu Val Asp Asp Lys Leu Gly Gly Ser
340 345 350
Gly Leu Thr Phe Arg Leu Ser
355

(2) INFORMATION FOR SEQ ID NO:930:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 354 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..354
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568367

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:930:

Met Lys Ser Ile Pro Met Ala Ile Pro Ser Phe Ser Met Cys His Lys
1 5 10 15
Leu Glu Leu Leu Lys Glu Gly Lys Thr Arg Asp Val Pro Lys Ala Glu
20 25 30
Glu Asp Glu Gly Leu Ser Cys Glu Phe Gln Glu Met Leu Asp Ser Leu
35 40 45
Pro Lys Glu Arg Gly Trp Arg Thr Arg Tyr Leu Tyr Leu Phe Gln Gly
50 55 60
Phe Trp Cys Gln Ala Lys Glu Ile Gln Ala Ile Met Ser Phe Gln Lys
65 70 75 80
His Phe Gln Ser Leu Glu Asn Asp Val Val Leu Ala Thr Ile Pro Lys

	85		90		95
Ser Gly Thr Thr Trp Leu Lys Ala Leu Thr Phe Thr Ile Leu Asn Arg	100		105		110
His Arg Phe Asp Pro Val Ala Ser Ser Thr Asn His Pro Leu Phe Thr	115		120		125
Ser Asn Pro His Asp Leu Val Pro Phe Phe Glu Tyr Lys Leu Tyr Ala	130		135		140
Asn Gly Asp Val Pro Asp Leu Ser Gly Leu Ala Ser Pro Arg Thr Phe	145		150		155
Ala Thr His Leu Pro Phe Gly Ser Leu Lys Glu Thr Ile Glu Lys Pro	165		170		175
Gly Val Lys Val Val Tyr Leu Cys Arg Asn Pro Phe Asp Thr Phe Ile	180		185		190
Ser Ser Trp His Tyr Thr Asn Asn Ile Lys Ser Glu Ser Val Ser Pro	195		200		205
Val Leu Leu Asp Gln Ala Phe Asp Leu Tyr Cys Arg Gly Val Ile Gly	210		215		220
Phe Gly Pro Phe Trp Glu His Met Leu Gly Tyr Trp Arg Glu Ser Leu	225		230		235
Lys Arg Pro Glu Lys Val Phe Phe Leu Arg Tyr Glu Asp Leu Lys Asp	245		250		255
Asp Ile Glu Thr Asn Leu Lys Arg Leu Ala Thr Phe Leu Glu Leu Pro	260		265		270
Phe Thr Glu Glu Glu Glu Arg Lys Gly Val Val Lys Ala Ile Ala Glu	275		280		285
Leu Cys Ser Phe Glu Asn Leu Lys Lys Leu Glu Val Asn Lys Ser Asn	290		295		300
Lys Ser Ile Lys Asn Phe Glu Asn Arg Phe Leu Phe Arg Lys Gly Glu	305		310		315
Val Ser Asp Trp Val Asn Tyr Leu Ser Pro Ser Gln Val Glu Arg Leu	325		330		335
Ser Ala Leu Val Asp Asp Lys Leu Gly Gly Ser Gly Leu Thr Phe Arg	340		345		350
Leu Ser					

(2) INFORMATION FOR SEQ ID NO:931:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 349 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..349

(D) OTHER INFORMATION: / Ceres Seq. ID 1568368

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:931:

Met Ala Ile Pro Ser Phe Ser Met Cys His Lys Leu Glu Leu Leu Lys	
1	5 10 15
Glu Gly Lys Thr Arg Asp Val Pro Lys Ala Glu Glu Asp Glu Gly Leu	
20	25 30
Ser Cys Glu Phe Gln Glu Met Leu Asp Ser Leu Pro Lys Glu Arg Gly	
35	40 45
Trp Arg Thr Arg Tyr Leu Tyr Leu Phe Gln Gly Phe Trp Cys Gln Ala	
50	55 60
Lys Glu Ile Gln Ala Ile Met Ser Phe Gln Lys His Phe Gln Ser Leu	
65	70 75
Glu Asn Asp Val Val Leu Ala Thr Ile Pro Lys Ser Gly Thr Thr Trp	
	85 90 95
Leu Lys Ala Leu Thr Phe Thr Ile Leu Asn Arg His Arg Phe Asp Pro	
	100 105 110

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Val Ala Ser Ser Thr Asn His Pro Leu Phe Thr Ser Asn Pro His Asp
      115              120              125
Leu Val Pro Phe Phe Glu Tyr Lys Leu Tyr Ala Asn Gly Asp Val Pro
      130              135              140
Asp Leu Ser Gly Leu Ala Ser Pro Arg Thr Phe Ala Thr His Leu Pro
      145              150              155              160
Phe Gly Ser Leu Lys Glu Thr Ile Glu Lys Pro Gly Val Lys Val Val
      165              170              175
Tyr Leu Cys Arg Asn Pro Phe Asp Thr Phe Ile Ser Ser Trp His Tyr
      180              185              190
Thr Asn Asn Ile Lys Ser Glu Ser Val Ser Pro Val Leu Leu Asp Gln
      195              200              205
Ala Phe Asp Leu Tyr Cys Arg Gly Val Ile Gly Phe Gly Pro Phe Trp
      210              215              220
Glu His Met Leu Gly Tyr Trp Arg Glu Ser Leu Lys Arg Pro Glu Lys
      225              230              235              240
Val Phe Phe Leu Arg Tyr Glu Asp Leu Lys Asp Asp Ile Glu Thr Asn
      245              250              255
Leu Lys Arg Leu Ala Thr Phe Leu Glu Leu Pro Phe Thr Glu Glu Glu
      260              265              270
Glu Arg Lys Gly Val Val Lys Ala Ile Ala Glu Leu Cys Ser Phe Glu
      275              280              285
Asn Leu Lys Lys Leu Glu Val Asn Lys Ser Asn Lys Ser Ile Lys Asn
      290              295              300
Phe Glu Asn Arg Phe Leu Phe Arg Lys Gly Glu Val Ser Asp Trp Val
      305              310              315              320
Asn Tyr Leu Ser Pro Ser Gln Val Glu Arg Leu Ser Ala Leu Val Asp
      325              330              335
Asp Lys Leu Gly Gly Ser Gly Leu Thr Phe Arg Leu Ser
      340              345

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(2) INFORMATION FOR SEQ ID NO:932:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 797 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..797

(D) OTHER INFORMATION: / Ceres Seq. ID 1568376

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:932:

```

aaattcgcat agcttgcaaa taacgctgac aaaaaaagaa acagtgaaga agaaaaaaaaa    60
aaaaggtcat ttctattttc tccatttgat ttttgccgac cggagaaaaa atcttctttgc    120
cgtctctctt ttcattttcag caggaaacttt tatttgaaat cggtttgatt tagccatggc    180
aaacgcggca tcgggaatgg ctgtgcatga tgattgcaag ctgaaattta tggaaactgaa    240
ggcgaaaaaga acattccgta ccatagttcta caagattgag gataagcaag tgattgtaga    300
gaaactcggg gaacctgaac aatcatatga tgactttgca gctagtcttc cagctgatga    360
tgcccgatatt tgcattttacg atttogaactt tGgtcactgc ggagaactgc cagaagagca    420
agatcttctt cattgcatgg tctccggaca ctgccaaaagt gagagacaag atgattttacg    480
cgagctctaa agatagggttc aagagagaac tagatggaat tcaagtggaa ctccaagcta    540
ctgatccaac agaaatgggt ctgtatgttt tcaaaagccg caccaactaa gtaaaaacaaa    600
accctgtaag ggcatttgaa taagttttgt tcttgagtg atatgttttc ctctgactgt    660
tatgaaaact ttttaacacc ttcaacttca ttctacttgg tattattgta tgcctttgat    720
gtgttatgtg tgcctttgta tggttttcaa ttagttttac atgtacaata ctgaaatca    780
gattgttgct aagcttc

```

(2) INFORMATION FOR SEQ ID NO:933:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:

(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..104
 (D) OTHER INFORMATION: / Ceres Seq. ID 1568377
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:933:
Met Ala Asn Ala Ala Ser Gly Met Ala Val His Asp Asp Cys Lys Leu
1 5 10 15
Lys Phe Met Glu Leu Lys Ala Lys Arg Thr Phe Arg Thr Ile Val Tyr
 20 25 30
Lys Ile Glu Asp Lys Gln Val Ile Val Glu Lys Leu Gly Glu Pro Glu
 35 40 45
Gln Ser Tyr Asp Asp Phe Ala Ala Ser Leu Pro Ala Asp Asp Cys Arg
 50 55 60
Tyr Cys Ile Tyr Asp Phe Asp Phe Gly His Cys Gly Glu Leu Pro Glu
65 70 75 80
Glu Gln Asp Leu Leu His Cys Met Val Ser Gly His Cys Gln Ser Glu
 85 90 95
Arg Gln Asp Asp Leu Arg Glu Leu
 100

(2) INFORMATION FOR SEQ ID NO:934:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 97 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..97
 (D) OTHER INFORMATION: / Ceres Seq. ID 1568378
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:934:
Met Ala Val His Asp Asp Cys Lys Leu Lys Phe Met Glu Leu Lys Ala
1 5 10 15
Lys Arg Thr Phe Arg Thr Ile Val Tyr Lys Ile Glu Asp Lys Gln Val
 20 25 30
Ile Val Glu Lys Leu Gly Glu Pro Glu Gln Ser Tyr Asp Asp Phe Ala
 35 40 45
Ala Ser Leu Pro Ala Asp Asp Cys Arg Tyr Cys Ile Tyr Asp Phe Asp
 50 55 60
Phe Gly His Cys Gly Glu Leu Pro Glu Glu Gln Asp Leu Leu His Cys
65 70 75 80
Met Val Ser Gly His Cys Gln Ser Glu Arg Gln Asp Asp Leu Arg Glu
 85 90 95
Leu

(2) INFORMATION FOR SEQ ID NO:935:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 87 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..87
 (D) OTHER INFORMATION: / Ceres Seq. ID 1568379
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:935:
Met Met Thr Leu Gln Leu Val Phe Gln Leu Met Ile Ala Asp Ile Ala
1 5 10 15

Phe Thr Ile Ser Thr Leu Val Thr Ala Glu Asn Cys Gln Lys Ser Lys
20 25 30
Ile Phe Phe Ile Ala Trp Ser Pro Asp Thr Ala Lys Val Arg Asp Lys
35 40 45
Met Ile Tyr Ala Ser Ser Lys Asp Arg Phe Lys Arg Glu Leu Asp Gly
50 55 60
Ile Gln Val Glu Leu Gln Ala Thr Asp Pro Thr Glu Met Gly Leu Asp
65 70 75 80
Val Phe Lys Ser Arg Thr Asn
85

(2) INFORMATION FOR SEQ ID NO:936:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1327 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1327
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568405

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:936:

actgggtcgt	ctctttcttc	gatttctctt	tctatctggt	ttccattttc	gtctcgtttg	60
tgttctcgtg	gggtttggtt	gtctctgttc	ttctatttgt	ggcgttattc	atcgtgtcaa	120
ttgtcatctt	catcgttttc	gtcgtgttat	ttggtgtttc	tcgtttgggt	cttctgaaca	180
ttcttcatct	ttctcttttt	gggtgtgtct	cccacgaaca	ggtagattga	tgaaaagcaa	240
ccatggatga	cctacatgga	agcaatgctc	gaatgcacat	tagagaagct	caagatccaa	300
tgcatgtgca	atttgaacat	catgctttgc	atcacatcca	caatggaagc	ggtaggtgtg	360
atgaccaggc	tgatgatggc	aatgctgggt	ggatgagtga	gggtgtggaa	acagacattc	420
cttctcacc	tggaagtgtg	actgacaatc	gtggtgaagt	gggtcaccgt	ggtagtgaac	480
aaggagatga	gttaacattg	tcttttcagg	gccaaagtcta	cggttttgac	agtgtcttgc	540
ctgagaaggt	tcaagctgtg	cttctattat	tgggtgtgtg	tgaattacct	cagcagcccc	600
tcctggccta	ggatcacctc	atcagaacaa	cagagtatcg	agtttacctg	gtactcctca	660
aagggttagt	attccgcagc	gattagcttc	tttggtcaga	tttcgagaga	aacggaagg	720
aaggaaattt	gataagaaga	ttcgtatata	agtcgccaa	gaggtagctt	tgaggatgca	780
acgcaataaa	ggtcagttca	catctgccaa	gtcaaaacat	gatgaagctg	catctgctgg	840
atctagctgg	gggtcgaaac	aaacctgggc	catagaaaat	agtgaagctc	agcatcaaga	900
gatctcatgt	ggcagctgtg	gaattggcga	gaagtcaact	ccaatgatgc	gacgtggacc	960
tgccggccca	agaaacattt	gcaatgcatt	tgggcaaaac	aggggtgctt		1020
tagggagcta	tccaagacct	ctcctcaaac	agcccagaat	cttcttttaa	ataagaatga	1080
agatgcaaat	cttgagactg	atcatcaaat	aatgataaca	gtggccaagt	acataagcaa	1140
ctcacagtga	gggcagttgt	gtcttcccca	ttacaagcaa	gagaagagat	tcaacagagt	1200
ttgcattccc	ttaggtttgt	tagctttatc	attccotttg	aaagaatctg	actcagattta	1260
ggttatcagg	atttgatcta	tgacaatgta	atctgagtga	taatgatctg	caatgttttg	1320
ctctcttc						

(2) INFORMATION FOR SEQ ID NO:937:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 122 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..122
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568406

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:937:

Met Asp Asp Leu His Gly Ser Asn Ala Arg Met His Ile Arg Glu Ala			
1 5 10 15			
Gln Asp Pro Met His Val Gln Phe Glu His His Ala Leu His His Ile			
20 25 30			

His Asn Gly Ser Gly Met Val Asp Asp Gln Ala Asp Asp Gly Asn Ala
35 40 45
Gly Gly Met Ser Glu Gly Val Glu Thr Asp Ile Pro Ser His Pro Gly
50 55 60
Asn Val Thr Asp Asn Arg Gly Glu Val Val Asp Arg Gly Ser Glu Gln
65 70 75 80
Gly Asp Gln Leu Thr Leu Ser Phe Gln Gly Gln Val Tyr Val Phe Asp
85 90 95
Ser Val Leu Pro Glu Lys Val Gln Ala Val Leu Leu Leu Leu Gly Gly
100 105 110
Arg Glu Leu Pro Gln Gln Pro Leu Leu Ala
115 120

(2) INFORMATION FOR SEQ ID NO:938:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 112 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..112
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568407

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:938:

Met His Ile Arg Glu Ala Gln Asp Pro Met His Val Gln Phe Glu His
1 5 10 15
His Ala Leu His His Ile His Asn Gly Ser Gly Met Val Asp Asp Gln
20 25 30
Ala Asp Asp Gly Asn Ala Gly Gly Met Ser Glu Gly Val Glu Thr Asp
35 40 45
Ile Pro Ser His Pro Gly Asn Val Thr Asp Asn Arg Gly Glu Val Val
50 55 60
Asp Arg Gly Ser Glu Gln Gly Asp Gln Leu Thr Leu Ser Phe Gln Gly
65 70 75 80
Gln Val Tyr Val Phe Asp Ser Val Leu Pro Glu Lys Val Gln Ala Val
85 90 95
Leu Leu Leu Leu Gly Gly Arg Glu Leu Pro Gln Gln Pro Leu Leu Ala
100 105 110

(2) INFORMATION FOR SEQ ID NO:939:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 124 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..124
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568408

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:939:

Met Gln Arg Asn Lys Gly Gln Phe Thr Ser Ala Lys Ser Asn Asn Asp
1 5 10 15
Glu Ala Ala Ser Ala Gly Ser Ser Trp Gly Ser Asn Gln Thr Trp Ala
20 25 30
Ile Glu Ser Ser Glu Ala Gln His Gln Glu Ile Ser Cys Arg His Cys
35 40 45
Gly Ile Gly Glu Lys Ser Thr Pro Met Met Arg Arg Gly Pro Ala Gly
50 55 60
Pro Arg Thr Leu Cys Asn Ala Cys Gly Leu Met Trp Ala Asn Lys Gly

65	70	75	80
Ala Phe Arg Asp Leu Ser Lys Ala Ser	Pro Gln Thr Ala Gln Asn Leu		
	85	90	95
Pro Leu Asn Lys Asn Glu Asp Ala Asn	Leu Glu Thr Asp His Gln Ile		
	100	105	110
Met Ile Thr Val Ala Asn Asp Ile Ser	Asn Ser Gln		
	115	120	

(2) INFORMATION FOR SEQ ID NO:940:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1289 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1289
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568409

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:940:

actaattaaa	tctctctataa	aacataagag	agtctaaaca	ctgtggtaga	aaaaaatata	60
gactttttaga	tatgtgtagt	aaaataacat	tagtgtaa	tttattttcc	agttatttca	120
tatcaacaga	tgctgtgaat	ggatcatttc	ctgcgctttt	ggctttttgga	gattcaattc	180
tcgatactgg	caacaacaa	tttctctga	cttttatgaa	agaaataatc	tgccatattg	240
gaaggagttt	cagcatgaga	agggcgacag	gaagatttgg	aaatggaaga	gttttctctg	300
atatagttgc	tgaaggttta	gggatcaaga	agattttacc	agcttatcgt	aagttgttca	360
attctccaag	tgaccttaga	actgggtgtt	gcttcgcatac	aggtggtgca	ggagttgacc	420
ctgttacatc	caaatgtgct	agagttttaa	cgccaaagga	tcaagttaac	gatttcaaac	480
ggtacataag	aaagctaaag	gccacagcag	gtccttcaag	agcaagtgtg	atagtttcaa	540
atgcagtgat	tctgttttct	caaggaaata	atgatattgg	aatctcatat	tttggaaact	600
caactgctgc	tttccgagga	tttaactcca	atagataatac	caactaaacta	gctgtgttga	660
acaaacaggt	tatgaagaag	ttatacgcag	aaggagcgag	aaaattcgcg	gtaatgggag	720
tgataccgtt	gggatgtttt	cctatgacaa	gaatcttctc	tggtgggttc	gtcatcacgt	780
gtaacttctt	cgcgaaataga	gtcgcagaa	agtacaaacg	aaaattgagg	agcggaacta	840
aaagtgtggg	acgtgaagca	ggttttaggg	gtacaaaatt	tgcttatgtc	gacatgtaca	900
acactcttat	ggatgttatt	aaaaattata	gaagatacgg	attttctaat	gagaaaaaatg	960
gggtgtgttg	tatgattacc	gctataatac	catgcgccaa	cccagataaa	tacgtctctt	1020
acgacttcgt	tcattccatc	gagaaaagctt	acagaacaat	ttctaaaaag	ctgtgccagg	1080
atatacaagaa	tggcccttgc	tgattttatta	tatatacaat	gctttatttt	aattttaata	1140
acagcctatg	tttaataatg	aaatgagaag	acaaaaatca	tacatggcca	ttctctgttt	1200
ttctcttatgt	taaagaatgt	ataatccagt	ttatgtattg	ttcactttat	ataatccacg	1260
aaacaacaaag	gagtttgttt	acaaCatgt				

(2) INFORMATION FOR SEQ ID NO:941:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 343 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..343
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568410

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:941:

Met Cys Ser Lys Ile Thr Leu Val Leu Thr Leu Phe Ser Ser Tyr Phe	
1	5
Ile Ser Thr Asp Ala Val Asn Gly Ser Phe Pro Ala Leu Leu Ala Phe	
	20
Gly Asp Ser Ile Leu Asp Thr Gly Asn Asn Asn Phe Leu Leu Thr Phe	
	35
Met Lys Gly Asn Ile Trp Pro Tyr Gly Arg Ser Phe Ser Met Arg Arg	
	50
	60

Ala Thr Gly Arg Phe Gly Asn Gly Arg Val Phe Ser Asp Ile Val Ala
65 70 75 80
Glu Gly Leu Gly Ile Lys Lys Ile Leu Pro Ala Tyr Arg Lys Leu Phe
85 90 95
Asn Ser Pro Ser Asp Leu Arg Thr Gly Val Cys Phe Ala Ser Gly Gly
100 105 110
Ala Gly Val Asp Pro Val Thr Ser Lys Leu Leu Arg Val Leu Thr Pro
115 120 125
Lys Asp Gln Val Asn Asp Phe Lys Gly Tyr Ile Arg Lys Leu Lys Ala
130 135 140
Thr Ala Gly Pro Ser Arg Ala Ser Ser Ile Val Ser Asn Ala Val Ile
145 150 155 160
Leu Val Ser Gln Gly Asn Asn Asp Ile Gly Ile Ser Tyr Phe Gly Thr
165 170 175
Pro Thr Ala Ala Phe Arg Gly Leu Thr Pro Asn Arg Tyr Thr Thr Lys
180 185 190
Leu Ala Gly Trp Asn Lys Gln Phe Met Lys Glu Leu Tyr Asp Gln Gly
195 200 205
Ala Arg Lys Phe Ala Val Met Gly Val Ile Pro Leu Gly Cys Leu Pro
210 215 220
Met Thr Arg Ile Phe Leu Gly Gly Phe Val Ile Thr Cys Asn Phe Phe
225 230 235 240
Ala Asn Arg Val Ala Glu Gln Tyr Asn Gly Lys Leu Arg Ser Gly Thr
245 250 255
Lys Ser Trp Gly Arg Glu Ala Gly Phe Arg Gly Thr Lys Phe Val Tyr
260 265 270
Val Asp Met Tyr Asn Thr Leu Met Asp Val Ile Lys Asn Tyr Arg Arg
275 280 285
Tyr Gly Phe Ser Asn Glu Lys Asn Gly Cys Cys Cys Met Ile Thr Ala
290 295 300
Ile Ile Pro Cys Pro Asn Pro Asp Lys Tyr Val Phe Tyr Asp Phe Val
305 310 315 320
His Pro Ser Glu Lys Ala Tyr Arg Thr Ile Ser Lys Lys Leu Val Gln
325 330 335
Asp Ile Lys Asn Gly Leu Ala
340

(2) INFORMATION FOR SEQ ID NO:942:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 295 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..295
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568411

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:942:

Met Lys Gly Asn Ile Trp Pro Tyr Gly Arg Ser Phe Ser Met Arg Arg
1 5 10 15
Ala Thr Gly Arg Phe Gly Asn Gly Arg Val Phe Ser Asp Ile Val Ala
20 25 30
Glu Gly Leu Gly Ile Lys Lys Ile Leu Pro Ala Tyr Arg Lys Leu Phe
35 40 45
Asn Ser Pro Ser Asp Leu Arg Thr Gly Val Cys Phe Ala Ser Gly Gly
50 55 60
Ala Gly Val Asp Pro Val Thr Ser Lys Leu Leu Arg Val Leu Thr Pro
65 70 75 80
Lys Asp Gln Val Asn Asp Phe Lys Gly Tyr Ile Arg Lys Leu Lys Ala
85 90 95
Thr Ala Gly Pro Ser Arg Ala Ser Ser Ile Val Ser Asn Ala Val Ile

100 105 110
Leu Val Ser Gln Gly Asn Asn Asp Ile Gly Ile Ser Tyr Phe Gly Thr
115 120 125
Pro Thr Ala Ala Phe Arg Gly Leu Thr Pro Asn Arg Tyr Thr Thr Lys
130 135 140
Leu Ala Gly Trp Asn Lys Gln Phe Met Lys Glu Leu Tyr Asp Gln Gly
145 150 155 160
Ala Arg Lys Phe Ala Val Met Gly Val Ile Pro Leu Gly Cys Leu Pro
165 170 175
Met Thr Arg Ile Phe Leu Gly Gly Phe Val Ile Thr Cys Asn Phe Phe
180 185 190
Ala Asn Arg Val Ala Glu Gln Tyr Asn Gly Lys Leu Arg Ser Gly Thr
195 200 205
Lys Ser Trp Gly Arg Glu Ala Gly Phe Arg Gly Thr Lys Phe Val Tyr
210 215 220
Val Asp Met Tyr Asn Thr Leu Met Asp Val Ile Lys Asn Tyr Arg Arg
225 230 235 240
Tyr Gly Phe Ser Asn Glu Lys Asn Gly Cys Cys Cys Met Ile Thr Ala
245 250 255
Ile Ile Pro Cys Pro Asn Pro Asp Lys Tyr Val Phe Tyr Asp Phe Val
260 265 270
His Pro Ser Glu Lys Ala Tyr Arg Thr Ile Ser Lys Lys Leu Val Gln
275 280 285
Asp Ile Lys Asn Gly Leu Ala
290 295

(2) INFORMATION FOR SEQ ID NO:943:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 282 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..282

(D) OTHER INFORMATION: / Ceres Seq. ID 1568412

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:943:

Met Arg Arg Ala Thr Gly Arg Phe Gly Asn Gly Arg Val Phe Ser Asp
1 5 10 15
Ile Val Ala Glu Gly Leu Gly Ile Lys Lys Ile Leu Pro Ala Tyr Arg
20 25 30
Lys Leu Phe Asn Ser Pro Ser Asp Leu Arg Thr Gly Val Cys Phe Ala
35 40 45
Ser Gly Gly Ala Gly Val Asp Pro Val Thr Ser Lys Leu Leu Arg Val
50 55 60
Leu Thr Pro Lys Asp Gln Val Asn Asp Phe Lys Gly Tyr Ile Arg Lys
65 70 75 80
Leu Lys Ala Thr Ala Gly Pro Ser Arg Ala Ser Ser Ile Val Ser Asn
85 90 95
Ala Val Ile Leu Val Ser Gln Gly Asn Asn Asp Ile Gly Ile Ser Tyr
100 105 110
Phe Gly Thr Pro Thr Ala Ala Phe Arg Gly Leu Thr Pro Asn Arg Tyr
115 120 125
Thr Thr Lys Leu Ala Gly Trp Asn Lys Gln Phe Met Lys Glu Leu Tyr
130 135 140
Asp Gln Gly Ala Arg Lys Phe Ala Val Met Gly Val Ile Pro Leu Gly
145 150 155 160
Cys Leu Pro Met Thr Arg Ile Phe Leu Gly Gly Phe Val Ile Thr Cys
165 170 175
Asn Phe Phe Ala Asn Arg Val Ala Glu Gln Tyr Asn Gly Lys Leu Arg
180 185 190

Ser Gly Thr Lys Ser Trp Gly Arg Glu Ala Gly Phe Arg Gly Thr Lys
195 200 205
Phe Val Tyr Val Asp Met Tyr Asn Thr Leu Met Asp Val Ile Lys Asn
210 215 220
Tyr Arg Arg Tyr Gly Phe Ser Asn Glu Lys Asn Gly Cys Cys Cys Met
225 230 235 240
Ile Thr Ala Ile Ile Pro Cys Pro Asn Pro Asp Lys Tyr Val Phe Tyr
245 250 255
Asp Phe Val His Pro Ser Glu Lys Ala Tyr Arg Thr Ile Ser Lys Lys
260 265 270
Leu Val Gln Asp Ile Lys Asn Gly Leu Ala
275 280

(2) INFORMATION FOR SEQ ID NO:944:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 593 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..593
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568425

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:944:

atcaaaatct	ttacaatatt	tatcatgtat	gattctatca	agtgagatgg	aacgggtatgc	60
aatttttccg	tttaataatg	tggtttcgct	tacagggttg	acaagtcact	ccagtagcac	120
tagagaagct	tgaggtagca	acaaagacac	tgaggagagac	agtggtggag	acagaggtga	180
cccaacagcc	ggaagaatcc	gtccccgcgc	tgacagaaca	aaaatccgaa	gcaccaattg	240
tagaaaacaa	cgaagaagtg	gttgtggaag	aggcagagaa	gaaagatgaa	gaaaccgaga	300
agaaaaacaga	ggagaaagac	gagaagacac	aagtgtcac	ggaactccg	gtagttgagg	360
aggagagagaa	gaagctgag	gaagtgaacc	aaactccggc	ggttgtggag	gaggagaaga	420
agacagaggt	ggttgaggag	aaacagactg	aggttgccgc	tgctgaggaa	gtgccctgtg	480
agaaggccga	ggagtaaaga	ggaaggaaga	agctatatat	gacctttttt	ggtctcatat	540
cgttttctgt	ttattttatt	ttatcaaWca	tttcataagt	attttctatg	ttt	

(2) INFORMATION FOR SEQ ID NO:945:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 146 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..146
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568426

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:945:

Met	Gln	Phe	Phe	Arg	Leu	Ile	Met	Cys	Phe	Arg	Leu	Gln	Val	Glu	Gln
1			5					10				15			
Val	Thr	Pro	Val	Ala	Val	Glu	Asn	Val	Glu	Val	Pro	Thr	Lys	Thr	Val
			20					25				30			
Glu	Glu	Thr	Val	Val	Glu	Thr	Glu	Val	Thr	Gln	Gln	Pro	Glu	Glu	Ser
			35				40				45				
Val	Pro	Ala	Val	Thr	Glu	Gln	Lys	Ser	Glu	Ala	Pro	Ile	Val	Glu	Thr
			50				55				60				
Asn	Glu	Glu	Val	Val	Val	Glu	Glu	Ala	Glu	Lys	Lys	Asp	Glu	Glu	Thr
			65				70			75			80		
Glu	Lys	Lys	Thr	Glu	Glu	Lys	Asp	Glu	Lys	Thr	Glu	Val	Ile	Thr	Glu
			85				90				95				
Thr	Pro	Val	Val	Glu	Glu	Glu	Lys	Lys	Ala	Glu	Glu	Val	Thr	Glu	
			100				105				110				
Thr	Pro	Ala	Val	Val	Glu	Glu	Lys	Lys	Thr	Glu	Val	Val	Glu	Glu	

115 120 125
Lys Gln Thr Glu Val Ala Ala Glu Glu Val Ala Val Glu Lys Ala
130 135 140
Glu Glu
145

(2) INFORMATION FOR SEQ ID NO:946:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 139 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide

- (B) LOCATION: 1..139

- (D) OTHER INFORMATION: / Ceres Seq. ID 1568427

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:946:

Met	Cys	Phe	Arg	Leu	Gln	Val	Glu	Gln	Val	Thr	Pro	Val	Ala	Val	Glu
1			5				10				15				
Asn	Val	Glu	Val	Pro	Thr	Lys	Thr	Val	Glu	Glu	Thr	Val	Val	Glu	Thr
			20				25				30				
Glu	Val	Thr	Gln	Gln	Pro	Glu	Glu	Ser	Val	Pro	Ala	Val	Thr	Glu	Gln
			35				40				45				
Lys	Ser	Glu	Ala	Pro	Ile	Val	Glu	Thr	Asn	Glu	Glu	Val	Val	Val	Glu
			50				55				60				
Glu	Ala	Glu	Lys	Lys	Asp	Glu	Glu	Thr	Glu	Lys	Lys	Thr	Glu	Glu	Lys
			65				70				75				80
Asp	Glu	Lys	Thr	Glu	Val	Ile	Thr	Glu	Thr	Pro	Val	Val	Glu	Glu	Glu
			85				90				95				
Glu	Lys	Lys	Ala	Glu	Glu	Val	Thr	Glu	Thr	Pro	Ala	Val	Val	Glu	Glu
			100				105				110				
Glu	Lys	Lys	Thr	Glu	Val	Val	Glu	Glu	Lys	Gln	Thr	Glu	Val	Ala	Ala
			115				120				125				
Ala	Glu	Glu	Val	Ala	Val	Glu	Lys	Ala	Glu	Glu					
			130				135								

(2) INFORMATION FOR SEQ ID NO:947:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1157 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -

- (B) LOCATION: 1..1157

- (D) OTHER INFORMATION: / Ceres Seq. ID 1568436

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:947:

cgagatatat	cgactccgcg	accctccact	actctgctga	cttcacacaca	cacacacaaa	60
cacaatcgcc	ggcaacaatg	gcgaagctca	cactctctct	cttcctttcc	ttctctcatct	120
tctctctatc	catcgctttc	caatcgagcg	agctctctgt	tgacgacgac	gaatttggtc	180
tagaaggagc	aaagcccgcc	tcaccgagtc	ttcacacatc	ttctctctct	tcgccacagc	240
agcagcaaca	gactcccaact	attcggagaa	gatactcaga	tcctaccgat	ctggattcaa	300
aagtccaatt	tactctcgaa	catgccttcg	gtgactctga	tttctcccc	gccggtactt	360
tctccgctcg	tctcaaaaac	tggagtcgat	gcggaaaagc	attaacgaag	ctgcgattct	420
ctagaaatga	ttttctgtct	gaagagaag	atgcattcaa	gaatctgctg	aaaggagatg	480
gcttttatcg	gattcggctt	ccatctaatt	tgggttagtc	accagggaga	gagtttgtga	540
ttgcatcagt	gagagctaga	tgtctaccac	gggatggctt	ggatgagcat	ttcattatag	600
acatgggaag	tgtcaaacat	tgggcagtta	gttatgggtc	tcttggggcg	tgtcaaatag	660
ctcgacaatt	gaaaacttcca	gcaaaatggt	cgtttaactc	tcacacaatt	ctgaaaaagca	720
gtgagcagcg	gccaaagaact	ccaattattca	ctgaggagat	tctaggchdK	tgagaatgta	780
gagggagaag	ttgaaccacc	accagagaga	tcattttggg	cgaaatattg	gatgtatttg	840

ataccgctgg gactcgtagt gatgaatgcc gtgacacaag catcaaacat ggctgaagaa 900
cCtgcggggtg gacaggcagg aggtgcacaa gtgcaaccag ctgccaggag aagatgattc 960
cacttttact tctcccaaag caatgaaagc tgcagctggg tagagatgat gattcaacag 1020
atcttcatgt aaaccatctt gccatcattt ggtttttatgt aacctttaat tttaatccctc 1080
gatcggtgtg ttttagtact caccaatcgg gaaatcaaaa atcttgtctt catgacatat 1140
caagaacaaa gacattt

(2) INFORMATION FOR SEQ ID NO:948:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 256 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..256

(D) OTHER INFORMATION: / Ceres Seq. ID 1568437

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:948:

Arg Tyr Ile Asp Ser Ala Thr Leu His Tyr Ser Ala Asp Leu His Thr
1 5 10 15
His Thr Gln Thr Gln Ser Pro Ala Thr Met Ala Lys Leu Thr Leu Leu
20 25 30
Phe Phe Leu Ser Phe Leu Ile Phe Ser Ser Ser Ile Ala Phe Gln Ser
35 40 45
Asp Glu Leu Leu Val Asp Asp Glu Phe Gly Leu Glu Gly Ala Lys
50 55 60
Pro Arg Ser Thr Asp Leu His Thr Ser Ser Ser Ser Pro Gln Gln
65 70 75 80
Gln Gln Gln Thr Pro Thr Ile Arg Arg Arg Tyr Ser Asp Pro Thr Asp
85 90 95
Leu Asp Ser Lys Val Gln Phe Thr Leu Glu His Ala Phe Gly Asp Ser
100 105 110
Asp Phe Ser Pro Ala Gly Thr Phe Ser Ala Arg Leu Lys Thr Trp Ser
115 120 125
His Gly Gly Lys Thr Leu Thr Lys Leu Arg Phe Ser Arg Asn Asp Phe
130 135 140
Ser Ala Glu Glu Lys Asp Ala Phe Lys Asn Leu Leu Lys Gly Asp Gly
145 150 155 160
Phe Tyr Arg Ile Arg Leu Pro Ser Asn Val Val Ser Pro Pro Gly Arg
165 170 175
Glu Phe Val Ile Ala Ser Val Arg Ala Arg Cys Leu Pro Arg Asp Gly
180 185 190
Leu Asp Glu His Phe Ile Ile His Met Glu Gly Ala Asn Ile Leu Ala
195 200 205
Val Ser Tyr Gly Ser Pro Gly Ala Cys Gln Tyr Pro Arg Gln Leu Lys
210 215 220
Leu Pro Ala Lys Trp Ser Phe Asn Ser His Thr Ile Leu Lys Ser Ser
225 230 235 240
Glu Gln Ala Pro Arg Thr Pro Ile Phe Thr Glu Glu Ile Leu Gly Xaa
245 250 255

(2) INFORMATION FOR SEQ ID NO:949:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 231 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..231

(D) OTHER INFORMATION: / Ceres Seq. ID 1568438

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:949:

Met Ala Lys Leu Thr Leu Leu Phe Phe Leu Ser Phe Leu Ile Phe Ser
1 5 10 15
Ser Ser Ile Ala Phe Gln Ser Asp Glu Leu Leu Val Asp Asp Asp Glu
20 25 30
Phe Gly Leu Glu Gly Ala Lys Pro Arg Ser Thr Asp Leu His Thr Ser
35 40 45
Ser Ser Ser Ser Pro Gln Gln Gln Gln Thr Pro Thr Ile Arg Arg
50 55 60
Arg Tyr Ser Asp Pro Thr Asp Leu Asp Ser Lys Val Gln Phe Thr Leu
65 70 75 80
Glu His Ala Phe Gly Asp Ser Asp Phe Ser Pro Ala Gly Thr Phe Ser
85 90 95
Ala Arg Leu Lys Thr Trp Ser His Gly Gly Lys Thr Leu Thr Lys Leu
100 105 110
Arg Phe Ser Arg Asn Asp Phe Ser Ala Glu Glu Lys Asp Ala Phe Lys
115 120 125
Asn Leu Leu Lys Gly Asp Gly Phe Tyr Arg Ile Arg Leu Pro Ser Asn
130 135 140
Val Val Ser Pro Pro Gly Arg Glu Phe Val Ile Ala Ser Val Arg Ala
145 150 155 160
Arg Cys Leu Pro Arg Asp Gly Leu Asp Glu His Phe Ile Ile His Met
165 170 175
Glu Gly Ala Asn Ile Leu Ala Val Ser Tyr Gly Ser Pro Gly Ala Cys
180 185 190
Gln Tyr Pro Arg Gln Leu Lys Leu Pro Ala Lys Trp Ser Phe Asn Ser
195 200 205
His Thr Ile Leu Lys Ser Ser Glu Gln Ala Pro Arg Thr Pro Ile Phe
210 215 220
Thr Glu Glu Ile Leu Gly Xaa
225 230

(2) INFORMATION FOR SEQ ID NO:950:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 501 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..501

(D) OTHER INFORMATION: / Ceres Seq. ID 1568490

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:950:

atatacCttc ttcttcttca ccttatgcaa gataatggac aaagtattatg gaatgtcgtc 60
cgaaaaagggt gtgggttatat ttaccaagag ctctgttgtt ttgtcctatg cggttcaagt 120
ttcttcttcaa gatcttggtg ttaaccctaa gatccacgag attgataagg accttgaatg 180
ccgagagata gagaaggctc ttatgaggct aggggtgttca aagcccggtcc cagccgtctt 240
cattgtgtgc aagctcgttg gttcgaccaa cgaagtaatg tccatgcacc taagcagctc 300
gctcgttccc ctagtgaagc catatttatg ttaacaacaa acgaaggagt atttatgata 360
ttaattagct atgtatatgt tattcaataa ggaacaaaat tgagccaaat ctttgaatg 420
tgttttttgg tattattatt gttgtataa cattgggaaa gtgtacgtat aattataaga 480
ctgttatatt gattcgaagg t

(2) INFORMATION FOR SEQ ID NO:951:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 110 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..110

(D) OTHER INFORMATION: / Ceres Seq. ID 1568491

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:951:

Tyr	Thr	Phe	Phe	Phe	Thr	Leu	Cys	Lys	Ile	Met	Asp	Lys	Val	Met
1				5				10					15	
Arg	Met	Ser	Ser	Glu	Lys	Gly	Val	Val	Ile	Phe	Thr	Lys	Ser	Cys
			20				25					30		
Cys	Leu	Ser	Tyr	Ala	Val	Gln	Val	Leu	Phe	Gln	Asp	Leu	Gly	Val
		35				40				45				
Pro	Lys	Ile	His	Glu	Ile	Asp	Lys	Asp	Pro	Glu	Cys	Arg	Glu	Ile
50				55				60						
Lys	Ala	Leu	Met	Arg	Leu	Gly	Cys	Ser	Lys	Pro	Val	Pro	Ala	Val
65				70				75					80	
Ile	Gly	Gly	Lys	Leu	Val	Gly	Ser	Thr	Asn	Glu	Val	Met	Ser	Met
			85					90				95		His
Leu	Ser	Ser	Ser	Leu	Val	Pro	Leu	Val	Lys	Pro	Tyr	Leu	Cys	
			100				105						110	

(2) INFORMATION FOR SEQ ID NO:952:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 99 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..99

(D) OTHER INFORMATION: / Ceres Seq. ID 1568492

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:952:

Met	Asp	Lys	Val	Met	Arg	Met	Ser	Ser	Glu	Lys	Gly	Val	Val	Ile	Phe
1				5				10						15	
Thr	Lys	Ser	Ser	Cys	Cys	Leu	Ser	Tyr	Ala	Val	Gln	Val	Leu	Phe	Gln
			20				25					30			
Asp	Leu	Gly	Val	Asn	Pro	Lys	Ile	His	Glu	Ile	Asp	Lys	Asp	Pro	Glu
		35				40					45				
Cys	Arg	Glu	Ile	Glu	Lys	Ala	Leu	Met	Arg	Leu	Gly	Cys	Ser	Lys	Pro
		50				55				60					
Val	Pro	Ala	Val	Phe	Ile	Gly	Gly	Lys	Leu	Val	Gly	Ser	Thr	Asn	Glu
65				70				75						80	
Val	Met	Ser	Met	His	Leu	Ser	Ser	Ser	Leu	Val	Pro	Leu	Val	Lys	Pro
			85					90				95			

Tyr Leu Cys

(2) INFORMATION FOR SEQ ID NO:953:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 95 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..95

(D) OTHER INFORMATION: / Ceres Seq. ID 1568493

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:953:

Met	Arg	Met	Ser	Ser	Glu	Lys	Gly	Val	Val	Ile	Phe	Thr	Lys	Ser	Ser
1				5				10					15		
Cys	Cys	Leu	Ser	Tyr	Ala	Val	Gln	Val	Leu	Phe	Gln	Asp	Leu	Gly	Val
			20				25					30			

Asn	Pro	Lys	Ile	His	Glu	Ile	Asp	Lys	Asp	Pro	Glu	Cys	Arg	Glu	Ile
		35				40					45				
Glu	Lys	Ala	Leu	Met	Arg	Leu	Gly	Cys	Ser	Lys	Pro	Val	Pro	Ala	Val
		50				55					60				
Phe	Ile	Gly	Gly	Lys	Leu	Val	Gly	Ser	Thr	Asn	Glu	Val	Met	Ser	Met
		65				70				75				80	
His	Leu	Ser	Ser	Ser	Leu	Val	Pro	Leu	Val	Lys	Pro	Tyr	Leu	Cys	
					85				90					95	

(2) INFORMATION FOR SEQ ID NO:954:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1075 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1075
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568494

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:954:

atgaaaccgg	atactcgaga	gtcgccggag	tgtccttccc	ttcttctatc	agctctgctt	60
ctcctttaga	aattagggtt	tttgagggaag	acgagtattc	acttcttttc	accgtgaagc	120
gattggtctt	ttgttcaagg	agcaagcaaa	gctctcagct	tatcgagata	gaagattttc	180
aggaacacaa	gaggagtttg	atgaagcggt	aagggcagct	acacgcggtt	acattggcaa	240
ttgtgttttt	tacactactg	aagaacagct	ttacgagctt	ttctctagag	ctggagaaat	300
caaaaagatc	atcatggggtt	tggataagaa	cactaaaaca	ccttggtgct	ttgttttctg	360
ccgtgtctac	tctagagagg	atactgaaga	tgcagtcag	tatataaagt	ggGactattc	420
tcgatgaccg	gccatttcgt	gtggattttg	attggggatt	ccaagaagga	agacataagg	480
gacgttgtag	aagcggtggt	caggttctgt	atgaataccg	tacagattac	gatcctgtct	540
gaggttatgg	gaaatttagtt	cagaaggaac	tcgaagcaca	aagcgagctc	gtggattaac	600
gtactggctc	attgggagct	tatcctcaag	Ctgcgccaac	gaattattga	aatggaaagg	660
gtggtgaggg	aaactatggt	caaggaggac	aaaatcgcca	tggaaagaga	ggagactacc	720
atcggaacg	acaaagagac	gatgatcgct	atggacgtga	taactcaaga	agaacacacg	780
atcatgagtc	taggagagac	actgatagtg	acatgagacc	ggagaagaac	ccagatttcc	840
gtgagagcgg	tgactccgat	gacgatgggt	aagatgatcg	gaagagaaga	tcttaaaaca	900
aaactttaga	agttgtcaat	gttgctgaat	ggtcaatgta	atcttttagt	tgatgagtct	960
gaactcagtt	tggtgtttct	agattttcat	tacaacggtt	cttaagtgtc	ttcgttcaat	1020
atcagtgtcc	tcattaaact	ttgtctcttg	atcaacagat	atgtcattac	tagtt	

(2) INFORMATION FOR SEQ ID NO:955:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..69
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568495

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:955:

Glu	Thr	Gly	Tyr	Ser	Arg	Val	Ala	Gly	Val	Ser	Phe	Pro	Ser	Ser	Ile
1			5					10					15		
Ser	Ser	Ala	Ser	Pro	Leu	Glu	Ile	Arg	Val	Phe	Glu	Glu	Asp	Glu	Tyr
			20					25				30			
Ser	Leu	Leu	Phe	Thr	Val	Lys	Arg	Trp	Leu	Leu	Cys	Ser	Arg	Ser	Lys
			35				40				45				
Gln	Ser	Ser	Gln	Leu	Ile	Glu	Ile	Glu	Asp	Phe	Gln	Glu	His	Lys	Arg
			50			55				60					
Ser	Leu	Met	Lys	Arg											
			65												

(2) INFORMATION FOR SEQ ID NO:956:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 101 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..101
(D) OTHER INFORMATION: / Ceres Seq. ID 1568496
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:956:
Met Ala Ser Leu Phe Lys Glu Gln Ala Lys Leu Ser Ala Tyr Arg Asp
1 5 10 15
Arg Arg Phe Ser Gly Thr Gln Glu Phe Asp Glu Ala Leu Arg Ala
20 25 30
Ser Thr Thr Val Tyr Ile Gly Asn Val Ser Phe Tyr Thr Thr Glu Glu
35 40 45
Gln Leu Tyr Glu Leu Phe Ser Arg Ala Gly Glu Ile Lys Lys Ile Ile
50 55 60
Met Gly Leu Asp Lys Asn Thr Lys Thr Pro Cys Gly Phe Cys Phe Val
65 70 75 80
Leu Phe Tyr Ser Arg Glu Asp Thr Glu Asp Ala Val Lys Tyr Ile Ser
85 90 95
Gly Asp Tyr Ser Arg
100

(2) INFORMATION FOR SEQ ID NO:957:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 56 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..56
(D) OTHER INFORMATION: / Ceres Seq. ID 1568497
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:957:
Met Glu Met Glu Gly Val Val Glu Glu Thr Met Val Lys Glu Asp Lys
1 5 10 15
Ile Ala Met Glu Glu Glu Thr Thr Ile Gly Asn Asp Lys Glu Thr
20 25 30
Met Ile Ala Met Asp Val Ile Thr Gln Glu Glu Thr Gln Ile Met Ser
35 40 45
Leu Gly Glu Thr Leu Ile Val Thr
50 55

(2) INFORMATION FOR SEQ ID NO:958:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1230 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..1230
(D) OTHER INFORMATION: / Ceres Seq. ID 1568508
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:958:
acgtcaaaaa ttcaaaaacc ccaaaacccat ataattctct atataaatat tcagccctag 60
atcttataat tcatcaatca aacaattctct tcaatcaaat ctcttcttca atcaaatctt 120
caaatccctt caaagatgcc ttcaatgcCa gaagagccgc tcctaacacc aacccagac 180
agattTctgt atgttcccaa ttactatccc acagatctgg gaaatgtaca aaaaagccga 240

agcatcattc	tggaccgcgc	aagaagtaga	tctatcacaa	gacaaccgcg	actgggaaaa	300
cagttctaac	gcaggtgaac	gtcacttcat	caaacacgtc	ctcgtctttc	tcgctgcac	360
tgaacgaatc	gtactagaga	atctcgcttc	tcgcttcatg	tcgcatgttc	aaagtctcga	420
ggcgctgtct	ttctacggtt	tccagatcgc	gattgaaaaa	atccactcgg	agatgtatag	480
tctctctctc	gatacttata	tcaaagataa	caaagagaga	gatcatctct	ttcgtgccat	540
tgaacaatc	ccttgcgtcg	ccaagaaagc	tcaatgggct	atgaatgga	tcgacgggttc	600
tcagactttc	gcgcaacgaa	tcatcgcttt	cgcttgcgtc	gaaggtatct	tcttctccgg	660
aaagctttgt	tcaatctctc	ggctgaagaa	acggggactc	atgcctggat	taacattctc	720
aaacgaattg	atctctcgtg	acgaagggtt	acactgcgac	ttcgttgttc	tactctcac	780
gtactcaaaa	acaaagctta	gcgaagaacg	cgtgaaatca	aNtcGtctgc	gacgcggtcg	840
aaatcgagag	agagttttgt	tgcgacgcgc	ttcgtgcgcg	gttggttggg	atgaaccgtg	900
atttgtagag	tcagtatatt	gagtttgttg	cgcataggct	tttggtgtacg	cttggtgtacg	960
ggaaggtgta	cggtgttact	aatccgtttg	attggatgga	acttatttcg	cttcaaggga	1020
aaacgaattt	cttcgagaaa	cgtgttgttg	attacaaaaa	ggcttcctgt	atgtctagcg	1080
ttaatggtaa	cggcgcgttt	gataaccatg	tcttctctct	cgacgaagat	ttttaagag	1140
cggtttgttt	gatgctataa	ttacgattct	actcttctgt	tattaccgtg	tattatcctt	1200
ggtttttgaa	ttaatgaata	attagttgcc				

(2) INFORMATION FOR SEQ ID NO:959:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 236 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..236

(D) OTHER INFORMATION: / Ceres Seq. ID 1568509

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:959:

Met	Phe	Pro	Ile	His	Tyr	Pro	Gln	Ile	Trp	Glu	Met	Tyr	Lys	Lys	Ala
1				5					10					15	
Glu	Ala	Ser	Phe	Trp	Thr	Ala	Glu	Glu	Val	Asp	Leu	Ser	Gln	Asp	Asn
		20						25					30		
Arg	Asp	Trp	Glu	Asn	Ser	Leu	Asn	Asp	Gly	Glu	Arg	His	Phe	Ile	Lys
		35					40				45				
His	Val	Leu	Ala	Phe	Phe	Ala	Ala	Ser	Asp	Gly	Ile	Val	Leu	Glu	Asn
		50				55				60					
Leu	Ala	Ser	Arg	Phe	Met	Ser	Asp	Val	Gln	Val	Ser	Glu	Ala	Arg	Ala
65				70					75					80	
Phe	Tyr	Gly	Phe	Gln	Ile	Ala	Ile	Glu	Asn	Ile	His	Ser	Glu	Met	Tyr
				85					90				95		
Ser	Leu	Leu	Leu	Asp	Thr	Tyr	Ile	Lys	Asp	Asn	Lys	Glu	Arg	Asp	His
		100						105				110			
Leu	Phe	Arg	Ala	Ile	Glu	Thr	Ile	Pro	Cys	Val	Ala	Lys	Lys	Ala	Gln
		115					120					125			
Trp	Ala	Met	Lys	Trp	Ile	Asp	Gly	Ser	Gln	Thr	Phe	Ala	Glu	Arg	Ile
		130				135					140				
Ile	Ala	Phe	Ala	Cys	Val	Glu	Gly	Ile	Phe	Phe	Ser	Gly	Ser	Phe	Cys
145				150					155					160	
Ser	Ile	Phe	Trp	Leu	Lys	Lys	Arg	Gly	Leu	Met	Pro	Gly	Leu	Thr	Phe
		165						170				175			
Ser	Asn	Glu	Leu	Ile	Ser	Arg	Asp	Glu	Gly	Leu	His	Cys	Asp	Phe	Ala
		180					185					190			
Cys	Leu	Leu	Tyr	Thr	Leu	Leu	Lys	Thr	Lys	Leu	Ser	Glu	Glu	Arg	Val
		195					200					205			
Lys	Ser	Xaa	Arg	Leu	Arg	Arg	Gly	Arg	Asn	Arg	Glu	Arg	Val	Cys	Val
		210					215					220			
Arg	Arg	Ala	Ser	Val	Arg	Val	Gly	Trp	Asp	Glu	Pro				
225				230					235						

(2) INFORMATION FOR SEQ ID NO:960:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 225 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..225
(D) OTHER INFORMATION: / Ceres Seq. ID 1568510
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:960:
Met Tyr Lys Lys Ala Glu Ala Ser Phe Trp Thr Ala Glu Glu Val Asp
1 5 10 15
Leu Ser Gln Asp Asn Arg Asp Trp Glu Asn Ser Leu Asn Asp Gly Glu
20 25 30
Arg His Phe Ile Lys His Val Leu Ala Phe Phe Ala Ala Ser Asp Gly
35 40 45
Ile Val Leu Glu Asn Leu Ala Ser Arg Phe Met Ser Asp Val Gln Val
50 55 60
Ser Glu Ala Arg Ala Phe Tyr Gly Phe Gln Ile Ala Ile Glu Asn Ile
65 70 75 80
His Ser Glu Met Tyr Ser Leu Leu Leu Asp Thr Tyr Ile Lys Asp Asn
85 90 95
Lys Glu Arg Asp His Leu Phe Arg Ala Ile Glu Thr Ile Pro Cys Val
100 105 110
Ala Lys Lys Ala Gln Trp Ala Met Lys Trp Ile Asp Gly Ser Gln Thr
115 120 125
Phe Ala Glu Arg Ile Ile Ala Phe Ala Cys Val Glu Gly Ile Phe Phe
130 135 140
Ser Gly Ser Phe Cys Ser Ile Phe Trp Leu Lys Lys Arg Gly Leu Met
145 150 155 160
Pro Gly Leu Thr Phe Ser Asn Glu Leu Ile Ser Arg Asp Glu Gly Leu
165 170 175
His Cys Asp Phe Ala Cys Leu Leu Tyr Thr Leu Leu Lys Thr Lys Leu
180 185 190
Ser Glu Glu Arg Val Lys Ser Xaa Arg Leu Arg Arg Gly Arg Asn Arg
195 200 205
Glu Arg Val Cys Val Arg Arg Ala Ser Val Arg Val Gly Trp Asp Glu
210 215 220
Pro
225
(2) INFORMATION FOR SEQ ID NO:961:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 167 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..167
(D) OTHER INFORMATION: / Ceres Seq. ID 1568511
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:961:
Met Ser Asp Val Gln Val Ser Glu Ala Arg Ala Phe Tyr Gly Phe Gln
1 5 10 15
Ile Ala Ile Glu Asn Ile His Ser Glu Met Tyr Ser Leu Leu Leu Asp
20 25 30
Thr Tyr Ile Lys Asp Asn Lys Glu Arg Asp His Leu Phe Arg Ala Ile
35 40 45
Glu Thr Ile Pro Cys Val Ala Lys Lys Ala Gln Trp Ala Met Lys Trp
50 55 60
Ile Asp Gly Ser Gln Thr Phe Ala Glu Arg Ile Ile Ala Phe Ala Cys

65		70		75		80
Val Glu Gly Ile	Phe Phe Ser Gly Ser	Phe Cys Ser Ile Phe Trp Leu				
	85	90	95			
Lys Lys Arg Gly Leu Met Pro Gly Leu Thr Phe Ser Asn Glu Leu Ile						
	100	105	110			
Ser Arg Asp Glu Gly Leu His Cys Asp Phe Ala Cys Leu Leu Tyr Thr						
	115	120	125			
Leu Leu Lys Thr Lys Leu Ser Glu Glu Arg Val Lys Ser Xaa Arg Leu						
	130	135	140			
Arg Arg Gly Arg Asn Arg Glu Arg Val Cys Val Arg Arg Ala Ser Val						
	145	150	155			160
Arg Val Gly Trp Asp Glu Pro						
	165					

(2) INFORMATION FOR SEQ ID NO:962:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1388 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1388
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568512

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:962:

```

cgaagattct cgttgatgac tatctcgatt cgtcttgatt cctctttttt cccagaaaaag      60
tcgctattgg aatcgaacga aagtgttgaa gattttacca gtcagaggta tatatatata      120
gagagagagt tatggtattg gatcaatgga ttccaaggt taaagatggt cagcatctct      180
ccgaagacga gcttcagcct ctctgcgaat acgtgaaaga gattctgatt gaggagtcac      240
acgtacacgc tgtaaaacgt ccagtcaccg tatgtggtga tatccatggc cagtttcatg      300
attctatgga gctttttcag accggagggtC atgttccoga caccaattac atttttatgg      360
gggacttcgt ggatagaggt tacaacagcc ttgaagtctt cactattctt ttacttctta      420
aagctagata tccagccaat attacacttt tgcgcggaaa tcatgaaagt aggcagctaa      480
cgcagggtga tggttttctat gacgaatgcc agaggaagta tggtaacgct aatgcgtggc      540
gatattgcac agatgttttt gactatctta cctctgcagc tattatagat ggcaacagttc      600
tatgtgttca cgttgccctt tccccggatg tccggacaat tgatcagata agactgatcg      660
agcgaatcgt cgaaattcct catgaagggc ccttttgoga tcttatgtgag atgfatccgtg      720
aagatattga aacatggggc gtttagtccac gtggagctgg ttggcttttc ggaaccaggg      780
ttaccactga gtttaaccat atcaacaagc tggatctagt atgcgcgtcg caccacagtt      840
tacaagaagg tcttaagtag atgttccaag ataaaggcct tgtaactgta tggctctcac      900
ctaataactg ttaccgctgt gggaaatgct cttctatatt gagtttcaat gcaacacatgg      960
aaagggaagt gaagtctctc acagagacag aagagaacaa tcaaatgaga ggcccaagga      1020
ctggagtctc gtatttccta tgaagaatca cacttattat attgctgtg atgatgaagc      1080
cttgctgtcc attggcaata tgttcagttc aatgtggaaa aggttaatat atgattatat      1140
atatattcta ctgatggggt togtctacta tcatattttt tgtccattag gttacatttc      1200
ccttttgaaa gttacaagtc aaacactttg gtaatagctc tagtcatttt gatctctcgc      1260
tctcttttct ttcccccaat ctttctcttg taatgttatt tttttcattg ttcaactgta      1320
ctgttctctc tgtttttctt gttgtgtgtg tgaagatgac attaatctta aaataatcaa      1380
acatcggt

```

(2) INFORMATION FOR SEQ ID NO:963:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 303 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..303
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568513

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:963:

Met Asp Leu Asp Gln Trp Ile Ser Lys Val Lys Asp Gly Gln His Leu
1 5 10 15
Ser Glu Asp Glu Leu Gln Leu Leu Cys Glu Tyr Val Lys Glu Ile Leu
20 25 30
Ile Glu Glu Ser Asn Val Gln Pro Val Asn Ser Pro Val Thr Val Cys
35 40 45
Gly Asp Ile His Gly Gln Phe His Asp Leu Met Lys Leu Phe Gln Thr
50 55 60
Gly Gly His Val Pro Asp Thr Asn Tyr Ile Phe Met Gly Asp Phe Val
65 70 75 80
Asp Arg Gly Tyr Asn Ser Leu Glu Val Phe Thr Ile Leu Leu Leu Leu
85 90 95
Lys Ala Arg Tyr Pro Ala Asn Ile Thr Leu Leu Arg Gly Asn His Glu
100 105 110
Ser Arg Gln Leu Thr Gln Val Tyr Gly Phe Tyr Asp Glu Cys Gln Arg
115 120 125
Lys Tyr Gly Asn Ala Asn Ala Trp Arg Tyr Cys Thr Asp Val Phe Asp
130 135 140
Tyr Leu Thr Leu Ser Ala Ile Ile Asp Gly Thr Val Leu Cys Val His
145 150 155 160
Gly Gly Leu Ser Pro Asp Val Arg Thr Ile Asp Gln Ile Arg Leu Ile
165 170 175
Glu Arg Asn Arg Glu Ile Pro His Glu Gly Pro Phe Cys Asp Leu Met
180 185 190
Trp Ser Asp Pro Glu Asp Ile Glu Thr Trp Ala Val Ser Pro Arg Gly
195 200 205
Ala Gly Trp Leu Phe Gly Ser Arg Val Thr Thr Glu Phe Asn His Ile
210 215 220
Asn Lys Leu Asp Leu Val Cys Arg Ser His Gln Leu Val Gln Glu Gly
225 230 235 240
Leu Lys Tyr Met Phe Gln Asp Lys Gly Leu Val Thr Val Trp Ser Ala
245 250 255
Pro Asn Asn Cys Tyr Arg Cys Gly Asn Val Ala Ser Ile Leu Ser Phe
260 265 270
Asn Asp Asn Met Glu Arg Glu Val Lys Phe Phe Thr Glu Thr Glu Glu
275 280 285
Asn Asn Gln Met Arg Gly Pro Arg Thr Gly Val Pro Tyr Phe Leu
290 295 300

(2) INFORMATION FOR SEQ ID NO:964:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 245 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..245

(D) OTHER INFORMATION: / Ceres Seq. ID 1568514

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:964:

Met Lys Leu Phe Gln Thr Gly Gly His Val Pro Asp Thr Asn Tyr Ile
1 5 10 15
Phe Met Gly Asp Phe Val Asp Arg Gly Tyr Asn Ser Leu Glu Val Phe
20 25 30
Thr Ile Leu Leu Leu Lys Ala Arg Tyr Pro Ala Asn Ile Thr Leu
35 40 45
Leu Arg Gly Asn His Glu Ser Arg Gln Leu Thr Gln Val Tyr Gly Phe
50 55 60
Tyr Asp Glu Cys Gln Arg Lys Tyr Gly Asn Ala Asn Ala Trp Arg Tyr
65 70 75 80
Cys Thr Asp Val Phe Asp Tyr Leu Thr Leu Ser Ala Ile Ile Asp Gly

Met	Gly	Asp	Phe	Val	Asp	Arg	Gly	Tyr	Asn	Ser	Leu	Glu	Val	Phe	Thr
1				5					10					15	
Ile	Leu	Leu	Leu	Leu	Lys	Ala	Arg	Tyr	Pro	Ala	Asn	Ile	Thr	Leu	Leu
			20					25					30		
Arg	Gly	Asn	His	Glu	Ser	Arg	Gln	Leu	Thr	Gln	Val	Tyr	Gly	Phe	Tyr
		35					40					45			
Asp	Glu	Cys	Gln	Arg	Lys	Tyr	Gly	Asn	Ala	Asn	Ala	Trp	Arg	Tyr	Cys
	50					55					60				
Thr	Asp	Val	Phe	Asp	Tyr	Leu	Thr	Leu	Ser	Ala	Ile	Ile	Asp	Gly	Thr
	65				70				75					80	
Val	Leu	Cys	Val	His	Gly	Gly	Leu	Ser	Pro	Asp	Val	Arg	Thr	Ile	Asp
				85					90					95	
Gln	Ile	Arg	Glu	Ile	Glu	Arg	Asn	Arg	Glu	Ile	Pro	His	Glu	Gly	Pro
			100					105					110		
Phe	Cys	Asp	Leu	Met	Trp	Ser	Asp	Pro	Glu	Asp	Ile	Glu	Thr	Trp	Ala
		115					120					125			
Val	Ser	Pro	Arg	Gly	Ala	Gly	Trp	Leu	Phe	Gly	Ser	Arg	Val	Thr	Thr
					135					140					
Glu	Phe	Asn	His	Ile	Asn	Lys	Leu	Asp	Leu	Val	Cys	Arg	Ser	His	Gln
	145				150					155				160	
Leu	Val	Gln	Glu	Gly	Leu	Lys	Tyr	Met	Phe	Gln	Asp	Lys	Gly	Leu	Val
			165						170					175	
Thr	Val	Trp	Ser	Ala	Pro	Asn	Asn	Cys	Tyr	Arg	Cys	Gly	Asn	Val	Ala
			180					185					190		
Ser	Ile	Leu	Ser	Phe	Asn	Asp	Asn	Met	Glu	Arg	Glu	Val	Lys	Phe	Phe
		195				200						205			
Thr	Glu	Thr	Glu	Glu	Asn	Asn	Gln	Met	Arg	Gly	Pro	Arg	Thr	Gly	Val
	210				215						220				

Pro Tyr Phe Leu
225

(2) INFORMATION FOR SEQ ID NO:966:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 660 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..660
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568528

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:966:

gaccaagaaa	tgtatacttt	ataagagaaa	tgtacttgat	attcaaaaaa	acaaaaaata	60
aactaggttg	gttaagatta	ttcaaaacttc	aaaggcaaaa	ccaaatgagc	ttcgtgtggt	120
ccgtcgcggt	ttgggtcata	gctgtagcgg	Anttgttgtg	attagcaaat	ggttataccg	180
atggtcgaaac	ccgaagtgc	atggtaagtt	accaccggga	tcaatgggtt	taccgatcat	240
cggagagaca	tgcgacttct	ttgagcccca	tggattatac	gagatcccac	cctttgtcaa	300
gaagaggatg	ttaaagtacg	ggccattgtt	tcggaacaac	attttcggat	ccaacaccgt	360
ggttttgaca	gaagctgata	tcattcttga	ggttttcocg	caagagaaca	agtcttttgt	420
gactagctat	ccagaggcca	ttctcaagcc	atttggaaaa	gaacgtgttt	cctcaaacat	480
ggaaaacatcc	acaagcacgt	caaacaatc	agtcttcaac	ttcttggctc	tgaggcttta	540
aaaaaacaga	tgataggaga	aatagacaga	gtaacctatg	agcatcttag	atcgaaagct	600
aacgagggta	gcttcgatgc	taaggaggca	gttaaaagtg	tacttacata	gtttcttaat	660

(2) INFORMATION FOR SEQ ID NO:967:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..52
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568529

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:967:

Pro	Arg	Asn	Val	Tyr	Phe	Ile	Arg	Glu	Met	Tyr	Leu	Ile	Phe	Lys	Lys
1		5						10						15	
Thr	Lys	Asn	Lys	Leu	Gly	Trp	Leu	Arg	Leu	Phe	Lys	Leu	Gln	Arg	Gln
		20					25						30		
Asn	Gln	Met	Ser	Phe	Val	Trp	Ser	Ala	Ala	Val	Trp	Val	Ile	Ala	Val
		35					40					45			
Ala	Xaa	Leu	Leu												
		50													

(2) INFORMATION FOR SEQ ID NO:968:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..105
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568530

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:968:

Met	Gly	Leu	Pro	Ile	Ile	Gly	Glu	Thr	Cys	Asp	Phe	Phe	Glu	Pro	His
1		5					10						15		
Gly	Leu	Tyr	Glu	Ile	Pro	Pro	Phe	Val	Lys	Arg	Met	Leu	Lys	Tyr	

	20		25		30										
Gly	Pro	Leu	Phe	Arg	Thr	Asn	Ile	Phe	Gly	Ser	Asn	Thr	Val	Val	Leu
	35						40					45			
Thr	Glu	Ala	Asp	Ile	Ile	Phe	Glu	Val	Phe	Arg	Gln	Glu	Asn	Lys	Ser
	50					55					60				
Phe	Val	Thr	Ser	Tyr	Pro	Glu	Ala	Ile	Leu	Lys	Pro	Phe	Gly	Lys	Glu
	65				70				75					80	
Thr	Cys	Ser	Ser	Asn	Met	Glu	Thr	Ser	Thr	Ser	Asn	Lys	Ser		
			85					90				95			
Val	Phe	Asn	Phe	Leu	Ala	Leu	Arg	Leu							
	100						105								

(2) INFORMATION FOR SEQ ID NO:969:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 77 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..77
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568531

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:969:

Met	Leu	Lys	Tyr	Gly	Pro	Leu	Phe	Arg	Thr	Asn	Ile	Phe	Gly	Ser	Asn
1			5					10					15		
Thr	Val	Val	Leu	Thr	Glu	Ala	Asp	Ile	Ile	Phe	Glu	Val	Phe	Arg	Gln
		20				25						30			
Glu	Asn	Lys	Ser	Phe	Val	Thr	Ser	Tyr	Pro	Glu	Ala	Ile	Leu	Lys	Pro
	35					40					45				
Phe	Gly	Lys	Glu	Thr	Cys	Ser	Ser	Asn	Met	Glu	Thr	Ser	Thr	Ser	Thr
	50				55					60					
Ser	Asn	Lys	Ser	Val	Phe	Asn	Phe	Leu	Ala	Leu	Arg	Leu			
65			70					75							

(2) INFORMATION FOR SEQ ID NO:970:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 468 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..468
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568576

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:970:

aataagtcca	tatttgttag	ctccaactcc	aaagtgaag	agagaaagag	atagagaatc	60
gccatggcaa	cgaagtcaag	actttctatc	tgcgccatc	ttaccatcgt	cgttctcggt	120
atctttgaaa	tacctgagat	agaagcacat	gatagcgagt	gtctgaaaga	atatgggggt	180
gatgttgggt	ttggcttctg	tgcgcctaag	atatttccga	cgatttgta	tagaaattgc	240
caaaaagaca	agggggctaa	tggtgaaaaa	tgcccttggg	gagagggtgg	taatgtgaaa	300
tgcttatgcg	acttctgcag	caaggaaatc	tttaatcagg	ttataatgct	tacttgaatc	360
ttgcattgtg	cgtgtgttaa	tttgtgtact	aattaagcaa	ggctaattgat	ccaagaataa	420
atgtaacaat	gaataagtaa	aataaagaaa	cgctaggctt	tgcttgtg		

(2) INFORMATION FOR SEQ ID NO:971:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 97 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1..97
(D) OTHER INFORMATION: / Ceres Seq. ID 1568577

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:971:

Met	Ala	Thr	Lys	Ser	Val	Leu	Ser	Ile	Phe	Ala	Ile	Phe	Thr	Ile	Val
1			5					10					15		
Val	Leu	Val	Ile	Phe	Glu	Ile	Pro	Glu	Ile	Glu	Ala	His	Asp	Ser	Glu
			20					25					30		
Cys	Leu	Lys	Glu	Tyr	Gly	Gly	Asp	Val	Gly	Phe	Gly	Phe	Cys	Ala	Pro
		35					40					45			
Lys	Ile	Phe	Pro	Thr	Ile	Cys	Tyr	Arg	Asn	Cys	Gln	Lys	Asp	Lys	Gly
		50				55					60				
Ala	Asn	Gly	Gly	Lys	Cys	Leu	Trp	Gly	Glu	Gly	Gly	Asn	Val	Lys	Cys
		65				70				75				80	
Leu	Cys	Asp	Phe	Cys	Ser	Lys	Glu	Ser	Phe	Asn	Gln	Phe	Ile	Ser	Leu
			85					90						95	

Thr

(2) INFORMATION FOR SEQ ID NO:972:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 676 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -
(B) LOCATION: 1..676
(D) OTHER INFORMATION: / Ceres Seq. ID 1568583

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:972:

agatacaaaag	ctttctttat	aaacgctgcg	tcacatcact	gaatcaaaaa	ccctagcgat	60
acttcacatc	tcgagccgga	gccgcgttgc	gaaagcattt	caatcgtagt	ctaagagaat	120
gtcgacagtg	ggagagctcg	cttgMagvta	cgctgttatg	atcctcgagg	atgagggtat	180
tgctatcacg	gctgacaaaa	tcgccacttt	ggtgaaagct	gctggtgtta	ccattgagtc	240
atactggcca	atgctatttc	ccaagatggc	tgagaaacgt	aatgtcactg	atctcatcat	300
gaacgttggt	gctggtgggt	gaggtggtgc	gcctgttgca	gctgctgctc	ctgctgctgg	360
cggtggtgct	gcgcgtgctg	ctcctgctgc	cgaggagaag	aagaaggacg	aaccagcaga	420
agagagtcat	ggagatttgg	gttttggcct	gttcgattaa	gtgcatttta	cttgttkttt	480
cttcttcgat	ttgagactat	ttttttttcg	tatcgagcta	ttactgtgtt	tggtctggct	540
gaagaactat	aattagttgt	ttctgaacc	atatgttgta	tgacacaaat	tttcaagcaa	600
accctatggc	tccttctttc	cttagaagt	attttgtcac	ctcttttttt	tttaattcat	660
tcgagatatt	agtgctg					

(2) INFORMATION FOR SEQ ID NO:973:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 113 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1..113
(D) OTHER INFORMATION: / Ceres Seq. ID 1568584

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:973:

Met	Ser	Thr	Val	Gly	Glu	Leu	Ala	Xaa	Xaa	Tyr	Ala	Val	Met	Ile	Leu
1				5						10				15	
Glu	Asp	Glu	Gly	Ile	Ala	Ile	Thr	Ala	Asp	Lys	Ile	Ala	Thr	Leu	Val
			20					25					30		
Lys	Ala	Ala	Gly	Val	Thr	Ile	Glu	Ser	Tyr	Trp	Pro	Met	Leu	Phe	Ala
		35					40					45			
Lys	Met	Ala	Glu	Lys	Arg	Asn	Val	Thr	Asp	Leu	Ile	Met	Asn	Val	Gly

50 55 60
Ala Gly Gly Gly Gly Gly Ala Pro Val Ala Ala Ala Pro Ala Ala
65 70 75 80
Gly Gly Gly Ala Ala Ala Ala Ala Pro Ala Ala Glu Glu Lys Lys Lys
85 90 95
Asp Glu Pro Ala Glu Glu Ser Asp Gly Asp Leu Gly Phe Gly Leu Phe
100 105 110
Asp

(2) INFORMATION FOR SEQ ID NO:974:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 100 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..100

(D) OTHER INFORMATION: / Ceres Seq. ID 1568585

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:974:

Met Ile Leu Glu Asp Glu Gly Ile Ala Ile Thr Ala Asp Lys Ile Ala
1 5 10 15
Thr Leu Val Lys Ala Ala Gly Val Thr Ile Glu Ser Tyr Trp Pro Met
20 25 30
Leu Phe Ala Lys Met Ala Glu Lys Arg Asn Val Thr Asp Leu Ile Met
35 40 45
Asn Val Gly Ala Gly Gly Gly Gly Ala Pro Val Ala Ala Ala Ala
50 55 60
Pro Ala Ala Gly Gly Gly Ala Ala Ala Ala Pro Ala Ala Glu Glu
65 70 75 80
Lys Lys Lys Asp Glu Pro Ala Glu Glu Ser Asp Gly Asp Leu Gly Phe
85 90 95
Gly Leu Phe Asp
100

(2) INFORMATION FOR SEQ ID NO:975:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 69 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..69

(D) OTHER INFORMATION: / Ceres Seq. ID 1568586

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:975:

Met Leu Phe Ala Lys Met Ala Glu Lys Arg Asn Val Thr Asp Leu Ile
1 5 10 15
Met Asn Val Gly Ala Gly Gly Gly Gly Ala Pro Val Ala Ala Ala
20 25 30
Ala Pro Ala Ala Gly Gly Gly Ala Ala Ala Ala Pro Ala Ala Glu
35 40 45
Glu Lys Lys Lys Asp Glu Pro Ala Glu Glu Ser Asp Gly Asp Leu Gly
50 55 60
Phe Gly Leu Phe Asp
65

(2) INFORMATION FOR SEQ ID NO:976:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 930 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..930
(D) OTHER INFORMATION: / Ceres Seq. ID 1568595
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:976:

gcgcaccata	gaaggagaaaa	caaatcttca	ttccagcaat	ggcgattcgt	tgtgtagcga	60
gtagaaaaac	cctagccggc	ttgaaggaga	catactcgag	gctattgagg	atcagaggga	120
ttcagacttt	tacgtctcct	gatcttctct	acgattatgg	cgcatgtgaa	ccggccatta	180
gtggagagat	catgcagatt	catcaccaga	agcatcacca	gccttatggt	actaattaca	240
ataatgctct	tgagcagctt	gatcaagctg	tgaacaaggg	agatgcttcc	actgttgtta	300
agttgcagag	cgccatcaaa	ttcaacggcg	gaggtcatgt	caaccattcg	attttctgga	360
agaaacctgc	tccctccagt	gaaggtgggt	gagagccacc	aaaaggatct	cttggtagtg	420
ccattgacgc	tcactttggc	tcccttgaag	gtctggtgaa	aaagatgagt	gctgaggggt	480
ctgcagtgtca	aggtctcagg	tgggtgtggc	tcggactaga	caaagaactg	aagaagctag	540
ttgttgacac	aactgccaat	caggatccat	tagtgacaaa	aggaggaagc	ttggtacctc	600
tgggtgggtat	agatgttttg	gagcacgcct	actacttgca	gtacaaaaat	gtgaggcctg	660
agtatctgaa	gaatgtatgg	aaagtgatca	actggaataa	tgaacgcgag	gtttatgaga	720
aggaagaacaa	ctgaatcggt	tacacgatga	cataaggaga	tgaaccagtt	ccagctcagc	780
ttttgtttta	aggtttgtctg	aaacaaactt	acagtgtctc	tttggttttt	aagatttgct	840
caactcagct	gtgtgggtacg	ttgttttaca	atgaaagttt	Kcaagaataa	aaatttgcta	900
ttattgtcag	aaagcgctat	tgtttattct				

(2) INFORMATION FOR SEQ ID NO:977:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 231 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..231
(D) OTHER INFORMATION: / Ceres Seq. ID 1568596
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:977:

Met	Ala	Ile	Arg	Cys	Val	Ala	Ser	Arg	Lys	Thr	Leu	Ala	Gly	Leu	Lys	
1				5					10					15		
Glu	Thr	Ser	Ser	Arg	Leu	Leu	Arg	Ile	Arg	Gly	Ile	Gln	Thr	Phe	Thr	
				20				25				30				
Leu	Pro	Asp	Leu	Pro	Tyr	Asp	Tyr	Gly	Ala	Leu	Glu	Pro	Ala	Ile	Ser	
				35				40				45				
Gly	Glu	Ile	Met	Gln	Ile	His	His	Gln	Lys	His	His	Gln	Ala	Tyr	Val	
				50				55				60				
Thr	Asn	Tyr	Asn	Asn	Ala	Leu	Glu	Gln	Leu	Asp	Gln	Ala	Val	Asn	Lys	
				65				70				75			80	
Gly	Asp	Ala	Ser	Thr	Val	Val	Lys	Leu	Gln	Ser	Ala	Ile	Lys	Phe	Asn	
				85				90						95		
Gly	Gly	Gly	His	Val	Asn	His	Ser	Ile	Phe	Trp	Lys	Asn	Leu	Ala	Pro	
				100				105					110			
Ser	Ser	Glu	Gly	Gly	Gly	Glu	Pro	Pro	Lys	Gly	Ser	Leu	Gly	Ser	Ala	
				115				120				125				
Ile	Asp	Ala	His	Phe	Gly	Ser	Leu	Glu	Gly	Leu	Val	Lys	Lys	Met	Ser	
				130				135				140				
Ala	Glu	Gly	Ala	Ala	Val	Gln	Gly	Ser	Gly	Trp	Val	Trp	Leu	Gly	Leu	
				145				150				155			160	
Asp	Lys	Glu	Leu	Lys	Lys	Leu	Val	Val	Asp	Thr	Thr	Ala	Asn	Gln	Asp	
				165				170					175			
Pro	Leu	Val	Thr	Lys	Gly	Gly	Ser	Leu	Val	Pro	Leu	Val	Gly	Ile	Asp	
				180				185					190			
Val	Trp	Glu	His	Ala	Tyr	Tyr	Leu	Gln	Tyr	Lys	Asn	Val	Arg	Pro	Glu	

195 200 205
Tyr Leu Lys Asn Val Trp Lys Val Ile Asn Trp Lys Tyr Ala Ser Glu
210 215 220
Val Tyr Glu Lys Glu Ser Asn
225 230

(2) INFORMATION FOR SEQ ID NO:978:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 180 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..180
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568597

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:978:

Met	Gln	Ile	His	His	Gln	Lys	His	His	Gln	Ala	Tyr	Val	Thr	Asn	Tyr
1			5						10					15	
Asn	Asn	Ala	Leu	Glu	Gln	Leu	Asp	Gln	Ala	Val	Asn	Lys	Gly	Asp	Ala
			20					25					30		
Ser	Thr	Val	Val	Lys	Leu	Gln	Ser	Ala	Ile	Lys	Phe	Asn	Gly	Gly	Gly
			35				40					45			
His	Val	Asn	His	Ser	Ile	Phe	Trp	Lys	Asn	Leu	Ala	Pro	Ser	Ser	Glu
			50				55					60			
Gly	Gly	Gly	Glu	Pro	Pro	Lys	Gly	Ser	Leu	Gly	Ser	Ala	Ile	Asp	Ala
			65			70				75			80		
His	Phe	Gly	Ser	Leu	Glu	Gly	Leu	Val	Lys	Lys	Met	Ser	Ala	Glu	Gly
			85					90					95		
Ala	Ala	Val	Gln	Gly	Ser	Gly	Trp	Val	Trp	Leu	Gly	Leu	Asp	Lys	Glu
			100				105					110			
Leu	Lys	Lys	Leu	Val	Val	Asp	Thr	Thr	Ala	Asn	Gln	Asp	Pro	Leu	Val
			115				120					125			
Thr	Lys	Gly	Gly	Ser	Leu	Val	Pro	Leu	Val	Gly	Ile	Asp	Val	Trp	Glu
			130				135					140			
His	Ala	Tyr	Tyr	Leu	Gln	Tyr	Lys	Asn	Val	Arg	Pro	Glu	Tyr	Leu	Lys
			145			150				155				160	
Asn	Val	Trp	Lys	Val	Ile	Asn	Trp	Lys	Tyr	Ala	Ser	Glu	Val	Trp	Glu
			165					170						175	
Lys	Glu	Ser	Asn												

(2) INFORMATION FOR SEQ ID NO:979:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1270 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1270
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568598

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:979:

cgaaaagcat	tgatttggct	ctccttctc	ttctattcta	ttcataaaga	acctaattctt	60
catcttctcc	atcttcttct	tcaaggactc	caactcgctc	atccaggaga	gtttattagt	120
agtaaccaat	ccaagtgttc	cttttgtttg	aagcaacaag	ctttgtgata	ttatcctgag	180
agacaatggt	tgggtttaag	aaatcacccg	caaatcttcc	caagcataac	tcagtcgacc	240
tcaagtcttc	caagccaaat	ctcttcgatt	cagatgatga	atctgacaac	aaacataccc	300
ttaaccYtTt	ctaagaggac	tacctctgaa	ccctctttgg	ctgatgatgc	aaacccctttt	360
ggtggtgaga	gagttcagaa	aggagatagt	agttcatcca	aacagtcatt	gttttcgaa	420
tccaaatacc	agtacaagaa	caatttccgt	gattctgggt	gtattgaaaa	ccagtcgggt	480

caggagcttg	aaggttatgc	tgtgtacaag	gctgaagaga	ctacgaaatc	tgtacaaggt	540
tggtttgaag	tagcagaaga	tataaggtct	gatgctacca	gaacttttgt	catgttacac	600
gatcaggcgc	agcaaatcac	taggacgcac	cataaagcgc	ttgaaatcga	ccatgatctc	660
agtcgtggtg	agaagctctt	tggaagcctt	ggaggcatgt	tttcaaagac	ttggaaacaa	720
aagaagactc	gttcctataa	tggtcccgct	gtaaccagag	atgactcacc	aacgagaaga	780
gttaaccact	tagagaaaag	ggaaaaactg	ggactgaact	cagaccaccg	aggacaatca	840
agaacccgag	aaccactccc	cgaatcagct	gatgcttacc	agagagtgga	gatggaaaaa	900
gctaagcaag	acgatgggct	ttcagacttg	agtgatatac	tcggcgagct	aaagaacatg	960
gctgtgtaca	tgggaaagcga	aatcgagaag	cagaacaaag	gacttgacca	tcttcctgat	1020
gatgtgtacg	aactcaactt	cagagtgcaa	caatcaaacg	aacgtggctg	ccgtttgtct	1080
ggaaagtaga	tgaacagagg	gtttatatgt	tcattacact	cattcctcgt	ttgtttttat	1140
ctctatgaag	ttgttcttta	aaactggaaa	gattctttac	atgttaaaata	cattatttgt	1200
atctgtgttt	gtatttgatc	ttgtgacaaa	aaaccaaata	acttattgat	caaacagaa	1260
caactttggc						

(2) INFORMATION FOR SEQ ID NO:980:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 271 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..271

(D) OTHER INFORMATION: / Ceres Seq. ID 1568599

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:980:

Met	Met	Asn	Leu	Thr	Thr	Asn	Ile	Pro	Leu	Thr	Xaa	Ser	Lys	Arg	Thr
1		5						10					15		
Thr	Ser	Glu	Pro	Ser	Leu	Ala	Asp	Met	Thr	Asn	Pro	Phe	Gly	Gly	Glu
		20						25					30		
Arg	Val	Gln	Lys	Gly	Asp	Ser	Ser	Ser	Lys	Gln	Ser	Leu	Phe	Ser	
		35				40					45				
Asn	Ser	Lys	Tyr	Gln	Tyr	Lys	Asn	Asn	Phe	Arg	Asp	Ser	Gly	Gly	Ile
		50				55					60				
Glu	Asn	Gln	Ser	Val	Gln	Glu	Leu	Glu	Gly	Tyr	Ala	Val	Tyr	Lys	Ala
		65			70				75				80		
Glu	Glu	Thr	Thr	Lys	Ser	Val	Gln	Gly	Cys	Leu	Lys	Val	Ala	Glu	Asp
		85						90					95		
Ile	Arg	Ser	Asp	Ala	Thr	Arg	Thr	Leu	Val	Met	Leu	His	Asp	Gln	Gly
		100					105						110		
Glu	Gln	Ile	Thr	Arg	Thr	His	His	Lys	Ala	Val	Glu	Ile	Asp	His	Asp
		115			120						125				
Leu	Ser	Arg	Gly	Glu	Lys	Leu	Leu	Gly	Ser	Leu	Gly	Met	Phe	Ser	
		130			135						140				
Lys	Thr	Trp	Lys	Pro	Lys	Lys	Thr	Arg	Pro	Ile	Asn	Gly	Pro	Val	Val
		145			150				155					160	
Thr	Arg	Asp	Asp	Ser	Pro	Thr	Arg	Arg	Val	Asn	His	Leu	Glu	Lys	Arg
		165						170					175		
Glu	Lys	Leu	Gly	Leu	Asn	Ser	Ala	Pro	Arg	Gly	Gln	Ser	Arg	Thr	Arg
		180					185						190		
Glu	Pro	Leu	Pro	Glu	Ser	Ala	Asp	Ala	Tyr	Gln	Arg	Val	Glu	Met	Glu
		195				200						205			
Lys	Ala	Lys	Gln	Asp	Asp	Gly	Leu	Ser	Asp	Leu	Ser	Asp	Ile	Leu	Gly
		210				215					220				
Glu	Leu	Lys	Asn	Met	Ala	Val	Asp	Met	Gly	Ser	Glu	Ile	Glu	Lys	Gln
		225			230				235						
Asn	Lys	Gly	Leu	Asp	His	Leu	His	Asp	Asp	Val	Asp	Glu	Leu	Asn	Phe
		245						250						255	
Arg	Val	Gln	Gln	Ser	Asn	Gln	Arg	Gly	Arg	Arg	Leu	Leu	Gly	Lys	
		260					265						270		

(2) INFORMATION FOR SEQ ID NO:981:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 270 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..270
 (D) OTHER INFORMATION: / Ceres Seq. ID 1568600
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:981:

Met	Asn	Leu	Thr	Thr	Asn	Ile	Pro	Leu	Thr	Xaa	Ser	Lys	Arg	Thr	Thr
1				5					10				-	15	
Ser	Glu	Pro	Ser	Leu	Ala	Asp	Met	Thr	Asn	Pro	Phe	Gly	Gly	Glu	Arg
				20				25					30		
Val	Gln	Lys	Gly	Asp	Ser	Ser	Ser	Lys	Gln	Ser	Leu	Phe	Ser	Asn	
			35				40				45				
Ser	Lys	Tyr	Gln	Tyr	Lys	Asn	Asn	Phe	Arg	Asp	Ser	Gly	Gly	Ile	Glu
	50				55					60					
Asn	Gln	Ser	Val	Gln	Glu	Leu	Glu	Gly	Tyr	Ala	Val	Tyr	Lys	Ala	Glu
65				70					75					80	
Glu	Thr	Thr	Lys	Ser	Val	Gln	Gly	Cys	Leu	Lys	Val	Ala	Glu	Asp	Ile
			85					90					95		
Arg	Ser	Asp	Ala	Thr	Arg	Thr	Leu	Val	Met	Leu	His	Asp	Gln	Gly	Glu
			100				105						110		
Gln	Ile	Thr	Arg	Thr	His	His	Lys	Ala	Val	Glu	Ile	Asp	His	Asp	Leu
	115				120					125					
Ser	Arg	Gly	Glu	Lys	Leu	Leu	Gly	Ser	Leu	Gly	Gly	Met	Phe	Ser	Lys
	130				135					140					
Thr	Trp	Lys	Pro	Lys	Lys	Thr	Arg	Pro	Ile	Asn	Gly	Pro	Val	Val	Thr
145				150				155						160	
Arg	Asp	Asp	Ser	Pro	Thr	Arg	Arg	Val	Asn	His	Leu	Glu	Lys	Arg	Glu
			165					170					175		
Lys	Leu	Gly	Leu	Asn	Ser	Ala	Pro	Arg	Gly	Gln	Ser	Arg	Thr	Arg	Glu
	180						185						190		
Pro	Leu	Pro	Glu	Ser	Ala	Asp	Ala	Tyr	Gln	Arg	Val	Glu	Met	Glu	Lys
	195						200					205			
Ala	Lys	Gln	Asp	Asp	Gly	Leu	Ser	Asp	Leu	Ser	Asp	Ile	Leu	Gly	Glu
	210				215						220				
Leu	Lys	Asn	Met	Ala	Val	Asp	Met	Gly	Ser	Glu	Ile	Glu	Lys	Gln	Asn
225				230						235				240	
Lys	Gly	Leu	Asp	His	Leu	His	Asp	Asp	Val	Asp	Glu	Leu	Asn	Phe	Arg
			245					250					255		
Val	Gln	Gln	Ser	Asn	Gln	Arg	Gly	Arg	Arg	Leu	Leu	Gly	Lys		
			260					265					270		

(2) INFORMATION FOR SEQ ID NO:982:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 247 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..247
 (D) OTHER INFORMATION: / Ceres Seq. ID 1568601
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:982:

Met	Thr	Asn	Pro	Phe	Gly	Gly	Glu	Arg	Val	Gln	Lys	Gly	Asp	Ser	Ser
1			5					10					15		
Ser	Ser	Lys	Gln	Ser	Leu	Phe	Ser	Asn	Ser	Lys	Tyr	Gln	Tyr	Lys	Asn
			20					25					30		


```

Asn Phe Arg Asp Ser Gly Gly Ile Glu Asn Gln Ser Val Gln Glu Leu
    35          40          45
Glu Gly Tyr Ala Val Tyr Lys Ala Glu Glu Thr Thr Lys Ser Val Gln
    50          55          60
Gly Cys Leu Lys Val Ala Glu Asp Ile Arg Ser Asp Ala Thr Arg Thr
    65          70          75          80
Leu Val Met Leu His Asp Gln Gly Glu Gln Ile Thr Arg Thr His His
    85          90          95
Lys Ala Val Glu Ile Asp His Asp Leu Ser Arg Gly Glu Lys Leu Leu
    100         105         110
Gly Ser Leu Gly Gly Met Phe Ser Lys Thr Trp Lys Pro Lys Lys Thr
    115         120         125
Arg Pro Ile Asn Gly Pro Val Val Thr Arg Asp Asp Ser Pro Thr Arg
    130         135         140
Arg Val Asn His Leu Glu Lys Arg Glu Lys Leu Gly Leu Asn Ser Ala
    145         150         155         160
Pro Arg Gly Gln Ser Arg Thr Arg Glu Pro Leu Pro Glu Ser Ala Asp
    165         170         175
Ala Tyr Gln Arg Val Glu Met Glu Lys Ala Lys Gln Asp Asp Gly Leu
    180         185         190
Ser Asp Leu Ser Asp Ile Leu Gly Glu Leu Lys Asn Met Ala Val Asp
    195         200         205
Met Gly Ser Glu Ile Glu Lys Gln Asn Lys Gly Leu Asp His Leu His
    210         215         220
Asp Asp Val Asp Glu Leu Asn Phe Arg Val Gln Gln Ser Asn Gln Arg
    225         230         235         240
Gly Arg Arg Leu Leu Gly Lys
    245

```

(2) INFORMATION FOR SEQ ID NO:983:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 678 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..678
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568602

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:983:

```

gatttttttag ggtttcaagt gaaaagagta atagcgcggc ggaGCcatgc ttetcaagac      60
tgagcttttgc cgattcagtg gccagaaaat ttacctctgt agaggggatca gatttatccg      120
atcggactct caggtgtttt tgtttctcaa ctccaaatgt aagaggtatt tccacaacaa      180
gttgaagcca tctaagcttt gctggactgc tatgtaccga aagcagcaca agaaggacgc      240
agcacaaagag gctgtgaaga gaaggagacg tgcaactaag aagccttact caaggtcgat      300
tgtcgtgtct actttggagg ttattcagaa gaagcgagca gagaagcctg aagttcgtga      360
tgccgctaga gaagctgccc tacgtgagat caaggagaga atcaagaaga ccaaggacga      420
gaagaaggca aagaaggtcg agtatgcac aaagcaaacag aagtcacaag tgaaggga      480
tatccccaag agtgcgtcac ccaaggctgc taagatgggt ggtgggtgag gcagacgttg      540
aatggagcta tagagtagcc cactcttctc tcttcaacta tctttctttc ttgktttgac      600
attgktttgt tttgtcagcc attttttagt tttgcaccag atctaataata ttcagtttat      660
gaaaactttt tgtttggc

```

(2) INFORMATION FOR SEQ ID NO:984:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 164 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide

(B) LOCATION: 1..164

(D) OTHER INFORMATION: / Ceres Seq. ID 1568603

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:984:

```
Met Val Leu Lys Thr Glu Leu Cys Arg Phe Ser Gly Gln Lys Ile Tyr
1      5      10      15
Pro Gly Arg Gly Ile Arg Phe Ile Arg Ser Asp Ser Gln Val Phe Leu
20      25      30
Phe Leu Asn Ser Lys Cys Lys Arg Tyr Phe His Asn Lys Leu Lys Pro
35      40      45
Ser Lys Leu Cys Trp Thr Ala Met Tyr Arg Lys Gln His Lys Lys Asp
50      55      60
Ala Ala Gln Glu Ala Val Lys Arg Arg Arg Ala Thr Lys Lys Pro
65      70      75      80
Tyr Ser Arg Ser Ile Val Gly Ala Thr Leu Glu Val Ile Gln Lys Lys
85      90      95
Arg Ala Glu Lys Pro Glu Val Arg Asp Ala Ala Arg Glu Ala Ala Leu
100      105      110
Arg Glu Ile Lys Glu Arg Ile Lys Lys Thr Lys Asp Glu Lys Lys Ala
115      120      125
Lys Lys Val Glu Tyr Ala Ser Lys Gln Gln Lys Ser Gln Val Lys Gly
130      135      140
Asn Ile Pro Lys Ser Ala Ala Pro Lys Ala Ala Lys Met Gly Gly Gly
145      150      155      160
Gly Gly Arg Arg
```

(2) INFORMATION FOR SEQ ID NO:985:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 109 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..109

(D) OTHER INFORMATION: / Ceres Seq. ID 1568604

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:985:

```
Met Tyr Arg Lys Gln His Lys Lys Asp Ala Ala Gln Glu Ala Val Lys
1      5      10      15
Arg Arg Arg Arg Ala Thr Lys Lys Pro Tyr Ser Arg Ser Ile Val Gly
20      25      30
Ala Thr Leu Glu Val Ile Gln Lys Lys Arg Ala Glu Lys Pro Glu Val
35      40      45
Arg Asp Ala Ala Arg Glu Ala Ala Leu Arg Glu Ile Lys Glu Arg Ile
50      55      60
Lys Lys Thr Lys Asp Glu Lys Lys Ala Lys Lys Val Glu Tyr Ala Ser
65      70      75      80
Lys Gln Gln Lys Ser Gln Val Lys Gly Asn Ile Pro Lys Ser Ala Ala
85      90      95
Pro Lys Ala Ala Lys Met Gly Gly Gly Gly Arg Arg
100      105
```

(2) INFORMATION FOR SEQ ID NO:986:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 344 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..344

(D) OTHER INFORMATION: / Ceres Seq. ID 1568605
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:986:
aaacttaatc acacacaagg agagaagaga gaaagagaga aagagagaca gagataatgg 60
cgtacagtg cgtgttttcta caccagagcg cattggcttc atcagccgca cgaatcatcat 120
cttcctctc atccacagcgt cacgtgtcgc tctccaaacc tgttcagatc atctgtaaaag 180
cacaagctgg agacaagagg tggttcaagg gagccaggaa atttgtcgag aqcgccagcCa 240
cttctttcag tgtgtcttga gtgaaagcaa cacaacgtaa caatgctctg cttgtctttc 300
tcatttgtct cttgtaaaaa atggaaaatg aaactgagct ttg

(2) INFORMATION FOR SEQ ID NO:987:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 58 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..58
(D) OTHER INFORMATION: / Ceres Seq. ID 1568606
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:987:
Asn Leu Ile Thr His Lys Glu Arg Arg Glu Lys Glu Arg Lys Arg Asp
1 5 10 15
Arg Asp Asn Gly Val Gln Cys Val Phe Pro Thr Pro Glu Arg Ile Gly
20 25 30
Phe Ile Ser Arg Thr Ile Ile Phe Leu Leu Ile Pro Ala Ser Arg
35 40 45
Val Ala Leu Gln Thr Cys Ser Asp His Leu
50 55

(2) INFORMATION FOR SEQ ID NO:988:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 67 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..67
(D) OTHER INFORMATION: / Ceres Seq. ID 1568607
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:988:
Met Ala Tyr Ser Ala Cys Phe Leu His Gln Ser Ala Leu Ala Ser Ser
1 5 10 15
Ala Ala Arg Ser Ser Ser Ser Ser Ser Gln Arg His Val Ser Leu
20 25 30
Ser Lys Pro Val Gln Ile Ile Cys Lys Ala Gln Ala Gly Asp Lys Arg
35 40 45
Trp Phe Lys Gly Ala Arg Lys Phe Val Glu Ser Ala Ala Thr Ser Phe
50 55 60
Ser Val Ala
65

(2) INFORMATION FOR SEQ ID NO:989:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1001 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..1001
(D) OTHER INFORMATION: / Ceres Seq. ID 1568614

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:989:

ctcacacaca	caccaacgca	aacctccaaa	acagggccgg	ggcgattcat	tcacaatctc	60
ggcgattctc	tcttcogtct	cgagtcgctg	agatccatca	gtaaaaggtc	tgcaaaatgg	120
ttgctcaggg	attcactgtg	gatcttaaaa	agcccccctgt	atttcagggt	ggtcactctg	180
gagaagatta	tgaggaatgg	gttcaccaac	ctatcgcgac	caaggaaggg	cctcggtttt	240
ttcagagtg	cttttgggag	ttcttgacac	ttacagtttg	gtgggcaggt	cctgtcattt	300
gggttcaggt	tgtagtctgg	tgcataatcaa	ggtcagtaag	tatgggagtg	tcactccag	360
aaatcgctcc	aattgtgtgc	atgggaatat	tcactgggac	attttttgaa	tacgtttctt	420
acccgttgt	ttccacata	aaaacgaaga	gttactgggg	aaacactgca	cactactcta	480
ttcacggatg	ccatcataag	caccogatgg	accacottcg	gctcgtcttt	cctcactagt	540
caacagcgat	tttatgcttt	ccgttctgga	acattcgggc	tatctcaact	ccttcaaccg	600
acactcgatt	gttttggtga	ggcatgctcg	gatattgtag	gtacgattgc	actctatttt	660
accttcacca	tgcccaacct	actagaccag	tgaccaaaaa	tctcaagaag	taccatttga	720
atcatcactt	caggattcag	gacaaaaggat	ttggtatAac	ttcgtcgtta	tgggacatag	780
ctcttggggac	acttccacc	acaaaagccc	ccagaaaaga	gcaatagtag	taaaaggcaa	840
aaactaaaaa	gatgttttga	atacatttaa	tttaattcta	agttattaat	catcctctgt	900
aaatttgaga	tggttaatct	gaggtttcat	ttggatcact	gtcttttgta	gtttgtaaat	960
caatacttca	caatccta	ataatattt	tctgcgaaag	t		

(2) INFORMATION FOR SEQ ID NO:990:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 236 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..236

(D) OTHER INFORMATION: / Ceres Seq. ID 1568615

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:990:

Met	Val	Ala	Gln	Gly	Phe	Thr	Val	Asp	Leu	Lys	Lys	Pro	Leu	Val	Phe
1			5					10					15		
Gln	Val	Gly	His	Leu	Gly	Glu	Asp	Tyr	Glu	Glu	Trp	Val	His	Gln	Pro
			20					25					30		
Ile	Ala	Thr	Lys	Glu	Gly	Pro	Arg	Phe	Phe	Gln	Ser	Asp	Phe	Trp	Glu
			35					40					45		
Phe	Leu	Thr	Leu	Thr	Val	Trp	Trp	Ala	Val	Pro	Val	Ile	Trp	Leu	Pro
			50					55				60			
Val	Val	Val	Trp	Cys	Ile	Ser	Arg	Ser	Val	Ser	Met	Gly	Cys	Ser	Leu
			65					70				75			80
Pro	Glu	Ile	Val	Pro	Ile	Val	Val	Met	Gly	Ile	Phe	Ile	Trp	Thr	Phe
			85					90					95		
Phe	Glu	Tyr	Val	Leu	His	Arg	Phe	Val	Phe	His	Ile	Lys	Thr	Lys	Ser
			100					105					110		
Tyr	Trp	Gly	Asn	Thr	Ala	His	Tyr	Leu	Ile	His	Gly	Cys	His	His	Lys
			115					120					125		
His	Pro	Met	Asp	His	Leu	Arg	Leu	Val	Phe	Pro	Pro	Thr	Ala	Thr	Ala
			130					135					140		
Ile	Leu	Cys	Phe	Pro	Phe	Trp	Asn	Ile	Ala	Ala	Ile	Ser	Thr	Pro	Ser
			145					150					155		160
Thr	Ala	Pro	Ala	Leu	Phe	Gly	Gly	Gly	Met	Leu	Gly	Tyr	Val	Met	Tyr
			165					170					175		
Asp	Val	Thr	His	Tyr	Tyr	Leu	His	His	Ala	Gln	Pro	Thr	Arg	Pro	Val
			180					185					190		
Thr	Lys	Asn	Leu	Lys	Lys	Tyr	His	Leu	Asn	His	His	Phe	Arg	Ile	Gln
			195					200					205		
Asp	Lys	Gly	Phe	Gly	Ile	Thr	Ser	Ser	Leu	Trp	Asp	Ile	Val	Phe	Gly
			210					215					220		
Thr	Leu	Pro	Thr	Thr	Lys	Ala	Pro	Arg	Lys	Glu	Gln				
			225					230					235		

(2) INFORMATION FOR SEQ ID NO:991:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 161 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..161
 (D) OTHER INFORMATION: / Ceres Seq. ID 1568616
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:991:

Met	Gly	Cys	Ser	Leu	Pro	Glu	Ile	Val	Pro	Ile	Val	Val	Met	Gly	Ile
1			5					10					15		
Phe	Ile	Trp	Thr	Phe	Phe	Glu	Tyr	Val	Leu	His	Arg	Phe	Val	Phe	His
			20				25					30			
Ile	Lys	Thr	Lys	Ser	Tyr	Trp	Gly	Asn	Thr	Ala	His	Tyr	Leu	Ile	His
			35				40					45			
Gly	Cys	His	His	Lys	His	Pro	Met	Asp	His	Leu	Arg	Leu	Val	Phe	Pro
	50				55					60					
Pro	Thr	Ala	Thr	Ala	Ile	Leu	Cys	Phe	Pro	His	Trp	Asn	Ile	Ala	Ala
65				70				75						80	
Ile	Ser	Thr	Pro	Ser	Thr	Ala	Pro	Ala	Leu	Phe	Gly	Gly	Gly	Met	Leu
				85					90					95	
Gly	Tyr	Val	Met	Tyr	Asp	Val	Thr	His	Tyr	Tyr	Leu	His	His	Ala	Gln
			100				105						110		
Pro	Thr	Arg	Pro	Val	Thr	Lys	Asn	Leu	Lys	Lys	Tyr	His	Leu	Asn	His
			115				120					125			
His	Phe	Arg	Ile	Gln	Asp	Lys	Gly	Phe	Gly	Ile	Thr	Ser	Ser	Leu	Trp
	130				135					140					
Asp	Ile	Val	Phe	Gly	Thr	Leu	Pro	Thr	Thr	Lys	Ala	Pro	Arg	Lys	Glu
145					150				155						160
Gln															

(2) INFORMATION FOR SEQ ID NO:992:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 148 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..148
 (D) OTHER INFORMATION: / Ceres Seq. ID 1568617
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:992:

Met	Gly	Ile	Phe	Ile	Trp	Thr	Phe	Phe	Glu	Tyr	Val	Leu	His	Arg	Phe
1			5						10				15		
Val	Phe	His	Ile	Lys	Thr	Lys	Ser	Tyr	Trp	Gly	Asn	Thr	Ala	His	Tyr
			20				25					30			
Leu	Ile	His	Gly	Cys	His	His	Lys	His	Pro	Met	Asp	His	Leu	Arg	Leu
			35				40					45			
Val	Phe	Pro	Pro	Thr	Ala	Thr	Ala	Ile	Leu	Cys	Phe	Pro	Phe	Trp	Asn
	50				55					60					
Ile	Ala	Ala	Ile	Ser	Thr	Pro	Ser	Thr	Ala	Pro	Ala	Leu	Phe	Gly	Gly
65				70				75						80	
Gly	Met	Leu	Gly	Tyr	Val	Met	Tyr	Asp	Val	Thr	His	Tyr	Tyr	Leu	His
			85				90						95		
His	Ala	Gln	Pro	Thr	Arg	Pro	Val	Thr	Lys	Asn	Leu	Lys	Lys	Tyr	His
		100					105					110			
Leu	Asn	His	His	Phe	Arg	Ile	Gln	Asp	Lys	Gly	Phe	Gly	Ile	Thr	Ser
		115					120					125			

Ser Leu Trp Asp Ile Val Phe Gly Thr Leu Pro Thr Thr Lys Ala Pro
130 135 140
Arg Lys Glu Gln
145

(2) INFORMATION FOR SEQ ID NO:993:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1112 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1112
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568635

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:993:

```
gagtttcaat ggcggaattt tttctctctt tctttttctt cttctctctt atcgtctctc 60
ttctcatcat cttatctttc atcgtagcgc caagatccgt cactgacccc atcaagtgtc 120
gccacgtgtt catcaccggt ggatacaagc gaatcggtct cgtctcgcgt caccgtgcgc 180
ttctccgaagg cgtcaaaagt tccatctctc ctcgttcaac tgaagaagtc gccgaagcca 240
aacgatccat ccagctagct accggtgtgc aggtcgccac gttctctcgc gacgttcgcg 300
attacgagcg cgtttcgaaa gcgattgatg aatcgggacc gatcgatgtg ttgattgtta 360
atacaggcgt gtttatggg aaagagattg agaaacagag tcttgaggag gttaaagtta 420
tgattgatgt gaactctgact gggagcttca atgtgattaa cctctatgtg cctcgtatga 480
aagctaggga aagtctgtgt tctgcttcca tttctcttgt gtcctctcaa gctggtcagg 540
caggtatata tggttacact gcataattcg cgagcaagtt tggggttcag ggtttagcgc 600
aagcattgca gccagaagtt atttctgatg acattcatgt gactctcttg tttctctcgt 660
acactgatac acccggtgtt gaacaagaac tgaagaagag gccagaacta acttcaatca 720
tagcgcgcat atcgggttca atgaaaacca aggaagtggc caagatatgt ttgatgtgta 780
tcaagcagc aaaattttaca gtgacatgcc attttattgg cttcttacta tcaattgcta 840
gcaccggcat gtccctctcag ggatcgtttt Gcgttcgcgt cattgaagtt atattcggtg 900
gtctaataag attcgtcagc ttggtttttc aatggcaatg gtacaaaacc atagaaaagt 960
ggagcaaaga aaaacaagta aatagtaagt tagcttagtg tatttgtac aatggtagta 1020
atactatatg atcagttctt tgtacagtga acagggtcat ggtgttgtag ttccaacttc 1080
ggcttctctg ttttcaattt gaataaattg tg
```

(2) INFORMATION FOR SEQ ID NO:994:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 331 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..331
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568636

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:994:

```
Val Ser Met Ala Ala Ile Phe Ser Leu Phe Leu Phe Phe Ile Leu Phe
1 5 10 15
Ile Val Ser Leu Leu Ile Ile Leu Ser Phe Ile Val Arg Pro Arg Ser
20 25 30
Val Thr Ile Pro Ile Lys Phe Arg His Val Phe Ile Thr Gly Gly Ser
35 40 45
Ser Gly Ile Gly Leu Ala Leu Ala His Arg Ala Val Ser Glu Gly Ala
50 55 60
Lys Val Ser Ile Leu Ala Arg Ser Thr Glu Lys Leu Ala Glu Ala Lys
65 70 75 80
Arg Ser Ile Gln Leu Ala Thr Gly Val Glu Val Ala Thr Phe Ser Ala
85 90 95
Asp Val Arg Asp Tyr Asp Ala Val Ser Lys Ala Ile Asp Glu Ser Gly
100 105 110
```

Pro Ile Asp Val Leu Ile Val Asn Gln Gly Val Phe Ile Gly Lys Glu
115 120 125
Ile Glu Lys Gln Ser Pro Glu Glu Val Lys Phe Met Ile Asp Val Asn
130 135 140
Leu Thr Gly Ser Phe Asn Val Ile Lys Ala Ala Leu Pro Ala Met Lys
145 150 155 160
Ala Arg Glu Ser Arg Gly Ser Ala Ser Ile Ser Leu Val Ser Ser Gln
165 170 175
Ala Gly Gln Ala Gly Ile Tyr Gly Tyr Thr Ala Tyr Ser Ala Ser Lys
180 185 190
Phe Gly Leu Gln Gly Leu Ala Gln Ala Leu Gln Gln Glu Val Ile Ser
195 200 205
Asp Asp Ile His Val Thr Leu Leu Phe Pro Pro Asp Thr Asp Thr Pro
210 215 220
Gly Phe Glu Gln Glu Leu Lys Lys Arg Pro Glu Leu Thr Ser Ile Ile
225 230 235 240
Ala Ala Ser Ser Gly Ser Met Lys Thr Lys Glu Val Ala Lys Ile Cys
245 250 255
Phe Asp Gly Ile Lys Ala Gly Lys Phe Thr Val Thr Cys His Phe Ile
260 265 270
Gly Phe Leu Leu Ser Ile Ala Ser Thr Gly Met Ser Pro Gln Gly Ser
275 280 285
Phe Trp Leu Ala Leu Ile Glu Val Ile Phe Gly Gly Leu Ile Arg Phe
290 295 300
Val Ser Leu Val Phe Gln Trp Gln Trp Tyr Lys Thr Ile Glu Lys Trp
305 310 315 320
Ser Lys Glu Lys Gln Val Asn Ser Lys Leu Ala
325 330

(2) INFORMATION FOR SEQ ID NO:995:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 329 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..329

(D) OTHER INFORMATION: / Ceres Seq. ID 1568637

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:995:

Met Ala Ala Ile Phe Ser Leu Phe Leu Phe Phe Ile Leu Phe Ile Val
1 5 10 15
Ser Leu Leu Ile Ile Leu Ser Phe Ile Val Arg Pro Arg Ser Val Thr
20 25 30
Ile Pro Ile Lys Phe Arg His Val Phe Ile Thr Gly Gly Ser Ser Gly
35 40 45
Ile Gly Leu Ala Leu Ala His Arg Ala Val Ser Glu Gly Ala Lys Val
50 55 60
Ser Ile Leu Ala Arg Ser Thr Glu Lys Leu Ala Glu Ala Lys Arg Ser
65 70 75 80
Ile Gln Leu Ala Thr Gly Val Glu Val Ala Thr Phe Ser Ala Asp Val
85 90 95
Arg Asp Tyr Asp Ala Val Ser Lys Ala Ile Asp Glu Ser Gly Pro Ile
100 105 110
Asp Val Leu Ile Val Asn Gln Gly Val Phe Ile Gly Lys Glu Ile Glu
115 120 125
Lys Gln Ser Pro Glu Glu Val Lys Phe Met Ile Asp Val Asn Leu Thr
130 135 140
Gly Ser Phe Asn Val Ile Lys Ala Ala Leu Pro Ala Met Lys Ala Arg
145 150 155 160
Glu Ser Arg Gly Ser Ala Ser Ile Ser Leu Val Ser Ser Gln Ala Gly

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1267 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..1267
(D) OTHER INFORMATION: / Ceres Seq. ID 1568645
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:997:

```

aaacaaaWWY WNaWccaaag acgagccaga gccacctcta acaccatcgg cgacttctcc 60
tctactect cegtgcgga cgtgttgat ttacaacgat tcggtggcta atcgttggta 120
gatttagaat taaagggtaa aggagacgac gacgagagat gccgtcaaac ggagatctcg 180
accgtcagat cgaacagcta atggagtgtta agccgttagg tgaagcagac gtgaagatgcc 240
tttgcgatca agctaaaagg attctcgttg aggaatataa tgttcaaccg gttaaagtgtc 300
cggttacagg atgcgcgcat atccatggac agttttatga cctaattgag ctatttcgta 360
ttgggtgtaa tgctcctgat actaattacc tctcatgggg agattatgta gtcgtggct 420
actattctgt agaacagctc tctctattgg tggcattgaa ggtgcgttac agggacagac 480
ttacgatcct gcgagggaat catgagagcc gtcagattac acaagctcat ggtttttatg 540
acgaatgctt gaggaaatac ggaaatgcaa atgtgtggaa gtattttacg gaccttttcg 600
attatctccc tctaacagca ctcatagaga gtcaggtttt ctgtttgcat ggaggccottt 660
caccttctct gaatactctt gacaatatcc gaagcttgga tcaatacaaa gaggttccac 720
acgaaggacc aatgtgcgat ctactctggt ctgatcccg cgtactgtgt ggatggggaa 780
tatctctcct tgggtcgttg tacacgtttg gacaggacat tgcactcag ttcaatcata 840
acaatggact gagtctgata tcaagagcgc atcaacttgt aatggaaggg tataattggt 900
gtcaggaaaa gaacgtagtg acagtgttta gtgcacaaaa ctactgttac agatgtggaa 960
acatggcgcc aattcttgag attggagaaa agatggaaca gaacttctct caattcgatc 1020
cagcacttag acaagtcgaa ccgataacca cagcagaagc cctgattat tttttgtgat 1080
ttcatttttt ttcttcaaaa gtttgtttgt tgetgtatca ttgtagatgt gtcctctgtt 1140
tatttgtttt ttctcagctc ctagatggaa tgtgatacca aagacgaaaa accatcatt 1200
ttttgttgga tgttgatact gaaacaggtt tgtagaagcc tcttcttatt atagaaaaatg 1260
tcttttg

```

(2) INFORMATION FOR SEQ ID NO:998:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 306 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..306
(D) OTHER INFORMATION: / Ceres Seq. ID 1568646
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:998:

```

Met Pro Ser Asn Gly Asp Leu Asp Arg Glu Ile Glu Gln Leu Met Glu
1      5      10      15
Cys Lys Pro Leu Gly Glu Ala Asp Val Lys Ile Leu Cys Asp Gln Ala
20     25     30
Lys Ala Ile Leu Val Glu Glu Tyr Asn Val Gln Pro Val Lys Cys Pro
35     40     45
Val Thr Val Cys Gly Asp Ile His Gly Gln Phe Tyr Asp Leu Ile Glu
50     55     60
Leu Phe Arg Ile Gly Gly Asn Ala Pro Asp Thr Asn Tyr Leu Phe Met
65     70     75
Gly Asp Tyr Val Asp Arg Gly Tyr Tyr Ser Val Glu Thr Val Ser Leu
85     90     95
Leu Val Ala Leu Lys Val Arg Tyr Arg Asp Arg Leu Thr Ile Leu Arg
100    105    110
Gly Asn His Glu Ser Arg Gln Ile Thr Gln Val Tyr Gly Phe Tyr Asp
115    120    125
Glu Cys Leu Arg Lys Tyr Gly Asn Ala Asn Val Trp Lys Tyr Phe Thr

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130 135 140
Asp Leu Phe Asp Tyr Leu Pro Leu Thr Ala Leu Ile Glu Ser Gln Val
145 150 155 160
Phe Cys Leu His Gly Gly Leu Ser Pro Ser Leu Asp Thr Leu Asp Asn
165 170 175
Ile Arg Ser Leu Asp Arg Ile Gln Glu Val Pro His Glu Gly Pro Met
180 185 190
Cys Asp Leu Leu Trp Ser Asp Pro Asp Asp Arg Cys Gly Trp Gly Ile
195 200 205
Ser Pro Arg Gly Ala Gly Tyr Thr Phe Gly Gln Asp Ile Ala Thr Gln
210 215 220
Phe Asn His Asn Asn Gly Leu Ser Leu Ile Ser Arg Ala His Gln Leu
225 230 235 240
Val Met Glu Gly Tyr Asn Trp Cys Gln Glu Lys Asn Val Val Thr Val
245 250 255
Phe Ser Ala Pro Asn Tyr Cys Tyr Arg Cys Gly Asn Met Ala Ala Ile
260 265 270
Leu Glu Ile Gly Glu Lys Met Glu Gln Asn Phe Leu Gln Phe Asp Pro
275 280 285
Ala Pro Arg Gln Val Glu Pro Asp Thr Thr Arg Lys Thr Pro Asp Tyr
290 295 300
Phe Leu
305

(2) INFORMATION FOR SEQ ID NO:999:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 292 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..292
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568647

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:999:

Met Glu Cys Lys Pro Leu Gly Glu Ala Asp Val Lys Ile Leu Cys Asp
1 5 10 15
Gln Ala Lys Ala Ile Leu Val Glu Glu Tyr Asn Val Gln Pro Val Lys
20 25 30
Cys Pro Val Thr Val Cys Gly Asp Ile His Gly Gln Phe Tyr Asp Leu
35 40 45
Ile Glu Leu Phe Arg Ile Gly Gly Asn Ala Pro Asp Thr Asn Tyr Leu
50 55 60
Phe Met Gly Asp Tyr Val Asp Arg Gly Tyr Tyr Ser Val Glu Thr Val
65 70 75 80
Ser Leu Leu Val Ala Leu Lys Val Arg Tyr Arg Asp Arg Leu Thr Ile
85 90 95
Leu Arg Gly Asn His Glu Ser Arg Gln Ile Thr Gln Val Tyr Gly Phe
100 105 110
Tyr Asp Glu Cys Leu Arg Lys Tyr Gly Asn Ala Asn Val Trp Lys Tyr
115 120 125
Phe Thr Asp Leu Phe Asp Tyr Leu Pro Leu Thr Ala Leu Ile Glu Ser
130 135 140
Gln Val Phe Cys Leu His Gly Gly Leu Ser Pro Ser Leu Asp Thr Leu
145 150 155 160
Asp Asn Ile Arg Ser Leu Asp Arg Ile Gln Glu Val Pro His Glu Gly
165 170 175
Pro Met Cys Asp Leu Leu Trp Ser Asp Pro Asp Asp Arg Cys Gly Trp
180 185 190
Gly Ile Ser Pro Arg Gly Ala Gly Tyr Thr Phe Gly Gln Asp Ile Ala
195 200 205

(2) INFORMATION FOR SEQ ID NO:1000:

(A) LENGTH: 227 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..227

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1000:

(2) INFORMATION FOR SEQ ID NO:1001:

(A) LENGTH: 1354 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1354

(D) OTHER INFORMATION: / Ceres Seq. ID 1568657

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1001:

acacacaaac	aacacatcca	ctcgaatttt	ctatttcgga	ataacaaaaa	cgatcgggcg	60
agacatgacg	ggggcacaag	ggaactctaa	cgagactctg	ttttcttctt	acaagatggg	120
aagattctgat	ctctctcatt	gagtggttct	ggcgccgatg	acgcggtgca	ggcggttgaa	180
cgagatacca	aacgcggcgt	tggcagagta	ttatgctcaa	cggaaccttc	ccggcggttt	240
ctctactccc	gaaggcacca	gtgtctctcc	cggaatcgca	Gggttccacc	atgtgcctgg	300
aattctattca	gatgaacaag	tagaagcatg	gaagcaagtt	gtggaagcag	ttcacgctaa	360
gggaggtttc	atcttttgtc	aattatggca	tggttgaactg	gcttctcatg	caagtgtatca	420
acctaatgga	ggatcaccaa	tatcgtcaac	gaacaaacca	atctcggaaa	acaggtggcg	480
agtttttggt	cccgatgggt	cccacgtgaa	gtacccgaaa	cctcggtgtt	tagaagcttc	540
cgagataacct	cggttggttg	aggattattg	cctttctgct	ttgaatcgca	ttcgagctgg	600
tttcgatggg	attgagatcc	acggggcgca	tggttacctc	attgatcagt	ttttgaaaga	660
cgggatcaat	gaccgtactg	accaatacgg	aggatccatt	gaaaaccgtt	gtagattctt	720
gaacaagaata	gtggcaaggtg	tagtttcagc	cataggagct	agtaaaagtt	gtgtgagggt	780
atctccagct	atagatcaat	tggacgcaac	tgattctaac	ccattatcac	tcgggctagt	840
ctgtgttgat	atgctcaata	agttacaaga	tgttaatggc	ttgaagctcg	cttaccttca	900
cgtttaccaa	cgtcgtctacc	acgcctacgg	gcaaacagag	tcgggaaggc	aagggaagtg	960
tgaggagaaga	gctaagctaa	tgaagagctt	gagaatggct	tataaaggaa	cctttatgtc	1020
cagtgaggaga	ttcaataaag	aactaggcat	gcaagctgtt	gttcgaaggc	atgctgattt	1080
ggtttccat	ggcaggcttt	ttatcgcaaa	cccgatttgg	gtttcggggt	tcaagattga	1140
tggaaagttg	aataaataata	atcgggaagc	gtttttacct	caagatccag	ttgttggtca	1200
cacggattat	cctttcttgg	ctcctttttc	cgccctctga	gtttgataat	cgaggagaga	1260
aattgtattga	tggtgtataa	agacaataata	ttaatatgta	aaatgacaa	gttattgtta	1320
tcacattaat	gaatagtcac	gtatcttatt	gttt			

(2) INFORMATION FOR SEQ ID NO:1002:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 412 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..412

(D) OTHER INFORMATION: / Ceres Seq. ID 1568658

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1002:

His	Asn	Asn	Asn	Thr	Ser	Thr	Arg	Ile	Phe	Tyr	Phe	Arg	Ile	Thr	Lys
1				5				10					15		
Pro	Ile	Gly	Gly	Asp	Met	Thr	Ala	Ala	Gln	Gly	Asn	Ser	Asn	Glu	Thr
				20				25					30		
Leu	Phe	Ser	Ser	Tyr	Lys	Met	Gly	Arg	Phe	Asp	Leu	Ser	His	Arg	Val
				35				40					45		
Val	Leu	Ala	Pro	Met	Thr	Arg	Cys	Arg	Ala	Leu	Asn	Gly	Val	Pro	Asn
				50				55					60		
Ala	Ala	Leu	Ala	Glu	Tyr	Tyr	Ala	Gln	Arg	Thr	Thr	Pro	Gly	Gly	Phe
65				70				75					80		
Leu	Ile	Ser	Glu	Gly	Thr	Met	Val	Ser	Pro	Gly	Ser	Ala	Gly	Phe	Pro
				85				90					95		
His	Val	Pro	Gly	Ile	Tyr	Ser	Asp	Glu	Gln	Val	Glu	Ala	Trp	Lys	Gln
				100				105					110		
Val	Val	Glu	Ala	Val	His	Ala	Lys	Gly	Gly	Phe	Ile	Phe	Cys	Gln	Leu
				115				120					125		
Trp	His	Val	Gly	Arg	Ala	Ser	His	Ala	Val	Tyr	Gln	Pro	Asn	Gly	Gly
				130				135					140		
Ser	Pro	Ile	Ser	Ser	Thr	Asn	Lys	Pro	Ile	Ser	Glu	Asn	Arg	Trp	Arg
145				150				155					160		
Val	Leu	Leu	Pro	Asp	Gly	Ser	His	Val	Lys	Tyr	Pro	Lys	Pro	Arg	Ala

Met	Thr	Ala	Ala	Gln	Gly	Asn	Ser	Asn	Glu	Thr	Leu	Phe	Ser	Ser	Tyr
1				5					10					15	
Lys	Met	Gly	Arg	Phe	Asp	Leu	Ser	His	Arg	Val	Val	Leu	Ala	Pro	Met
			20					25					30		
Thr	Arg	Cys	Arg	Ala	Leu	Asn	Gly	Val	Pro	Asn	Ala	Ala	Leu	Ala	Glu
		35					40					45			
Tyr	Tyr	Ala	Gln	Arg	Thr	Thr	Pro	Gly	Gly	Phe	Leu	Ile	Ser	Glu	Gly
	50					55					60				
Thr	Met	Val	Ser	Pro	Gly	Ser	Ala	Gly	Phe	Pro	His	Val	Pro	Gly	Ile
65					70					75					80
Tyr	Ser	Asp	Glu	Gln	Val	Glu	Ala	Trp	Lys	Gln	Val	Val	Glu	Ala	Val
			85						90					95	
His	Ala	Lys	Gly	Gly	Phe	Ile	Phe	Cys	Gln	Leu	Trp	His	Val	Gly	Arg
			100					105					110		
Ala	Ser	His	Ala	Val	Tyr	Gln	Pro	Asn	Gly	Gly	Ser	Pro	Ile	Ser	Ser
		115					120					125			
Thr	Asn	Lys	Pro	Ile	Ser	Glu	Asn	Arg	Trp	Arg	Val	Leu	Leu	Pro	Asp
	130					135					140				

Gly Ser His Val Lys Tyr Pro Lys Pro Arg Ala Leu Glu Ala Ser Glu
145 150 155 160
Ile Pro Arg Val Val Glu Asp Tyr Cys Leu Ser Ala Leu Asn Ala Ile
165 170 175
Arg Ala Gly Phe Asp Gly Ile Glu Ile His Gly Ala His Gly Tyr Leu
180 185 190
Ile Asp Gln Phe Leu Lys Asp Gly Ile Asn Asp Arg Thr Asp Gln Tyr
195 200 205
Gly Gly Ser Ile Glu Asn Arg Cys Arg Phe Leu Lys Gln Val Val Glu
210 215 220
Gly Val Val Ser Ala Ile Gly Ala Ser Lys Val Gly Val Arg Val Ser
225 230 235 240
Pro Ala Ile Asp His Leu Asp Ala Thr Asp Ser Asn Pro Leu Ser Leu
245 250 255
Gly Leu Ala Val Val Asp Met Leu Asn Lys Leu Gln Asp Val Asn Gly
260 265 270
Leu Lys Leu Ala Tyr Leu His Val Thr Gln Pro Arg Tyr His Ala Tyr
275 280 285
Gly Gln Thr Glu Ser Gly Arg Gln Gly Ser Asp Glu Glu Ala Lys
290 295 300
Leu Met Lys Ser Leu Arg Met Ala Tyr Lys Gly Thr Phe Met Ser Ser
305 310 315 320
Gly Gly Phe Asn Lys Glu Leu Gly Met Gln Ala Val Gln Gln Gly Asp
325 330 335
Ala Asp Leu Val Ser Tyr Gly Arg Leu Phe Ile Ala Asn Pro Asp Leu
340 345 350
Val Ser Arg Phe Lys Ile Asp Gly Lys Leu Asn Lys Tyr Asn Arg Lys
355 360 365
Thr Phe Tyr Thr Gln Asp Pro Val Val Gly Tyr Thr Asp Tyr Pro Phe
370 375 380
Leu Ala Pro Phe Ser Arg Leu
385 390

(2) INFORMATION FOR SEQ ID NO:1004:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 374 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..374

(D) OTHER INFORMATION: / Ceres Seq. ID 1568660

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1004:

Met Gly Arg Phe Asp Leu Ser His Arg Val Val Leu Ala Pro Met Thr
1 5 10
Arg Cys Arg Ala Leu Asn Gly Val Pro Asn Ala Ala Leu Ala Glu Tyr
20 25 30
Tyr Ala Gln Arg Thr Thr Pro Gly Gly Phe Leu Ile Ser Glu Gly Thr
35 40 45
Met Val Ser Pro Gly Ser Ala Gly Phe Pro His Val Pro Gly Ile Tyr
50 55 60
Ser Asp Glu Gln Val Glu Ala Trp Lys Gln Val Val Glu Ala Val His
65 70 75 80
Ala Lys Gly Gly Phe Ile Phe Cys Gln Leu Trp His Val Gly Arg Ala
85 90 95
Ser His Ala Val Tyr Gln Pro Asn Gly Gly Ser Pro Ile Ser Ser Thr
100 105 110
Asn Lys Pro Ile Ser Glu Asn Arg Trp Arg Val Leu Leu Pro Asp Gly
115 120 125
Ser His Val Lys Tyr Pro Lys Pro Arg Ala Leu Glu Ala Ser Glu Ile

130	135	140
Pro Arg Val Val Glu Asp Tyr Cys Leu Ser Ala Leu Asn Ala Ile Arg		
145	150	155
Ala Gly Phe Asp Gly Ile Glu Ile His Gly Ala His Gly Tyr Leu Ile		
	165	170
Asp Gln Phe Leu Lys Asp Gly Ile Asn Asp Arg Thr Asp Gln Tyr Gly		
	180	185
Gly Ser Ile Glu Asn Arg Cys Arg Phe Leu Lys Gln Val Val Glu Gly		
	195	200
Val Val Ser Ala Ile Gly Ala Ser Lys Val Gly Val Arg Val Ser Pro		
	210	215
Ala Ile Asp His Leu Asp Ala Thr Asp Ser Asn Pro Leu Ser Leu Gly		
	225	230
Leu Ala Val Val Asp Met Leu Asn Lys Leu Gln Asp Val Asn Gly Leu		
	245	250
Lys Leu Ala Tyr Leu His Val Thr Gln Pro Arg Tyr His Ala Tyr Gly		
	260	265
Gln Thr Glu Ser Gly Arg Gln Gly Ser Asp Glu Glu Glu Ala Lys Leu		
	275	280
Met Lys Ser Leu Arg Met Ala Tyr Lys Gly Thr Phe Met Ser Ser Gly		
	290	295
Gly Phe Asn Lys Glu Leu Gly Met Gln Ala Val Gln Gln Gly Asp Ala		
	305	310
Asp Leu Val Ser Tyr Gly Arg Leu Phe Ile Ala Asn Pro Asp Leu Val		
	325	330
Ser Arg Phe Lys Ile Asp Gly Lys Leu Asn Lys Tyr Asn Arg Lys Thr		
	340	345
Phe Tyr Thr Gln Asp Pro Val Val Gly Tyr Thr Asp Tyr Pro Phe Leu		
	355	360
Ala Pro Phe Ser Arg Leu		
370		

(2) INFORMATION FOR SEQ ID NO:1005:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1223 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1223
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568669

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1005:

acaaaccccttt	ccacaagaag	ttataaaacca	atacatagaa	gaaaaacttc	aaactcaaaa	60
aatgatgaag	ggtgcacaagt	tttcatctct	tcttgtgctt	ttctttattt	ttccgatcgc	120
atttgctcaa	ctgagagtcg	ggtttttatag	tcaatcatgc	ccccaagccg	agactatcgt	180
acgcaatctg	gtgcgccaac	ggtttggtgt	taccccaacc	gttacccgcg	ctttgctcgc	240
tatgcatttc	cacgactggt	tcgttaaggg	ctgtgacgct	ttctctctca	ttgattcaac	300
caattccgag	aaaactgcgt	gaccaaaacg	aagcgtcagg	gaatttgacc	tgatagaccg	360
gatcaaggct	cagctagaag	ctgcatgccc	ttccacagtc	tcattgtgctg	acatcgctac	420
attggccaca	ctgactcggg	tggccttagc	cggaggccca	agctacagca	tcaccaacgg	480
aaggcgtgac	ggtagggtct	caaaacaatc	tgatgtaacc	ttaccgggct	caacgactct	540
cgctctctgga	gccgctagtt	tattcacgaa	caaaagggatg	aaacagcttc	atgcagtagc	600
tcttttgggt	gcaacacatg	ttggtcaagg	aaattgtggt	ctcttttagt	acagaaatcac	660
tagcttccaa	ggaactggac	gaccgcagcc	gtccatggac	cccgcctttg	ttaccagcct	720
aagggaacaa	tgcagaaaata	gcgcgacggc	ggcactagac	cagtcgagtc	cattgagatt	780
cgacaaccag	ttcttcaaac	aaatccgtaa	aaggagagga	gtgttgcaag	ttgaccaaac	840
ctctgcctac	gaccacacaaa	ctcgtgggat	tgtggctcgc	tatgctaata	acaacgcctt	900
cttcaagcgt	cagttcgttta	gagcaatggt	gaagatggga	gcggtctagt	tgcttaactgc	960
tcgtaacggt	gagatcagaa	ggaactcgag	aagattcaac	taatgaacta	cagaagcgtg	1020
gatataaat	tacatttgat	acaatatatt	tcaaatcttc	tttatatttt	tactaattca	1080

tttttgggtt tgggtggggt tttcttgcac aaataaggct tttcttaaat tggatggttt 1140
cgattttcga gaagatttac tatgtactat attgttggct tgcatttggg ggatgtatct 1200
taagttttaca aataattgt ggc

(2) INFORMATION FOR SEQ ID NO:1006:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 333 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..333

(D) OTHER INFORMATION: / Ceres Seq. ID 1568670

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1006:

Gln	Pro	Phe	Pro	Gln	Glu	Val	Ile	Asn	Gln	Tyr	Ile	Glu	Glu	Asn	Phe
1			5						10					15	
Gln	Pro	Gln	Lys	Met	Met	Lys	Gly	Ala	Lys	Phe	Ser	Ser	Leu	Leu	Val
			20					25					30		
Leu	Phe	Phe	Ile	Phe	Pro	Ile	Ala	Phe	Ala	Gln	Leu	Arg	Val	Gly	Phe
		35					40					45			
Tyr	Ser	Gln	Ser	Cys	Pro	Gln	Ala	Glu	Thr	Ile	Val	Arg	Asn	Leu	Val
	50					55					60				
Arg	Gln	Arg	Phe	Gly	Val	Thr	Pro	Thr	Val	Thr	Ala	Ala	Leu	Leu	Arg
	65				70					75				80	
Met	His	Phe	His	Asp	Cys	Phe	Val	Lys	Gly	Cys	Asp	Ala	Ser	Leu	Leu
			85						90					95	
Ile	Asp	Ser	Thr	Asn	Ser	Glu	Lys	Thr	Ala	Gly	Pro	Asn	Gly	Ser	Val
			100					105					110		
Arg	Glu	Phe	Asp	Leu	Ile	Asp	Arg	Ile	Lys	Ala	Gln	Leu	Glu	Ala	Ala
		115					120						125		
Cys	Pro	Ser	Thr	Val	Ser	Cys	Ala	Asp	Ile	Val	Thr	Leu	Ala	Thr	Arg
	130					135					140				
Asp	Ser	Val	Ala	Leu	Ala	Gly	Gly	Pro	Ser	Tyr	Ser	Ile	Pro	Thr	Gly
	145				150					155				160	
Arg	Arg	Asp	Gly	Arg	Val	Ser	Asn	Asn	Leu	Asp	Val	Thr	Leu	Pro	Gly
			165						170					175	
Pro	Thr	Ile	Ser	Val	Ser	Gly	Ala	Val	Ser	Leu	Phe	Thr	Asn	Lys	Gly
			180					185						190	
Met	Asn	Thr	Phe	Asp	Ala	Val	Ala	Leu	Leu	Gly	Ala	His	Thr	Val	Gly
		195					200						205		
Gln	Gly	Asn	Cys	Gly	Leu	Phe	Ser	Asp	Arg	Ile	Thr	Ser	Phe	Gln	Gly
	210						215						220		
Thr	Gly	Arg	Pro	Asp	Pro	Ser	Met	Asp	Pro	Ala	Leu	Val	Thr	Ser	Leu
			230							235					240
Arg	Asn	Thr	Cys	Arg	Asn	Ser	Ala	Thr	Ala	Ala	Leu	Asp	Gln	Ser	Ser
			245						250					255	
Pro	Leu	Arg	Phe	Asp	Asn	Gln	Phe	Phe	Lys	Gln	Ile	Arg	Lys	Arg	Arg
			260					265					270		
Gly	Val	Leu	Gln	Val	Asp	Gln	Arg	Leu	Ala	Ser	Asp	Pro	Gln	Thr	Arg
		275					280					285			
Gly	Ile	Val	Ala	Arg	Tyr	Ala	Asn	Asn	Ala	Phe	Phe	Lys	Arg	Gln	
	290					295				300					
Phe	Val	Arg	Ala	Met	Val	Lys	Met	Gly	Ala	Val	Asp	Val	Leu	Thr	Gly
			310						315					320	
Arg	Asn	Gly	Glu	Ile	Arg	Arg	Asn	Cys	Arg	Arg	Phe	Asn			
			325						330						

(2) INFORMATION FOR SEQ ID NO:1007:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 313 amino acids
- (B) TYPE: amino acid

- (C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..313
(D) OTHER INFORMATION: / Ceres Seq. ID 1568671
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1007:

Met Met Lys Gly Ala Lys Phe Ser Ser Leu Leu Val Leu Phe Phe Ile
1 5 10 15
Phe Pro Ile Ala Phe Ala Gln Leu Arg Val Gly Phe Tyr Ser Gln Ser
20 25 30
Cys Pro Gln Ala Glu Thr Ile Val Arg Asn Leu Val Arg Gln Arg Phe
35 40 45
Gly Val Thr Pro Thr Val Thr Ala Ala Leu Leu Arg Met His Phe His
50 55 60
Asp Cys Phe Val Lys Gly Cys Asp Ala Ser Leu Leu Ile Asp Ser Thr
65 70 75 80
Asn Ser Glu Lys Thr Ala Gly Pro Asn Gly Ser Val Arg Glu Phe Asp
85 90 95
Leu Ile Asp Arg Ile Lys Ala Gln Leu Glu Ala Ala Cys Pro Ser Thr
100 105 110
Val Ser Cys Ala Asp Ile Val Thr Leu Ala Thr Arg Asp Ser Val Ala
115 120 125
Leu Ala Gly Gly Pro Ser Tyr Ser Ile Pro Thr Gly Arg Arg Asp Gly
130 135 140
Arg Val Ser Asn Asn Leu Asp Val Thr Leu Pro Gly Pro Thr Ile Ser
145 150 155 160
Val Ser Gly Ala Val Ser Leu Phe Thr Asn Lys Gly Met Asn Thr Phe
165 170 175
Asp Ala Val Ala Leu Leu Gly Ala His Thr Val Gly Gln Gly Asn Cys
180 185 190
Gly Leu Phe Ser Asp Arg Ile Thr Ser Phe Gln Gly Thr Gly Arg Pro
195 200 205
Asp Pro Ser Met Asp Pro Ala Leu Val Thr Ser Leu Arg Asn Thr Cys
210 215 220
Arg Asn Ser Ala Thr Ala Ala Leu Asp Gln Ser Ser Pro Leu Arg Phe
225 230 235 240
Asp Asn Gln Phe Phe Lys Gln Ile Arg Lys Arg Arg Gly Val Leu Gln
245 250 255
Val Asp Gln Arg Leu Ala Ser Asp Pro Gln Thr Arg Gly Ile Val Ala
260 265 270
Arg Tyr Ala Asn Asn Asn Ala Phe Phe Lys Arg Gln Phe Val Arg Ala
275 280 285
Met Val Lys Met Gly Ala Val Asp Val Leu Thr Gly Arg Asn Gly Glu
290 295 300
Ile Arg Arg Asn Cys Arg Arg Phe Asn
305 310

(2) INFORMATION FOR SEQ ID NO:1008:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 312 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..312
(D) OTHER INFORMATION: / Ceres Seq. ID 1568672

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1008:

Met Lys Gly Ala Lys Phe Ser Ser Leu Leu Val Leu Phe Phe Ile Phe

1	5	10	15
Pro Ile Ala Phe	Ala Gln Leu Arg	Val Gly Phe Tyr	Ser Gln Ser Cys
20	25	30	
Pro Gln Ala Glu	Thr Ile Val Arg	Asn Leu Val Arg	Gln Arg Phe Gly
35	40	45	
Val Thr Pro Thr	Val Thr Ala Ala	Leu Leu Arg Met	His Phe His Asp
50	55	60	
Cys Phe Val Lys	Gly Cys Asp Ala	Ser Leu Leu Ile	Asp Ser Thr Asn
65	70	75	80
Ser Glu Lys Thr	Ala Gly Pro Asn	Gly Ser Val Arg	Glu Phe Asp Leu
85	90	95	
Ile Asp Arg Ile	Lys Ala Gln Leu	Glu Ala Ala Cys	Pro Ser Thr Val
100	105	110	
Ser Cys Ala Asp	Ile Val Thr Leu	Ala Thr Arg Asp	Ser Val Ala Leu
115	120	125	
Ala Gly Gly Pro	Ser Tyr Ser Ile	Pro Thr Gly Arg	Asp Gly Arg
130	135	140	
Val Ser Asn Asn	Leu Asp Val Thr	Leu Pro Gly Pro	Thr Ile Ser Val
145	150	155	160
Ser Gly Ala Val	Ser Leu Phe Thr	Asn Lys Gly Met	Asn Thr Phe Asp
165	170	175	
Ala Val Ala Leu	Leu Gly Ala His	Thr Val Gly Gln	Gly Asn Cys Gly
180	185	190	
Leu Phe Ser Asp	Arg Ile Thr Ser	Phe Gln Gly Thr	Gly Arg Pro Asp
195	200	205	
Pro Ser Met Asp	Pro Ala Leu Val	Thr Ser Leu Arg	Asn Thr Cys Arg
210	215	220	
Asn Ser Ala Thr	Ala Ala Leu Asp	Gln Ser Ser Pro	Leu Arg Phe Asp
225	230	235	240
Asn Gln Phe Phe	Lys Gln Ile Arg	Lys Arg Arg Gly	Val Leu Gln Val
245	250	255	
Asp Gln Arg Leu	Ala Ser Asp Pro	Gln Thr Arg Gly	Ile Val Ala Arg
260	265	270	
Tyr Ala Asn Asn	Asn Ala Phe Phe	Lys Arg Gln Phe	Val Arg Ala Met
275	280	285	
Val Lys Met Gly	Ala Val Asp Val	Leu Thr Gly Arg	Asn Gly Glu Ile
290	295	300	
Arg Arg Asn Cys	Arg Arg Phe Asn		
305	310		

(2) INFORMATION FOR SEQ ID NO:1009:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 604 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..604
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568673

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1009:

aattcactat tAtgggagaa	agaactaaaa	acaccaagaa	aataaaaaaa	gagaaagagg	60
atgggagaaag	agttacatga	atccaaggtg	gctactttaca	cggaaagagg	cattggatca
60	120				
caagactcat	cgctgaaaaa	ggagaaggaa	aaatctcata	agcatagagg	attattccac
120	180				
ctccatcact	caaaagatga	gaaagatgga	gacaaaaaga	aagaagatc	aaagagagag
180	240				
aagatagctg	cagcaatggt	tggtcttga	gccactttta	tgaagaagaa	gcacaaaggt
240	300				
ggtggaaaaa	agggaaaaag	aggaggagga	ggaggaaaaa	aggaagaagg	aggaggagaa
300	360				
gaggaggagg	aagaagaaga	ggagtcgtct	tcatcgagg	aggaagaaga	agaagaagaa
360	420				
ggaggaggtg	gtggttgaga	tgaagaagag	ggaggaggca	agttttagtc	tttcattaca
420	480				
atgatcgccg	aagcctttga	agaatgaaaa	tttaatttgt	gatcactttc	ttgtcatttt
480	540				
tttttttttc	aaatttgcta	tcaaatata	gcatttgtaa	tgttttatat	gggatgttga
540	600				

attg

(2) INFORMATION FOR SEQ ID NO:1010:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 148 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..148

(D) OTHER INFORMATION: / Ceres Seq. ID 1568674

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1010:

Met	Glu	Lys	Glu	Leu	His	Glu	Ser	Lys	Val	Ala	Thr	Tyr	Thr	Glu	Arg
1			5						10					15	
Gly	Ile	Gly	Ser	His	Asp	Ser	Ser	Pro	Glu	Lys	Glu	Lys	Glu	Lys	Ser
			20					25						30	
His	Lys	His	Arg	Gly	Leu	Phe	His	Leu	His	Ser	Lys	Asp	Glu	Lys	
			35				40				45				
Asp	Gly	Asp	Lys	Lys	Lys	Glu	Gly	Ser	Lys	Arg	Glu	Lys	Ile	Ala	Ala
			50				55				60				
Ala	Met	Val	Gly	Leu	Gly	Ala	Thr	Phe	Met	Lys	Lys	Lys	His	Lys	Gly
			65				70			75				80	
Gly	Gly	Lys	Lys	Glu	Lys	Arg	Gly	Gly	Gly	Gly	Gly	Lys	Glu	Glu	Glu
				85					90					95	
Gly	Gly	Gly	Glu	Glu	Glu	Gly	Glu	Glu	Glu	Glu	Glu	Ser	Ser	Ser	Ser
				100					105					110	
Glu	Glu	Glu	Glu	Glu	Glu	Glu	Glu	Gly	Gly	Gly	Gly	Gly	Gly	Asp	Glu
				115				120					125		
Glu	Glu	Gly	Gly	Gly	Lys	Phe	Ser	Ala	Phe	Ile	Thr	Met	Ile	Ala	Glu
				130			135					140			
Ala	Phe	Glu	Glu												
				145											

(2) INFORMATION FOR SEQ ID NO:1011:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 83 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..83

(D) OTHER INFORMATION: / Ceres Seq. ID 1568675

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1011:

Met	Val	Gly	Leu	Gly	Ala	Thr	Phe	Met	Lys	Lys	Lys	His	Lys	Gly	Gly
1				5							10			15	
Gly	Lys	Lys	Glu	Lys	Arg	Gly	Gly	Gly	Gly	Lys	Glu	Glu	Glu	Gly	
				20					25					30	
Gly	Gly	Glu	Glu	Glu	Gly	Glu	Glu	Glu	Glu	Ser	Ser	Ser	Ser	Glu	
				35					40				45		
Glu	Glu	Glu	Glu	Glu	Glu	Glu	Gly	Gly	Gly	Gly	Gly	Asp	Glu	Glu	
				50			55				60				
Glu	Gly	Gly	Gly	Lys	Phe	Ser	Ala	Phe	Ile	Thr	Met	Ile	Ala	Glu	Ala
				65			70			75				80	
Phe	Glu	Glu													

(2) INFORMATION FOR SEQ ID NO:1012:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 75 amino acids
- (B) TYPE: amino acid

(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..75
(D) OTHER INFORMATION: / Ceres Seq. ID 1568676
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1012:
Met Lys Lys Lys His Lys Gly Gly Gly Lys Lys Glu Lys Arg Gly Gly
1 5 10 15
Gly Gly Gly Lys Glu Glu Glu Gly Gly Glu Glu Glu Glu Glu Glu
20 25 30
Glu Glu Glu Ser Ser Ser Ser Glu Glu Glu Glu Glu Glu Glu Gly
35 40 45
Gly Gly Gly Gly Gly Asp Glu Glu Glu Gly Gly Gly Lys Phe Ser Ala
50 55 60
Phe Ile Thr Met Ile Ala Glu Ala Phe Glu Glu
65 70 75

(2) INFORMATION FOR SEQ ID NO:1013:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1437 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1437

(D) OTHER INFORMATION: / Ceres Seq. ID 1568683

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1013:

tataaacggtc aggtgtgtcgt tgacacttca ttgtctctaa aaagtctgta ttatagtcac 60
atcattagcgt ttaaacccgt tgctatagct gcaacggaga aggtctcaatt tacagttaaa 120
ggcatgaatc tccgtcggcg tgccacaagg ttactttggt ctgttgaaag aaaaactctg 180
attcaggaaa caacacacga ttcgacgacc agggaggatg acgatttcaa ggacaacaag 240
agattgttga gtgtgttaaac ttctcttggt atatgcctat atagtgtggt cgaggattca 300
tggagattga agaccaagga ctccagttaga gcttcttccc ttctcttagt gttgaagatg 360
acgatgtttg ttctgaaatc cgtatacttg aaaccacatt agagtctcact ggaactgatt 420
ctgctaagca agctatggat ttcatatcat aaatcgggtg gcttcttcac agaagtaaac 480
ttgggggaatc agaccacaaat ccaggcggtt tccattaat acgcttccag tggctaactg 540
agttctcaat ggatcgagag ttggtgcgctg tgatcagaaa gctattaaac atgttctttg 600
atggagctgt tgggtgaatt ttctctccct ctaatgccac actgtcagaa ctgtgccttc 660
ttcacagagc cgtgaggaaa aactcctaag ctatggttga aatgctcttg agatatattc 720
ccaagcaaca aagaacaacg ttgttttagc ccgatgctgc tggctccagc gcccttaaac 780
ctcttcatat tgcagctggt aaagacggtt cagaagatgt gttggatgct ctaacagaa 840
atcctgcaat ggtggggagt gaagcgtgga agacatgtgc agacagcaca ggttTcaca 900
ccagaagact acgactttac ggggtcactt ctcalacatc cacttgattc aacgcaagat 960
caataaaaaa tcaacaactg aagatcatgt tgtgggtcaa atccccagtt cttctctaga 1020
cagagagcag aagaacacaa aatcaggtcc gatgggttca gccctggaga tcacacagat 1080
tccatgcaag ctctgtgacc ataaactggt gtatgggaca acacgcaggt ctgtagcgtg 1140
cagacacgct atgttgttcaa ttgtggcgat tgctgcggtt tgcgtctgtg ttgaccttct 1200
gtttaagagt tgcctgggaa tgctctatgt gtttcaaccg ttcaagtggt agttatgtga 1260
ctatggaaca agctgagtggt aagttcactt tgaaagatct tctaagatat atatatgaat 1320
gttacttata taaaacccat agagggttga tttctatatg taactatatg agtataagat 1380
atagagacat gttggagaa agattgtttg ttattattgt tgttgttgtt gttgtg

(2) INFORMATION FOR SEQ ID NO:1014:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 224 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..224

(D) OTHER INFORMATION: / Ceres Seq. ID 1568684

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1014:

Met	Pro	Ile	Leu	Ser	Gly	Arg	Gly	Phe	Met	Glu	Ile	Glu	Asp	Gln	Gly	
1				5					10					15		
Leu	Ser	Ser	Ser	Phe	Phe	Pro	Phe	Leu	Val	Val	Glu	Asp	Asp	Asp	Val	
			20					25					30			
Cys	Ser	Glu	Ile	Arg	Ile	Leu	Glu	Thr	Thr	Leu	Glu	Phe	Thr	Gly	Thr	
		35					40					45				
Asp	Ser	Ala	Lys	Gln	Ala	Met	Asp	Phe	Ile	His	Glu	Ile	Gly	Trp	Leu	
		50				55					60					
Leu	His	Arg	Ser	Lys	Leu	Gly	Glu	Ser	Asp	Pro	Asn	Pro	Gly	Val	Phe	
		65			70				75					80		
Pro	Leu	Ile	Arg	Phe	Gln	Trp	Leu	Ile	Glu	Phe	Ser	Met	Asp	Arg	Glu	
			85						90				95			
Trp	Cys	Ala	Val	Ile	Arg	Lys	Leu	Leu	Asn	Met	Phe	Phe	Asp	Gly	Ala	
			100					105					110			
Val	Gly	Glu	Phe	Ser	Ser	Ser	Ser	Asn	Ala	Thr	Leu	Ser	Glu	Leu	Cys	
		115						120				125				
Leu	Leu	His	Arg	Ala	Val	Arg	Lys	Asn	Ser	Lys	Pro	Met	Val	Glu	Met	
		130				135					140					
Leu	Leu	Arg	Tyr	Ile	Pro	Lys	Gln	Gln	Arg	Asn	Ser	Leu	Phe	Arg	Pro	
		145			150				155					160		
Asp	Ala	Ala	Gly	Pro	Ala	Gly	Leu	Thr	Pro	Leu	His	Ile	Ala	Ala	Gly	
			165					170					175			
Lys	Asp	Gly	Ser	Glu	Asp	Val	Leu	Asp	Ala	Leu	Thr	Glu	Asp	Pro	Ala	
			180				185					190				
Met	Val	Gly	Ile	Glu	Ala	Trp	Lys	Thr	Cys	Arg	Asp	Ser	Thr	Gly	Phe	
		195				200					205					
His	Thr	Arg	Arg	Leu	Arg	Thr	Tyr	Ala	Val	Thr	Ser	His	Thr	Ser	Thr	
		210				215					220					

(2) INFORMATION FOR SEQ ID NO:1015:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 215 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..215

(D) OTHER INFORMATION: / Ceres Seq. ID 1568685

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1015:

Met	Glu	Ile	Glu	Asp	Gln	Gly	Leu	Ser	Ser	Ser	Phe	Phe	Pro	Phe	Leu	
1				5				10					15			
Val	Val	Glu	Asp	Asp	Val	Cys	Ser	Glu	Ile	Arg	Ile	Leu	Glu	Thr		
		20				25						30				
Thr	Leu	Glu	Phe	Thr	Gly	Thr	Asp	Ser	Ala	Lys	Gln	Ala	Met	Asp	Phe	
		35				40					45					
Ile	His	Glu	Ile	Gly	Trp	Leu	His	Arg	Ser	Lys	Leu	Gly	Glu	Ser		
		50			55					60						
Asp	Pro	Asn	Pro	Gly	Val	Phe	Pro	Leu	Ile	Arg	Phe	Gln	Trp	Leu	Ile	
		65			70			75					80			
Glu	Phe	Ser	Met	Asp	Arg	Glu	Trp	Cys	Ala	Val	Ile	Arg	Lys	Leu	Leu	
			85					90				95				
Asn	Met	Phe	Phe	Asp	Gly	Ala	Val	Gly	Glu	Phe	Ser	Ser	Ser	Ser	Asn	
			100					105					110			

Ala Thr Leu Ser Glu Leu Cys Leu Leu His Arg Ala Val Arg Lys Asn
115 120 125
Ser Lys Pro Met Val Glu Met Leu Leu Arg Tyr Ile Pro Lys Gln Gln
130 135 140
Arg Asn Ser Leu Phe Arg Pro Asp Ala Ala Gly Pro Ala Gly Leu Thr
145 150 155 160
Pro Leu His Ile Ala Ala Gly Lys Asp Gly Ser Glu Asp Val Leu Asp
165 170 175
Ala Leu Thr Glu Asp Pro Ala Met Val Gly Ile Glu Ala Trp Lys Thr
180 185 190
Cys Arg Asp Ser Thr Gly Phe His Thr Arg Arg Leu Arg Thr Tyr Ala
195 200 205
Val Thr Ser His Thr Ser Thr
210 215

(2) INFORMATION FOR SEQ ID NO:1016:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..170
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568686

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1016:

Met Asp Phe Ile His Glu Ile Gly Trp Leu Leu His Arg Ser Lys Leu
1 5 10 15
Gly Glu Ser Asp Pro Asn Pro Gly Val Phe Pro Leu Ile Arg Phe Gln
20 25 30
Trp Leu Ile Glu Phe Ser Met Asp Arg Glu Trp Cys Ala Val Ile Arg
35 40 45
Lys Leu Leu Asn Met Phe Phe Asp Gly Ala Val Gly Glu Phe Ser Ser
50 55 60
Ser Ser Asn Ala Thr Leu Ser Glu Leu Cys Leu Leu His Arg Ala Val
65 70 75 80
Arg Lys Asn Ser Lys Pro Met Val Glu Met Leu Leu Arg Tyr Ile Pro
85 90 95
Lys Gln Gln Arg Asn Ser Leu Phe Arg Pro Asp Ala Ala Gly Pro Ala
100 105 110
Gly Leu Thr Pro Leu His Ile Ala Ala Gly Lys Asp Gly Ser Glu Asp
115 120 125
Val Leu Asp Ala Leu Thr Glu Asp Pro Ala Met Val Gly Ile Glu Ala
130 135 140
Trp Lys Thr Cys Arg Asp Ser Thr Gly Phe His Thr Arg Arg Leu Arg
145 150 155 160
Thr Tyr Ala Val Thr Ser His Thr Ser Thr
165 170

(2) INFORMATION FOR SEQ ID NO:1017:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1748 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1748
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568715

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1017:

aaatgtcatc tccttcacatc ctcaggtaaa aaaactgagt cGgagatttg gcgacgtgat

gaatcatttg	gtgataatct	ctgtgttctt	gagctcagtg	ttgttatata	gaggagaatc	120
tggaatcaca	agtagtttta	ttcgaatcga	atggcctgcg	gttgatatac	cacttgatca	180
tcattgtttc	aattgtccaa	aaggatataa	tgaccacaaa	caagtacata	taactcaagg	240
tgattatgat	ggtaaaagctg	ttatcatctc	ttgggttaca	cctgatgaac	ctggttctag	300
ccaagtacat	tacgggtgcg	ttcaggggaa	atatgagttt	gttgctcaag	ggacttacca	360
taactacacg	ttttacaagt	ataagtcctg	ctttattcat	cactgccttg	tctctgacct	420
tgagcatgat	acaaaatact	attacaagat	tgaaagcggg	gaatcttctc	gagagttttg	480
gtttgtttta	ccaccacatg	tacatccaga	tgcttccctac	aagtttggtg	ttataggcca	540
tatgggtcag	acattcaact	cgttatccac	gttggaacat	tacatggaga	gtggagctca	600
ggctgtttta	ttctctggag	atctttctta	tgctgataga	tatcagtata	atcacgttgg	660
tgtagagatg	gatagctggg	gtcgttttgt	ggagcgtagt	accgcttctc	aaccgtggct	720
ttgtctgcga	ggaaatcact	aagtagatta	catgccatcc	atgggcgagg	tgacaccttt	780
cagggaattac	cttcagcggt	acactacgcc	ttacttagcc	tcaaaaaagta	gcagtcctct	840
ttggtaacgt	gttaggcggt	catctgtcca	tatcattgtc	ctctccagct	attgcctttt	900
tgtagaagat	accccgcaat	ggcactggct	tagtgaagag	cttacaagag	ttgataggga	960
gaaacacact	tggtcaattg	ttttgatgca	cgtcccaata	tacaacagta	atgaagcaca	1020
tttctgggag	ggtgaaaagca	tgcgagcagc	ttttgaagag	gtgtttgtct	aacacaaagt	1080
tgtgttaact	tttgcctggc	atgttctatc	ctacgagaga	tcgtaccgaa	tatcaaatgt	1140
ggcgtataac	gtgtcaagcg	gagatcgtta	cccagttcca	gataaagtcg	cgctgtttta	1200
tatcacagtt	ggagacggag	gaaatcaaga	aggtctggct	ggaaggttta	cggaaccaca	1260
gccagatgat	tctgcatttc	gggaagctag	ctatggccac	tctactctgg	atataaagaa	1320
ccgaacacac	gctatatacc	actggaacgc	caatgatgat	gggaagaaag	tggcaacgga	1380
tgaattttgt	ttacacaacc	agtaactggg	aaagaacatt	gcagcgagaa	agcttaagaa	1440
gcattatata	agagagtgtg	ttgggtggct	gatcgccact	taattcacta	agtcctgctc	1500
atgtttttgt	tcaaaagtgt	tgaggatatt	cttttaactc	ggaacttatt	acttaatttg	1560
atgttaaatc	tctttccgcg	ttaaagtttc	agcaactctg	aatatgaagg	gaattatgta	1620
ttcttatcag	tcttttgatg	aagtgaagtc	tattctctgg	attatggatt	tggtgaataa	1680
tgtattcctt	agaacgggtg	taaggaaatt	tttcacatgg	gtgtgaattg	agaagtcatt	1740
ttgtgttt						

(2) INFORMATION FOR SEQ ID NO:1018:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 493 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..493
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568716

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1018:

Asn	Val	Ile	Ser	Phe	Ile	Ser	Gln	Val	Lys	Lys	Leu	Ser	Arg	Arg	Phe
1			5						10				15		
Gly	Asp	Val	Met	Asn	His	Leu	Val	Ile	Ile	Ser	Val	Phe	Leu	Ser	Ser
			20						25				30		
Val	Leu	Leu	Tyr	Arg	Gly	Glu	Ser	Gly	Ile	Thr	Ser	Ser	Phe	Ile	Arg
			35						40				45		
Ser	Glu	Trp	Pro	Ala	Val	Asp	Ile	Pro	Leu	Asp	His	His	Val	Phe	Asn
			50						55				60		
Val	Pro	Lys	Gly	Tyr	Asn	Ala	Pro	Gln	Gln	Val	His	Ile	Thr	Gln	Gly
			65						70				75		
Asp	Tyr	Asp	Gly	Lys	Ala	Val	Ile	Ile	Ser	Trp	Val	Thr	Pro	Asp	Glu
			85						90				95		
Pro	Gly	Ser	Ser	Gln	Val	His	Tyr	Gly	Ala	Val	Gln	Gly	Lys	Tyr	Glu
			100						105				110		
Phe	Val	Ala	Gln	Gly	Thr	Tyr	His	Asn	Tyr	Thr	Phe	Tyr	Lys	Tyr	Lys
			115						120				125		
Ser	Gly	Phe	Ile	His	His	Cys	Leu	Val	Ser	Asp	Leu	Glu	His	Asp	Thr
			130						135				140		
Lys	Tyr	Tyr	Tyr	Lys	Ile	Glu	Ser	Gly	Glu	Ser	Ser	Arg	Glu	Phe	Trp
			145						150				155		

Phe Val Thr Pro Pro His Val His Pro Asp Ala Ser Tyr Lys Phe Gly
165 170 175
Ile Ile Gly Asp Met Gly Gln Thr Phe Asn Ser Leu Ser Thr Leu Glu
180 185 190
His Tyr Met Glu Ser Gly Ala Gln Ala Val Leu Phe Leu Gly Asp Leu
195 200 205
Ser Tyr Ala Asp Arg Tyr Gln Tyr Asn Asp Val Gly Val Arg Trp Asp
210 215 220
Ser Trp Gly Arg Phe Val Glu Arg Ser Thr Ala Tyr Gln Pro Trp Leu
225 230 235 240
Trp Ser Ala Gly Asn His Glu Val Asp Tyr Met Pro Tyr Met Gly Glu
245 250 255
Val Thr Pro Phe Arg Asn Tyr Leu Gln Arg Tyr Thr Thr Pro Tyr Leu
260 265 270
Ala Ser Lys Ser Ser Ser Pro Leu Trp Tyr Ala Val Arg Arg Ala Ser
275 280 285
Ala His Ile Ile Val Leu Ser Ser Tyr Ser Pro Phe Val Lys Tyr Thr
290 295 300
Pro Gln Trp His Trp Leu Ser Glu Glu Leu Thr Arg Val Asp Arg Glu
305 310 315 320
Lys Thr Pro Trp Leu Ile Val Leu Met His Val Pro Ile Tyr Asn Ser
325 330 335
Asn Glu Ala His Phe Met Glu Gly Glu Ser Met Arg Ala Ala Phe Glu
340 345 350
Glu Trp Phe Val Gln His Lys Val Asp Val Ile Phe Ala Gly His Val
355 360 365
His Ala Tyr Glu Arg Ser Tyr Arg Ile Ser Asn Val Arg Tyr Asn Val
370 375 380
Ser Ser Gly Asp Arg Tyr Pro Val Pro Asp Lys Ser Ala Pro Val Tyr
385 390 395 400
Ile Thr Val Gly Asp Gly Gly Asn Gln Glu Gly Leu Ala Gly Arg Phe
405 410 415
Thr Glu Pro Gln Pro Asp Tyr Ser Ala Phe Arg Glu Ala Ser Tyr Gly
420 425 430
His Ser Thr Leu Asp Ile Lys Asn Arg Thr His Ala Ile Tyr His Trp
435 440 445
Asn Arg Asn Asp Asp Gly Lys Lys Val Ala Thr Asp Glu Phe Val Leu
450 455 460
His Asn Gln Tyr Trp Gly Lys Asn Ile Arg Arg Arg Lys Leu Lys Lys
465 470 475 480
His Tyr Ile Arg Ser Val Val Gly Gly Trp Ile Ala Thr
485 490

(2) INFORMATION FOR SEQ ID NO:1019:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 474 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..474

(D) OTHER INFORMATION: / Ceres Seq. ID 1568717

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1019:

Met Asn His Leu Val Ile Ile Ser Val Phe Leu Ser Ser Val Leu Leu
1 5 10
Tyr Arg Gly Glu Ser Gly Ile Thr Ser Ser Phe Ile Arg Ser Glu Trp
20 25 30
Pro Ala Val Asp Ile Pro Leu Asp His His Val Phe Asn Val Pro Lys
35 40 45
Gly Tyr Asn Ala Pro Gln Gln Val His Ile Thr Gln Gly Asp Tyr Asp

(ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1.1313
(D) OTHER INFORMATION: / Ceres Seq. ID 1568718

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1020:

Met	Gly	Gln	Thr	Phe	Asn	Ser	Leu	Ser	Thr	Leu	Glu	His	Tyr	Met	Glu
1				5					10					15	
Ser	Gly	Ala	Gln	Ala	Val	Leu	Phe	Leu	Gly	Asp	Leu	Ser	Tyr	Ala	Asp
			20					25					30		
Arg	Tyr	Gln	Tyr	Asn	Asp	Val	Gly	Val	Arg	Trp	Asp	Ser	Trp	Gly	Arg
		35				40					45				
Phe	Val	Glu	Arg	Ser	Thr	Ala	Tyr	Gln	Pro	Trp	Leu	Trp	Ser	Ala	Gly
	50				55					60					
Asn	His	Glu	Val	Asp	Tyr	Met	Pro	Tyr	Met	Gly	Glu	Val	Thr	Pro	Phe
65				70					75					80	
Arg	Asn	Tyr	Leu	Gln	Arg	Tyr	Thr	Thr	Pro	Tyr	Leu	Ala	Ser	Lys	Ser
			85					90					95		
Ser	Ser	Pro	Leu	Trp	Tyr	Ala	Val	Arg	Arg	Ala	Ser	Ala	His	Ile	Ile
			100					105					110		
Val	Leu	Ser	Ser	Tyr	Ser	Pro	Phe	Val	Lys	Tyr	Thr	Pro	Gln	Trp	His
			115				120					125			
Trp	Leu	Ser	Glu	Glu	Leu	Thr	Arg	Val	Asp	Arg	Glu	Lys	Thr	Pro	Trp
	130					135					140				
Leu	Ile	Val	Leu	Met	His	Val	Pro	Ile	Tyr	Asn	Ser	Asn	Glu	Ala	His
145					150					155				160	
Phe	Met	Glu	Gly	Glu	Ser	Met	Arg	Ala	Ala	Phe	Glu	Glu	Trp	Phe	Val
			165					170						175	
Gln	His	Lys	Val	Asp	Val	Ile	Phe	Ala	Gly	His	Val	His	Ala	Tyr	Glu
			180				185						190		
Arg	Ser	Tyr	Arg	Ile	Ser	Asn	Val	Arg	Tyr	Asn	Val	Ser	Ser	Gly	Asp
			195				200					205			
Arg	Tyr	Pro	Val	Pro	Asp	Lys	Ser	Ala	Pro	Val	Tyr	Ile	Thr	Val	Gly
	210					215									
Asp	Gly	Gly	Asn	Gln	Glu	Gly	Leu	Ala	Gly	Arg	Phe	Thr	Glu	Pro	Gln
225					230					235				240	
Pro	Asp	Tyr	Ser	Ala	Phe	Arg	Glu	Ala	Ser	Tyr	Gly	His	Ser	Thr	Leu
			245					250					255		
Asp	Ile	Lys	Asn	Arg	Thr	His	Ala	Ile	Tyr	His	Trp	Asn	Arg	Asn	Asp
			260				265						270		
Asp	Gly	Lys	Lys	Val	Ala	Thr	Asp	Glu	Phe	Val	Leu	His	Asn	Gln	Tyr
			275				280						285		
Trp	Gly	Lys	Asn	Ile	Arg	Arg	Arg	Lys	Leu	Lys	Lys	His	Tyr	Ile	Arg
	290					295					300				
Ser	Val	Val	Gly	Gly	Trp	Ile	Ala	Thr							
305					310										

(2) INFORMATION FOR SEQ ID NO:1021:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 596 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -
(B) LOCATION: 1..596
(D) OTHER INFORMATION: / Ceres Seq. ID 1568741

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1021:

gaataatttc	attctcttat	ggcatatggt	gctataaaaca	aacacactta	ccacgcttga	60
tcttacaaca	catgaaccat	gggtttctta	accactcttt	acttcaccac	tttagcacta	120
accctaactc	tgatcttttcg	tctcatacca	gaacaccacg	catcacgcca	tctgaatgga	180
aagaatccgg	cggtaatttg	agttaccact	actagcgaga	aatacattgt	tctacgccc	240
ttaccacggt	ttttacgacc	ctttttccca	cogttacagt	ttgccgctgc	accgttcgga	300

gggaatatcc cacaaccacc gttacottca ccacctccaa cattttctacc gtgtctccca 360
ggtttcaagt ttctcccttt tcagtcctcga aagcctacgc cgcgctaacc gtatatagct 420
tgacggcatc aagtctaaaa ctgtaatgaa atattaaact atctacttta atgtattatc 480
tatctctata tatcacogtt gatcatctat aaataattga tggtaatatc atggtatgaa 540
actgtaataa agatactagg ttagtaatt aataaaYtga ataaatacta tgttag

(2) INFORMATION FOR SEQ ID NO:1022:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 70 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..70
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568742

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1022:

Ile Ile Ser Phe Ser Tyr Gly Ile Trp Cys Tyr Lys Gln Thr His Leu
1 5 10 15
Pro Arg Leu Ile Leu Gln His Met Asn His Gly Phe Phe Asn Pro Leu
20 25 30
Leu Leu His His Phe Ser Thr Asn Pro Asn Leu Asp Leu Ser Ser His
35 40 45
Thr Arg Asn His Arg Ile Thr Pro Ser Glu Trp Lys Glu Ser Gly Gly
50 55 60
Asn Trp Ser Tyr His Tyr
65 70

(2) INFORMATION FOR SEQ ID NO:1023:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 109 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..109
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568743

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1023:

Met Ala Ser Ser Thr His Ser Tyr Phe Thr Thr Leu Ala Leu Thr Leu
1 5 10 15
Ile Leu Ile Phe Arg Leu Ile Pro Glu Thr Thr Ala Ser Arg His Leu
20 25 30
Asn Gly Lys Asn Pro Ala Val Ile Gly Val Thr Thr Thr Ser Glu Lys
35 40 45
Tyr Ile Val Pro Thr Pro Leu Pro Pro Phe Leu Arg Pro Phe Phe Pro
50 55 60
Pro Leu Gln Phe Ala Ala Ala Pro Phe Gly Gly Asn Ile Pro Gln Pro
65 70 75 80
Pro Leu Pro Ser Pro Pro Pro Thr Phe Leu Pro Cys Leu Pro Gly Phe
85 90 95
Lys Phe Pro Pro Phe Gln Ser Arg Lys Pro Thr Pro Pro
100 105

(2) INFORMATION FOR SEQ ID NO:1024:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 447 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..447

(D) OTHER INFORMATION: / Ceres Seq. ID 1568751

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1024:

aaWactgata gtagaaaaaa aaagagagaa gaaaaatggt gttgacaatc tatgctccat	60
tattcgcttc ttcaaaagaga gctgttgtga cattgtgtgga gaagggagta tcattcgaaa	120
ctgtcaatgt cgaatctcatg aaaggagaac agagacagcc tgagtatctc gcgattcagg	180
ttccgatttt ccctcttttt tactaaaatgt ttcttttttt ccggtgacta ttccgatca	240
tgatcccttt ttccgatcga tgcagccttt cggtaaaatc ccagtcctcg tcgacggaga	300
ctacaaaatc ttccgtacac ttcttctctt ttaagctact actacacgag tcgatgctcg	360
ataatggatc tgatcattg cgaatcatgat caatgaatca catgatcttt aagatttttt	420
tgattgtttg gaagagattg tttaggt	

(2) INFORMATION FOR SEQ ID NO:1025:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 53 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..53

(D) OTHER INFORMATION: / Ceres Seq. ID 1568752

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1025:

Xaa	Leu	Ile	Val	Glu	Lys	Lys	Arg	Glu	Lys	Lys	Asn	Gly	Val	Asp	Asn
1				5					10					15	
Leu	Cys	Ser	Ile	Ile	Arg	Phe	Phe	Lys	Glu	Ser	Cys	Cys	Asp	Ile	Gly
			20					25					30		
Gly	Glu	Gly	Ser	Ile	Ile	Arg	Asn	Cys	Gln	Cys	Arg	Ser	His	Glu	Arg
			35				40						45		
Arg	Thr	Glu	Thr	Ala											
			50												

(2) INFORMATION FOR SEQ ID NO:1026:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 56 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..56

(D) OTHER INFORMATION: / Ceres Seq. ID 1568753

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1026:

Met	Val	Leu	Thr	Ile	Tyr	Ala	Pro	Leu	Phe	Ala	Ser	Ser	Lys	Arg	Ala
1				5					10				15		
Val	Val	Thr	Leu	Val	Glu	Lys	Gly	Val	Ser	Phe	Glu	Thr	Val	Asn	Val
			20				25					30			
Asp	Leu	Met	Lys	Gly	Glu	Gln	Arg	Gln	Pro	Glu	Tyr	Leu	Ala	Ile	Gln
			35				40					45			
Val	Pro	Ile	Phe	Pro	Leu	Phe	Thr								
			50				55								

(2) INFORMATION FOR SEQ ID NO:1027:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 38 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..38

(D) OTHER INFORMATION: / Ceres Seq. ID 1568754

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1027:

Met Ile Pro Phe Ser Asp Arg Cys Ser Leu Ser Val Lys Ser Gln Ser
1 5 10 15
Ser Ser Thr Glu Thr Thr Lys Ser Ser Val His Phe Phe Ser Phe Lys
20 25 30
Leu Leu Leu His Glu Ser
35

(2) INFORMATION FOR SEQ ID NO:1028:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1592 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1592

(D) OTHER INFORMATION: / Ceres Seq. ID 1568758

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1028:

aaagactctct ctgcttttcga ccmAaaaacc ttctctctct ctctgggaga tctccatctt 60
cttcgcttct tgccttcccc gcttgaacaa attactcgat ctgcgcggcg gaacaagctc 120
tcgctttctc ttctccggcag atcgattctt ccaattccct attcctttct aggtcttctc 180
taagaaaccc ttaactttct caaaatctgc atttatggcg attagggtta ccttcaccta 240
ctccagctat gttgctagga cgaattgctc atccgcggcg actcgtgtcg gtaccggcga 300
cgttagatca tgccttcgaaa catgggttctg tcccagggtc tgcggccaca atcagatacc 360
agatattgtt gataaatctc ccggatccaa cacatggggt ccaagctcag gccctcgtgc 420
tcgaccagct tcatcaatgt atagcaccaa tgcgagggaa atcctcgaag aaggctgcga 480
gagtcacatt gtcttgggta tgatctctct catgaatttg actggagctc cacagtcttc 540
gggtgtgacc ggtctcggga tctctccctt taagactctc tctgtcatcc cgttccattg 600
gggttccaaq tggatgcctt gtgattcttc ggcgacgtta tcaacggata ttgctgagg 660
tgatagagga gaaagggtct gtgatcctaa agtgaagttg gagttgagtg ataaagtctc 720
gaatggtgga aacggatggg ttaataagct gttgaatctc tgcctcggag atgctaagtc 780
tgctttcaag cgggttaact ttctctctct ttcccgatcg gctttggccg agccaaagtc 840
tataccttca acatctatgc ttctactctc cgaatgtggg gatcgtgtta tagccagaaa 900
ggtctcctac tttttcagga agccagaggt ttccagacata gttatcttca aggtcctctc 960
tatttttggt gaacatgggt acagttgtgc tgatgttttc ataaaaagga tagttgtcag 1020
cgaagggtgac tgggttgaag ttgtgtatgg aaagctctta tgaattgaca ctgttcaagc 1080
agaggatttt gtcttagagc caattgacta tgaatggaa ccaatgtttg tccctgaagg 1140
ttatgtcttc gtcttaggag acaaccgcga caaaagcttt gattctcata actggggctcc 1200
acttccaata aagaacatca tagggagatc tgtgtttcgc tattggccac caaagcaagt 1260
gtcagacata atacaccatg aacaagttag ccaaaagaga gctgtgtgat ttcttgcacc 1320
aacgcagatg gtatcttagg attaagcaga aaatttgatt agatgagctg tgcattgcc 1380
accattttgg cgtcgaagcg aacagagcaa ttctttctc ctgtctaggc ttgatggcgg 1440
acatggaatg cactgggaaa tccatataaa aagaacaaag aaattgatat ttgtcttgg 1500
attttttttg atgtgttgaa acctaaatgc atccagtga attggcagta gctgtcaaac 1560

(2) INFORMATION FOR SEQ ID NO:1029:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 367 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..367

(D) OTHER INFORMATION: / Ceres Seq. ID 1568759

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1029:

Met Ala Ile Arg Val Thr Phe Thr Tyr Ser Ser Tyr Val Ala Arg Ser

1	5	10	15
Ile Ala Ser Ser Ala Gly Thr Arg Val Gly Thr Gly Asp Val Arg Ser			
20	25	30	
Cys Phe Glu Thr Trp Val Arg Pro Arg Phe Cys Gly His Asn Gln Ile			
35	40	45	
Pro Asp Ile Val Asp Lys Ser Pro Gly Ser Asn Thr Trp Gly Pro Ser			
50	55	60	
Ser Gly Pro Arg Ala Arg Pro Ala Ser Ser Met Tyr Ser Thr Ile Ala			
65	70	75	80
Arg Glu Ile Leu Glu Glu Gly Cys Lys Ser Pro Leu Val Leu Gly Met			
85	90	95	
Ile Ser Leu Met Asn Leu Thr Gly Ala Pro Gln Phe Ser Gly Val Thr			
100	105	110	
Gly Leu Gly Ile Ser Pro Phe Lys Thr Ser Ser Val Ile Pro Phe Leu			
115	120	125	
Arg Gly Ser Lys Trp Met Pro Cys Ser Ile Pro Ala Thr Leu Ser Thr			
130	135	140	
Asp Ile Ala Glu Val Asp Arg Gly Gly Lys Val Cys Asp Pro Lys Val			
145	150	155	160
Lys Leu Glu Leu Ser Asp Lys Val Ser Asn Gly Gly Asn Gly Trp Val			
165	170	175	
Asn Lys Leu Leu Asn Ile Cys Ser Glu Asp Ala Lys Ala Ala Phe Thr			
180	185	190	
Ala Val Thr Phe Ser Leu Leu Phe Arg Ser Ala Leu Ala Glu Pro Lys			
195	200	205	
Ser Ile Pro Ser Thr Ser Met Leu Pro Thr Leu Asp Val Gly Asp Arg			
210	215	220	
Val Ile Ala Glu Lys Val Ser Tyr Phe Phe Arg Lys Pro Glu Val Ser			
225	230	235	240
Asp Ile Val Ile Phe Lys Ala Pro Pro Ile Leu Val Glu His Gly Tyr			
245	250	255	
Ser Cys Ala Asp Val Phe Ile Lys Arg Ile Val Ala Ser Glu Gly Asp			
260	265	270	
Trp Val Glu Val Cys Asp Gly Lys Leu Leu Val Asn Asp Thr Val Gln			
275	280	285	
Ala Glu Asp Phe Val Leu Glu Pro Ile Asp Tyr Glu Met Glu Pro Met			
290	295	300	
Phe Val Pro Glu Gly Tyr Val Phe Val Leu Gly Asp Asn Arg Asn Lys			
305	310	315	320
Ser Phe Asp Ser His Asn Trp Gly Pro Leu Pro Ile Lys Asn Ile Ile			
325	330	335	
Gly Arg Ser Val Phe Arg Tyr Trp Pro Pro Ser Lys Val Ser Asp Ile			
340	345	350	
Ile His His Glu Gln Val Ser Gln Lys Arg Ala Val Asp Val Ser			
355	360	365	

(2) INFORMATION FOR SEQ ID NO:1030:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 293 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..293
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568760

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1030:

Met Tyr Ser Thr Ile Ala Arg Glu Ile Leu Glu Glu Gly Cys Lys Ser		
1	5	10
Pro Leu Val Leu Gly Met Ile Ser Leu Met Asn Leu Thr Gly Ala Pro		
20	25	30

Gln Phe Ser Gly Val Thr Gly Leu Gly Ile Ser Pro Phe Lys Thr Ser
35 40 45
Ser Val Ile Pro Phe Leu Arg Gly Ser Lys Trp Met Pro Cys Ser Ile
50 55 60
Pro Ala Thr Leu Ser Thr Asp Ile Ala Glu Val Asp Arg Gly Gly Lys
65 70 75 80
Val Cys Asp Pro Lys Val Lys Leu Glu Leu Ser Asp Lys Val Ser Asn
85 90 95
Gly Gly Asn Gly Trp Val Asn Lys Leu Leu Asn Ile Cys Ser Glu Asp
100 105 110
Ala Lys Ala Ala Phe Thr Ala Val Thr Phe Ser Leu Leu Phe Arg Ser
115 120 125
Ala Leu Ala Glu Pro Lys Ser Ile Pro Ser Thr Ser Met Leu Pro Thr
130 135 140
Leu Asp Val Gly Asp Arg Val Ile Ala Glu Lys Val Ser Tyr Phe Phe
145 150 155 160
Arg Lys Pro Glu Val Ser Asp Ile Val Ile Phe Lys Ala Pro Pro Ile
165 170 175
Leu Val Glu His Gly Tyr Ser Cys Ala Asp Val Phe Ile Lys Arg Ile
180 185 190
Val Ala Ser Glu Gly Asp Trp Val Glu Val Cys Asp Gly Lys Leu Leu
195 200 205
Val Asn Asp Thr Val Gln Ala Glu Asp Phe Val Leu Glu Pro Ile Asp
210 215 220
Tyr Glu Met Glu Pro Met Phe Val Pro Glu Gly Tyr Val Phe Val Leu
225 230 235 240
Gly Asp Asn Arg Asn Lys Ser Phe Asp Ser His Asn Trp Gly Pro Leu
245 250 255
Pro Ile Lys Asn Ile Ile Gly Arg Ser Val Phe Arg Tyr Trp Pro Pro
260 265 270
Ser Lys Val Ser Asp Ile Ile His His Glu Gln Val Ser Gln Lys Arg
275 280 285
Ala Val Asp Val Ser
290

(2) INFORMATION FOR SEQ ID NO:1031:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 272 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..272

(D) OTHER INFORMATION: / Ceres Seq. ID 1568761

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1031:

Met Ile Ser Leu Met Asn Leu Thr Gly Ala Pro Gln Phe Ser Gly Val
1 5 10 15
Thr Gly Leu Gly Ile Ser Pro Phe Lys Thr Ser Ser Val Ile Pro Phe
20 25 30
Leu Arg Gly Ser Lys Trp Met Pro Cys Ser Ile Pro Ala Thr Leu Ser
35 40 45
Thr Asp Ile Ala Glu Val Asp Arg Gly Gly Lys Val Cys Asp Pro Lys
50 55 60
Val Lys Leu Glu Leu Ser Asp Lys Val Ser Asn Gly Gly Asn Gly Trp
65 70 75 80
Val Asn Lys Leu Leu Asn Ile Cys Ser Glu Asp Ala Lys Ala Ala Phe
85 90 95
Thr Ala Val Thr Phe Ser Leu Leu Phe Arg Ser Ala Leu Ala Glu Pro
100 105 110
Lys Ser Ile Pro Ser Thr Ser Met Leu Pro Thr Leu Asp Val Gly Asp

	Arg	Val	Ile	Ala	Glu	Lys	Val	Ser	Tyr	Phe	Phe	Arg	Lys	Pro	Glu	Val
115	130						135					140				
	Ser	Asp	Ile	Val	Ile	Phe	Lys	Ala	Pro	Pro	Ile	Leu	Val	Glu	His	Gly
145	Tyr	Ser	Cys	Ala	Asp	Val	Phe	Ile	Lys	Arg	Ile	Val	Ala	Ser	Glu	Gly
					165					170					175	
	Asp	Trp	Val	Glu	Glu	Val	Cys	Asp	Gly	Lys	Leu	Leu	Val	Asn	Asp	Thr
					180					185					190	
	Gln	Ala	Glu	Glu	Asp	Phe	Val	Leu	Glu	Pro	Ile	Asp	Tyr	Glu	Met	Glu
				195					200					205		Pro
	Met	Phe	Val	Pro	Glu	Gly	Tyr	Val	Phe	Val	Leu	Gly	Asp	Asn	Arg	Asn
		210					215						220			
	Lys	Ser	Phe	Asp	Ser	His	Asn	Trp	Gly	Pro	Leu	Pro	Ile	Lys	Asn	Ile
225						230					235					240
	Ile	Gly	Arg	Ser	Val	Phe	Arg	Tyr	Trp	Pro	Pro	Ser	Lys	Val	Ser	Asp
					245					250					255	
	Ile	Ile	His	His	Glu	Gln	Val	Ser	Gln	Lys	Arg	Ala	Val	Asp	Val	Ser
				260					265					270		

(2) INFORMATION FOR SEQ ID NO:1032:

(i) SEQUENCE CHARACTERISTIC

- (A) LENGTH: 1188 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..1188
(D) OTHER INFORMATION: / Ceres Seq. ID 1568777

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1032:

tctggtttga	taaaaattct	tgaattctct	caagctctct	tctctacaac	catgtgacct	60
tcaagatatt	gtccaaagtac	tctttacaac	tctctccttt	taccaccaac	ccttgatgct	120
cctgtattga	acacaacaact	ctccatgacc	gttggaacca	gaggtctcat	ccttcttgag	180
gattacatac	tctgttgagaa	ctgtgccaat	ttcagacagg	aacggatctc	agagcgtgtg	240
gttcatgcga	gaggagccag	tgctaaagg	tcttttggag	tactcatgta	tatctctaac	300
ctcaactctg	ctgactttct	ccgaagctcc	gggtctga	ctctcgtcat	tgctcgggtc	360
tccaccgtta	tccatgagcg	tggaaattcc	gagaccttga	gagaccctcg	tggttttgac	420
ctcaagttct	acaccagaga	ggggaaactt	gatcttgtt	gaacaaactt	tctctgtttc	480
ttcatccgct	atgggatgaa	gttccctgac	atgttcacgc	ctcttaagcc	gaacccaaac	540
tctcacatcc	aagagaacctg	gagaattcct	gactcttctc	cccaccacac	tgaaagtgtt	600
aacatgtctc	ctttctctct	cgatgatata	ggtatcccat	aagatataac	gcacatgat	660
ggttcagggt	tcaacacata	catgttgatc	aaacaaagct	gc aaagctgc	ctacgttgat	720
ttccattgga	aaccaacctg	ttgtgctca	tctcttttgg	aagaagatgc	aattcgtggt	780
ggaggaaacca	accacagctca	tgcgaactca	gacttgtatg	actctatctg	tgctggaacc	840
taccttgtaa	ggaagtctctt	tatccaaatc	atgtgatcct	ctgatgaaga	caagctgcag	900
tttgaccgcc	tcgatgtaac	caagacgtct	ctcgaagata	tcttgctcct	ccaactcgtt	960
ggacgatatt	tgttgaaacca	gaacattgac	aactctcttg	cagagaatga	gcaactctgc	1020
ttctgtctcg	caattattgt	tccaggagta	caactactac	acgacaaagt	ctctctaaac	1080
ctgtctctct	ccctatgcga	tactcagaga	caacgctctg	gcacaaatac	ccttcagcta	1140
ccgGtcaat	actccaaaat	atctccacca	caacaaccac	catgaagg		

(2) INFORMATION FOR SEQ ID NO

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 394 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1.1394
(D) OTHER INFORMATION: / Ceres Seq. ID 1568778

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1033:

Leu	Val	Leu	Ile	Lys	Ile	Ser	Glu	Ser	Leu	Gln	Ala	Leu	Phe	Ser	Ser
1				5					10					15	
Thr	Met	Asp	Pro	Tyr	Lys	Tyr	Arg	Pro	Ala	Ser	Ser	Tyr	Asn	Ser	Pro
			20					25					30		
Phe	Phe	Thr	Thr	Asn	Ser	Gly	Ala	Pro	Val	Trp	Asn	Asn	Asn	Ser	Ser
			35				40					45			
Met	Thr	Val	Gly	Pro	Arg	Gly	Pro	Ile	Leu	Leu	Glu	Asp	Tyr	His	Leu
	50					55					60				
Val	Glu	Lys	Leu	Ala	Asn	Phe	Asp	Arg	Glu	Arg	Ile	Pro	Glu	Arg	Val
	65				70					75					80
Val	His	Ala	Arg	Gly	Ala	Ser	Ala	Lys	Gly	Phe	Glu	Val	Thr	His	
				85					90				95		
Asp	Ile	Ser	Asn	Leu	Thr	Cys	Ala	Asp	Phe	Leu	Arg	Ala	Pro	Gly	Val
			100					105					110		
Gln	Thr	Pro	Val	Ile	Val	Arg	Phe	Ser	Thr	Val	Ile	His	Glu	Arg	Gly
			115					120				125			
Ser	Pro	Glu	Thr	Leu	Arg	Asp	Pro	Arg	Gly	Phe	Ala	Val	Lys	Phe	Tyr
	130					135					140				
Thr	Arg	Glu	Gly	Asn	Phe	Asp	Leu	Val	Gly	Asn	Asn	Phe	Pro	Val	Phe
	145				150					155					160
Phe	Ile	Arg	Asp	Gly	Met	Lys	Phe	Pro	Asp	Met	Val	His	Ala	Leu	Lys
				165					170					175	
Pro	Asn	Pro	Lys	Ser	His	Ile	Gln	Glu	Asn	Trp	Arg	Ile	Leu	Asp	Phe
			180					185					190		
Phe	Ser	His	His	Pro	Glu	Ser	Leu	Asn	Met	Phe	Thr	Phe	Leu	Phe	Asp
			195					200				205			
Asp	Ile	Gly	Ile	Pro	Gln	Asp	Tyr	Arg	His	Met	Asp	Gly	Ser	Gly	Val
	210					215					220				
Asn	Thr	Tyr	Met	Leu	Ile	Asn	Lys	Ala	Gly	Lys	Ala	His	Tyr	Val	Lys
	225					230				235					240
Phe	His	Trp	Lys	Pro	Thr	Cys	Gly	Val	Lys	Ser	Leu	Leu	Glu	Glu	Asp
			245						250					255	
Ala	Ile	Arg	Val	Gly	Gly	Thr	Asn	His	Ser	His	Ala	Thr	Gln	Asp	Leu
			260					265					270		
Tyr	Asp	Ser	Ile	Ala	Ala	Gly	Asn	Tyr	Pro	Glu	Trp	Lys	Leu	Phe	Ile
			275					280				285			
Gln	Ile	Ile	Asp	Pro	Ala	Asp	Glu	Asp	Lys	Phe	Asp	Phe	Asp	Pro	Leu
	290					295					300				
Asp	Val	Thr	Lys	Thr	Trp	Pro	Glu	Asp	Ile	Leu	Pro	Leu	Gln	Pro	Val
	305					310				315				320	
Gly	Arg	Met	Val	Leu	Asn	Lys	Asn	Ile	Asp	Asn	Phe	Phe	Ala	Glu	Asn
			325						330					335	
Glu	Gln	Leu	Ala	Phe	Cys	Pro	Ala	Ile	Ile	Val	Pro	Gly	Ile	His	Tyr
			340					345					350		
Ser	Asp	Asp	Lys	Leu	Leu	Gln	Thr	Arg	Val	Phe	Ser	Tyr	Ala	Asp	Thr
			355					360				365			
Gln	Arg	His	Arg	Leu	Gly	Pro	Asn	Tyr	Leu	Gln	Leu	Pro	Gly	Gln	Cys
	370					375					380				
Ser	Lys	Met	Cys	Ser	Pro	Gln	Gln	Pro	Pro						
	385				390										

(2) INFORMATION FOR SEQ ID NO:1034:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 377 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..377

(D) OTHER INFORMATION: / Ceres Seq. ID 1568779

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1034:

Met	Asp	Pro	Tyr	Lys	Tyr	Arg	Pro	Ala	Pro	Ala	Pro	Val	Trp	Asn	Asn	Asn	Asn	Ser	Pro	Phe
1				5								10							15	
Phe	Thr	Thr	Asn	Ser	Gly	Ala	Pro	Val	Trp	Asn	Asn	Asn	Asn	Ser	Ser	Ser	Met			
			20					25						30						
Thr	Val	Gly	Pro	Arg	Gly	Pro	Ile	Leu	Leu	Glu	Asp	Tyr	His	Leu	Val					
		35					40				45									
Glu	Lys	Leu	Ala	Asn	Phe	Asp	Arg	Glu	Arg	Ile	Pro	Glu	Arg	Val	Val					
		50				55					60									
His	Ala	Arg	Gly	Ala	Ser	Ala	Lys	Gly	Phe	Phe	Glu	Val	Thr	His	Asp					
65					70				75					80						
Ile	Ser	Asn	Leu	Thr	Cys	Ala	Asp	Phe	Leu	Arg	Ala	Pro	Gly	Val	Gln					
			85						90					95						
Thr	Pro	Val	Ile	Val	Arg	Phe	Ser	Thr	Val	Ile	His	Glu	Arg	Gly	Ser					
		100						105						110						
Pro	Glu	Thr	Leu	Arg	Asp	Pro	Arg	Gly	Phe	Ala	Val	Lys	Phe	Tyr	Thr					
		115					120						125							
Arg	Glu	Gly	Asn	Phe	Asp	Leu	Val	Gly	Asn	Asn	Phe	Pro	Val	Phe	Phe					
		130				135					140									
Ile	Arg	Asp	Gly	Met	Lys	Phe	Pro	Asp	Met	Val	His	Ala	Leu	Lys	Pro					
145				150					155					160						
Asn	Pro	Lys	Ser	His	Ile	Gln	Glu	Asn	Trp	Arg	Ile	Leu	Asp	Phe	Phe					
			165						170					175						
Ser	His	His	Pro	Glu	Ser	Leu	Asn	Met	Phe	Thr	Phe	Leu	Phe	Asp	Asp					
			180					185					190							
Ile	Gly	Ile	Pro	Gln	Asp	Tyr	Arg	His	Met	Asp	Gly	Ser	Gly	Val	Asn					
		195				200						205								
Thr	Tyr	Met	Leu	Ile	Asn	Lys	Ala	Gly	Lys	Ala	His	Tyr	Val	Lys	Phe					
		210				215						220								
His	Trp	Lys	Pro	Thr	Cys	Gly	Val	Lys	Ser	Leu	Glu	Glu	Asp	Ala						
225					230				235					240						
Ile	Arg	Val	Gly	Gly	Thr	Asn	His	Ser	His	Ala	Thr	Gln	Asp	Leu	Tyr					
			245						250					255						
Asp	Ser	Ile	Ala	Ala	Gly	Asn	Tyr	Pro	Glu	Trp	Lys	Leu	Phe	Ile	Gln					
		260						265					270							
Ile	Ile	Asp	Pro	Ala	Asp	Glu	Asp	Lys	Phe	Asp	Phe	Asp	Pro	Leu	Asp					
		275					280					285								
Val	Thr	Lys	Thr	Trp	Pro	Glu	Asp	Ile	Leu	Pro	Leu	Gln	Pro	Val	Gly					
		290				295					300									
Arg	Met	Val	Leu	Asn	Lys	Asn	Ile	Asp	Asn	Phe	Phe	Ala	Glu	Asn	Glu					
				310					315					320						
Gln	Leu	Ala	Phe	Cys	Pro	Ala	Ile	Ile	Val	Pro	Gly	Ile	His	Tyr	Ser					
			325						330					335						
Asp	Asp	Lys	Leu	Leu	Gln	Thr	Arg	Val	Phe	Ser	Tyr	Ala	Asp	Thr	Gln					
			340				345						350							
Arg	His	Arg	Leu	Gly	Pro	Asn	Tyr	Leu	Gln	Leu	Pro	Gly	Gln	Cys	Ser					
		355				360						365								
Lys	Met	Cys	Ser	Pro	Gln	Gln	Pro	Pro												
		370				375														

(2) INFORMATION FOR SEQ ID NO:1035:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 346 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1..346
(D) OTHER INFORMATION: / Ceres Seq. ID 1568780

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1035:

Met	Thr	Val	Gly	Pro	Arg	Gly	Pro	Ile	Leu	Leu	Glu	Asp	Tyr	His	Leu
1			5					10					15		
Val	Glu	Lys	Leu	Ala	Asn	Phe	Asp	Arg	Glu	Arg	Ile	Pro	Glu	Arg	Val
			20					25				30			
Val	His	Ala	Arg	Gly	Ala	Ser	Ala	Lys	Gly	Phe	Phe	Glu	Val	Thr	His
			35					40				45			
Asp	Ile	Ser	Asn	Leu	Thr	Cys	Ala	Asp	Phe	Leu	Arg	Ala	Pro	Gly	Val
			50					55				60			
Gln	Thr	Pro	Val	Ile	Val	Arg	Phe	Ser	Thr	Val	Ile	His	Glu	Arg	Gly
			65					70				75			80
Ser	Pro	Glu	Thr	Leu	Arg	Asp	Pro	Arg	Gly	Phe	Ala	Val	Lys	Phe	Tyr
Thr	Arg	Glu	Gly	Asn	Phe	Asp	Leu	Val	Gly	Asn	Asn	Phe	Pro	Val	Phe
Phe	Ile	Arg	Asp	Gly	Met	Lys	Phe	Pro	Asp	Met	Val	His	Ala	Leu	Lys
Pro	Asn	Pro	Lys	Ser	His	Ile	Gln	Glu	Asn	Trp	Arg	Ile	Leu	Asp	Phe
Phe	Ser	His	His	Pro	Glu	Ser	Leu	Asn	Met	Phe	Thr	Phe	Leu	Phe	Asp
Asp	Ile	Gly	Ile	Pro	Gln	Asp	Tyr	Arg	His	Met	Asp	Gly	Ser	Gly	Val
Asn	Thr	Tyr	Met	Leu	Ile	Asn	Lys	Ala	Gly	Lys	Ala	His	Tyr	Val	Lys
Phe	His	Trp	Lys	Pro	Thr	Cys	Gly	Val	Lys	Ser	Leu	Leu	Glu	Glu	Asp
Ala	Ile	Arg	Val	Gly	Gly	Thr	Asn	His	Ser	His	Ala	Thr	Gln	Asp	Leu
Tyr	Asp	Ser	Ile	Ala	Ala	Gly	Asn	Tyr	Pro	Glu	Trp	Lys	Leu	Phe	Ile
Gln	Ile	Ile	Asp	Pro	Ala	Asp	Glu	Asp	Lys	Phe	Asp	Phe	Asp	Pro	Leu
Asp	Val	Thr	Lys	Thr	Trp	Pro	Glu	Asp	Ile	Leu	Pro	Leu	Gln	Pro	Val
Gly	Arg	Met	Val	Leu	Asn	Lys	Asn	Ile	Asp	Asn	Phe	Phe	Ala	Glu	Asn
Glu	Gln	Leu	Ala	Phe	Cys	Pro	Ala	Ile	Ile	Val	Pro	Gly	Ile	His	Tyr
Ser	Asp	Asp	Lys	Leu	Leu	Gln	Thr	Arg	Val	Phe	Ser	Tyr	Ala	Asp	Thr
Gln	Arg	His	Arg	Leu	Gly	Pro	Asn	Tyr	Leu	Gln	Leu	Pro	Gly	Gln	Cys
Ser	Lys	Met	Cys	Ser	Pro	Gln	Gln	Pro	Pro						

(2) INFORMATION FOR SEQ ID NO:1036:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1466 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -
(B) LOCATION: 1..1466
(D) OTHER INFORMATION: / Ceres Seq. ID 1568781

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1036:

tgtagttagg tcaatggaac agacaaagga tgattctgat ttgaggatg attttgaaac

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gaagaagatg gagactgata catcagctca agaggcaagg aatggtaaag acatacaagg 120
gattcagtgga gaagggttta agtatactac agacgagttt cgtgacacta ggttgaaca 180
ttatgataaac tttgtttaata tcttaaggcc tagctctcga gaaaagcttg ataaggaaca 240
tgggcaagata gttgagaaga gaaagaactt ttatgacttc caattcaata caaggcttgt 300
cacttccact attgtgcatt ttcagttggg agtactgtct gagcagccag cagcataaag 360
atatggcttc ggaatttggg atggggcgaca tctaaagcatg atgtatatct agtcaaaa 420
tattcaactca tgcacttgct atctctactc cagagagggga aagaagtagt taatgtcgc 480
agatcagatta cccccactca gaaactacct ggattgtttt ctgagccact ctctagggtg 540
caagttagca gcatggcagt caaagaaaat ctgactcctt taggaggggt cgacggggag 600
cttctctgca agtgtgtaaa tcagccctggg gttgcttttt gcacaagatt atcaacggaa 660
gataatgcca tcacacacag ttgatataata ccgagaccca agtggctccc ttaggcttat 720
aaccgcaaat aacgactgta aaatccgggt attcgatgct cagagottta cacgtgtcag 780
tgaatttact tttgattggt ctgtcaataa tacctcagtt agcccggatg ggaagctact 840
cgctgtactc ggggacagta cagaatgctt gatctctgat tccattctg aaaaagttat 900
ttcaagccctc agaggccaca aagactactc atttgcatc gcttgggacc cgaattggtct 960
aatcttagca acgggaaacc aagacacgac atgcccgtctc tgggacattc gtaaccgcgtc 1020
agaatcattc gctgtcctga aaggaacatc gggagccatc agaggactga agttcacacc 1080
agaagggcggt tttcttgcaa tggctgagcc tcgacacttt gttcacatct tcgacacgca 1140
gtccgggttt ctacagtcoc aagagattga tctgtttgga gaaatagccg ggaattcctt 1200
cagcccccac ccagagcgac tatatgttgg gtcgcagac cgacttatg gaagtgttat 1260
ggagtataag aggagtaagc ataataccta tatggactcc tttactgag aaaaaggtaaa 1320
tggaagataa aaagcatcta atattgtgtc acaagttggg tttacccta ttagtgtgta 1380
tatgtagaca gaattggtag tttcttgggt tatgtatggt gtatgtaacc cataatatat 1440
cttgccaac ttttaagtat ttttgt

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(2) INFORMATION FOR SEQ ID NO:1037:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 118 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..118
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1568782

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1037:

```

Val Val Arg Ser Met Glu Gln Thr Lys Asp Asp Ser Asp Phe Glu Asp
1 5 10 15
Asp Phe Glu Thr Lys Lys Met Glu Thr Asp Thr Ser Ala Gln Glu Ala
20 25 30
Arg Asn Gly Lys Asp Ile Gln Gly Ile Gln Trp Glu Gly Phe Lys Tyr
35 40 45
Thr Thr Asp Glu Phe Arg Asp Thr Arg Leu Lys His Tyr Asp Asn Phe
50 55 60
Val Asn Ile Leu Arg Pro Ser Ser Arg Glu Lys Leu Asp Lys Glu His
65 70 75 80
Gly Gln Val Val Glu Lys Gly Lys Asn Phe Tyr Asp Phe Gln Phe Asn
85 90 95
Thr Arg Leu Val Thr Ser Thr Ile Val His Phe Gln Leu Glu Val Leu
100 105 110
Ser Glu Gln Pro Ala Ala
115

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(2) INFORMATION FOR SEQ ID NO:1038:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 114 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide

(B) LOCATION: 1..114

(D) OTHER INFORMATION: / Ceres Seq. ID 1568783

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1038:

Met Glu Gln Thr Lys Asp Asp Ser Asp Phe Glu Asp Asp Phe Glu Thr
1 5 10 15
Lys Lys Met Glu Thr Asp Thr Ser Ala Gln Glu Ala Arg Asn Gly Lys
20 25 30
Asp Ile Gln Gly Ile Gln Trp Glu Gly Phe Lys Tyr Thr Thr Asp Glu
35 40 45
Phe Arg Asp Thr Arg Leu Lys His Tyr Asp Asn Phe Val Asn Ile Leu
50 55 60
Arg Pro Ser Ser Arg Glu Lys Leu Asp Lys Glu His Gly Gln Val Val
65 70 75 80
Glu Lys Gly Lys Asn Phe Tyr Asp Phe Gln Phe Asn Thr Arg Leu Val
85 90 95
Thr Ser Thr Ile Val His Phe Gln Leu Gly Val Leu Ser Glu Gln Pro
100 105 110
Ala Ala

(2) INFORMATION FOR SEQ ID NO:1039:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 214 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..214

(D) OTHER INFORMATION: / Ceres Seq. ID 1568784

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1039:

Met Pro Ser His Thr Val Asp Ile Tyr Arg Asp Pro Ser Gly Ser Leu
1 5 10 15
Arg Leu Ile Thr Ala Asn Asn Asp Cys Lys Ile Arg Val Phe Asp Ala
20 25 30
Gln Ser Phe Thr Arg Val Ser Glu Phe Thr Phe Asp Trp Ser Val Asn
35 40 45
Asn Thr Ser Val Ser Pro Asp Gly Lys Leu Leu Ala Val Leu Gly Asp
50 55 60
Ser Thr Glu Cys Leu Ile Ser Asp Ser His Ser Glu Lys Val Ile Ser
65 70 75 80
Ser Leu Arg Gly His Lys Asp Tyr Ser Phe Ala Ser Ala Trp His Pro
85 90 95
Asn Gly Leu Ile Leu Ala Thr Gly Asn Gln Asp Thr Thr Cys Arg Leu
100 105 110
Trp Asp Ile Arg Asn Pro Ser Glu Ser Phe Ala Val Leu Lys Gly Asn
115 120 125
Met Gly Ala Ile Arg Gly Leu Lys Phe Thr Pro Glu Gly Arg Phe Leu
130 135 140
Ala Met Ala Glu Pro Ala Asp Phe Val His Ile Phe Asp Thr Gln Ser
145 150 155 160
Gly Phe Leu Gln Ser Gln Glu Ile Asp Leu Phe Gly Glu Ile Ala Gly
165 170 175
Ile Ser Phe Ser Pro Asp Ser Glu Ala Leu Tyr Val Gly Val Ala Asp
180 185 190
Arg Thr Tyr Gly Ser Leu Met Glu Tyr Lys Arg Ser Lys Asp Asn His
195 200 205
Tyr Met Asp Ser Phe Tyr
210

(2) INFORMATION FOR SEQ ID NO:1040:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1129 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1129

(D) OTHER INFORMATION: / Ceres Seq. ID 1568803

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1040:

ctatccgatt	cgtctctctc	acgccctcac	gtttctccac	ctatctctca	aactaaccac	60
aagacctctt	ttttagagta	accaatcaca	gagagataga	gagagagaac	agagtcacatg	120
tcaatggcgt	ctatagcttc	ttctctctcc	accacctcac	ctctctctct	taggggtctt	180
cttctctcaa	agtcctctct	tttatctctt	accgtctctg	tcctccagaac	ctctacactct	240
tcctgggaat	catctctctt	ctctctgttc	gggtctctca	gtctcggttc	ctctaccacc	300
agccgctccg	ctctacgcgc	gaactctgcc	gtcaaggctc	aggctgatga	tttaccactg	360
gtcggtaata	agggcctctg	ttttgaagca	gaggcagttt	ttgatcaaga	gttcataaag	420
gtgaagctct	ctgagtagat	tggcaaaaag	tatgtttatc	tattctctca	ccctttggac	480
ttcacttttg	ctctgcccac	tgagattact	gccttcagtg	accgttatga	agaatttgag	540
aaagctaaaca	ccgaagtatt	aggggtctct	gtcgcagctg	tgttctcgca	ctctcgctgg	600
gtcccaacag	acagaaagtc	gggagggtct	gggtgatctga	attatctctt	tgtttcogtat	660
atcactaaat	catcttcaaa	atcgttttga	gtgctcatcc	ctgatcaggg	catctgcactg	720
agagggtctt	tcactcatga	caaggaagga	gtcattcaagc	attccacatt	caacaacctc	780
gggtattggc	gaagtgttga	tgagacaatg	agaacctctc	aggcattaca	gtatgttcaa	840
gaaaaccogg	atgaagtggt	ccctgcggga	tgggaagccag	gggagaaatc	aatgaaacct	900
gaaccccaag	tcagcaaaaga	atacttttca	gctatctaga	ggctaagatt	gaacacatgt	960
ttgggtgaaa	ttagcaatca	gagttgtttt	attcatcttt	tcaaggttgg	agcagagttg	1020
ttattttttg	ccaaagaacc	tttgtatcta	ctctatcttt	ctcctgtttc	tgctatgtga	1080
ttctctctaa	attgaatcaa	aaataaagaa	atctctcttt	ctcttttggc		

(2) INFORMATION FOR SEQ ID NO:1041:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 273 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..273

(D) OTHER INFORMATION: / Ceres Seq. ID 1568804

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1041:

Met	Ser	Met	Ala	Ser	Ile	Ala	Ser	Ser	Ser	Ser	Thr	Thr	Leu	Leu	Ser
1			5					10					15		
Ser	Ser	Arg	Val	Leu	Leu	Pro	Ser	Lys	Ser	Ser	Leu	Leu	Ser	Pro	Thr
			20					25					30		
Val	Ser	Val	Pro	Arg	Thr	Leu	His	Ser	Ser	Ser	Ala	Ser	Ser	Ser	Ser
			35					40					45		
Leu	Cys	Ser	Gly	Phe	Ser	Ser	Leu	Gly	Ser	Leu	Thr	Thr	Ser	Arg	Ser
			50					55					60		
Ala	Ser	Arg	Arg	Asn	Phe	Ala	Val	Lys	Ala	Gln	Ala	Asp	Asp	Leu	Pro
Leu	Val	Gly	Asn	Lys	Ala	Pro	Asp	Phe	Glu	Ala	Glu	Ala	Val	Phe	Asp
Gln	Glu	Phe	Ile	Lys	Val	Lys	Leu	Ser	Glu	Tyr	Ile	Gly	Lys	Lys	Tyr
Val	Ile	Leu	Phe	Phe	Tyr	Pro	Leu	Asp	Phe	Thr	Phe	Val	Cys	Pro	Thr
Glu	Ile	Thr	Ala	Phe	Ser	Asp	Arg	Tyr	Glu	Glu	Phe	Glu	Lys	Leu	Asn
Thr	Glu	Val	Leu	Gly	Val	Ser	Val	Asp	Ser	Val	Phe	Ser	His	Leu	Ala
145								150							

Trp	Val	Gln	Thr	Asp	Arg	Lys	Ser	Gly	Gly	Leu	Gly	Asp	Leu	Asn	Tyr	
				165					170					175		
Pro	Leu	Val	Ser	Asp	Ile	Thr	Lys	Ser	Ile	Ser	Lys	Ser	Phe	Gly	Val	
				180					185					190		
Leu	Ile	Pro	Asp	Gln	Gly	Ile	Ala	Leu	Arg	Gly	Leu	Phe	Ile	Ile	Asp	
		195					200					205				
Lys	Glu	Gly	Val	Ile	Gln	His	Ser	Thr	Ile	Asn	Asn	Leu	Gly	Ile	Gly	
		210				215					220					
Arg	Ser	Val	Asp	Glu	Thr	Met	Arg	Thr	Leu	Gln	Ala	Leu	Gln	Tyr	Val	
		225				230				235					240	
Gln	Glu	Asn	Pro	Asp	Glu	Val	Cys	Pro	Ala	Gly	Trp	Lys	Pro	Gly	Glu	
				245					250					255		
Lys	Ser	Met	Lys	Pro	Asp	Pro	Lys	Leu	Ser	Lys	Glu	Tyr	Phe	Ser	Ala	
			260					265					270			
Ile																

(2) INFORMATION FOR SEQ ID NO:1042:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 271 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..271

(D) OTHER INFORMATION: / Ceres Seq. ID 1568805

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1042:

Met	Ala	Ser	Ile	Ala	Ser	Ser	Ser	Ser	Thr	Thr	Leu	Leu	Ser	Ser	Ser	
1			5						10				15			
Arg	Val	Leu	Leu	Pro	Ser	Lys	Ser	Ser	Leu	Leu	Ser	Pro	Thr	Val	Ser	
			20					25					30			
Val	Pro	Arg	Thr	Leu	His	Ser	Ser	Ser	Ala	Ser	Ser	Ser	Ser	Leu	Cys	
			35					40					45			
Ser	Gly	Phe	Ser	Ser	Leu	Gly	Ser	Leu	Thr	Thr	Ser	Arg	Ser	Ala	Ser	
			50			55					60					
Arg	Arg	Asn	Phe	Ala	Val	Lys	Ala	Gln	Ala	Asp	Asp	Leu	Pro	Leu	Val	
			65		70				75					80		
Gly	Asn	Lys	Ala	Pro	Asp	Phe	Glu	Ala	Glu	Ala	Val	Phe	Asp	Gln	Glu	
			85					90					95			
Phe	Ile	Lys	Val	Lys	Leu	Ser	Glu	Tyr	Ile	Gly	Lys	Lys	Tyr	Val	Ile	
			100				105					110				
Leu	Phe	Phe	Tyr	Pro	Leu	Asp	Phe	Thr	Phe	Val	Cys	Pro	Thr	Glu	Ile	
			115				120					125				
Thr	Ala	Phe	Ser	Asp	Arg	Tyr	Glu	Glu	Phe	Glu	Lys	Leu	Asn	Thr	Glu	
			130				135					140				
Val	Leu	Gly	Val	Ser	Val	Asp	Ser	Val	Phe	Ser	His	Leu	Ala	Trp	Val	
			145			150				155				160		
Gln	Thr	Asp	Arg	Lys	Ser	Gly	Gly	Leu	Gly	Asp	Leu	Asn	Tyr	Pro	Leu	
				165					170				175			
Val	Ser	Asp	Ile	Thr	Lys	Ser	Ile	Ser	Lys	Ser	Phe	Gly	Val	Leu	Ile	
			180				185						190			
Pro	Asp	Gln	Gly	Ile	Ala	Leu	Arg	Gly	Leu	Phe	Ile	Ile	Asp	Lys	Glu	
			195				200					205				
Gly	Val	Ile	Gln	His	Ser	Thr	Ile	Asn	Asn	Leu	Gly	Ile	Gly	Arg	Ser	
			210				215					220				
Val	Asp	Glu	Thr	Met	Arg	Thr	Leu	Gln	Ala	Leu	Gln	Tyr	Val	Gln	Glu	
			225			230				235					240	
Asn	Pro	Asp	Glu	Val	Cys	Pro	Ala	Gly	Trp	Lys	Pro	Gly	Glu	Lys	Ser	
				245					250				255			
Met	Lys	Pro	Asp	Pro	Lys	Leu	Ser	Lys	Glu	Tyr	Phe	Ser	Ala	Ile		

260 265 270
(2) INFORMATION FOR SEQ ID NO:1043:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1510 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..1510
(D) OTHER INFORMATION: / Ceres Seq. ID 1568826

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1043:

aattattttt	ccattctct	tcactatctc	tctccctaga	aaattgccag	aagaagaagg	60
ttctccaatt	caaaaaaata	gaacctcgct	accattcatt	tcaaaaaatt	tcttggttaa	120
ttacgttttt	ttcttttttt	ttgcttcttt	cggttcttatt	gtcttagaag	acaaaagaga	180
ctagagagga	tagaaaaatg	gaagcttcaa	gcacaagaag	cgagaagaag	aagaagaaga	240
agacgataca	gagagaaaaa	accgatactc	aaaagaaaaa	aaagctaccc	agtgtttggt	300
tttcaattaa	gaaatctctc	ccctgcaaat	ctgatgtctc	cgatgtccac	attccgagat	360
ccaaaaaaga	gtcagtctcc	atatccaacta	agagaacaac	aacctctctc	ggcgccgggg	420
tcggcgccag	gtccggttgt	tcaagatcca	tagccaatct	taaagacgta	atccatggaa	480
accaacggca	tttagagaa	cgctttgtcg	ctagccctcg	ttctatagga	agcagcga	540
ttctcaatcc	cattactcac	gatgtaatct	ttagcaactc	cacctgcgag	ctcaagatca	600
ccgcgcgcgg	agcaacagaa	ttcgtcgga	atcttagacc	agggacgcg	gtcaattact	660
ctcttctcag	ccgtagccaa	acttcgagaa	aggcttcttc	tttagataga	gaaggattag	720
ggtttccaca	gagcagaaga	gagaatgata	gagaagccgc	cattaacgca	gacaattctc	780
ctgtttcttg	ccatacaatg	ggcgagaaat	ttagcaaatc	cgaagctgca	gaagctcatt	840
atctaaccaa	acacgcgcgt	actgagctaa	tggaaaggaga	ctcgtcgag	agaaatagtGg	900
agataatctg	cagaacaacg	tgggttaaaga	cagagaatca	aggagggaga	atcgatcgga	960
ttttgaagt	acacaacatg	caaaaaacct	tagcgagatt	cgaagaatac	agagatacac	1020
tgaagatcag	agcaagcaag	ttacaaaaaa	aacatccgag	atgtatcgcc	gacggaaaacg	1080
agcttctcag	gttttcacgg	accactgtgg	cttgccgttt	gggataaac	gggtcgacga	1140
gtctgtgttc	gtcgaaaaag	tgttcgcttt	gtcgattat	acgaaatggg	ttctcgcgga	1200
aacgggagat	gaataacgga	attgggggtt	ttactgcgtc	gacgagtga	agggcggttg	1260
agctctattg	gattggagat	gggtgtgtgt	gtgatcgga	ggcgttgatt	gtgtgtcgag	1320
tgattgcggg	gagggttcat	cggccggtgg	agaaatgaga	ggagatgggt	gggttgtttg	1380
gtgggtttga	ttcattgttg	ggtaaaagtg	gggtgtacac	aaatgttga	gagctctatt	1440
tgctcaattc	tcgagctttg	cttctctgtt	tgtgctaatt	tgcaaacctt	aaatcaaat	1500
tttaggtcgt						

(2) INFORMATION FOR SEQ ID NO:1044:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 426 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..426
(D) OTHER INFORMATION: / Ceres Seq. ID 1568827

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1044:

Met	Glu	Ala	Ser	Ser	Thr	Arg	Ser	Glu	Lys	Lys	Lys	Lys	Thr
1			5					10					15
Ile	Gln	Arg	Glu	Asn	Thr	Asp	Thr	Gln	Lys	Lys	Lys	Lys	Leu
			20					25					30
Val	Trp	Phe	Ser	Leu	Lys	Lys	Ser	Leu	Pro	Cys	Lys	Ser	Asp
			35					40					45
Asp	Val	His	Ile	Pro	Arg	Ser	Lys	Lys	Glu	Leu	Ala	Pro	Ile
			50					55					60
Lys	Arg	Thr	Thr	Thr	Ser	Ser	Gly	Gly	Gly	Val	Gly	Gly	Gly
65					70					75			80

Cys Ser Arg Ser Ile Ala Asn Leu Lys Asp Val Ile His Gly Asn Gln
85 90 95
Arg His Leu Glu Lys Pro Leu Cys Ser Ser Pro Arg Ser Ile Gly Ser
100 105 110
Ser Glu Phe Leu Asn Pro Ile Thr His Asp Val Ile Phe Ser Asn Ser
115 120 125
Thr Cys Glu Leu Lys Ile Thr Ala Ala Gly Ala Thr Glu Phe Val Gly
130 135 140
Asn Leu Arg Pro Gly Thr Pro Val Asn Tyr Ser Ser Ser Arg Arg Ser
145 150 155 160
Gln Thr Ser Arg Lys Ala Ser Ser Leu Asp Arg Glu Gly Leu Gly Phe
165 170 175
His Gln Ser Arg Arg Glu Asn Asp Arg Glu Ala Ala Ile Asn Gly Asp
180 185 190
Asn Ser Ser Val Ser Cys His Lys Cys Gly Glu Lys Phe Ser Lys Leu
195 200 205
Glu Ala Ala Glu Ala His His Leu Thr Lys His Ala Val Thr Glu Leu
210 215 220
Met Glu Gly Asp Ser Ser Arg Arg Ile Val Glu Ile Ile Cys Arg Thr
225 230 235 240
Ser Trp Leu Lys Thr Glu Asn Gln Gly Gly Arg Ile Asp Arg Ile Leu
245 250 255
Lys Val His Asn Met Gln Lys Thr Leu Ala Arg Phe Glu Glu Tyr Arg
260 265 270
Asp Thr Val Lys Ile Arg Ala Ser Lys Leu Gln Lys Lys His Pro Arg
275 280 285
Cys Ile Ala Asp Gly Asn Glu Leu Leu Arg Phe His Gly Thr Thr Val
290 295 300
Ala Cys Ala Leu Gly Ile Asn Gly Ser Thr Ser Leu Cys Ser Ser Glu
305 310 315 320
Lys Cys Cys Val Cys Arg Ile Ile Arg Asn Gly Phe Ser Ala Lys Arg
325 330 335
Glu Met Asn Asn Gly Ile Gly Val Phe Thr Ala Ser Thr Ser Glu Arg
340 345 350
Ala Phe Glu Ser Ile Val Ile Gly Asp Gly Gly Gly Gly Asp Arg Lys
355 360 365
Ala Leu Ile Val Cys Arg Val Ile Ala Gly Arg Val His Arg Pro Val
370 375 380
Glu Asn Val Glu Glu Met Gly Gly Leu Leu Ser Gly Phe Asp Ser Leu
385 390 395 400
Ala Gly Lys Val Gly Leu Tyr Thr Asn Val Glu Leu Tyr Leu Leu
405 410 415
Asn Ser Arg Ala Leu Leu Pro Val Leu Cys
420 425

(2) INFORMATION FOR SEQ ID NO:1045:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1088 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1088
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568859

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1045:

aaaagathct ataatagtag agatcaaga cctgagcaaa aactgaaaaa aaaaaaaaaa	60
aaaaaagact tctctctcaaa aatggcggtt acactagggt gaagagctgc tgcgtctagtc	120
ctctgcaacat caattcatca aaatggtttgc ttacacaaac tgcaacaaat tggatcggat	180
cgggtttcagc ttggtgaagc aaaagcaata agattactac ccaggagaaac aaacatggtt	240
caagaattag gaatcaggga agaatttatg gatccaacaa gagaacacaga gacaagtatt	300

1	Lys	Arg	Asp	Lys	5	Ser	Arg	Asp	Gln	Arg	Pro	Glu	Gln	Lys	15	Lys
Lys	Lys	Lys	Lys	Lys	Lys	Lys	Asp	Phe	Ser	Ser	Lys	Met	Ala	Phe	Thr	Leu
Gly	Gly	Arg	Ala	Arg	Arg	Leu	Val	Ser	Ala	Thr	Ser	Ile	His	Gln	Asn	
Gly	Cys	Leu	His	Lys	Leu	Gln	Gln	Ile	Gly	Ser	Asp	Arg	Phe	Gln	Leu	
65	Gly	Glu	Ala	Lys	Ala	Ile	Arg	Leu	Leu	Pro	Arg	Arg	Thr	Asn	Met	Val
Gln	Glu	Leu	Gly	Ile	Arg	Glu	Glu	Phe	Met	Asp	Pro	Asn	Arg	Glu	Thr	80
Glu	Thr	Ser	Tyr	Asp	Phe	Leu	Asp	Glu	Met	Arg	His	Arg	Phe	Leu	Lys	
Phe	Lys	Arg	Gln	Lys	Tyr	Leu	Pro	Glu	Ile	Glu	Lys	Phe	Lys	Ala	Leu	
Ala	Ile	Ala	Gln	Ser	Pro	Lys	Val	Met	Val	Ile	Gly	Cys	Ala	Asp	Ser	
Arg	Val	Cys	Pro	Ser	Tyr	Val	Leu	Gly	Phe	Gln	Pro	Gly	Glu	Ala	Phe	
Thr	Ile	Arg	Asn	Val	Ala	Asn	Leu	Val	Thr	Pro	Val	Gln	Asn	Gly	Pro	
Thr	Glu	Thr	Asn	Ser	Ala	Leu	Glu	Phe	Ala	Val	Thr	Thr	Leu	Gln	Val	
Glu	Asn	Ile	Ile	Val	Met	Gly	His	Ser	Asn	Cys	Gly	Gly	Ile	Ala	Ala	
Leu	Met	Ser	His	Gln	Asn	His	Gln	Gly	Gln	His	Ser	Ser	Leu	Val	Glu	
225	Arg	Trp	Val	Met	Asn	Gly	Lys	Ala	Ala	Lys	Leu	Arg	Thr	Gln	Leu	Ala
Ser	Ser	His	Leu	Ser	Phe	Asp	Glu	Gln	Cys	Arg	Asn	Cys	Glu	Lys	Glu	240
Ser	Ile	Lys	Asp	Ser	Val	Met	Asn	Leu	Ile	Thr	Tyr	Ser	Trp	Ile	Arg	
Asp	Arg	Val	Lys	Arg	Gly	Glu	Val	Lys	Ile	His	Gly	Cys	Tyr	Tyr	Asn	

275 280 285
Leu Ser Asp Cys Ser Leu Glu Lys Trp Arg Leu Ser Ser Asp Lys Thr
290 295 300
Asn Tyr Gly Phe Tyr Ile Ser Asp Arg Glu Ile Trp Ser
305 310 315

(2) INFORMATION FOR SEQ ID NO:1047:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 290 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..290

(D) OTHER INFORMATION: / Ceres Seq. ID 1568861

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1047:

Met Ala Phe Thr Leu Gly Gly Arg Ala Arg Arg Leu Val Ser Ala Thr
1 5 10 15
Ser Ile His Gln Asn Gly Cys Leu His Lys Leu Gln Gln Ile Gly Ser
20 25 30
Asp Arg Phe Gln Leu Gly Glu Ala Lys Ala Ile Arg Leu Leu Pro Arg
35 40 45
Arg Thr Asn Met Val Gln Gly Leu Gly Ile Arg Glu Glu Phe Met Asp
50 55 60
Pro Asn Arg Glu Thr Glu Thr Ser Tyr Asp Phe Leu Asp Glu Met Arg
65 70 75 80
His Arg Phe Leu Lys Phe Lys Arg Gln Lys Tyr Leu Pro Glu Ile Glu
85 90 95
Lys Phe Lys Ala Leu Ala Ile Ala Gln Ser Pro Lys Val Met Val Ile
100 105 110
Gly Cys Ala Asp Ser Arg Val Cys Pro Ser Tyr Val Leu Gly Phe Gln
115 120 125
Pro Gly Glu Ala Phe Thr Ile Arg Asn Val Ala Asn Leu Val Thr Pro
130 135 140
Val Gln Asn Gly Pro Thr Glu Thr Asn Ser Ala Leu Glu Phe Ala Val
145 150 155 160
Thr Thr Leu Gln Val Glu Asn Ile Ile Val Met Gly His Ser Asn Cys
165 170 175
Gly Gly Ile Ala Ala Leu Met Ser His Gln Asn His Gln Gly Gln His
180 185 190
Ser Ser Leu Val Glu Arg Trp Val Met Asn Gly Lys Ala Ala Lys Leu
195 200 205
Arg Thr Gln Leu Ala Ser Ser His Leu Ser Phe Asp Glu Gln Cys Arg
210 215 220
Asn Cys Glu Lys Glu Ser Ile Lys Asp Ser Val Met Asn Leu Ile Thr
225 230 235 240
Tyr Ser Trp Ile Arg Asp Arg Val Lys Arg Gly Glu Val Lys Ile His
245 250 255
Gly Cys Tyr Tyr Asn Leu Ser Asp Cys Ser Leu Glu Lys Trp Arg Leu
260 265 270
Ser Ser Asp Lys Thr Asn Tyr Gly Phe Tyr Ile Ser Asp Arg Glu Ile
275 280 285
Trp Ser
290

(2) INFORMATION FOR SEQ ID NO:1048:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 239 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..239

(D) OTHER INFORMATION: / Ceres Seq. ID 1568862

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1048:

Met	Val	Gln	Glu	Leu	Gly	Ile	Arg	Glu	Glu	Phe	Met	Asp	Pro	Asn	Arg
1			5					10					15		
Glu	Thr	Glu	Thr	Ser	Tyr	Asp	Phe	Leu	Asp	Glu	Met	Arg	His	Arg	Phe
			20					25					30		
Leu	Lys	Phe	Lys	Arg	Gln	Lys	Tyr	Leu	Pro	Glu	Ile	Glu	Lys	Phe	Lys
		35					40					45			
Ala	Leu	Ala	Ile	Ala	Gln	Ser	Pro	Lys	Val	Met	Val	Ile	Gly	Cys	Ala
		50				55				60					
Asp	Ser	Arg	Val	Cys	Pro	Ser	Tyr	Val	Leu	Gly	Phe	Gln	Pro	Gly	Glu
		65			70					75				80	
Ala	Phe	Thr	Ile	Arg	Asn	Val	Ala	Asn	Leu	Val	Thr	Pro	Val	Gln	Asn
			85						90					95	
Gly	Pro	Thr	Glu	Thr	Asn	Ser	Ala	Leu	Glu	Phe	Ala	Val	Thr	Thr	Leu
			100						105				110		
Gln	Val	Glu	Asn	Ile	Ile	Val	Met	Gly	His	Ser	Asn	Cys	Gly	Gly	Ile
		115				120						125			
Ala	Ala	Leu	Met	Ser	His	Gln	Asn	His	Gln	Gly	Gln	His	Ser	Ser	Leu
		130				135						140			
Val	Glu	Arg	Trp	Val	Met	Asn	Gly	Lys	Ala	Ala	Lys	Leu	Arg	Thr	Gln
		145			150					155				160	
Leu	Ala	Ser	Ser	His	Leu	Ser	Phe	Asp	Glu	Gln	Cys	Arg	Asn	Cys	Glu
			165						170					175	
Lys	Glu	Ser	Ile	Lys	Asp	Ser	Val	Met	Asn	Leu	Ile	Thr	Tyr	Ser	Trp
		180					185						190		
Ile	Arg	Asp	Arg	Val	Lys	Arg	Gly	Glu	Val	Lys	Ile	His	Gly	Cys	Tyr
		195					200					205			
Tyr	Asn	Leu	Ser	Asp	Cys	Ser	Leu	Glu	Lys	Trp	Arg	Leu	Ser	Ser	Asp
		210				215						220			
Lys	Thr	Asn	Tyr	Gly	Phe	Tyr	Ile	Ser	Asp	Arg	Glu	Ile	Trp	Ser	
		225			230					235					

(2) INFORMATION FOR SEQ ID NO:1049:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1540 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1540

(D) OTHER INFORMATION: / Ceres Seq. ID 1568863

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1049:

acaatctgac	caattcaatg	aaggcaattg	gtgttgacat	attgactgga	tttggcagtg	60
tctctgggtcc	acaaaagggt	aaatatggga	aggacaatat	tattactgca	aaagatataa	120
tcattgtccac	tgatctctgtg	ccgtttgtcc	ctaaaggaaat	tgaagttgat	ggaaagactg	180
tgatcaccag	tgaccatgct	ttgaaaattag	agtctgtccc	tgagttggatt	gcaattgtag	240
gaagtgggta	tattggtctt	gagttcagtg	atgtttcacac	agctcttgga	agtgaagtga	300
cttttataga	agcactggat	cagctaatgc	ctggatttga	tcctgagatc	agtaagctag	360
ctcagagggt	tttgataaat	ccaagaaaga	ttgactatca	tactggagtc	tttgcaagca	420
aaattactcc	ggcaagggat	gggaaaccag	ttctgattga	gcttattgat	gccaaaacca	480
aggaacctaa	ggatactttg	gaggtagatg	ctgctcttat	tgctactggg	agagctccat	540
tcaccaatgg	acttggcttg	gaaaatgtca	atgtttgtgac	gcagagaggt	ttcataccag	600
ttgatgagcg	aatgcgtgtg	atcgatggaa	aggggactct	gggtccgaac	ttgtactgca	660
ttggtgatgc	caatggtaaa	ttgatgcttg	cacatgcagc	cagtgcccaa	ggaatttctg	720
tggtcgagca	agtcagcgcc	agagatcatg	tgcttaatac	tcttagcatc	ccagctgctt	780

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gctttactca tctctAaaat cagcatgggtg ggattaacag agcctcaagc aaaagaaaaa 840
ggcgagaagg aaggatttaa agttagtgtt gtcaagacaa gtttcaaggc taacacaaag 900
ggcctagctg aaatgaagg agaaggaata gctaagatga tataccgacc tgacaacggg 960
gaaattcttag gagttcatat atttggaactg catgcagctg accttatcca tgaagcttct 1020
aatgcgattg ctctaggaac gcgtattcag gacataaaat tggcgagtta tgacacatcca 1080
acactctctg aggtctctga cgaactgttc aaagcagcca aggttgaag tcattgctacg 1140
acaaggacag taagtgaaaa agtggttgta taataagaaa ccaaaaaact attggggtgg 1200
ggagaacat ctggaagaaa gaaaatttgt gattgtactt tagggagatg caaagataaa 1260
gctaaacacg aaccaggaag atcgaaaagg aagaagaaga ggagagagatg atgagaacaa 1320
accttcogta agtaaaagact tgaagatat atctacaagg ccttcttctt tctttgagaa 1380
tatttctgtt ggagctctgt ctctgctttc acgtatatctt gtttaattgt tccatgggtt 1440
caattagtg agattgtgg tttgtgtatt gtatgtttgt ttgatgtgaa cgattttgga 1500
tgattctctt cttttacta gtaaaatcac ttgtctgtcc

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(2) INFORMATION FOR SEQ ID NO:1050:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 285 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..285
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568864

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1050:

```

Asn Leu Thr Asn Ser Met Lys Ala Ile Gly Val Asp Ile Leu Thr Gly
1      5      10
Phe Gly Ser Val Leu Gly Pro Gln Lys Val Lys Tyr Gly Lys Asp Asn
20     25     30
Ile Ile Thr Ala Lys Asp Ile Ile Ala Thr Gly Ser Val Pro Phe
35     40     45
Val Pro Lys Gly Ile Glu Val Asp Gly Lys Thr Val Ile Thr Ser Asp
50     55     60
His Ala Leu Lys Leu Glu Ser Val Pro Glu Trp Ile Ala Ile Val Gly
65     70     75     80
Ser Gly Tyr Ile Gly Leu Glu Phe Ser Asp Val Tyr Thr Ala Leu Gly
85     90     95
Ser Glu Val Thr Phe Ile Glu Ala Leu Asp Gln Leu Met Pro Gly Phe
100    105    110
Asp Pro Glu Ile Ser Lys Leu Ala Gln Arg Val Leu Ile Asn Pro Arg
115    120    125
Lys Ile Asp Tyr His Thr Gly Val Phe Ala Ser Lys Ile Thr Pro Ala
130    135    140
Arg Asp Gly Lys Pro Val Leu Ile Glu Leu Ile Asp Ala Lys Thr Lys
145    150    155    160
Glu Pro Lys Asp Thr Leu Glu Val Asp Ala Ala Leu Ile Ala Thr Gly
165    170    175
Arg Ala Pro Phe Thr Asn Gly Leu Gly Leu Glu Asn Val Asn Val Val
180    185    190
Thr Gln Arg Gly Phe Ile Pro Val Asp Glu Arg Met Arg Val Ile Asp
195    200    205
Gly Lys Gly Thr Leu Val Pro Asn Leu Tyr Cys Ile Gly Asp Ala Asn
210    215    220
Gly Lys Leu Met Leu Ala His Ala Ala Ser Ala Gln Gly Ile Ser Val
225    230    235    240
Val Glu Gln Val Ser Gly Arg Asp His Val Leu Asn His Leu Ser Ile
245    250    255
Pro Ala Ala Cys Phe Thr His Pro Glu Asn Gln His Gly Gly Ile Asn
260    265    270
Arg Ala Ser Ser Lys Arg Lys Arg Arg Glu Gly Arg Ile
275    280    285

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(2) INFORMATION FOR SEQ ID NO:1051:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 280 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..280
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568865

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1051:

Met Lys Ala Ile Gly Val Asp Ile Leu Thr Gly Phe Gly Ser Val Leu
1 5 10 15
Gly Pro Gln Lys Val Lys Tyr Gly Lys Asp Asn Ile Ile Thr Ala Lys
20 25 30
Asp Ile Ile Ile Ala Thr Gly Ser Val Pro Phe Val Pro Lys Gly Ile
35 40 45
Glu Val Asp Gly Lys Lys Thr Val Ile Thr Ser Asp His Ala Leu Lys Leu
50 55 60
Glu Ser Val Pro Glu Trp Ile Ala Ile Val Gly Ser Gly Tyr Ile Gly
65 70 75 80
Leu Glu Phe Ser Asp Val Tyr Thr Ala Leu Gly Ser Glu Val Thr Phe
85 90 95
Ile Glu Ala Leu Asp Gln Leu Met Pro Gly Phe Asp Pro Glu Ile Ser
100 105 110
Lys Leu Ala Gln Arg Val Leu Ile Asn Pro Arg Lys Ile Asp Tyr His
115 120 125
Thr Gly Val Phe Ala Ser Lys Ile Thr Pro Ala Arg Asp Gly Lys Pro
130 135 140
Val Leu Ile Glu Leu Ile Asp Ala Lys Thr Lys Glu Pro Lys Asp Thr
145 150 155 160
Leu Glu Val Asp Ala Ala Leu Ile Ala Thr Gly Arg Ala Pro Phe Thr
165 170 175
Asn Gly Leu Gly Leu Glu Asn Val Asn Val Val Thr Gln Arg Gly Phe
180 185 190
Ile Pro Val Asp Glu Arg Met Arg Val Ile Asp Gly Lys Gly Thr Leu
195 200 205
Val Pro Asn Leu Tyr Cys Ile Gly Asp Ala Asn Gly Lys Leu Met Leu
210 215 220
Ala His Ala Ala Ser Ala Gln Gly Ile Ser Val Val Glu Gln Val Ser
225 230 235 240
Gly Arg Asp His Val Val Leu Asn His Leu Ser Ile Pro Ala Ala Cys Phe
245 250 255
Thr His Pro Glu Asn Gln His Gly Gly Ile Asn Arg Ala Ser Ser Lys
260 265 270
Arg Lys Arg Arg Glu Gly Arg Ile
275 280

(2) INFORMATION FOR SEQ ID NO:1052:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 177 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..177
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568866

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1052:

Met Pro Gly Phe Asp Pro Glu Ile Ser Lys Leu Ala Gln Arg Val Leu

1	5	10	15
Ile Asn Pro Arg Lys Ile Asp Tyr His Thr Gly Val Phe Ala Ser Lys			
	20	25	30
Ile Thr Pro Ala Arg Asp Gly Lys Pro Val Leu Ile Glu Leu Ile Asp			
	35	40	45
Ala Lys Thr Lys Glu Pro Lys Asp Thr Leu Glu Val Asp Ala Ala Leu			
	50	55	60
Ile Ala Thr Gly Arg Ala Pro Phe Thr Asn Gly Leu Gly Leu Glu Asn			
65	70	75	80
Val Asn Val Val Thr Gln Arg Gly Phe Ile Pro Val Asp Glu Arg Met			
	85	90	95
Arg Val Ile Asp Gly Lys Gly Thr Leu Val Pro Asn Leu Tyr Cys Ile			
	100	105	110
Gly Asp Ala Asn Gly Lys Leu Met Leu Ala His Ala Ser Ala Gln			
	115	120	125
Gly Ile Ser Val Val Glu Gln Val Ser Gly Arg Asp His Val Leu Asn			
	130	135	140
His Leu Ser Ile Pro Ala Ala Cys Phe Thr His Pro Glu Asn Gln His			
145	150	155	160
Gly Gly Ile Asn Arg Ala Ser Ser Lys Arg Lys Arg Arg Glu Gly Arg			
	165	170	175
Ile			

(2) INFORMATION FOR SEQ ID NO:1053:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1326 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1326
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568867

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1053:

actcccatca aagcaaaact atctttctcc ttctcattcc tttttctctc actctctctcc	60
attaaagctc tgcactttct caaagagaat gttcatgggt aagatggggtc ttttgggaat	120
tgctctgttg tgtttttgct caatgtgttg ctctgttcat ggatatgacg ctggatgggt	180
caatgctcat gctaccttct atggtggaag tgatgcttca ggaacaatgg ttggagcttg	240
tggtcacggg aacctctaca gtcaagggtta cgggaccaac acggcggcgct tgagcactgc	300
ctcgttcaac aacgggtctta gctgcggggc gtgttttgag atcaaatgtc agagcgacgc	360
cgcgtgtgtg ttacctgtgt ctatcatgtg cacagccacc aatttctgtc ctccatacaa	420
cgtctctccc aataacgctg gtggttggtg taaccctcgc ctccatcatt tcatctctcc	480
tcagccctgt ttccaacgca ttgctcagta caaagctggg gtgtgccctg ttctctacag	540
aagggttcgc tgtatgagaa gaggaggtat aagattcaca atcaacggct actcttactt	600
caacctgtgc ttggtgacca atgttggtgg tgcgtgagat gtccattcgg ttgcggttaa	660
aggttctagg acaaggtggc aacaaatgtc aagaaaatgg ggcagaact ggcaagcaaa	720
caatctctta aacggtcaag cattgtcatt taaggtgact gctagtgatg gtcgtaccgt	780
cgtctctaac aacattgctc cagctagtgt gtcccttgga caaaccttca ccggccgcta	840
attccgttaa aatttgagta agttcggttt tatatagttt taggggtttg tagtagttg	900
gttgaggaaa gagttagaaa agagagaggg tttaaaggctt tttaggtgtt ttaagtggag	960
agccttgaaa ctctctcttt gactcttgag ggttaaaatg gagaaaagag cttgttttat	1020
aagggtcctt tttagcatgt taaggattag ggttttagta agtgggtgtt gagtagtaga	1080
gtggtgtgtc ttaagggaac tctatgttcc accaatgggt tcctttgttt tatcaacttt	1140
ttattttgtt ttatctcttt ttccaagctc tctgtcttgt ggtttaaaaa gcagaagtgg	1200
gtaggggcag agggagaatt tcaccaccgc cctatgtgtt ttctcttttg ggtcggtttg	1260
gtttatgtta tgaagtgtta attgtaattg agatcaacca atgggtttga taagtgtttt	1320
gttacc	

(2) INFORMATION FOR SEQ ID NO:1054:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 282 amino acids

(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..282
 (D) OTHER INFORMATION: / Ceres Seq. ID 1568868
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1054:
Leu Pro Ser Lys Gln Asn Tyr Leu Ser Pro Ser His Ser Phe Phe Ser
1 5 10 15
His Ser Pro Pro Leu Lys Leu Cys Thr Phe Ser Lys Arg Met Phe Met
 20 25 30
Gly Lys Met Gly Leu Leu Gly Ile Ala Leu Leu Cys Phe Ala Ala Met
 35 40 45
Val Cys Ser Val His Gly Tyr Asp Ala Gly Trp Val Asn Ala His Ala
 50 55 60
Thr Phe Tyr Gly Gly Ser Asp Ala Ser Gly Thr Met Gly Gly Ala Cys
65 70 75 80
Gly Tyr Gly Asn Leu Tyr Ser Gln Gly Tyr Gly Thr Asn Thr Ala Ala
 85 90 95
Leu Ser Thr Ala Leu Phe Asn Asn Gly Leu Ser Cys Gly Ala Cys Phe
 100 105 110
Glu Ile Lys Cys Gln Ser Asp Gly Ala Trp Cys Leu Pro Gly Ala Ile
 115 120 125
Ile Val Thr Ala Thr Asn Phe Cys Pro Pro Asn Asn Ala Leu Pro Asn
 130 135 140
Asn Ala Gly Gly Trp Cys Asn Pro Pro Leu His His Phe Asp Leu Ser
145 150 155 160
Gln Pro Val Phe Gln Arg Ile Ala Gln Tyr Lys Ala Gly Val Val Pro
 165 170 175
Val Ser Tyr Arg Arg Val Pro Cys Met Arg Arg Gly Gly Ile Arg Phe
 180 185 190
Thr Ile Asn Gly His Ser Tyr Phe Asn Leu Val Val Thr Asn Val
 195 200 205
Gly Gly Ala Gly Asp Val His Ser Val Ala Val Lys Gly Ser Arg Thr
 210 215 220
Arg Trp Gln Gln Met Ser Arg Asn Trp Gly Gln Asn Trp Gln Ser Asn
225 230 235 240
Asn Leu Leu Asn Gly Gln Ala Leu Ser Phe Lys Val Thr Ala Ser Asp
 245 250 255
Gly Arg Thr Val Val Ser Asn Asn Ile Ala Pro Ala Ser Trp Ser Phe
 260 265 270
Gly Gln Thr Phe Thr Gly Arg Gln Phe Arg
 275 280
(2) INFORMATION FOR SEQ ID NO:1055:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 253 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..253
 (D) OTHER INFORMATION: / Ceres Seq. ID 1568869
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1055:
Met Phe Met Gly Lys Met Gly Leu Leu Gly Ile Ala Leu Leu Cys Phe
1 5 10 15
Ala Ala Met Val Cys Ser Val His Gly Tyr Asp Ala Gly Trp Val Asn
 20 25 30

Ala His Ala Thr Phe Tyr Gly Gly Ser Asp Ala Ser Gly Thr Met Gly
35 40 45
Gly Ala Cys Gly Tyr Gly Asn Leu Tyr Ser Gln Gly Tyr Gly Thr Asn
50 55 60
Thr Ala Ala Leu Ser Thr Ala Leu Phe Asn Asn Gly Leu Ser Cys Gly
65 70 75 80
Ala Cys Phe Glu Ile Lys Cys Gln Ser Asp Gly Ala Trp Cys Leu Pro
85 90 95
Gly Ala Ile Ile Val Thr Ala Thr Asn Phe Cys Pro Pro Asn Asn Ala
100 105 110
Leu Pro Asn Asn Ala Gly Gly Trp Cys Asn Pro Pro Leu His His Phe
115 120 125
Asp Leu Ser Gln Pro Val Phe Gln Arg Ile Ala Gln Tyr Lys Ala Gly
130 135 140
Val Val Pro Val Ser Tyr Arg Arg Val Pro Cys Met Arg Arg Gly Gly
145 150 155 160
Ile Arg Phe Thr Ile Asn Gly His Ser Tyr Phe Asn Leu Val Leu Val
165 170 175
Thr Asn Val Gly Gly Ala Gly Asp Val His Ser Val Ala Val Lys Gly
180 185 190
Ser Arg Thr Arg Trp Gln Gln Met Ser Arg Asn Trp Gly Gln Asn Trp
195 200 205
Gln Ser Asn Asn Leu Leu Asn Gly Gln Ala Leu Ser Phe Lys Val Thr
210 215 220
Ala Ser Asp Gly Arg Thr Val Val Ser Asn Asn Ile Ala Pro Ala Ser
225 230 235 240
Trp Ser Phe Gly Gln Thr Phe Thr Gly Arg Gln Phe Arg
245 250

(2) INFORMATION FOR SEQ ID NO:1056:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 251 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..251

(D) OTHER INFORMATION: / Ceres Seq. ID 1568870

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1056:

Met Gly Lys Met Gly Leu Leu Gly Ile Ala Leu Leu Cys Phe Ala Ala
1 5 10 15
Met Val Cys Ser Val His Gly Tyr Asp Ala Gly Trp Val Asn Ala His
20 25 30
Ala Thr Phe Tyr Gly Gly Ser Asp Ala Ser Gly Thr Met Gly Gly Ala
35 40 45
Cys Gly Tyr Gly Asn Leu Tyr Ser Gln Gly Tyr Gly Thr Asn Thr Ala
50 55 60
Ala Leu Ser Thr Ala Leu Phe Asn Asn Gly Leu Ser Cys Gly Ala Cys
65 70 75 80
Phe Glu Ile Lys Cys Gln Ser Asp Gly Ala Trp Cys Leu Pro Gly Ala
85 90 95
Ile Ile Val Thr Ala Thr Asn Phe Cys Pro Pro Asn Asn Ala Leu Pro
100 105 110
Asn Asn Ala Gly Gly Trp Cys Asn Pro Pro Leu His His Phe Asp Leu
115 120 125
Ser Gln Pro Val Phe Gln Arg Ile Ala Gln Tyr Lys Ala Gly Val Val
130 135 140
Pro Val Ser Tyr Arg Arg Val Pro Cys Met Arg Arg Gly Gly Ile Arg
145 150 155 160
Phe Thr Ile Asn Gly His Ser Tyr Phe Asn Leu Val Leu Val Thr Asn

581 15 88.22 110

Lys Val Asp Ala Lys Gly Gly Leu Ser Lys Lys Leu Phe Asp Phe Ala
35 40 45
Tyr Ala Arg Arg Leu Ser Ala Ile Asn Gly Ser Trp Phe Gly Ala Trp
50 55 60
Gly Leu Glu Lys Leu Leu Trp Asp Val Leu Val Phe Arg Lys Ile Arg
65 70 75 80
Ala Val Leu Gly Gly Gln Ile Arg Tyr Leu Leu Ser Gly Gly Ala Pro
85 90 95
Leu Ser Gly Asp Thr Gln Arg Phe Ile Asn Ile Cys Val Gly Ala Pro
100 105 110
Ile Gly Gln Gly Tyr Gly Leu Thr Glu Thr Cys Ala Gly Gly Thr Phe
115 120 125
Ser Glu Phe Glu Asp Thr Ser Val Gly Arg Val Gly Ala Pro Leu Pro
130 135 140
Cys Ser Phe Val Lys Leu Val Asp Trp Ala Glu Gly Gly Tyr Leu Thr
145 150 155 160
Ser Asp Lys Pro Met Pro Arg Gly Glu Ile Val Ile Gly Gly Ser Asn
165 170 175
Ile Thr Leu Gly Tyr Phe Lys Asn Glu Glu Lys Thr Lys Glu Val Tyr
180 185 190
Lys Val Asp Glu Lys Gly Met Arg Trp Phe Tyr Thr Gly Asp Ile Gly
195 200 205
Arg Phe His Pro Asp Gly Cys Leu Glu Ile Ile Asp Arg Lys Lys Asp
210 215 220
Ile Val Lys Leu Gln His Gly Glu Tyr Val Ser Leu Gly Lys Val Glu
225 230 235 240
Ala Ala Leu Ser Ile Ser Pro Tyr Val Glu Asn Ile Met Val His Ala
245 250 255
Asp Ser Phe Tyr Ser Tyr Cys Val Ala Leu Val Val Ala Ser Gln His
260 265 270
Thr Val Glu Gly Trp Ala Ser Lys Xaa Gly Ile Xaa Phe Ala Asn Phe
275 280 285
Glu Glu Leu Cys Thr Lys Glu Gln Ala Val Lys Glu Val Tyr Ala Tyr
290 295 300
Leu Val Lys Ala Ala Lys Gln Ser Arg Leu Glu Lys Phe Glu Ile Xaa
305 310 315 320
Ala Lys Ile Lys Leu Leu Ala Ser Pro Trp Thr Pro Glu Ser Gly Leu
325 330 335
Val Thr Ala Ala Leu Lys Leu Lys Arg Asp Val Ile Arg Arg Glu Phe
340 345 350
Ser Glu Asp Leu Thr Lys Leu Tyr Ala
355 360

(2) INFORMATION FOR SEQ ID NO:1059:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 346 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..346

(D) OTHER INFORMATION: / Ceres Seq. ID 1568873

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1059:

Met Thr Ala Val Pro Ala Ile Leu Asp Arg Val Arg Asp Gly Val Arg
1 5 10 15
Lys Lys Val Asp Ala Lys Gly Gly Leu Ser Lys Lys Leu Phe Asp Phe
20 25 30
Ala Tyr Ala Arg Arg Leu Ser Ala Ile Asn Gly Ser Trp Phe Gly Ala
35 40 45
Trp Gly Leu Glu Lys Leu Leu Trp Asp Val Leu Val Phe Arg Lys Ile

50	55	60
Arg Ala Val Leu Gly Gly Gln Ile Arg Tyr	Leu Leu Ser Gly Gly Ala	
65	70	75
Pro Leu Ser Gly Asp Thr Gln Arg Phe Ile Asn Ile Cys Val Gly Ala		80
85	90	95
Pro Ile Gly Gln Gly Tyr Gly Leu Thr Glu Thr Cys Ala Gly Gly Thr		100
100	105	110
Phe Ser Glu Phe Glu Asp Thr Ser Val Gly Arg Val Gly Ala Pro Leu		115
115	120	125
Pro Cys Ser Phe Val Lys Leu Val Asp Trp Ala Glu Gly Gly Tyr Leu		130
130	135	140
Thr Ser Asp Lys Pro Met Pro Arg Gly Glu Ile Val Ile Gly Gly Ser		145
145	150	155
Asn Ile Thr Leu Gly Tyr Phe Lys Asn Glu Lys Thr Lys Glu Val		160
165	170	175
Tyr Lys Val Asp Glu Lys Gly Met Arg Trp Phe Tyr Thr Gly Asp Ile		180
180	185	190
Gly Arg Phe His Pro Asp Gly Cys Leu Glu Ile Ile Asp Arg Lys Lys		195
195	200	205
Asp Ile Val Lys Leu Gln His Gly Glu Tyr Val Ser Leu Gly Lys Val		210
210	215	220
Glu Ala Ala Leu Ser Ile Ser Pro Tyr Val Glu Asn Ile Met Val His		225
225	230	235
Ala Asp Ser Phe Tyr Ser Tyr Cys Val Ala Leu Val Val Ala Ser Gln		240
245	250	255
His Thr Val Glu Gly Trp Ala Ser Lys Xaa Gly Ile Xaa Phe Ala Asn		260
260	265	270
Phe Glu Glu Leu Cys Thr Lys Glu Gln Ala Val Lys Glu Val Tyr Ala		275
275	280	285
Tyr Leu Val Lys Ala Ala Lys Gln Ser Arg Leu Glu Lys Phe Glu Ile		290
290	295	300
Xaa Ala Lys Ile Lys Leu Leu Ala Ser Pro Trp Thr Pro Glu Ser Gly		305
305	310	315
Leu Val Thr Ala Ala Leu Lys Leu Lys Arg Asp Val Ile Arg Arg Glu		320
325	330	335
Phe Ser Glu Asp Leu Thr Lys Leu Tyr Ala		340
340	345	

(2) INFORMATION FOR SEQ ID NO:1060:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 197 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..197

(D) OTHER INFORMATION: / Ceres Seq. ID 1568874

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1060:

Met Pro Arg Gly Glu Ile Val Ile Gly Gly Ser Asn Ile Thr Leu Gly		
1	5	10
Tyr Phe Lys Asn Glu Lys Thr Lys Glu Val Tyr Lys Val Asp Glu		15
20	25	30
Lys Gly Met Arg Trp Phe Tyr Thr Gly Asp Ile Gly Arg Phe His Pro		35
35	40	45
Asp Gly Cys Leu Glu Ile Ile Asp Arg Lys Lys Asp Ile Val Lys Leu		50
50	55	60
Gln His Gly Glu Tyr Val Ser Leu Gly Lys Val Glu Ala Ala Leu Ser		65
65	70	75
Ile Ser Pro Tyr Val Glu Asn Ile Met Val His Ala Asp Ser Phe Tyr		80
85	90	95

Ser Tyr Cys Val Ala Leu Val Val Ala Ser Gln His Thr Val Glu Gly
100 105 110
Trp Ala Ser Lys Xaa Gly Ile Xaa Phe Ala Asn Phe Glu Glu Leu Cys
115 120 125
Thr Lys Glu Gln Ala Val Lys Glu Val Tyr Ala Tyr Leu Val Lys Ala
130 135 140
Ala Lys Gln Ser Arg Leu Glu Lys Phe Glu Ile Xaa Ala Lys Ile Lys
145 150 155 160
Leu Leu Ala Ser Pro Trp Thr Pro Glu Ser Gly Leu Val Thr Ala Ala
165 170 175
Leu Lys Leu Lys Arg Asp Val Ile Arg Arg Glu Phe Ser Glu Asp Leu
180 185 190
Thr Lys Leu Tyr Ala
195

(2) INFORMATION FOR SEQ ID NO:1061:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1133 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1133

(D) OTHER INFORMATION: / Ceres Seq. ID 1568883

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1061:

gtgtctcaca	tctctttgtc	ttctccgcct	cctccgatct	cactccgatc	tctctacgat	60
tcattctctc	atggcttcac	ttgctacttc	tgtctctact	tctctccaat	ctcgtctctc	120
tcaactgggtg	attgggggcta	aacaagttaa	aagcttttagc	tatggaagca	gaagcaatct	180
ttcttttaat	cttgccacgc	ttctacccgc	cttgactgtt	tactgcgctg	caaaacctga	240
gacagtggac	aaggtgtgtg	cagttgtcag	aaagcaactc	tcaactaaa	aggctgacga	300
aattaccgct	gccaccaaat	ttgctgcaat	tggtgctgat	tccttgata	cgttgagat	360
agttatggga	ttagaggaag	agtttgggat	tgaatggct	tcaacgatgt	ttctaaatta	420
cctgacttgg	aagagaagca	tgtctccaaa	ggggcacata	ccagaagcag	agattgcaaa	480
tgatctatcg	cataacaaga	tgtgtatgca	aggtcatgac	aagatgggtc	gacctatcgc	540
tgttgccatt	gggaacagac	ataacccttc	caaaaggcaac	cctgacgagt	tcaagcgttt	600
tgttgtctac	acgctcgaga	agatttggct	tagaatgcgc	agaggtcga	agaaattcgt	660
agcaattgga	gatctgcaag	gctggggata	ttctaattgt	gacatccgtg	gctaccttgc	720
tgctctttcc	actttgcagg	attgttacc	agagagatta	gggaacctct	atatagttca	780
tgccccctac	attttcatga	cgcgatggaa	ggctcattat	ctctttatcg	acgccaaacac	840
caagaaaaag	attgttttgc	tggagaaaca	gaactcact	ccaacgctgc	ttagagacat	900
agacgaaagc	caactctccg	Gacatctacg	gaggcaaaAt	tgccacttgt	tcctattcag	960
gagacctgat	tataggtcatt	actTaaggGc	ccacctctat	ttccaaatta	ttacttacta	1020
gtatcttttt	ttttatttga	ataaaatgaa	aaacatattg	agtgctgcga	aatgccaaaca	1080
attatataatt	tactgtcaaa	gaagctaaaa	gatataatat	tgaatcacc	ttt	

(2) INFORMATION FOR SEQ ID NO:1062:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..339

(D) OTHER INFORMATION: / Ceres Seq. ID 1568884

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1062:

Cys	Leu	Thr	Ser	Leu	Cys	Leu	Leu	Arg	Leu	Arg	Ser	His	Ser	Asp
1				5				10				15		
Leu	Ser	Thr	Ile	His	Ser	Ser	Met	Ala	Ser	Ile	Ala	Thr	Ser	Ala
				20				25				30		

Thr Ser Leu Gln Ala Arg Pro Arg Gln Leu Val Ile Gly Ala Lys Gln
35 40 45
Val Lys Ser Phe Ser Tyr Gly Ser Arg Ser Asn Leu Ser Phe Asn Leu
50 55 60
Arg Gln Leu Pro Thr Arg Leu Thr Val Tyr Cys Ala Ala Lys Pro Glu
65 70 75 80
Thr Val Asp Lys Val Cys Ala Val Val Arg Lys Gln Leu Ser Leu Lys
85 90 95
Glu Ala Asp Glu Ile Thr Ala Ala Thr Lys Phe Ala Ala Leu Gly Ala
100 105 110
Asp Ser Leu Asp Thr Val Glu Ile Val Met Gly Leu Glu Glu Glu Phe
115 120 125
Gly Ile Glu Met Ala Ser Thr Met Phe Leu Asn Tyr Leu Thr Trp Lys
130 135 140
Arg Ser Met Leu Pro Lys Gly His Ile Pro Glu Ala Glu Ile Ala Asn
145 150 155 160
Asp Leu Ser His Asn Lys Met Cys Met Gln Gly His Asp Lys Met Gly
165 170 175
Arg Pro Ile Ala Val Ala Ile Gly Asn Arg His Asn Pro Ser Lys Gly
180 185 190
Asn Pro Asp Glu Phe Lys Arg Phe Val Val Tyr Thr Leu Glu Lys Ile
195 200 205
Cys Ala Arg Met Pro Arg Gly Gln Glu Lys Phe Val Ala Ile Gly Asp
210 215 220
Leu Gln Gly Trp Gly Tyr Ser Asn Cys Asp Ile Arg Gly Tyr Leu Ala
225 230 235 240
Ala Leu Ser Thr Leu Gln Asp Cys Tyr Pro Glu Arg Leu Gly Lys Leu
245 250 255
Tyr Ile Val His Ala Pro Tyr Ile Phe Met Thr Ala Trp Lys Val Ile
260 265 270
Tyr Pro Phe Ile Asp Ala Asn Thr Lys Lys Lys Ile Val Phe Val Glu
275 280 285
Asn Lys Lys Leu Thr Pro Thr Leu Leu Glu Asp Ile Asp Glu Ser Gln
290 295 300
Leu Pro Gly His Leu Arg Arg Gln Asn Cys His Leu Phe Leu Phe Arg
305 310 315 320
Arg Pro Asp Tyr Arg Ser Tyr Leu Arg Ala His Leu Tyr Phe Gln Ile
325 330 335
Ile Thr Tyr

(2) INFORMATION FOR SEQ ID NO:1063:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 316 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..316

(D) OTHER INFORMATION: / Ceres Seq. ID 1568885

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1063:

Met Ala Ser Ile Ala Thr Ser Ala Ser Thr Ser Leu Gln Ala Arg Pro
1 5 10 15
Arg Gln Leu Val Ile Gly Ala Lys Gln Val Lys Ser Phe Ser Tyr Gly
20 25 30
Ser Arg Ser Asn Leu Ser Phe Asn Leu Arg Gln Leu Pro Thr Arg Leu
35 40 45
Thr Val Tyr Cys Ala Ala Lys Pro Glu Thr Val Asp Lys Val Cys Ala
50 55 60
Val Val Arg Lys Gln Leu Ser Leu Lys Glu Ala Asp Glu Ile Thr Ala

65		70		75		80
Ala Thr Lys Phe	Ala Ala Leu Gly Ala Asp Ser Leu Asp Thr Val Glu					
	85			90		95
Ile Val Met Gly	Leu Glu Glu Glu Phe Gly Ile Glu Met Ala Ser Thr					
	100			105		110
Met Phe Leu Asn Tyr	Leu Thr Trp Lys Arg Ser Met Leu Pro Lys Gly					
	115			120		125
His Ile Pro Glu Ala	Glu Ile Ala Asn Asp Leu Ser His Asn Lys Met					
	130			135		140
Cys Met Gln Gly His	Asp Lys Met Gly Arg Pro Ile Ala Val Ala Ile					
	145			150		155
Gly Asn Arg His Asn	Pro Ser Lys Gly Asn Pro Asp Glu Phe Lys Arg					
	165			170		175
Phe Val Val Tyr Thr	Leu Glu Lys Ile Cys Ala Arg Met Pro Arg Gly					
	180			185		190
Gln Glu Lys Phe Val	Ala Ile Gly Asp Leu Gln Gly Trp Gly Tyr Ser					
	195			200		205
Asn Cys Asp Ile Arg	Gly Tyr Leu Ala Ala Leu Ser Thr Leu Gln Asp					
	210			215		220
Cys Tyr Pro Glu Arg	Leu Gly Lys Leu Tyr Ile Val His Ala Pro Tyr					
	225			230		235
Ile Phe Met Thr Ala	Trp Lys Val Ile Tyr Pro Phe Ile Asp Ala Asn					
	245			250		255
Thr Lys Lys Lys Ile	Val Phe Val Glu Asn Lys Lys Leu Thr Pro Thr					
	260			265		270
Leu Leu Glu Asp Ile	Asp Glu Ser Gln Leu Pro Gly His Leu Arg Arg					
	275			280		285
Gln Asn Cys His Leu	Phe Leu Phe Arg Arg Pro Asp Tyr Arg Ser Tyr					
	290			295		300
Leu Arg Ala His Leu	Tyr Phe Gln Ile Ile Thr Tyr					
	305			310		315

(2) INFORMATION FOR SEQ ID NO:1064:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 218 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..218

(D) OTHER INFORMATION: / Ceres Seq. ID 1568886

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1064:

Met Gly Leu Glu Glu Glu Phe Gly Ile Glu Met Ala Ser Thr Met Phe	
1	5
Leu Asn Tyr Leu Thr Trp Lys Arg Ser Met Leu Pro Lys Gly His Ile	
	20
Pro Glu Ala Glu Ile Ala Asn Asp Leu Ser His Asn Lys Met Cys Met	
	35
Gln Gly His Asp Lys Met Gly Arg Pro Ile Ala Val Ala Ile Gly Asn	
	50
Arg His Asn Pro Ser Lys Gly Asn Pro Asp Glu Phe Lys Arg Phe Val	
65	70
Val Tyr Thr Leu Glu Lys Ile Cys Ala Arg Met Pro Arg Gly Gln Glu	
	85
Lys Phe Val Ala Ile Gly Asp Leu Gln Gly Trp Gly Tyr Ser Asn Cys	
	100
Asp Ile Arg Gly Tyr Leu Ala Ala Leu Ser Thr Leu Gln Asp Cys Tyr	
	115
Pro Glu Arg Leu Gly Lys Leu Tyr Ile Val His Ala Pro Tyr Ile Phe	
	130
	135
	140

Met Thr Ala Trp Lys Val Ile Tyr Pro Phe Ile Asp Ala Asn Thr Lys
145 150 155 160
Lys Lys Ile Val Phe Val Glu Asn Lys Lys Leu Thr Pro Thr Leu Leu
165 170 175
Glu Asp Ile Asp Glu Ser Gln Leu Pro Gly His Leu Arg Arg Gln Asn
180 185 190
Cys His Leu Phe Leu Phe Arg Arg Pro Asp Tyr Arg Ser Tyr Leu Arg
195 200 205
Ala His Leu Tyr Phe Gln Ile Ile Thr Tyr
210 215

(2) INFORMATION FOR SEQ ID NO:1065:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1790 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1790

(D) OTHER INFORMATION: / Ceres Seq. ID 1568887

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1065:

ccctcgcgca	tcttcggtgc	tataaaacaa	actcacgact	agatcatctt	ggagtggagt	60
ttacgtttga	tagactacta	caatgaagga	gccaacgacg	gagatagaga	ttgaaacttc	120
agctgtcaca	acgactcctgc	ctcctcctct	tcctccgacg	gcgtcacctc	atcaggcggt	180
gggtggagagg	ctcaaggatt	atggacagga	agatgttttc	tcctctctgg	atgaactctc	240
accggaagag	cgagatctcc	tcctccgaga	tatcgagaat	ttggatcttc	caaggataga	300
tcggatcatc	agatgctcac	ttcaactaca	aggggttgcca	gtggcgccaa	tagaacgggt	360
gcggagagaat	tgtgtgtcaa	cggtggagga	aagaactaag	gaagacagag	aaaaatgggt	420
gaaaatggga	ttaaaagcta	tactcgaagg	caaatgggtg	gtgggtgctt	tatctgggtg	480
acagggaaca	agacttggaa	gttcagatcc	aaaagggtgt	tataatatcg	gactgccatc	540
tgggaaatca	ctttttcaga	ttcaagctga	gaggatctta	tgtgtccaaa	ggcttgcttc	600
tcaggcaaatg	agtgaaggcaa	gtccaaactcg	cccagttaca	atacagtggg	atataatgac	660
cagtcacatt	actcatgaac	caacacaaaa	attcttcgag	agtcacaaat	attttggcct	720
tgaaaccagat	caagtccact	ttttttcaac	aaggagctct	gccttgcat	tcaaaaggatg	780
gcaagtttat	catggagaca	cttttcagcc	tatccaaggc	gccggatggg	aacggggagg	840
tttatcacgc	tttaaaatct	tcaagggttat	tagaagatat	ggcttcgagg	gggattaaat	900
atgtggattg	ctatggtggt	gacaatgttc	tggttcgagt	agctgaccct	acttttctgg	960
gatacttcat	cgacaaaagt	gcagcttcag	ctgcacaaagt	agtgcgcaag	gcataccac	1020
aggaaaaagt	tgaggatttt	gtaaggaggg	gaaaagggtg	gcctttgact	gtagtttgat	1080
acacagagct	tgaccagctt	atggctcttg	caactaatca	acaaacagga	cgcttctcaat	1140
attgtctggg	taacgtgtgc	ttacacatgt	tcactctgga	tttccctaac	caagttgcga	1200
attggctgaa	aaagacacgg	tttaccattt	ggcgGagaag	aagataccgt	ctataaatgt	1260
cgacatagtg	ggGactaaaa	actagaacag	ttcatattcg	attgcttttc	ttatgctcct	1320
tcgactgcaac	tttttgagggt	gttgaggagg	gaagagtttg	caccgggtgaa	gaacgcacaa	1380
gggtgcgaatt	acgacacacc	ggaaaacgca	agactgttgg	ttctacagct	gcatacacgt	1440
tggtgtcatag	caagctgtgtg	attttcaaca	cattccgttg	cttttatatg	gactggtgtg	1500
gaagtgtcac	catgtgtctc	gtacgctgga	gaaaactctag	aagcgatttg	tcgggggaaga	1560
acctttcacg	caacatgtga	aatctccctc	taattctctt	ctttcttttt	cttatctatt	1620
cttgtaattt	tgtcattgtc	tttgcttttt	cttttggctt	ggttctctct	ttgtgttggg	1680
gtttgtgtct	tatatatgaa	ctgtaaactg	cggaggtggt	cagtagcttc	ttttcaatgt	1740
gttactcttc	attattgcga	caatagtga	gtctccgaaa	ttttggtggt		

(2) INFORMATION FOR SEQ ID NO:1066:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 271 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..271

(D) OTHER INFORMATION: / Ceres Seq. ID 1568888

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1066:

Met Lys Glu Pro Thr Thr Glu Ile Glu Ile Glu Thr Ser Ala Val Thr
1 5 10 15
Thr Ile Leu Pro Pro Pro Leu Pro Pro Thr Ala Ser Pro His Gln Ala
20 25 30
Leu Val Glu Arg Leu Lys Asp Tyr Gly Gln Glu Asp Val Phe Ser Leu
35 40 45
Trp Asp Glu Leu Ser Pro Glu Glu Arg Asp Leu Leu Leu Arg Asp Ile
50 55 60
Glu Asn Leu Asp Leu Pro Arg Ile Asp Arg Ile Ile Arg Cys Ser Leu
65 70 75 80
His Ser Gln Gly Leu Pro Val Ala Ala Ile Glu Pro Val Pro Glu Asn
85 90 95
Cys Val Ser Thr Val Glu Glu Arg Thr Lys Glu Asp Arg Glu Lys Trp
100 105 110
Trp Lys Met Gly Leu Lys Ala Ile Tyr Glu Gly Lys Leu Gly Val Val
115 120 125
Leu Leu Ser Gly Gly Gln Gly Thr Arg Leu Gly Ser Ser Asp Pro Lys
130 135 140
Gly Cys Tyr Asn Ile Gly Leu Pro Ser Gly Lys Ser Leu Phe Gln Ile
145 150 155 160
Gln Ala Glu Arg Ile Leu Cys Val Gln Arg Leu Ala Ser Gln Ala Met
165 170 175
Ser Glu Ala Ser Pro Thr Arg Pro Val Thr Ile Gln Trp Tyr Ile Met
180 185 190
Thr Ser Pro Phe Thr His Glu Pro Thr Gln Lys Phe Phe Glu Ser His
195 200 205
Lys Tyr Phe Gly Leu Glu Pro Asp Gln Val Thr Phe Phe Ser Thr Arg
210 215 220
Ser Ser Ala Leu His Phe Lys Gly Trp Gln Val Tyr His Gly Asp Thr
225 230 235 240
Phe Gln Pro Ile Gln Gly Ala Gly Trp Glu Arg Gly Ser Leu Tyr Ser
245 250 255
Phe Lys Ile Phe Lys Val Ile Arg Arg Tyr Gly Phe Glu Gly Asp
260 265 270

(2) INFORMATION FOR SEQ ID NO:1067:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 157 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..157

(D) OTHER INFORMATION: / Ceres Seq. ID 1568889

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1067:

Met Gly Leu Lys Ala Ile Tyr Glu Gly Lys Leu Gly Val Val Leu Leu
1 5 10 15
Ser Gly Gly Gln Gly Thr Arg Leu Gly Ser Ser Asp Pro Lys Gly Cys
20 25 30
Tyr Asn Ile Gly Leu Pro Ser Gly Lys Ser Leu Phe Gln Ile Gln Ala
35 40 45
Glu Arg Ile Leu Cys Val Gln Arg Leu Ala Ser Gln Ala Met Ser Glu
50 55 60
Ala Ser Pro Thr Arg Pro Val Thr Ile Gln Trp Tyr Ile Met Thr Ser
65 70 75 80
Pro Phe Thr His Glu Pro Thr Gln Lys Phe Phe Glu Ser His Lys Tyr
85 90 95

Phe Gly Leu Glu Pro Asp Gln Val Thr Phe Phe Ser Thr Arg Ser Ser
100 105 110
Ala Leu His Phe Lys Gly Trp Gln Val Tyr His Gly Asp Thr Phe Gln
115 120 125
Pro Ile Gln Gly Ala Gly Trp Glu Arg Gly Ser Leu Tyr Ser Phe Lys
130 135 140
Ile Phe Lys Val Ile Arg Arg Tyr Gly Phe Glu Gly Asp
145 150 155

(2) INFORMATION FOR SEQ ID NO:1068:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 193 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..193

(D) OTHER INFORMATION: / Ceres Seq. ID 1568890

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1068:

Met Asn Gln His Lys Asn Ser Ser Arg Val Thr Ser Ile Leu Ala Leu
1 5 10 15
Asn Gln Ile Lys Ser Pro Phe Phe Gln Gln Gly Ala Leu Pro Cys Ile
20 25 30
Ser Lys Asp Gly Lys Phe Ile Met Glu Thr Pro Phe Ser Leu Ser Lys
35 40 45
Ala Pro Asp Gly Asn Gly Gly Val Tyr Thr Ala Leu Lys Ser Ser Arg
50 55 60
Leu Leu Glu Asp Met Ala Ser Arg Gly Ile Lys Tyr Val Asp Cys Tyr
65 70 75 80
Gly Val Asp Asn Val Leu Val Arg Val Ala Asp Pro Thr Phe Leu Gly
85 90 95
Tyr Phe Ile Asp Lys Ser Ala Ala Ser Ala Ala Lys Val Val Arg Lys
100 105 110
Ala Tyr Pro Gln Glu Lys Val Gly Val Phe Val Arg Arg Gly Lys Gly
115 120 125
Gly Pro Leu Thr Val Val Glu Tyr Thr Glu Leu Asp Gln Ser Met Ala
130 135 140
Ser Ala Thr Asn Gln Gln Thr Gly Arg Leu Gln Tyr Cys Trp Ser Asn
145 150 155 160
Val Cys Leu His Met Phe Thr Leu Asp Phe Leu Asn Gln Val Ala Asn
165 170 175
Gly Leu Lys Lys Thr Ala Phe Thr Ile Trp Arg Arg Arg Arg Tyr Arg
180 185 190
Leu

(2) INFORMATION FOR SEQ ID NO:1069:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1575 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1575

(D) OTHER INFORMATION: / Ceres Seq. ID 1568891

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1069:

aaagagcaaa actatctaat tccatggcgt tctccctct cttccaatt cctcaacctg	60
cctctctttt ttctactctc tccgcattta ccgtttctaa taatgcttcc tctctctctc	120
tctcccgctet ttactcttta tatcacccca aaggaaacctt acgaaccaga accgcgacct	180

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cgtttttcgg agcttctggg aacttgagga ttgtttccat ggcggagaat aggcaattgg 240
ttttaggatt tgggtggcga gcCggCtgcg gaattggatg atattggatga aggtgaaatc 300
cagaggaattg gaaatgaaga cgaagacgac gatgaattca tacaagtcca tgcataaatac 360
tcctctgctg cttcgctcga gagatgggat gttttgggtc tcggccaagc catggtagat 420
ttctctggag ttgtggatga tgagtttcta aagaaacttg gtttataaaa gggaaacaagg 480
aaactgatta atcacgagga gaggggtaaa ttattacaag caatggatgg ttgtagctat 540
aaRgcgcagc ctggaggctc attgtccaaac actttagttg ccttcgcaag attaggtttc 600
caatccatct gtgaccggcc ttgtaattgt gcaatggcgt gcagtattgg aggtgacctc 660
ctcggtagct tttacgggac taaactacga cgagcaaatg taaattttct tctctgtcca 720
atcaaggacg gaacaacagg aacagtgata gttctcacaa ctccgtgatg acaacgtact 780
atgcttgcat atcagggaac atcctctgtc gtttaattat attctgtttt ggctagtttg 840
tagtccaaga caaatgtctt ttgttggtaa ggctatttgt ttgagcttcc tgatactata 900
agaaccataa caaaagcctg cgaagaagcc cacagaaacg gggcacttgt tgctgtgaca 960
gcatcagatg tgtcctgcat agagaggcat tatgatgatt tctgggacat tgtggggaac 1020
tatgcggata ttgtatttgc aatatagcga gaagcaagag cgttttgtca cttttccgca 1080
gaggaagctc caatttcacg gacaagatac atgagccact ttgttccgtt tgtttctgtt 1140
accgtaggaa tcaacgggtc atatatggga gtaaaaggag agggccatcta cattctccg 1200
tccccatgcg tgccagttga tacatgttgt gctggagatg catatgtctc agggatctta 1260
tacggtagct tgagggggtg ctctgacttg aaaggaaatg gagatattgc tgcaacgatt 1320
cgagcaactg tgggtgggtca acaaggaacc aggccttaggg ttcaggagcg gggtgagctt 1380
gctcgtcac atgccttcg tctcaatggt tctggtgttc gaacagatgt tgggtcttga 1440
tgaaacctct ttagcttggt atttttagct ttttgattca ttcctttgct tcatgtagta 1500
gtgcctttt caattgact gtaacttgt atgtaacatt ttagtatata gatatgttt 1560
cgcgaaagt ttgag

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(2) INFORMATION FOR SEQ ID NO:1070:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 385 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..385

(D) OTHER INFORMATION: / Ceres Seq. ID 1568892

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1070:

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Met Asp Glu Gly Ile Gln Arg Ile Gly Asn Glu Asp Glu Asp Asp
1 5 10 15
Asp Glu Phe Ile Gln Val His Ala Asn Asn Ser Ser Ala Ala Ser Pro
20 25 30
Glu Arg Trp Asp Val Leu Gly Leu Gly Gln Ala Met Val Asp Phe Ser
35 40 45
Gly Val Val Asp Asp Glu Phe Leu Lys Lys Leu Gly Leu Lys Gly
50 55 60
Thr Arg Lys Leu Ile Asn His Glu Glu Arg Gly Lys Leu Leu Gln Ala
65 70 75 80
Met Asp Gly Cys Ser Tyr Xaa Ala Ala Ala Gly Gly Ser Leu Ser Asn
85 90 95
Thr Leu Val Ala Leu Ala Arg Leu Gly Ser Gln Ser Ile Cys Asp Arg
100 105 110
Pro Leu Asn Val Ala Met Ala Gly Ser Ile Gly Gly Asp Pro Leu Gly
115 120 125
Ser Phe Tyr Gly Thr Lys Leu Arg Arg Ala Asn Val Asn Phe Leu Ser
130 135 140
Ala Pro Ile Lys Asp Gly Thr Thr Gly Thr Val Ile Val Leu Thr Thr
145 150 155 160
Pro Asp Ala Gln Arg Thr Met Leu Ala Tyr Gln Gly Thr Ser Ser Val
165 170 175
Val Asn Tyr Asp Ser Cys Leu Ala Ser Leu Ile Ala Lys Thr Asn Val
180 185 190
Phe Val Val Glu Gly Tyr Leu Phe Glu Leu Pro Asp Thr Ile Arg Thr

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195	200	205
Ile Thr Lys Ala Cys Glu Glu Ala His Arg Asn Gly Ala Leu Val Ala		
210	215	220
Val Thr Ala Ser Asp Val Ser Cys Ile Glu Arg His Tyr Asp Asp Phe		
225	230	235
Trp Asp Ile Val Gly Asn Tyr Ala Asp Ile Val Phe Ala Asn Ser Asp		
245	250	255
Glu Ala Arg Ala Phe Cys His Phe Ser Ala Glu Glu Ser Pro Ile Ser		
260	265	270
Ala Thr Arg Tyr Met Ser His Phe Val Pro Phe Val Ser Val Thr Asp		
275	280	285
Gly Ile Asn Gly Ser Tyr Ile Gly Val Lys Gly Glu Ala Ile Tyr Ile		
290	295	300
Pro Pro Ser Pro Cys Val Pro Val Asp Thr Cys Gly Ala Gly Asp Ala		
305	310	315
Tyr Ala Ser Gly Ile Leu Tyr Gly Ile Leu Arg Gly Val Ser Asp Leu		
325	330	335
Lys Gly Met Gly Asp Met Ala Ala Thr Ile Ala Ala Thr Val Val Gly		
340	345	350
Gln Gln Gly Thr Arg Leu Arg Val Gln Asp Ala Val Glu Leu Ala Arg		
355	360	365
Ser His Ala Phe Arg Leu Asn Gly Ser Gly Val Arg Thr Asp Val Gly		
370	375	380

Ser
385

(2) INFORMATION FOR SEQ ID NO:1071:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 342 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..342

(D) OTHER INFORMATION: / Ceres Seq. ID 1568893

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1071:

Met Val Asp Phe Ser Gly Val Val Asp Asp Glu Phe Leu Lys Lys Leu	
1	15
Gly Leu Lys Lys Gly Thr Arg Lys Leu Ile Asn His Glu Glu Arg Gly	
20	30
Lys Leu Leu Gln Ala Met Asp Gly Cys Ser Tyr Xaa Ala Ala Ala Gly	
35	45
Gly Ser Leu Ser Asn Thr Leu Val Ala Leu Ala Arg Leu Gly Ser Gln	
50	60
Ser Ile Cys Asp Arg Pro Leu Asn Val Ala Met Ala Gly Ser Ile Gly	
65	75
Gly Asp Pro Leu Gly Ser Phe Tyr Gly Thr Lys Leu Arg Arg Ala Asn	
85	95
Val Asn Phe Leu Ser Ala Pro Ile Lys Asp Gly Thr Thr Gly Thr Val	
100	110
Ile Val Leu Thr Thr Pro Asp Ala Gln Arg Thr Met Leu Ala Tyr Gln	
115	125
Gly Thr Ser Ser Val Val Asn Tyr Asp Ser Cys Leu Ala Ser Leu Ile	
130	140
Ala Lys Thr Asn Val Phe Val Val Glu Gly Tyr Leu Phe Glu Leu Pro	
145	155
Asp Thr Ile Arg Thr Ile Thr Lys Ala Cys Glu Glu Ala His Arg Asn	
165	175
Gly Ala Leu Val Ala Val Thr Ala Ser Asp Val Ser Cys Ile Glu Arg	
180	190

His Tyr Asp Asp Phe Trp Asp Ile Val Gly Asn Tyr Ala Asp Ile Val
195 200 205
Phe Ala Asn Ser Asp Glu Ala Arg Ala Phe Cys His Phe Ser Ala Glu
210 215 220
Glu Ser Pro Ile Ser Ala Thr Arg Tyr Met Ser His Phe Val Pro Phe
225 230 235 240
Val Ser Val Thr Asp Gly Ile Asn Gly Ser Tyr Ile Gly Val Lys Gly
245 250 255
Glu Ala Ile Tyr Ile Pro Pro Ser Pro Cys Val Pro Val Asp Thr Cys
260 265 270
Gly Ala Gly Asp Ala Tyr Ala Ser Gly Ile Leu Tyr Gly Ile Leu Arg
275 280 285
Gly Val Ser Asp Leu Lys Gly Met Gly Asp Met Ala Ala Thr Ile Ala
290 295 300
Ala Thr Val Val Gly Gln Gln Gly Thr Arg Leu Arg Val Gln Asp Ala
305 310 315 320
Val Glu Leu Ala Arg Ser His Ala Phe Arg Leu Asn Gly Ser Gly Val
325 330 335
Arg Thr Asp Val Gly Ser
340

(2) INFORMATION FOR SEQ ID NO:1072:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 305 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..305

(D) OTHER INFORMATION: / Ceres Seq. ID 1568894

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1072:

Met Asp Gly Cys Ser Tyr Xaa Ala Ala Ala Gly Gly Ser Leu Ser Asn
1 5 10 15
Thr Leu Val Ala Leu Ala Arg Leu Gly Ser Gln Ser Ile Cys Asp Arg
20 25 30
Pro Leu Asn Val Ala Met Ala Gly Ser Ile Gly Gly Asp Pro Leu Gly
35 40 45
Ser Phe Tyr Gly Thr Lys Leu Arg Arg Ala Asn Val Asn Phe Leu Ser
50 55 60
Ala Pro Ile Lys Asp Gly Thr Thr Gly Thr Val Ile Val Leu Thr Thr
65 70 75 80
Pro Asp Ala Gln Arg Thr Met Leu Ala Tyr Gln Gly Thr Ser Ser Val
85 90 95
Val Asn Tyr Asp Ser Cys Leu Ala Ser Leu Ile Ala Lys Thr Asn Val
100 105 110
Phe Val Val Glu Gly Tyr Leu Phe Glu Leu Pro Asp Thr Ile Arg Thr
115 120 125
Ile Thr Lys Ala Cys Glu Glu Ala His Arg Asn Gly Ala Leu Val Ala
130 135 140
Val Thr Ala Ser Asp Val Ser Cys Ile Glu Arg His Tyr Asp Asp Phe
145 150 155 160
Trp Asp Ile Val Gly Asn Tyr Ala Asp Ile Val Phe Ala Asn Ser Asp
165 170 175
Glu Ala Arg Ala Phe Cys His Phe Ser Ala Glu Glu Ser Pro Ile Ser
180 185 190
Ala Thr Arg Tyr Met Ser His Phe Val Pro Phe Val Ser Val Thr Asp
195 200 205
Gly Ile Asn Gly Ser Tyr Ile Gly Val Lys Gly Glu Ala Ile Tyr Ile
210 215 220
Pro Pro Ser Pro Cys Val Pro Val Asp Thr Cys Gly Ala Gly Asp Ala

225	230	235	240
Tyr Ala Ser Gly Ile Leu Tyr Gly Ile Leu Arg Gly Val Ser Asp Leu			
	245	250	255
Lys Gly Met Gly Asp Met Ala Ala Thr Ile Ala Ala Thr Val Val Gly			
	260	265	270
Gln Gln Gly Thr Arg Leu Arg Val Gln Asp Ala Val Glu Leu Ala Arg			
	275	280	285
Ser His Ala Phe Arg Leu Asn Gly Ser Gly Val Arg Thr Asp Val Gly			
	290	295	300

Ser
305

(2) INFORMATION FOR SEQ ID NO:1073:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1374 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1374
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568895

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1073:

attatggtgta	atttctgctg	ccattgctgc	tcctctctcc	ggagatacaa	aggcgaaatct	60
gaccagtaag	aaagatggca	gtcgagatgg	ccctctcagtc	tcagggttttg	gtggaagaga	120
aatcgagtgt	tagaattcttg	acactaaaca	gaccaaaagca	gctgaatgct	ctgtcccttcc	180
acatgatctc	tcgattgctg	caactgttcc	ttgcatttga	ggaggaccct	agtgtgaaac	240
ttgtcatcct	aaagggtcat	gggagagcct	tttgtgctgg	tgccgatgtt	gcagctgttg	300
ttcgtgacat	caatcaaggt	aactggagac	tcggtgccaa	ttactttcca	ctgtaataca	360
tgctcaacta	tggtatggcc	acatatagca	aagctcaggt	ttcaatcttg	aatgggtatcg	420
tcattggagg	cggagctggt	gtatccgtcc	atggtcgatt	tcgtattgca	actgagaaca	480
cgggtttttg	catgcctcag	acagctctgg	ggctctttcc	agatgtaggc	gcctctact	540
tcctgtcaag	gctccctggg	ttttttgggg	agtatgttgg	cctcacacga	gctagattag	600
atgggtgctga	aatgcttgct	tggtggcctg	caactcattt	tgttcctcca	acgaggttga	660
ctgcattaga	agcagatctt	tgacagaatta	attcaaatga	ttcaactttt	gcctcaacaa	720
ttctcgatgc	atacaccacg	catccgcgcc	tgaacacagca	gagtgcttac	cgcaggttag	780
atgttattga	taggtgtttc	tcaaggagaa	cagtcgaaga	aattatatct	gcacttgaga	840
gagagggcac	tcaagaagca	gatggttgga	tctcagctac	cattcaagca	ttgaagaagg	900
gttcaccagc	aagccttaaa	atctctctta	gatcgataag	ggaaggggcg	gtgcagggggg	960
tggggacagt	tccttatccg	gagtatagaa	tggtgtgtca	tgatgatga	ggagaataca	1020
gcaaaagtatt	tggtggagggg	tcagagaccca	tattgttaga	caaaagataa	aaccacaaagt	1080
gggagccaa	gcgactggag	gacatgaagg	atagcatggt	ggagcagtag	ttcagagagag	1140
tggaacggga	ggatgatcta	aagcttccgc	caaggaaata	cttcgctgct	ttagggtatcg	1200
caaaagctgtg	aagtggagaa	ggtgatggag	cactattgtt	tacgtctgtg	ggaaagaaaa	1260
aagaaaaata	atgtaaacac	actgtgtgtg	aataggactt	gcatacata	cataaatcat	1320
tattgtattt	gagaattgac	accaaagcag	cagagcagaa	tttgtttaag	attc	

(2) INFORMATION FOR SEQ ID NO:1074:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 378 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..378
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568896

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1074:

Met Ala Val Glu Met Ala Ser Gln Ser Gln Val Leu Val Glu Glu Lys			
1	5	10	15
Ser Ser Val Arg Ile Leu Thr Leu Asn Arg Pro Lys Gln Leu Asn Ala			

	20		25		30
Leu Ser Phe His Met Ile Ser Arg Leu Leu Gln Leu Phe Leu Ala Phe	35		40		45
Glu Glu Asp Pro Ser Val Lys Leu Val Ile Leu Lys Gly His Gly Arg	50		55		60
Ala Phe Cys Ala Gly Gly Asp Val Ala Ala Val Val Arg Asp Ile Asn	65		70		75
Gln Gly Asn Trp Arg Leu Gly Ala Asn Tyr Phe Ser Ser Glu Tyr Met	85		90		95
Leu Asn Tyr Val Met Ala Thr Tyr Ser Lys Ala Gln Val Ser Ile Leu	100		105		110
Asn Gly Ile Val Met Gly Gly Gly Ala Gly Val Ser Val His Gly Arg	115		120		125
Phe Arg Ile Ala Thr Glu Asn Thr Val Phe Ala Met Pro Glu Thr Ala	130		135		140
Leu Gly Leu Phe Pro Asp Val Gly Ala Ser Tyr Phe Leu Ser Arg Leu	145		150		155
Pro Gly Phe Phe Gly Glu Tyr Val Gly Leu Thr Arg Ala Arg Leu Asp	165		170		175
Gly Ala Glu Met Leu Ala Cys Gly Leu Ala Thr His Phe Val Pro Ser	180		185		190
Thr Arg Leu Thr Ala Leu Glu Ala Asp Leu Cys Arg Ile Asn Ser Asn	195		200		205
Asp Pro Thr Phe Ala Ser Thr Ile Leu Asp Ala Tyr Thr Gln His Pro	210		215		220
Arg Leu Lys Gln Gln Ser Ala Tyr Arg Arg Leu Asp Val Ile Asp Arg	225		230		235
Cys Phe Ser Arg Arg Thr Val Glu Glu Ile Ile Ser Ala Leu Glu Arg	245		250		255
Glu Ala Thr Gln Glu Ala Asp Gly Trp Ile Ser Ala Thr Ile Gln Ala	260		265		270
Leu Lys Lys Gly Ser Pro Ala Ser Leu Lys Ile Ser Leu Arg Ser Ile	275		280		285
Arg Glu Gly Arg Leu Gln Gly Val Gly Gln Cys Leu Ile Arg Glu Tyr	290		295		300
Arg Met Val Cys His Val Met Lys Gly Glu Ile Ser Lys Asp Phe Val	305		310		315
Glu Gly Cys Arg Ala Ile Leu Val Asp Lys Asp Lys Asn Pro Lys Trp	325		330		335
Glu Pro Arg Arg Leu Glu Asp Met Lys Asp Ser Met Val Glu Gln Tyr	340		345		350
Phe Glu Arg Val Glu Arg Glu Asp Asp Leu Lys Leu Pro Pro Arg Asn	355		360		365
Asn Leu Pro Ala Leu Gly Ile Ala Lys Leu	370		375		

(2) INFORMATION FOR SEQ ID NO:1075:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 374 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..374
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568897

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1075:

Met Ala Ser Gln Ser Gln Val Leu Val Glu Glu Lys Ser Ser Val Arg		
1	5	10
Ile Leu Thr Leu Asn Arg Pro Lys Gln Leu Asn Ala Leu Ser Phe His		
20	25	30

```

Met Ile Ser Arg Leu Leu Gln Leu Phe Leu Ala Phe Glu Glu Asp Pro
    35          40          45
Ser Val Lys Leu Val Ile Leu Lys Gly His Gly Arg Ala Phe Cys Ala
    50          55          60
Gly Gly Asp Val Ala Ala Val Val Arg Asp Ile Asn Gln Gly Asn Trp
    65          70          75          80
Arg Leu Gly Ala Asn Tyr Phe Ser Ser Glu Tyr Met Leu Asn Tyr Val
    85          90          95
Met Ala Thr Tyr Ser Lys Ala Gln Val Ser Ile Leu Asn Gly Ile Val
    100          105          110
Met Gly Gly Gly Ala Gly Val Ser Val His Gly Arg Phe Arg Ile Ala
    115          120          125
Thr Glu Asn Thr Val Phe Ala Met Pro Glu Thr Ala Leu Gly Leu Phe
    130          135          140
Pro Asp Val Gly Ala Ser Tyr Phe Leu Ser Arg Leu Pro Gly Phe Phe
    145          150          155          160
Gly Glu Tyr Val Gly Leu Thr Arg Ala Arg Leu Asp Gly Ala Glu Met
    165          170          175
Leu Ala Cys Gly Leu Ala Thr His Phe Val Pro Ser Thr Arg Leu Thr
    180          185          190
Ala Leu Glu Ala Asp Leu Cys Arg Ile Asn Ser Asn Asp Pro Thr Phe
    195          200          205
Ala Ser Thr Ile Leu Asp Ala Tyr Thr Gln His Pro Arg Leu Lys Gln
    210          215          220
Gln Ser Ala Tyr Arg Arg Leu Asp Val Ile Asp Arg Cys Phe Ser Arg
    225          230          235          240
Arg Thr Val Glu Glu Ile Ile Ser Ala Leu Glu Arg Glu Ala Thr Gln
    245          250          255
Glu Ala Asp Gly Trp Ile Ser Ala Thr Ile Gln Ala Leu Lys Lys Gly
    260          265          270
Ser Pro Ala Ser Leu Lys Ile Ser Leu Arg Ser Ile Arg Glu Gly Arg
    275          280          285
Leu Gln Gly Val Gly Gln Cys Leu Ile Arg Glu Tyr Arg Met Val Cys
    290          295          300
His Val Met Lys Gly Glu Ile Ser Lys Asp Phe Val Glu Gly Cys Arg
    305          310          315          320
Ala Ile Leu Val Asp Lys Asp Lys Asn Pro Lys Trp Glu Pro Arg Arg
    325          330          335
Leu Glu Asp Met Lys Asp Ser Met Val Glu Gln Tyr Phe Glu Arg Val
    340          345          350
Glu Arg Glu Asp Asp Leu Lys Leu Pro Pro Arg Asn Asn Leu Pro Ala
    355          360          365
Leu Gly Ile Ala Lys Leu
    370

```

(2) INFORMATION FOR SEQ ID NO:1076:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 342 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..342
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568898

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1076:

```

Met Ile Ser Arg Leu Leu Gln Leu Phe Leu Ala Phe Glu Glu Asp Pro
1          5          10          15
Ser Val Lys Leu Val Ile Leu Lys Gly His Gly Arg Ala Phe Cys Ala
    20          25          30
Gly Gly Asp Val Ala Ala Val Val Arg Asp Ile Asn Gln Gly Asn Trp

```


35	40	45	
Arg Leu Gly Ala Asn Tyr Phe Ser Ser Glu Tyr Met Leu Asn Tyr Val			
50	55	60	
Met Ala Thr Tyr Ser Lys Ala Gln Val Ser Ile Leu Asn Gly Ile Val			
65	70	75	80
Met Gly Gly Gly Ala Gly Val Ser Val His Gly Arg Phe Arg Ile Ala			
85	90	95	
Thr Glu Asn Thr Val Phe Ala Met Pro Glu Thr Ala Leu Gly Leu Phe			
100	105	110	
Pro Asp Val Gly Ala Ser Tyr Phe Leu Ser Arg Leu Pro Gly Phe Phe			
115	120	125	
Gly Glu Tyr Val Gly Leu Thr Arg Ala Arg Leu Asp Gly Ala Glu Met			
130	135	140	
Leu Ala Cys Gly Leu Ala Thr His Phe Val Pro Ser Thr Arg Leu Thr			
145	150	155	160
Ala Leu Glu Ala Asp Leu Cys Arg Ile Asn Ser Asn Asp Pro Thr Phe			
165	170	175	
Ala Ser Thr Ile Leu Asp Ala Tyr Thr Gln His Pro Arg Leu Lys Gln			
180	185	190	
Gln Ser Ala Tyr Arg Arg Leu Asp Val Ile Asp Arg Cys Phe Ser Arg			
195	200	205	
Arg Thr Val Glu Glu Ile Ile Ser Ala Leu Glu Arg Glu Ala Thr Gln			
210	215	220	
Glu Ala Asp Gly Trp Ile Ser Ala Thr Ile Gln Ala Leu Lys Lys Gly			
225	230	235	240
Ser Pro Ala Ser Leu Lys Ile Ser Leu Arg Ser Ile Arg Glu Gly Arg			
245	250	255	
Leu Gln Gly Val Gly Gln Cys Leu Ile Arg Glu Tyr Arg Met Val Cys			
260	265	270	
His Val Met Lys Gly Glu Ile Ser Lys Asp Phe Val Glu Gly Cys Arg			
275	280	285	
Ala Ile Leu Val Asp Lys Asp Lys Asn Pro Lys Trp Glu Pro Arg Arg			
290	295	300	
Leu Glu Asp Met Lys Asp Ser Met Val Glu Gln Tyr Phe Glu Arg Val			
305	310	315	320
Glu Arg Glu Asp Asp Leu Lys Leu Pro Pro Arg Asn Asn Leu Pro Ala			
325	330	335	
Leu Gly Ile Ala Lys Leu			
340			

(2) INFORMATION FOR SEQ ID NO:1077:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1180 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1180

(D) OTHER INFORMATION: / Ceres Seq. ID 1568902

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1077:

aatatagtac	caactccatt	gaatgttaaa	actcagaaga	aagtggagtg	atcatataac	60
gacaatgaag	aattctcttta	acttgttctt	tatgttkttc	tttgcaatgc	caattctttc	120
actctccgag	aatccaacca	atttcagcga	gagttgcgaa	gacgggagtg	gagaaaccgg	180
ttcaagcttt	ggcatagggt	tcgatttggt	tcttgatttt	ggtttatacc	ggaatagctg	240
ccccgaagca	gagtcctatcg	tctactcgtg	gggtggaacc	acggtgttag	aggatccaag	300
aatggctgct	tctcttctcc	gtcttcattt	ccacgactgt	tttgctcaatg	gatgtgatgc	360
ttcgggtgtg	ttagatgaca	cagaaggact	ggttgggtgaa	aaaacggcgc	ctcctaattc	420
aaattctcta	cgagggttcg	aagtgatgta	ttcgataaag	tctgatattg	aagtctgatg	480
tcacagagacc	gtctcatcgc	cagacattct	tgccatggct	gctagagatt	cagtcgtgtg	540
gtcgggtgga	ccaaggtggg	aggtggaagt	aggaagaaaa	gacagtagaa	cagcaagcaa	600

acaggcgacga acaaatggct tacccctcacc aaactcaacc gatatcaactc tcatctctac 660
tttccagaatt cttggccttt cacaaccgga catggctgcct cttccgggtgacacatatt 720
gggaaaggcga cggNgcAct cgttttacag ctgggttgca gccactgcaa actgggacaac 780
cagctaacca cggagacaac cttgagttcc tcgagtcact gcaacagtta tgctgcagct 840
ttggcccccag ttaggtatc actcagcttg acttggtgac tccatcaaca ttggacaacc 900
agtactatgt aaacctcctc tcgggtgagg gattgcttcc atcagaccag gcttttagcgg 960
ttcaagaccc agggacaagg gcgattgttg agacctacgc aacagatcag tcgggttttt 1020
ttgaggattt taagaacgct atggttaaaa tgggagggat atccggtggt agtaaatagcg 1080
agattaggaa gaattgtaga atgattaaat aaaaataaaa gcccgactta ttgaatgata 1140
tctaattatc tatataaaaa ttaagaagt ccacctacgt

(2) INFORMATION FOR SEQ ID NO:1078:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 254 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..254

(D) OTHER INFORMATION: / Ceres Seq. ID 1568903

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1078:

Met	Leu	Lys	Leu	Arg	Arg	Lys	Trp	Ser	Asp	His	Ile	Thr	Thr	Met	Lys
1			5						10					15	
Asn	Leu	Phe	Asn	Leu	Phe	Leu	Met	Xaa	Phe	Phe	Ala	Met	Pro	Ile	Leu
			20					25					30		
Ser	Leu	Ser	Glu	Asn	Pro	Thr	Asn	Phe	Ser	Glu	Ser	Cys	Glu	Asp	Gly
		35					40					45			
Ser	Gly	Glu	Thr	Gly	Ser	Ser	Phe	Gly	Ile	Gly	Phe	Asp	Leu	Val	Leu
		50				55				60					
Asp	Phe	Gly	Leu	Tyr	Arg	Asn	Ser	Cys	Pro	Glu	Ala	Glu	Ser	Ile	Val
65					70				75					80	
Tyr	Ser	Trp	Val	Glu	Thr	Thr	Val	Leu	Glu	Asp	Pro	Arg	Met	Ala	Ala
			85						90				95		
Ser	Leu	Leu	Arg	Leu	His	Phe	His	Asp	Cys	Phe	Val	Asn	Gly	Cys	Asp
			100					105					110		
Ala	Ser	Val	Leu	Leu	Asp	Asp	Thr	Glu	Gly	Leu	Val	Gly	Glu	Lys	Thr
			115				120					125			
Ala	Pro	Pro	Asn	Leu	Asn	Ser	Leu	Arg	Gly	Phe	Glu	Val	Ile	Asp	Ser
			130			135					140				
Ile	Lys	Ser	Asp	Ile	Glu	Ser	Val	Cys	Pro	Glu	Thr	Val	Ser	Cys	Ala
145				150					155					160	
Asp	Ile	Leu	Ala	Met	Ala	Ala	Arg	Asp	Ser	Val	Val	Val	Ser	Gly	Gly
			165					170					175		
Pro	Arg	Trp	Glu	Val	Glu	Val	Gly	Arg	Lys	Asp	Ser	Arg	Thr	Ala	Ser
			180				185						190		
Lys	Gln	Ala	Ala	Thr	Asn	Gly	Leu	Pro	Ser	Pro	Asn	Ser	Thr	Val	Ser
			195				200					205			
Thr	Leu	Ile	Ser	Thr	Phe	Gln	Asn	Leu	Gly	Leu	Ser	Gln	Thr	Asp	Met
			210			215					220				
Val	Ala	Leu	Ser	Gly	Gly	His	Thr	Leu	Gly	Lys	Ala	Arg	Xaa	His	Phe
225				230					235					240	
Val	Tyr	Ser	Ser	Val	Ala	Ala	Thr	Ala	Asn	Trp	Thr	Thr	Ser		
			245						250						

(2) INFORMATION FOR SEQ ID NO:1079:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 240 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..240

(D) OTHER INFORMATION: / Ceres Seq. ID 1568904

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1079:

```
Met Lys Asn Leu Phe Asn Leu Phe Leu Met Xaa Phe Phe Ala Met Pro
1      5      10      15
Ile Leu Ser Leu Ser Glu Asn Pro Thr Asn Phe Ser Glu Ser Cys Glu
20      25      30
Asp Gly Ser Gly Glu Thr Gly Ser Ser Phe Gly Ile Gly Phe Asp Leu
35      40      45
Val Leu Asp Phe Gly Leu Tyr Arg Asn Ser Cys Pro Glu Ala Glu Ser
50      55      60
Ile Val Tyr Ser Trp Val Glu Thr Thr Val Leu Glu Asp Pro Arg Met
65      70      75
Ala Ala Ser Leu Leu Arg Leu His Phe His Asp Cys Phe Val Asn Gly
85      90      95
Cys Asp Ala Ser Val Leu Leu Asp Asp Thr Glu Gly Leu Val Asn Gly
100     105     110
Lys Thr Ala Pro Pro Asn Leu Asn Ser Leu Arg Gly Phe Glu Val Ile
115     120     125
Asp Ser Ile Lys Ser Asp Ile Glu Ser Val Cys Pro Glu Thr Val Ser
130     135     140
Cys Ala Asp Ile Leu Ala Met Ala Ala Arg Asp Ser Val Val Val Ser
145     150     155
Gly Gly Pro Arg Trp Glu Val Glu Val Gly Arg Lys Asp Ser Arg Thr
165     170     175
Ala Ser Lys Gln Ala Ala Thr Asn Gly Leu Pro Ser Pro Asn Ser Thr
180     185     190
Val Ser Thr Leu Ile Ser Thr Phe Gln Asn Leu Gly Leu Ser Gln Thr
195     200     205
Asp Met Val Ala Leu Ser Gly Gly His Thr Leu Gly Lys Ala Arg Xaa
210     215     220
His Phe Val Tyr Ser Ser Val Ala Ala Thr Ala Asn Trp Thr Thr Ser
225     230     235     240
```

(2) INFORMATION FOR SEQ ID NO:1080:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 231 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..231

(D) OTHER INFORMATION: / Ceres Seq. ID 1568905

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1080:

```
Met Xaa Phe Phe Ala Met Pro Ile Leu Ser Leu Ser Glu Asn Pro Thr
1      5      10      15
Asn Phe Ser Glu Ser Cys Glu Asp Gly Ser Gly Glu Thr Gly Ser Ser
20      25      30
Phe Gly Ile Gly Phe Asp Leu Val Leu Asp Phe Gly Leu Tyr Arg Asn
35      40      45
Ser Cys Pro Glu Ala Glu Ser Ile Val Tyr Ser Trp Val Glu Thr Thr
50      55      60
Val Leu Glu Asp Pro Arg Met Ala Ala Ser Leu Leu Arg Leu His Phe
65      70      75      80
His Asp Cys Phe Val Asn Gly Cys Asp Ala Ser Val Leu Leu Asp Asp
85      90      95
```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1082:

```

Met Gly Asn Leu Phe Cys Cys Val Gln Val Asp Gln Ser Thr Val Ala
1      5      10      15
Ile Lys Glu Thr Phe Gly Lys Phe Glu Asp Val Leu Glu Pro Gly Cys
20      25      30
His Phe Leu Pro Trp Cys Leu Gly Ser Gln Val Ala Gly Tyr Leu Ser
35      40      45
Leu Arg Val Gln Gln Leu Asp Val Arg Cys Glu Thr Lys Thr Lys Asp
50      55      60
Asn Val Phe Val Asn Val Val Ala Ser Ile Gln Tyr Arg Ala Leu Ala
65      70      75      80
Asn Lys Ala Asn Asp Ala Tyr Tyr Lys Leu Ser Asn Thr Arg Gly Gln
85      90      95
Ile Gln Ala Tyr Val Phe Asp Val Ile Arg Ala Ser Val Pro Lys Leu
100      105      110
Leu Leu Asp Asp Val Phe Glu Gln Lys Asn Asp Ile Ala Lys Ala Val
115      120      125
Glu Glu Glu Leu Glu Lys Ala Met Ser Ala Tyr Gly Tyr Glu Ile Val
130      135      140
Gln Thr Leu Ile Val Asp Ile Glu Pro Asp Glu His Val Lys Arg Ala
145      150      155      160
Met Asn Glu Ile Asn Ala Ala Ala Arg Met Arg Leu Ala Ala Asn Glu
165      170      175
Lys Ala Glu Ala Glu Lys Ile Leu Gln Ile Lys Arg Ala Glu Gly Glu
180      185      190
Ala Glu Ser Lys Tyr Leu Ser Gly Leu Gly Ile Ala Arg Gln Arg Gln
195      200      205
Ala Ile Val Asp Gly Leu Arg Asp Ser Val Leu Gly Phe Ala Val Asn
210      215      220
Val Pro Gly Thr Thr Ala Lys Asp Val Met Asp Met Val Leu Val Thr
225      230      235      240
Gln Tyr Phe Asp Thr Met Lys Glu Ile Gly Ala Ser Ser Lys Ser Ser
245      250      255
Ala Val Phe Ile Pro His Gly Pro Gly Ala Val Arg Asp Val Ala Ser
260      265      270
Gln Ile Arg Asp Gly Leu Leu Gln Gly Ser Ser Ala Asn Leu
275      280      285

```

(2) INFORMATION FOR SEQ ID NO:1083:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 151 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..151
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568908

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1083:

```

Met Ser Ala Tyr Gly Tyr Glu Ile Val Gln Thr Leu Ile Val Asp Ile
1      5      10      15
Glu Pro Asp Glu His Val Lys Arg Ala Met Asn Glu Ile Asn Ala Ala
20      25      30
Ala Arg Met Arg Leu Ala Ala Asn Glu Lys Ala Glu Ala Glu Lys Ile
35      40      45
Leu Gln Ile Lys Arg Ala Glu Gly Glu Ala Glu Ser Lys Tyr Leu Ser
50      55      60
Gly Leu Gly Ile Ala Arg Gln Arg Gln Ala Ile Val Asp Gly Leu Arg
65      70      75      80
Asp Ser Val Leu Gly Phe Ala Val Asn Val Pro Gly Thr Thr Ala Lys
85      90      95
Asp Val Met Asp Met Val Leu Val Thr Gln Tyr Phe Asp Thr Met Lys

```

100 105 110
Glu Ile Gly Ala Ser Ser Lys Ser Ser Ala Val Phe Ile Pro His Gly
115 120 125
Pro Gly Ala Val Arg Asp Val Ala Ser Gln Ile Arg Asp Gly Leu Leu
130 135 140
Gln Gly Ser Ser Ala Asn Leu
145 150

(2) INFORMATION FOR SEQ ID NO:1084:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1391 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1391
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568928

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1084:

```

gaaaaagaga ggcagcgatg aacagtatct tctccattga cgatttctcc gatcctttct 60
gggaaactcc tccgattcct ctcaatccctg acttctctaa gccgtgttacg gcggtatgaag 120
ttagccagag tcacaccggaa tggactttcg agatgtttct cgaagagatt tcttcgtcgg 180
cggtgagctc tgagccactt ggtaacaaca acaacgcgat cgtcggtgtt tcttcggcgc 240
aatctcttcc tctgttttcc ggacagaatg atttcgagga tgaatagcga ttctgtgatc 300
gcgattcggg aaatttggat tgtgctgctc ccatgacgac gaagacgggtg attgttgatt 360
ccgatgatta tcgttcgtgtt ttaagaaca agcttgagac tgagtgcgct aotgttggtt 420
ctcttcgggt tgggtctgtg aagcctgaag attcgactag ttctccagaa actcaacttc 480
aaccagttca atocagtcct ctactcaag gagaacttgg tttacttct tcttaccag 540
ctgaggtGaa aaaaactgggt gtatcaatga agcaggttac tagtgatcg tcgagagaat 600
attctgata cgaggacctt gatgaagaga atgaaccac cggttccttg aagccagagg 660
acgttaaaaa acttagaagg atgctgtcaa atcgtgagto agctaggcga tctagaagga 720
gaaagcagga gcaaacaaagt gacctcgaaa cacagggttaa tgatctaaaa ggtgagcatt 780
catcacttct taacaacactg agcaacatga atcacaagta tgacgaggct gctgttgcca 840
atagaatact aaaggctgac attgagacat taagagctaa ggtgaaaatg gcggaagaaa 900
ccgtgaagag agtaacagga atgaatccga tgcttctcgg aagatcaagt ggacataaag 960
acaacaacag aatgccaaata actggttaaca acaggatgga tctctctagc attattccag 1020
cttatcaacc acactcaaac ctaaacacaca tgtcaaacca aaacatcggg attaccaaca 1080
ttctacttcc aagactcgga aacaatttcc ctgctctccc atcccaaac agctctctcc 1140
tgcaagaaat tagaataagg caaaatcacc atgtttactcc aagcgccaac ccgatggct 1200
ggcaatccga actcagaac gattcagcat ggccgaaaaa atgcgtggac tgatcaaaaa 1260
agaagcgggt ttgcactat attaatgtct atgcactctg aatttgaag ttattataag 1320
ttacgaatca tgagaaaaaa tcttgtgaaa atacagttct atgcttata tatatataag 1380
ctctgtctta t

```

(2) INFORMATION FOR SEQ ID NO:1085:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 416 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..416
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568929

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1085:

```

Lys Arg Glu Arg Ala Met Asn Ser Ile Phe Ser Ile Asp Asp Phe Ser
1 5 10 15
Asp Pro Phe Trp Glu Thr Pro Pro Ile Pro Leu Asn Pro Asp Ser Ser
20 25 30
Lys Pro Val Thr Ala Asp Glu Val Ser Gln Ser Gln Pro Glu Trp Thr
35 40 45

```

Phe	Glu	Met	Phe	Leu	Glu	Glu	Ile	Ser	Ser	Ser	Ala	Val	Ser	Ser	Glu
50					55						60				
Pro	Leu	Gly	Asn	Asn	Asn	Asn	Ala	Ile	Val	Gly	Val	Ser	Ser	Ala	Gln
65					70					75				80	
Ser	Leu	Pro	Ser	Val	Ser	Gly	Gln	Asn	Asp	Phe	Glu	Asp	Asp	Ser	Arg
			85						90					95	
Phe	Arg	Asp	Arg	Asp	Ser	Gly	Asn	Leu	Asp	Cys	Ala	Ala	Pro	Met	Thr
			100					105					110		
Thr	Lys	Thr	Val	Ile	Val	Asp	Ser	Asp	Asp	Tyr	Arg	Arg	Val	Leu	Lys
			115					120					125		
Asn	Lys	Leu	Glu	Thr	Glu	Cys	Ala	Thr	Val	Val	Ser	Leu	Arg	Val	Gly
			130				135					140			
Ser	Val	Lys	Pro	Glu	Asp	Ser	Thr	Ser	Ser	Pro	Glu	Thr	Gln	Leu	Gln
			145				150				155				160
Pro	Val	Gln	Ser	Ser	Pro	Leu	Thr	Gln	Gly	Glu	Leu	Gly	Val	Thr	Ser
				165					170						175
Ser	Leu	Pro	Ala	Glu	Val	Lys	Lys	Thr	Gly	Val	Ser	Met	Lys	Gln	Val
			180					185					190		
Thr	Ser	Gly	Ser	Ser	Arg	Glu	Tyr	Ser	Asp	Asp	Glu	Asp	Leu	Asp	Glu
			195				200					205			
Glu	Asn	Glu	Thr	Thr	Gly	Ser	Leu	Lys	Pro	Glu	Asp	Val	Lys	Lys	Ser
			210				215				220				
Arg	Arg	Met	Leu	Ser	Asn	Arg	Glu	Ser	Ala	Arg	Arg	Ser	Arg	Arg	Arg
			225			230				235					240
Lys	Gln	Glu	Gln	Thr	Ser	Asp	Leu	Glu	Thr	Gln	Val	Asn	Asp	Leu	Lys
				245						250					255
Gly	Glu	His	Ser	Ser	Leu	Leu	Lys	Gln	Leu	Ser	Asn	Met	Asn	His	Lys
			260					265					270		
Tyr	Asp	Glu	Ala	Ala	Val	Gly	Asn	Arg	Ile	Leu	Lys	Ala	Asp	Ile	Glu
			275				280						285		
Thr	Leu	Arg	Ala	Lys	Val	Lys	Met	Ala	Glu	Glu	Thr	Val	Lys	Arg	Val
			290				295					300			
Thr	Gly	Met	Asn	Pro	Met	Leu	Leu	Gly	Arg	Ser	Ser	Gly	His	Asn	Asn
			305			310				315				320	
Asn	Asn	Arg	Met	Pro	Ile	Thr	Gly	Asn	Asn	Arg	Met	Asp	Ser	Ser	Ser
				325						330				335	
Ile	Ile	Pro	Ala	Tyr	Gln	Pro	His	Ser	Asn	Leu	Asn	His	Met	Ser	Asn
			340					345					350		
Gln	Asn	Ile	Gly	Ile	Pro	Thr	Ile	Leu	Pro	Pro	Arg	Leu	Gly	Asn	Asn
			355					360				365			
Phe	Ala	Ala	Pro	Pro	Ser	Gln	Thr	Ser	Ser	Pro	Leu	Gln	Arg	Ile	Arg
			370				375				380				
Asn	Gly	Gln	Asn	His	His	Val	Thr	Pro	Ser	Ala	Asn	Pro	Tyr	Gly	Trp
			385			390				395					400
Asn	Thr	Glu	Pro	Gln	Asn	Asp	Ser	Ala	Trp	Pro	Lys	Lys	Cys	Val	Asp
				405					410					415	

(2) INFORMATION FOR SEQ ID NO:1086:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 411 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..411

(D) OTHER INFORMATION: / Ceres Seq. ID 1568930

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1086:

Met Asn Ser Ile Phe Ser Ile Asp Asp Phe Ser Asp Pro Phe Trp Glu

1	5	10	15
Thr Pro Pro	Ile Pro Leu Asn Pro Asp	Ser Ser Lys Pro Val Thr Ala	
20	20	25	30
Asp Glu Val	Ser Gln Ser Gln Pro Glu	Trp Thr Phe Glu Met Phe Leu	
35	40	45	50
Glu Glu Ile	Ser Ser Ser Ala Val Ser Ser	Glu Pro Leu Gly Asn Asn	
50	55	60	65
Asn Asn Ala	Ile Val Gly Val Ser Ser	Ala Gln Ser Leu Pro Ser Val	
70	75	80	85
Ser Gly Gln	Asn Asp Phe Glu Asp Asp	Ser Arg Phe Arg Asp Arg Asp	
90	95	100	105
Ser Gly Asn	Leu Asp Cys Ala Ala Pro	Met Thr Thr Lys Thr Val Ile	
110	115	120	125
Val Asp Ser	Asp Asp Tyr Arg Arg Val	Leu Lys Asn Lys Leu Glu Thr	
130	135	140	145
Glu Cys Ala	Thr Val Val Ser Leu Arg	Val Gly Ser Val Lys Pro Glu	
150	155	160	165
Asp Ser Thr	Ser Ser Pro Glu Thr Gln	Leu Gln Pro Val Gln Ser Ser	
170	175	180	185
Pro Leu Thr	Gln Gly Glu Leu Gly Val Thr	Ser Ser Leu Pro Ala Glu	
190	195	200	205
Val Lys Lys	Thr Gly Val Ser Met Lys	Gln Val Thr Ser Gly Ser Ser	
210	215	220	225
Arg Glu Tyr	Ser Asp Asp Glu Asp Leu	Asp Glu Glu Asn Glu Thr Thr	
230	235	240	245
Gly Ser Leu	Lys Pro Glu Asp Val Lys	Lys Ser Arg Arg Met Leu Ser	
250	255	260	265
Asn Arg Glu	Ser Ala Arg Arg Ser Arg	Arg Lys Gln Glu Gln Thr	
270	275	280	285
Ser Asp Leu	Glu Thr Gln Val Asn Asp	Leu Lys Gly Glu His Ser Ser	
290	295	300	305
Leu Leu Lys	Gln Leu Ser Asn Met Asn	His Lys Tyr Asp Glu Ala Ala	
310	315	320	325
Val Gly Asn	Arg Ile Leu Lys Ala Asp	Ile Glu Thr Leu Arg Ala Lys	
330	335	340	345
Val Lys Met	Ala Glu Glu Thr Val	Lys Arg Val Thr Gly Met Asn Pro	
350	355	360	365
Met Leu Leu	Gly Arg Ser Ser Gly His	Asn Asn Asn Arg Met Pro	
370	375	380	385
Ile Thr Gly	Asn Asn Arg Met Asp Ser	Ser Ser Ile Ile Pro Ala Tyr	
390	395	400	405
Gln Pro His	Ser Asn Leu Asn His Met	Ser Asn Gln Asn Ile Gly Ile	
410	415	420	425
Pro Thr Ile	Leu Pro Pro Arg Leu Gly	Asn Asn Phe Ala Ala Pro Pro	
430	435	440	445
Ser Gln Thr	Ser Ser Pro Leu Gln Arg	Ile Arg Asn Gly Gln Asn His	
450	455	460	465
His Val Thr	Pro Ser Ala Asn Pro Tyr	Gly Trp Asn Thr Glu Pro Gln	
470	475	480	485
Asn Asp Ser	Ala Trp Pro Lys Lys Cys	Val Asp	
490	495	500	505

(2) INFORMATION FOR SEQ ID NO:1087:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 366 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..366

(D) OTHER INFORMATION: / Ceres Seq. ID 1568931

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1087:

Met	Phe	Leu	Glu	Glu	Ile	Ser	Ser	Ser	Ser	Ala	Val	Ser	Ser	Glu	Pro	Leu
1			5						10						15	
Gly	Asn	Asn	Asn	Asn	Ala	Ile	Val	Gly	Val	Ser	Ser	Ala	Gln	Ser	Leu	
			20				25						30			
Pro	Ser	Val	Ser	Gly	Gln	Asn	Asp	Phe	Glu	Asp	Asp	Ser	Arg	Phe	Arg	
		35				40						45				
Asp	Arg	Asp	Ser	Gly	Asn	Leu	Asp	Cys	Ala	Ala	Pro	Met	Thr	Thr	Lys	
	50				55						60					
Thr	Val	Ile	Val	Asp	Ser	Asp	Asp	Tyr	Arg	Arg	Val	Leu	Lys	Asn	Lys	
65				70				75						80		
Leu	Glu	Thr	Glu	Cys	Ala	Thr	Val	Val	Ser	Leu	Arg	Val	Gly	Ser	Val	
			85				90						95			
Lys	Pro	Glu	Asp	Ser	Thr	Ser	Ser	Pro	Glu	Thr	Gln	Leu	Gln	Pro	Val	
		100					105						110			
Gln	Ser	Ser	Pro	Leu	Thr	Gln	Gly	Glu	Leu	Gly	Val	Thr	Ser	Ser	Leu	
		115				120						125				
Pro	Ala	Glu	Val	Lys	Lys	Thr	Gly	Val	Ser	Met	Lys	Gln	Val	Thr	Ser	
	130					135					140					
Gly	Ser	Ser	Arg	Glu	Tyr	Ser	Asp	Asp	Glu	Asp	Leu	Asp	Glu	Glu	Asn	
145				150					155					160		
Glu	Thr	Thr	Gly	Ser	Leu	Lys	Pro	Glu	Asp	Val	Lys	Lys	Ser	Arg	Arg	
			165					170						175		
Met	Leu	Ser	Asn	Arg	Glu	Ser	Ala	Arg	Arg	Ser	Arg	Arg	Arg	Lys	Gln	
			180				185							190		
Glu	Gln	Thr	Ser	Asp	Leu	Glu	Thr	Gln	Val	Asn	Asp	Leu	Lys	Gly	Glu	
		195				200						205				
His	Ser	Ser	Leu	Leu	Lys	Gln	Leu	Ser	Asn	Met	Asn	His	Lys	Tyr	Asp	
	210					215					220					
Glu	Ala	Ala	Val	Gly	Asn	Arg	Ile	Leu	Lys	Ala	Asp	Ile	Glu	Thr	Leu	
225				230					235						240	
Arg	Ala	Lys	Val	Lys	Met	Ala	Glu	Glu	Thr	Val	Lys	Arg	Val	Thr	Gly	
			245					250						255		
Met	Asn	Pro	Met	Leu	Leu	Gly	Arg	Ser	Ser	Gly	His	Asn	Asn	Asn	Asn	
			260				265							270		
Arg	Met	Pro	Ile	Thr	Gly	Asn	Asn	Arg	Met	Asp	Ser	Ser	Ser	Ile	Ile	
		275					280					285				
Pro	Ala	Tyr	Gln	Pro	His	Ser	Asn	Leu	Asn	His	Met	Ser	Asn	Gln	Asn	
		290				295					300					
Ile	Gly	Ile	Pro	Thr	Ile	Leu	Pro	Pro	Arg	Leu	Gly	Asn	Asn	Phe	Ala	
305				310					315					320		
Ala	Pro	Pro	Ser	Gln	Thr	Ser	Ser	Pro	Leu	Gln	Arg	Ile	Arg	Asn	Gly	
			325					330						335		
Gln	Asn	His	His	Val	Thr	Pro	Ser	Ala	Asn	Pro	Tyr	Gly	Trp	Asn	Thr	
		340					345						350			
Glu	Pro	Gln	Asn	Asp	Ser	Ala	Trp	Pro	Lys	Lys	Cys	Val	Asp			
		355				360						365				

(2) INFORMATION FOR SEQ ID NO:1088:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1213 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1213

(D) OTHER INFORMATION: / Ceres Seq. ID 1568944

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1088:

gtctcctttc cagaacaatc taacgctttc tgaacatct tcttctcttt cttctctgaa

attatttttc	cagtgatcaa	tttcttctct	tctagatttt	tacaggaact	aattttctgc	120
tctgaggtat	cagatgagta	gccgatggaa	tcgtacgac	tacgttggtga	atttgctctg	180
agatattcgc	aagtgtgag	ttgaagatct	ctctacaag	tatggaccaa	ttgtggacat	240
tgatttgaag	attccaccga	gacctctctg	ttatgctctt	gtcagatttg	aagatcctcg	300
tgatgcagac	gatgcaattt	atggacgtga	tggttatgat	tttgatgggt	gtcgactctg	360
ggttgagatt	gcacatgggt	gtcgtagatt	ttcaccatca	gttgataggt	acagcagcag	420
ctacagtgcg	agccgtgcac	cttcaagacg	ctctgactat	cgcgtgcttg	tgaccggatt	480
accgctctct	gcttctgtgc	aggaccttaa	ggatcacatg	cgcaaaagctg	gagatgctct	540
cttctctgaa	gttttccctg	accgtaaaag	catgtctctg	gttgctggatt	atagcaacta	600
tgatgatgat	aagtacgcga	taaggaaact	tgatgccact	gaatttcgaa	atgctttctc	660
tgatgcttat	agtcgggtga	gggaatatga	gtcgaggagt	gtgagtcgaa	gccagcatga	720
ttctaagaag	tatagaagca	ggagtcggag	ccgtggtcca	agctgtagct	atagtagcaa	780
gagcaggagt	gtgtcacctg	ctagatccat	ttcccccggt	tcacggcccc	ttagtctgtc	840
tcgtctgccca	tacagctctc	ttctcaaggct	ccaatcaaga	tcaaaatcaa	gatCAACAYc	900
aGgatcaaga	tcgaattctc	cagtttcacc	gtgatattct	ggatgaaaaa	gaaaactggc	960
cactggctgt	accggaatct	ttctcaagctt	ctcaggtctc	actgctaata	gaatttgatt	1020
ccgatttggg	attattatac	tggtcttctt	gtatgggaag	accaatatgt	ctttctagatt	1080
ctagtgttga	acctggaatt	ggtctgttat	tggtctcatta	aaaagccgga	aactctgtct	1140
cggtgctata	ataaagtcca	ctcagcgttg	gtgtgggtgt	ggtgaggttt	ttccatacat	1200
atacatttac	att					

(2) INFORMATION FOR SEQ ID NO:1089:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 270 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..270
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568945

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1089:

Met	Ser	Ser	Arg	Trp	Asn	Arg	Thr	Ile	Tyr	Val	Gly	Asn	Leu	Pro	Gly
1			5						10					15	
Asp	Ile	Arg	Lys	Cys	Glu	Val	Glu	Asp	Leu	Phe	Tyr	Lys	Tyr	Gly	Pro
			20						25				30		
Ile	Val	Asp	Ile	Asp	Leu	Lys	Ile	Pro	Pro	Arg	Pro	Pro	Gly	Tyr	Ala
			35				40					45			
Phe	Val	Glu	Phe	Glu	Asp	Pro	Arg	Asp	Ala	Asp	Asp	Ala	Ile	Tyr	Gly
			50				55				60				
Arg	Asp	Gly	Tyr	Asp	Phe	Asp	Gly	Cys	Arg	Leu	Arg	Val	Glu	Ile	Ala
					70				75					80	
His	Gly	Gly	Arg	Arg	Phe	Ser	Pro	Ser	Val	Asp	Arg	Tyr	Ser	Ser	Ser
					85				90					95	
Tyr	Ser	Ala	Ser	Arg	Ala	Pro	Ser	Arg	Arg	Ser	Asp	Tyr	Arg	Val	Leu
					100				105					110	
Val	Thr	Gly	Leu	Pro	Pro	Ser	Ala	Ser	Trp	Gln	Asp	Leu	Lys	Asp	His
					115				120					125	
Met	Arg	Lys	Ala	Gly	Asp	Val	Cys	Phe	Ser	Glu	Val	Phe	Pro	Asp	Arg
						130			135			140			
Lys	Gly	Met	Ser	Gly	Val	Val	Asp	Tyr	Ser	Asn	Tyr	Asp	Asp	Met	Lys
						145				150				155	
Tyr	Ala	Ile	Arg	Lys	Leu	Asp	Ala	Thr	Glu	Phe	Arg	Asn	Ala	Phe	Ser
						165			170					175	
Ser	Ala	Tyr	Ile	Arg	Val	Arg	Glu	Tyr	Glu	Ser	Arg	Ser	Val	Ser	Arg
						180			185					190	
Ser	Pro	Asp	Asp	Ser	Lys	Ser	Tyr	Arg	Ser	Arg	Ser	Arg	Ser	Arg	Gly
						195			200					205	
Pro	Ser	Cys	Ser	Tyr	Ser	Ser	Lys	Ser	Arg	Ser	Val	Ser	Pro	Ala	Arg
						210			215					220	
Ser	Ile	Ser	Pro	Arg	Ser	Arg	Pro	Leu	Ser	Arg	Ser	Arg	Ser	Pro	Tyr

225		230		235		240									
Ser	Ser	Val	Ser	Arg	Ser	Gln	Ser	Arg	Ser	Lys	Ser	Arg	Ser	Thr	Xaa
				245						250				255	
Arg	Ser	Arg	Ser	Asn	Ser	Pro	Val	Ser	Pro	Val	Ile	Ser	Gly		
				260						265				270	

(2) INFORMATION FOR SEQ ID NO:1090:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 142 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..142
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568946

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1090:

Met	Arg	Lys	Ala	Gly	Asp	Val	Cys	Phe	Ser	Glu	Val	Phe	Pro	Asp	Arg
1			5						10				15		
Lys	Gly	Met	Ser	Gly	Val	Val	Asp	Tyr	Ser	Asn	Tyr	Asp	Asp	Met	Lys
			20				25						30		
Tyr	Ala	Ile	Arg	Lys	Leu	Asp	Ala	Thr	Glu	Phe	Arg	Asn	Ala	Phe	Ser
		35				40						45			
Ser	Ala	Tyr	Ile	Arg	Val	Arg	Glu	Tyr	Glu	Ser	Arg	Ser	Val	Ser	Arg
		50				55					60				
Ser	Pro	Asp	Asp	Ser	Lys	Ser	Tyr	Arg	Ser	Arg	Ser	Arg	Ser	Arg	Gly
		65			70				75				80		
Pro	Ser	Cys	Ser	Tyr	Ser	Ser	Lys	Ser	Arg	Ser	Val	Ser	Pro	Ala	Arg
			85						90				95		
Ser	Ile	Ser	Pro	Arg	Ser	Arg	Pro	Leu	Ser	Arg	Ser	Arg	Ser	Pro	Tyr
			100				105						110		
Ser	Ser	Val	Ser	Arg	Ser	Gln	Ser	Arg	Ser	Lys	Ser	Arg	Ser	Thr	Xaa
		115				120						125			
Arg	Ser	Arg	Ser	Asn	Ser	Pro	Val	Ser	Pro	Val	Ile	Ser	Gly		
		130			135						140				

(2) INFORMATION FOR SEQ ID NO:1091:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1204 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1204
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568962

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1091:

atataaaata	accatatctc	tcactttctc	ttctttctct	tcttatcact	attcgctcat	60
ttccctctct	ctgttgtttac	agaagtcgac	ggcgagttagc	ttcaaccaaa	aagaaacacc	120
agtatctgtc	tcagcaatgg	agtttttcca	gaaagcaaaa	gctattcgaa	tgcgtaacag	180
tcacaacaag	tatctaacag	cagacgcaga	tgaagaaacc	gtaactcaaa	accgtaacgg	240
atctaccaaa	aaagttcgat	ggaccgtcga	acgggttcgt	gattctttcc	atgttattcg	300
tctttaaagc	gtttacggta	agtaacttaac	cgcttctaac	gagcggttct	tgctcgaggc	360
tacgggggaag	aaagtgtatt	agttgaaact	gagtcggggt	gattcttctg	ttgagtgga	420
accggttaga	gaaggatcta	agattaagct	taggaactaga	tctggtaact	atttacgagg	480
taatgtgtgt	cttctctctt	ggagaaactc	ggtcacacac	gaagttcttc	atttgtctgc	540
tactacaggat	tggattttct	gggatgttga	tgtttgttag	atcttgactg	attccgaatt	600
ccagacggag	tctgcgaaa	cgccgcacac	gaagacgaag	tctccaccgc	cgcatcgagg	660
accgacgagt	tcgcggtgtg	cggtcgagtc	tccaaggact	tcgtcttctc	tttcagacag	720
atccgattca	gattcgggtg	agtcctccgc	taaatctgat	ggacgaacca	tatatattca	780
tgtcgctgac	gaggaaggac	acgtggaaga	tgaacaacac	ggttgatatg	ctttcacggt	840

(2) INFORMATION FOR SEQ ID NO:1092:

(A) LENGTH: 338 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

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(ix) FEATURE:
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(A) NAME/KEY: peptide

(B) LOCATION: 1..338

(D) OTHER INFORMATION: / Ceres Seq. ID 1568963

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1092:

Tyr	Leu	Ile	Thr	Ile	Ser	Leu	Thr	Ser	Ser	Ser	Ser	Ser	Ser	Tyr	His
1	5	10	15	20	25	30	35	40	45	50	55	60	65	70	75
Tyr	Ser	Leu	Ile	Ser	Pro	Ser	Leu	Leu	Leu	Gln	Lys	Ser	Thr	Ala	Ser
Ser	Phe	Asn	Gln	Lys	Glu	Thr	Pro	Val	Ser	Val	Ser	Ala	Met	Glu	Phe
Phe	Gln	Lys	Ala	Lys	Ala	Ile	Arg	Met	Arg	Asn	Ser	His	Asn	Lys	Tyr
Leu	Thr	Ala	Asp	Asp	Asp	Glu	Glu	Thr	Val	Thr	Gln	Asn	Arg	Asn	Gly
65	70	75	80	85	90	95	100	105	110	115	120	125	130	135	140
Ser	Thr	Lys	Asn	Val	Arg	Trp	Thr	Val	Glu	Pro	Val	Arg	Asp	Ser	Phe
His	Val	Ile	Arg	Leu	Lys	Ser	Cys	Tyr	Gly	Lys	Tyr	Leu	Thr	Ala	Ser
Asn	Glu	Arg	Phe	Leu	Lys	Gly	Ala	Thr	Gly	Lys	Lys	Val	Ile	Gln	Leu
Lys	Leu	Ser	Arg	Val	Asp	Ser	Ser	Val	Glu	Trp	Glu	Pro	Val	Arg	Glu
Gly	Ser	Lys	Ile	Lys	Leu	Arg	Thr	Arg	Ser	Gly	Asn	Tyr	Leu	Arg	Gly
145	150	155	160	165	170	175	180	185	190	195	200	205	210	215	220
Asn	Gly	Gly	Leu	Pro	Pro	Trp	Arg	Asn	Ser	Val	Thr	His	Asp	Val	Pro
His	Leu	Ser	Ala	Thr	Gln	Asp	Ser	Ile	Ser	Trp	Asp	Val	Asp	Val	Val
Glu	Ile	Leu	Thr	Asp	Ser	Glu	Phe	Gln	Thr	Glu	Ser	Ala	Lys	Ala	Pro
Pro	Pro	Lys	Thr	Thr	Ser	Pro	Pro	Pro	His	Arg	Arg	Pro	Thr	Ser	Ser
225	230	235	240	245	250	255	260	265	270	275	280	285	290	295	300
Pro	Leu	Ser	Ala	Glu	Ser	Pro	Arg	Thr	Ser	Ser	Ser	Leu	Ser	Asp	Arg
Ser	Asp	Ser	Asp	Ser	Val	Glu	Ser	Pro	Pro	Lys	Ser	Asp	Gly	Arg	Thr
Ile	Tyr	Tyr	His	Val	Ala	Asp	Glu	Glu	Gly	His	Val	Glu	Asp	Glu	Thr
Thr	Val	Gly	Tyr	Ala	Phe	Thr	Phe	Lys	Gly	Asn	Ser	Val	Ala	Glu	Leu
Thr	Gln	Thr	Leu	Arg	Glu	Glu	Thr	Cys	Met	Glu	Asp	Ala	Val	Val	Cys
Thr	Arg	Ser	Pro	Leu	Asn	Gly	Lys	Leu	Phe	Pro	Leu	Arg	Leu	Gln	Leu
305	310	315	320	325	330	335	340	345	350	355	360	365	370	375	380
Pro	Pro	Asn	Asn	Gly	Thr	Leu	His	Val	Ile	Leu	Leu	Pro	Ser	Ser	Ala

Ser Leu

(2) INFORMATION FOR SEQ ID NO:1093:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 293 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..293
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568964

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1093:

Met	Glu	Phe	Phe	Gln	Lys	Ala	Lys	Ala	Ile	Arg	Met	Arg	Asn	Ser	His
1				5					10					15	
Asn	Lys	Tyr	Leu	Thr	Ala	Asp	Asp	Asp	Glu	Glu	Thr	Val	Thr	Gln	Asn
			20					25					30		
Arg	Asn	Gly	Ser	Thr	Lys	Asn	Val	Arg	Trp	Thr	Val	Glu	Pro	Val	Arg
		35					40					45			
Asp	Ser	Phe	His	Val	Ile	Arg	Leu	Lys	Ser	Cys	Tyr	Gly	Lys	Tyr	Leu
	50					55				60					
Thr	Ala	Ser	Asn	Glu	Arg	Phe	Leu	Leu	Gly	Ala	Thr	Gly	Lys	Lys	Val
	65				70				75					80	
Ile	Gln	Leu	Lys	Leu	Ser	Arg	Val	Asp	Ser	Ser	Val	Glu	Trp	Glu	Pro
			85					90						95	
Val	Arg	Glu	Gly	Ser	Lys	Ile	Lys	Leu	Arg	Thr	Arg	Ser	Gly	Asn	Tyr
			100					105					110		
Leu	Arg	Gly	Asn	Gly	Gly	Leu	Pro	Pro	Trp	Arg	Asn	Ser	Val	Thr	His
		115					120					125			
Asp	Val	Pro	His	Leu	Ser	Ala	Thr	Gln	Asp	Ser	Ile	Ser	Trp	Asp	Val
	130						135				140				
Asp	Val	Val	Glu	Ile	Leu	Thr	Asp	Ser	Glu	Phe	Gln	Thr	Glu	Ser	Ala
	145				150				155					160	
Lys	Ala	Pro	Pro	Pro	Lys	Thr	Thr	Ser	Pro	Pro	Pro	His	Arg	Arg	Pro
			165					170					175		
Thr	Ser	Ser	Pro	Leu	Ser	Ala	Glu	Ser	Pro	Arg	Thr	Ser	Ser	Ser	Leu
			180					185					190		
Ser	Asp	Arg	Ser	Asp	Ser	Asp	Ser	Val	Glu	Ser	Pro	Pro	Lys	Ser	Asp
		195					200					205			
Gly	Arg	Thr	Ile	Tyr	Tyr	His	Val	Ala	Asp	Glu	Glu	Gly	His	Val	Glu
	210					215					220				
Asp	Glu	Thr	Thr	Val	Gly	Tyr	Ala	Phe	Thr	Phe	Lys	Gly	Asn	Ser	Val
	225				230				235					240	
Ala	Glu	Leu	Thr	Gln	Thr	Leu	Arg	Glu	Glu	Thr	Cys	Met	Glu	Asp	Ala
			245					250					255		
Val	Val	Cys	Thr	Arg	Ser	Pro	Leu	Asn	Gly	Lys	Leu	Phe	Pro	Leu	Arg
		260					265						270		
Leu	Gln	Leu	Pro	Pro	Asn	Asn	Gly	Thr	Leu	His	Val	Ile	Leu	Leu	Pro
	275						280						285		

Ser Ser Ala Ser Leu
290

(2) INFORMATION FOR SEQ ID NO:1094:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 282 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide

(B) LOCATION: 1..282

(D) OTHER INFORMATION: / Ceres Seq. ID 1568965

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1094:

```
Met Arg Asn Ser His Asn Lys Tyr Leu Thr Ala Asp Asp Asp Glu Glu
1      5      10      15
Thr Val Thr Gln Asn Arg Asn Gly Ser Thr Lys Asn Val Arg Trp Thr
20     25     30
Val Glu Pro Val Arg Asp Ser Phe His Val Ile Arg Leu Lys Ser Cys
35     40     45
Tyr Gly Lys Tyr Leu Thr Ala Ser Asn Glu Arg Phe Leu Leu Gly Ala
50     55     60
Thr Gly Lys Lys Val Ile Gln Leu Lys Leu Ser Arg Val Asp Ser Ser
65     70     75     80
Val Glu Trp Glu Pro Val Arg Glu Gly Ser Lys Ile Lys Leu Arg Thr
85     90     95
Arg Ser Gly Asn Tyr Leu Arg Gly Asn Gly Gly Leu Pro Trp Arg
100    105    110
Asn Ser Val Thr His Asp Val Pro His Leu Ser Ala Thr Gln Asp Ser
115    120    125
Ile Ser Trp Asp Val Asp Val Val Glu Ile Leu Thr Asp Ser Glu Phe
130    135    140
Gln Thr Glu Ser Ala Lys Ala Pro Pro Pro Lys Thr Thr Ser Pro Pro
145    150    155    160
Pro His Arg Arg Pro Thr Ser Ser Pro Leu Ser Ala Glu Ser Pro Arg
165    170    175
Thr Ser Ser Ser Leu Ser Asp Arg Ser Asp Ser Asp Ser Val Glu Ser
180    185    190
Pro Pro Lys Ser Asp Gly Arg Thr Ile Tyr Tyr His Val Ala Asp Glu
195    200    205
Glu Gly His Val Glu Asp Glu Thr Thr Val Gly Tyr Ala Phe Thr Phe
210    215    220
Lys Gly Asn Ser Val Ala Glu Leu Thr Gln Thr Leu Arg Glu Glu Thr
225    230    235    240
Cys Met Glu Asp Ala Val Val Cys Thr Arg Ser Pro Leu Asn Gly Lys
245    250    255
Leu Phe Pro Leu Arg Leu Gln Leu Pro Pro Asn Asn Gly Thr Leu His
260    265    270
Val Ile Leu Leu Pro Ser Ser Ala Ser Leu
275    280
```

(2) INFORMATION FOR SEQ ID NO:1095:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1043 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1043

(D) OTHER INFORMATION: / Ceres Seq. ID 1568966

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1095:

```
aaaagtgtggc cactaagtgg tgtaagaata ataaattgtc aatatcaatt gactgattct 60
tattgttcat atacggacac aaatcttttc gttaagttag tgttttgatac aaaaaaagt 120
gaaaacttta aagccatgcc atcacttttg tctaacgaat ccgatggatac attacgagag 180
catcttgtgg atgtgttgtt gtctgtttca gaaccaaaga ttcgggtaca tgactgacc 240
cgagtcgccc atgatggatc tcggatcttg aaaggagtta cgtatagatat accaaaaggt 300
atgatcgttg gtgtgattgg acctagtgga agtgaaagt caacgttttt gagatctctg 360
aatcgtcttt ggggaaccac ggagtcgaact gtgtctcttg accggtgaaga taaaaccaac 420
gttgatgtta ttgctctctg tcgtagagtt ggaatgcctt tcagcttcc tggtcttttt 480
caagggaactg ttgcggataa tgtgagatat ggtccgaatt tgagagggga gaaactaagt 540
gacgaagaggg tttaataagc gctaagtcct gcagacacttg atgcttctct tgctaagaag 600
```

```

actgggtgcag agttatctgt gggtaacgt caacgagtag cacttgcaag gactctagcc 660
aacgagcctg aggtgttctt gctcgatgaa caacaacgtg ctcttgatcc gatatcgaca 720
gagaaacatt aggatgttat agtgaaactg aagaagcaga gagggattac tactgtgatt 780
gtttctcaca gtatcaagca gattcagaaa gttgctgata tcgtttgcct tgttctcgac 840
ggagagattg ttgaagttct taaaccaagt gagctttcgc acgCtacgca tccaatggca 900
cagaggtttc ttcaactcag ttcttgagac cattttctca ttgattggttc ctgcaagtta 960
tttgctatct tgcttgaaac ttaataatct ctttcaagag aggaacaaa gctgggtgaa 1020
tgtaacaaca cctttcatgg ttt

```

(2) INFORMATION FOR SEQ ID NO:1096:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 263 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..263

(D) OTHER INFORMATION: / Ceres Seq. ID 1568967

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1096:

```

Met Pro Ser Leu Trp Ser Asn Glu Ser Asp Gly Ser Leu Arg Glu His
1      5      10      15
Leu Val Asp Val Val Ser Gly Ser Glu Pro Lys Ile Arg Val His
20      25      30
Asp Leu Thr Arg Val Ala Asp Asp Gly Ser Arg Ile Leu Lys Gly Val
35      40      45
Thr Ile Asp Ile Pro Lys Gly Met Ile Val Gly Val Ile Gly Pro Ser
50      55      60
Gly Ser Gly Lys Ser Thr Phe Leu Arg Ser Leu Asn Arg Leu Trp Glu
65      70      75      80
Pro Pro Glu Ser Thr Val Phe Leu Asp Gly Glu Asp Ile Thr Asn Val
85      90      95
Asp Val Ile Ala Leu Arg Arg Arg Val Gly Met Leu Phe Gln Leu Pro
100     105     110
Val Leu Phe Gln Gly Thr Val Ala Asp Asn Val Arg Tyr Gly Pro Asn
115     120     125
Leu Arg Gly Glu Lys Leu Ser Asp Glu Glu Val Tyr Lys Leu Leu Ser
130     135     140
Leu Ala Asp Leu Asp Ala Ser Phe Ala Lys Lys Thr Gly Ala Glu Leu
145     150     155
Ser Val Gly Gln Ala Gln Arg Val Ala Leu Ala Arg Thr Leu Ala Asn
160     165     170     175
Glu Pro Glu Val Leu Leu Asp Glu Pro Thr Ser Ala Leu Asp Pro
180     185     190
Ile Ser Thr Glu Asn Ile Glu Asp Val Ile Val Lys Leu Lys Lys Gln
195     200     205
Arg Gly Ile Thr Thr Val Ile Val Ser His Ser Ile Lys Gln Ile Gln
210     215     220
Lys Val Ala Asp Ile Val Cys Leu Val Val Asp Gly Glu Ile Val Glu
225     230     235     240
Val Leu Lys Pro Ser Glu Leu Ser His Ala Thr His Pro Met Ala Gln
245     250     255
Arg Phe Leu Gln Leu Ser Ser
260

```

(2) INFORMATION FOR SEQ ID NO:1097:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 208 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..208

(D) OTHER INFORMATION: / Ceres Seq. ID 1568968

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1097:

```
Met Ile Val Gly Val Ile Gly Pro Ser Gly Ser Gly Lys Ser Thr Phe
1      5      10      15
Leu Arg Ser Leu Asn Arg Leu Trp Glu Pro Pro Glu Ser Thr Val Phe
20      25      30
Leu Asp Gly Glu Asp Ile Thr Asn Val Asp Val Ile Ala Leu Arg Arg
35      40      45
Arg Val Gly Met Leu Phe Gln Leu Pro Val Leu Phe Gln Gly Thr Val
50      55      60
Ala Asp Asn Val Arg Tyr Gly Pro Asn Leu Arg Gly Glu Lys Leu Ser
65      70      75      80
Asp Glu Glu Val Tyr Lys Leu Leu Ser Leu Ala Asp Leu Asp Ala Ser
85      90      95
Phe Ala Lys Lys Thr Gly Ala Glu Leu Ser Val Gly Gln Ala Gln Arg
100      105      110
Val Ala Leu Ala Arg Thr Leu Ala Asn Glu Pro Glu Val Leu Leu Leu
115      120      125
Asp Glu Pro Thr Ser Ala Leu Asp Pro Ile Ser Thr Glu Asn Ile Glu
130      135      140
Asp Val Ile Val Lys Leu Lys Lys Gln Arg Gly Ile Thr Thr Val Ile
145      150      155      160
Val Ser His Ser Ile Lys Gln Ile Gln Lys Val Ala Asp Ile Val Cys
165      170      175
Leu Val Val Asp Gly Glu Ile Val Glu Val Leu Lys Pro Ser Glu Leu
180      185      190
Ser His Ala Thr His Pro Met Ala Gln Arg Phe Leu Gln Leu Ser Ser
195      200      205
```

(2) INFORMATION FOR SEQ ID NO:1098:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 157 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..157

(D) OTHER INFORMATION: / Ceres Seq. ID 1568969

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1098:

```
Met Leu Phe Gln Leu Pro Val Leu Phe Gln Gly Thr Val Ala Asn
1      5      10      15
Val Arg Tyr Gly Pro Asn Leu Arg Gly Glu Lys Leu Ser Asp Glu Glu
20      25      30
Val Tyr Lys Leu Leu Ser Leu Ala Asp Leu Asp Ala Ser Phe Ala Lys
35      40      45
Lys Thr Gly Ala Glu Leu Ser Val Gly Gln Ala Gln Arg Val Ala Leu
50      55      60
Ala Arg Thr Leu Ala Asn Glu Pro Glu Val Leu Leu Leu Asp Glu Pro
65      70      75      80
Thr Ser Ala Leu Asp Pro Ile Ser Thr Glu Asn Ile Glu Asp Val Ile
85      90      95
Val Lys Leu Lys Lys Gln Arg Gly Ile Thr Thr Val Ile Val Ser His
100      105      110
Ser Ile Lys Gln Ile Gln Lys Val Ala Asp Ile Val Cys Leu Val Val
115      120      125
```


Asp Gly Glu Ile Val Glu Val Leu Lys Pro Ser Glu Leu Ser His Ala
130 135 140
Thr His Pro Met Ala Gln Arg Phe Leu Gln Leu Ser Ser
145 150 155

(2) INFORMATION FOR SEQ ID NO:1099:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1218 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1218
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568974

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1099:

atgtccacca	cttcacctct	ctctctcttt	cttctccact	gtaacctccc	aattcaaaaa	60
caattataaa	ccaaacttga	ttaatatata	tttctttatc	atcatctctt	cgaatgcaa	120
gatattcatg	atttctccat	gaacggagtt	ggtggtgggg	gaggaggagg	agggagggtt	180
ttcgggtggag	gaatcgccgg	cggaggaggt	ggtgatcgaa	ggatgagagc	tcatcagaac	240
aatatactta	accatcatca	atctctcaag	tgtcctcggt	gtaattctct	taacacaaag	300
ttctgttact	acaacaatta	caatctttct	cagcctcgct	acttttgcaa	gaactgtcgt	360
cgttactcga	ctaaagggtg	tgttctcgt	aacgttccc	tcggagggtg	ttgccggaaa	420
gctaaacggt	cgaaaaacaa	acaggttccg	tctgtctcat	cagccgacaa	accaacgacg	480
acgcaagatg	atcatcacgt	ggaggagaaa	tcgagtacag	gatctcaact	tagcacgga	540
agctctcttc	tcacgcgttc	taactctacc	acogtgcg	ccgtctccgt	caccgcggcg	600
gcggaagtgt	cttcgctcgt	tattccaggt	tttgatagc	ctaataatga	aatttacggt	660
aacgggatcg	agtgtcgac	gttacttgga	caaggctcat	cggccggtg	tggtttctcg	720
gagatcggtg	gttttcggcg	ggtttcagct	attgaaacta	caccgttttg	attcgggggt	780
aaattcgtaa	atcaaatgta	tcactcgaag	tagaagggtg	aaactgtaca	gcagcaacag	840
tttggaacgt	gaacggctca	ggttgagttt	caagggaagt	cttcgatcc	gaatatggga	900
tttgaacgtg	tggattgggg	aagtgccggt	ggagatcaaa	caactgttga	tttaaccagt	960
accgttgatc	atgcatactg	gagtcacaa	caatggacgt	cgtctgacca	agatcagagt	1020
ggtctctacc	ttccttgatt	ctgatcatag	cttcttcttc	tttaaccocaa	aatatatatt	1080
ttatacacat	aaggtaaagt	tcgatgaagt	ggttttttwa	attttTattt	gatggGtCta	1140
aaAcgggatt	Tattatataa	ttatatgact	gottgtaaat	ttttTccca	aatatacaat	1200
ttacctctct	tttttttt					

(2) INFORMATION FOR SEQ ID NO:1100:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 307 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..307
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568975

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1100:

Met	Gln	Asp	Ile	His	Asp	Phe	Ser	Met	Asn	Gly	Val	Gly	Gly	Gly	Gly
1		5						10				15			
Gly	Gly	Gly	Gly	Arg	Phe	Phe	Gly	Gly	Gly	Ile	Gly	Gly	Gly	Gly	Gly
		20					25				30				
Gly	Asp	Arg	Arg	Met	Arg	Ala	His	Gln	Asn	Asn	Ile	Leu	Asn	His	His
		35					40				45				
Gln	Ser	Leu	Lys	Cys	Pro	Arg	Cys	Asn	Ser	Leu	Asn	Thr	Lys	Phe	Cys
		50				55				60					
Tyr	Tyr	Asn	Asn	Tyr	Asn	Leu	Ser	Gln	Pro	Arg	His	Phe	Cys	Lys	Asn
		65				70			75					80	
Cys	Arg	Arg	Tyr	Trp	Thr	Lys	Gly	Gly	Val	Leu	Arg	Asn	Val	Pro	Val
			85				90						95		

Tyr Leu Pro
305

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 299 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

{ix} FEATURE:

(B) LOCATION: 1..299

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1101:

Met	Asn	Gly	Val	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Arg	Phe	Phe	Gly
1				5					10					15	
Gly	Gly	Ile	Gly	Gly	Gly	Gly	Gly	Asp	Arg	Arg	Met	Arg	Ala	His	
			20					25					30		
Gln	Asn	Asn	Ile	Leu	Asn	His	His	Gln	Ser	Leu	Lys	Cys	Pro	Arg	Cys
		35					40					45			
Asn	Ser	Leu	Asn	Thr	Lys	Phe	Cys	Tyr	Tyr	Asn	Asn	Tyr	Asn	Leu	Ser
	50					55					60				
Gln	Pro	Arg	His	Phe	Cys	Lys	Asn	Cys	Arg	Arg	Tyr	Trp	Thr	Lys	Gly
65					70					75				80	
Gly	Val	Leu	Arg	Asn	Val	Pro	Val	Gly	Gly	Gly	Cys	Arg	Lys	Ala	Lys
			85						90					95	
Arg	Ser	Lys	Thr	Lys	Gln	Val	Pro	Ser	Ser	Ser	Ser	Ala	Asp	Lys	Pro
			100					105					110		
Thr	Thr	Thr	Gln	Asp	Asp	His	His	Val	Glu	Glu	Lys	Ser	Ser	Thr	Gly
			115				120					125			
Ser	His	Ser	Ser	Ser	Glu	Ser	Ser	Ser	Leu	Thr	Ala	Ser	Asn	Ser	Thr
	130					135					140				
Thr	Val	Ala	Ala	Val	Ser	Val	Thr	Ala	Ala	Ala	Glu	Val	Ala	Ser	Ser
145					150				155					160	
Val	Ile	Pro	Gly	Phe	Asp	Met	Pro	Asn	Met	Lys	Ile	Tyr	Gly	Asn	Gly

(2) INFORMATION FOR SEQ ID NO:1102:

(A) LENGTH: 271 amino acids

(ii) MOLECULE TYPE: peptide

(A) NAME/KEY: peptide

(B) LOCATION: 1..271

(D) OTHER INFORMATION: / Ceres Seq. ID 1568977

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1102:

Met	Arg	Ala	His	Gln	Asn	Asn	Ile	Leu	Asn	His	His	Gln	Ser	Leu	Lys
1				5					10					15	
Cys	Pro	Arg	Cys	Asn	Ser	Leu	Asn	Thr	Lys	Phe	Cys	Tyr	Tyr	Asn	Asn
			20					25					30		
Tyr	Asn	Leu	Ser	Gln	Pro	Arg	His	Phe	Cys	Lys	Asn	Cys	Arg	Arg	Tyr
		35					40					45			
Trp	Thr	Lys	Gly	Val	Leu	Arg	Asn	Val	Pro	Val	Gly	Gly	Gly	Cys	
	50				55					60					
Arg	Lys	Ala	Lys	Arg	Ser	Lys	Thr	Lys	Gln	Val	Pro	Ser	Ser	Ser	Ser
65					70					75					80
Ala	Asp	Lys	Pro	Thr	Thr	Thr	Gln	Asp	His	His	Val	Glu	Glu	Lys	
				85				90					95		
Ser	Ser	Thr	Thr	Gly	Ser	His	Ser	Ser	Ser	Glu	Ser	Ser	Ser	Leu	Thr
			100					105					110		Ala
Ser	Asn	Ser	Thr	Thr	Val	Ala	Ala	Val	Ser	Val	Thr	Ala	Ala	Ala	Glu
			115				120					125			
Val	Ala	Ser	Ser	Val	Ile	Pro	Gly	Phe	Asp	Met	Pro	Asn	Met	Lys	Ile
						135									140
Tyr	Gly	Asn	Gly	Ile	Glu	Trp	Ser	Thr	Leu	Leu	Gly	Gln	Gly	Ser	Ser
145					150					155					160
Ala	Gly	Gly	Val	Phe	Ser	Ser	Glu	Ile	Gly	Gly	Phe	Pro	Ala	Val	Ser
				165						170					175
Ile	Glu	Thr	Thr	Pro	Phe	Gly	Phe	Gly	Gly	Lys	Phe	Val	Asn	Gln	Asp
			180					185					190		
Asp	His	Leu	Lys	Leu	Glu	Gly	Glu	Thr	Val	Gln	Gln	Gln	Gln	Phe	Gly
		195					200					205			
Asp	Arg	Thr	Ala	Gln	Val	Glu	Phe	Gln	Gly	Arg	Ser	Ser	Asp	Pro	Asn
		210				215					220				
Met	Gly	Phe	Glu	Pro	Leu	Asp	Trp	Gly	Ser	Gly	Gly	Gly	Asp	Gln	Thr
225					230					235					240
Leu	Phe	Asp	Leu	Thr	Ser	Thr	Val	Asp	His	Ala	Tyr	Trp	Ser	Gln	Ser
				245					250					255	

Gln Trp Thr Ser Ser Asp Gln Asp Gln Ser Gly Leu Tyr Leu Pro
260 265 270

(2) INFORMATION FOR SEQ ID NO:1103:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1484 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1484
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568978

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1103:

acgggtcaat	ttgatttgga	taataattct	ctttttctct	ggaaagtctg	aatttttttt	60
tgtttggaag	ctctggagaaa	atattatact	cttctcattg	aatgatcaat	ttacaaatcc	120
tcatttgatc	gatctttgtca	atttttgaaa	aaaaaaatct	gaactttgag	aaagatttat	180
gagttttgat	atctgtcggg	catggtttga	ttgtggctgt	tgggtaagac	aacaaattag	240
ggtttttgaa	tagttttgtg	attgaagatt	gtctgaaatg	gaagcagcta	ttactcagag	300
gattcagtac	ccatcatggg	ttgattgtag	aaaagttaga	tgtaaagcgc	agcgtgggtc	360
attgcggtat	ttctcagcag	ttaaaggtaga	tgaaggtttt	agaggtcttt	ctttggctcg	420
cttgcaacct	gaagaagaaa	tgtatcaacg	aagacagatt	ttctcagcgg	ttctcgtgtc	480
tgataacaat	ttctcagcgt	tgttggagac	tggaaagtgt	tatccatttg	atgaagatat	540
ttcacaagaga	aaagcagaag	aggttaaacc	gtatttgaat	ggacgatcta	tgtaccttgt	600
cggaaatgat	gggttctggga	aaacaactgt	gggaaagtta	atgtccaaag	tgctcggtta	660
tacgttcttt	gactgcgaca	ctttgattga	gggcgatgaa	tggaaactct	gttgacagaga	720
tatttgttca	tcacggagag	aattttttta	gaggaaagga	gaccgatcgc	cttaagaagc	780
ttcttctcag	tgtatcaagt	gttgtttcca	caggtggagg	tgacgttata	agaccctata	840
actggaagta	tatgcataaa	ggaatcacga	tttggtctaga	tgtgcctcta	gaagcattag	900
cccatagaa	cgtctcgtgt	ggaactgatt	cacgaccact	gtacacagat	gaatcaggag	960
atgcatactc	agtgctcttc	aaacgtctct	cggctatttg	ggacgagcgc	ggtgaagcat	1020
acacaaacgc	aaatgccaga	gtctccttag	aaaataattg	agcaaaagct	ggctataaaa	1080
atgtctcaga	ttctcacacca	actgaaattt	gtatcgaggc	cttcagacaa	gttctgagct	1140
ttctagagaa	agaagaaaact	atggagatcc	cagacggcga	ctctaatatt	ccacgccttc	1200
tgttctcogt	ctcttcattt	atctgtttta	tcaactaaac	gaagcaatca	ctcatcacca	1260
ggccattgag	caagttcaga	gacaaagaag	acctctagtt	actggttccg	gttcatttga	1320
gcttacacga	gcctaatatt	gactggaaac	atggtttatt	gaagaagatg	tcaatacatg	1380
tatatataaa	atataatact	ttttttttgt	ttcagtatca	ttctttctct	cttttccctta	1440
caataagaat	taaggaaaaa	tagccgtgtt	tgtaaacatg	ggcc		

(2) INFORMATION FOR SEQ ID NO:1104:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 157 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..157
- (D) OTHER INFORMATION: / Ceres Seq. ID 1568979

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1104:

Met	Glu	Ala	Ala	Ile	Thr	Gln	Arg	Ile	Gln	Tyr	Pro	Ser	Trp	Val	Asp	
1				5				10						15		
Cys	Arg	Lys	Val	Glu	Cys	Lys	Pro	Gln	Arg	Gly	Ser	Leu	Arg	Tyr	Ser	
				20				25						30		
Gln	Gln	Val	Lys	Val	Asp	Arg	Arg	Phe	Arg	Gly	Leu	Ser	Leu	Ala	Arg	
				35				40						45		
Leu	Gln	Pro	Glu	Arg	Arg	Ile	Asp	Gln	Arg	Arg	Ala	Val	Ser	Pro	Ala	
				50				55						60		
Val	Ser	Cys	Ser	Asp	Asn	Asn	Ser	Ser	Ala	Leu	Leu	Glu	Thr	Gly	Ser	
65				70				75						80		

Val	Tyr	Pro	Phe	Asp	Glu	Asp	Ile	Leu	Lys	Arg	Lys	Ala	Glu	Glu	Val
				85					90					95	
Lys	Pro	Tyr	Leu	Asn	Gly	Arg	Ser	Met	Tyr	Leu	Val	Gly	Met	Met	Gly
			100					105					110		
Ser	Gly	Lys	Thr	Thr	Val	Gly	Lys	Leu	Met	Ser	Lys	Val	Leu	Gly	Tyr
			115					120					125		
Thr	Phe	Phe	Asp	Cys	Asp	Thr	Leu	Ile	Glu	Gly	Asp	Glu	Trp	Asn	Phe
			130				135				140				
Cys	Cys	Arg	Asp	Ile	Cys	Ser	Ser	Arg	Arg	Glu	Phe	Phe			
			145			150				155					

(2) INFORMATION FOR SEQ ID NO:1105:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 163 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..163

(D) OTHER INFORMATION: / Ceres Seq. ID 1568980

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1105:

Met	Asn	Gly	Thr	Ser	Val	Ala	Glu	Ile	Phe	Val	His	His	Gly	Glu	Asn
1				5					10					15	
Phe	Phe	Arg	Gly	Lys	Glu	Thr	Asp	Ala	Leu	Lys	Lys	Leu	Ser	Ser	Arg
			20					25					30		
Tyr	Gln	Val	Val	Val	Ser	Thr	Gly	Gly	Gly	Ala	Val	Ile	Arg	Pro	Ile
			35				40					45			
Asn	Trp	Lys	Tyr	Met	His	Lys	Gly	Ile	Ser	Ile	Trp	Leu	Asp	Val	Pro
			50			55					60				
Leu	Glu	Ala	Leu	Ala	His	Arg	Ile	Ala	Ala	Val	Gly	Thr	Asp	Ser	Arg
			65			70				75				80	
Pro	Leu	Leu	His	Asp	Glu	Ser	Gly	Asp	Ala	Tyr	Ser	Val	Ala	Phe	Lys
			85						90				95		
Arg	Leu	Ser	Ala	Ile	Trp	Asp	Glu	Arg	Gly	Glu	Ala	Tyr	Thr	Asn	Ala
			100					105					110		
Asn	Ala	Arg	Val	Ser	Leu	Glu	Asn	Ile	Ala	Ala	Lys	Arg	Gly	Tyr	Lys
			115				120					125			
Asn	Val	Ser	Asp	Leu	Thr	Pro	Thr	Glu	Ile	Cys	Ile	Glu	Ala	Phe	Glu
			130			135					140				
Gln	Val	Leu	Ser	Phe	Leu	Glu	Lys	Glu	Glu	Thr	Met	Glu	Ile	Pro	Asp
					150					155				160	
Gly	Asp	Leu													

(2) INFORMATION FOR SEQ ID NO:1106:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 111 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..111

(D) OTHER INFORMATION: / Ceres Seq. ID 1568981

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1106:

Met	His	Lys	Gly	Ile	Ser	Ile	Trp	Leu	Asp	Val	Pro	Leu	Glu	Ala	Leu
1				5					10					15	
Ala	His	Arg	Ile	Ala	Ala	Val	Gly	Thr	Asp	Ser	Arg	Pro	Leu	Leu	His
			20				25						30		
Asp	Glu	Ser	Gly	Asp	Ala	Tyr	Ser	Val	Ala	Phe	Lys	Arg	Leu	Ser	Ala

35 40 45
Ile Trp Asp Glu Arg Gly Glu Ala Tyr Thr Asn Ala Asn Ala Arg Val
50 55 60
Ser Leu Glu Asn Ile Ala Ala Lys Arg Gly Tyr Lys Asn Val Ser Asp
65 70 75 80
Leu Thr Pro Thr Glu Ile Cys Ile Glu Ala Phe Glu Gln Val Leu Ser
85 90 95
Phe Leu Glu Lys Glu Glu Thr Met Glu Ile Pro Asp Gly Asp Leu
100 105 110

(2) INFORMATION FOR SEQ ID NO:1107:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1196 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1196

(D) OTHER INFORMATION: / Ceres Seq. ID 1569006

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1107:

tccccaattc	gtctctctcca	acagttttct	tcttctcttc	ttctttgggt	gttccttcca	60
ccaacggcag	aaatcgattt	ggcttaaatc	tcccctctct	ctgactctct	ctgategccg	120
cggggaacat	taattttccc	ggtagttcaa	caaaaaaaaa	actctccgtt	tttatttttc	180
cccccttttc	acgggtggaa	gtttccggag	atgggtgtcac	ccgaaaaacg	taattggatt	240
tgtgacttga	tcgactgtga	ttacgggaag	ttcacaaatc	aaggtcctgg	tttctcttgg	300
ctcgttccag	aacctattgg	tgtttcttct	aactccagtg	ctggagtgtg	tggctcggct	360
ggaaactcga	aacgtagcaa	agaacctgga	tccaaaaaga	gggggagatg	tgaatcatcc	420
tctgccaatc	gctcgaaagc	atgtagagag	aagcagcgac	gggacaggtt	gaatgacaag	480
tttatggaa	tgggtgcaat	tttggagcct	ggaaatcctc	ccaaaacaga	caaggctcgt	540
atcttggttg	atgctgtccg	catggtgaca	cagctacggg	gcgaggccca	gaagctgaag	600
gactccaatt	caagtcctca	ggacaaaatc	aaagagttaa	agactgagaa	aaacgagctg	660
cgagatgaga	aacagaggct	gaagacagag	aaagaaaagc	tggagcagca	gctgaaagcc	720
attaatgctc	ctcaaccaag	ttttttccca	gccccacctc	tgatgcttac	tgttttgtct	780
tcagcgcaag	gccaaagctc	tggaaaacag	atgggtgccaa	tcatacagta	cccaggagtt	840
gccatctggc	agttcatgcc	tcctgtcttc	gtcgataact	ctcaggatca	tgtccttctg	900
ctctctgttg	cttaatacaag	aaaaatcatc	aaccggtttg	cttcttgctt	ccgcttaaaa	960
gaaaagcttc	catttgtttt	gctctctctc	ctttctcgcg	tttcttagtc	ttatcctttt	1020
gctttgtcgt	gtttatcatg	taactgttat	ctgttgaaaca	atgatataac	attgtaacct	1080
ccaattgCtt	cgcgcaatgt	tatctattca	catgtaaatt	taagttagat	ttggcagatc	1140
gtctctcaat	ttatgtgttc	ttacataatt	acatagaatt	tggttacttc	ctcgcc	

(2) INFORMATION FOR SEQ ID NO:1108:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 234 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..234

(D) OTHER INFORMATION: / Ceres Seq. ID 1569007

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1108:

Met	Val	Ser	Pro	Glu	Asn	Ala	Asn	Trp	Ile	Cys	Asp	Leu	Ile	Asp	Ala
1				5				10				15			
Asp	Tyr	Gly	Ser	Phe	Thr	Ile	Gln	Gly	Pro	Gly	Phe	Ser	Trp	Pro	Val
			20				25					30			
Gln	Gln	Pro	Ile	Gly	Val	Ser	Ser	Asn	Ser	Ser	Ala	Gly	Val	Asp	Gly
		35					40				45				
Ser	Ala	Gly	Asn	Ser	Glu	Ala	Ser	Lys	Glu	Pro	Gly	Ser	Lys	Lys	Arg
	50						55				60				

Gly Arg Cys Glu Ser Ser Ser Ala Thr Ser Ser Lys Ala Cys Arg Glu
65 70 75 80
Lys Gln Arg Arg Asp Arg Leu Asn Asp Lys Phe Met Glu Leu Gly Ala
85 90 95
Ile Leu Glu Pro Gly Asn Pro Pro Lys Thr Asp Lys Ala Ala Ile Leu
100 105 110
Val Asp Ala Val Arg Met Val Thr Gln Leu Arg Gly Glu Ala Gln Lys
115 120 125
Leu Lys Asp Ser Asn Ser Ser Leu Gln Asp Lys Ile Lys Glu Leu Lys
130 135 140
Thr Glu Lys Asn Glu Leu Arg Asp Glu Lys Gln Arg Leu Lys Thr Glu
145 150 155 160
Lys Glu Lys Leu Glu Gln Gln Leu Lys Ala Ile Asn Ala Pro Gln Pro
165 170 175
Ser Phe Phe Pro Ala Pro Pro Met Met Pro Thr Ala Phe Ala Ser Ala
180 185 190
Gln Gly Gln Ala Pro Gly Asn Lys Met Val Pro Ile Ile Ser Tyr Pro
195 200 205
Gly Val Ala Met Trp Gln Phe Met Pro Pro Ala Ser Val Asp Thr Ser
210 215 220
Gln Asp His Val Leu Arg Pro Pro Val Ala
225 230

(2) INFORMATION FOR SEQ ID NO:1109:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 143 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..143

(D) OTHER INFORMATION: / Ceres Seq. ID 1569008

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1109:

Met Glu Leu Gly Ala Ile Leu Glu Pro Gly Asn Pro Pro Lys Thr Asp
1 5 10 15
Lys Ala Ala Ile Leu Val Asp Ala Val Arg Met Val Thr Gln Leu Arg
20 25 30
Gly Glu Ala Gln Lys Leu Lys Asp Ser Asn Ser Ser Leu Gln Asp Lys
35 40 45
Ile Lys Glu Leu Lys Thr Glu Lys Asn Glu Leu Arg Asp Glu Lys Gln
50 55 60
Arg Leu Lys Thr Glu Lys Glu Lys Leu Glu Gln Gln Leu Lys Ala Ile
65 70 75 80
Asn Ala Pro Gln Pro Ser Phe Phe Pro Ala Pro Pro Met Met Pro Thr
85 90 95
Ala Phe Ala Ser Ala Gln Gly Gln Ala Pro Gly Asn Lys Met Val Pro
100 105 110
Ile Ile Ser Tyr Pro Gly Val Ala Met Trp Gln Phe Met Pro Pro Ala
115 120 125
Ser Val Asp Thr Ser Gln Asp His Val Leu Arg Pro Pro Val Ala
130 135 140

(2) INFORMATION FOR SEQ ID NO:1110:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 117 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..117

(D) OTHER INFORMATION: / Ceres Seq. ID 1569009

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1110:

```
Met Val Thr Gln Leu Arg Gly Glu Ala Gln Lys Leu Lys Asp Ser Asn
1      5      10      15
Ser Ser Leu Gln Asp Lys Ile Lys Glu Leu Lys Thr Glu Lys Asn Glu
20     25     30
Leu Arg Asp Glu Lys Gln Arg Leu Lys Thr Glu Lys Glu Lys Leu Glu
35     40     45
Gln Gln Leu Lys Ala Ile Asn Ala Pro Gln Pro Ser Phe Phe Pro Ala
50     55     60
Pro Pro Met Met Pro Thr Ala Phe Ala Ser Ala Gln Gly Gln Ala Pro
65     70     75     80
Gly Asn Lys Met Val Pro Ile Ile Ser Tyr Pro Gly Val Ala Met Trp
85     90     95
Gln Phe Met Pro Pro Ala Ser Val Asp Thr Ser Gln Asp His Val Leu
100    105    110
Arg Pro Pro Val Ala
115
```

(2) INFORMATION FOR SEQ ID NO:1111:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1936 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1936

(D) OTHER INFORMATION: / Ceres Seq. ID 1569025

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1111:

```
gaagtagatg ttctgtaaca acaatggcca aaacacagag gtcttgttgt ctgcgtcaacg      60
ctctaatacgc tatagctttt ttggcgacag Cccatttgtg tgaagctggc ttgtctcaga      120
aagaacagga caaggtctcg aaattgccctg tgcagaattt ttgtctcaact      180
actctggggt ttgtctact aatgagcaat tgggaagagc tctcttttac tggttatttg      240
aagccgttga agatgctaag tctaagcctc ttgttctctg gctcaatgga ggaccaggat      300
gttcattctgt tgcataatgg gaagcagaag agataggacc atttcacatt aaggcagatg      360
ggaaaactct ttaccttaat caatattctt ggaacaaagc tgcaaatatt ttgttctctg      420
atgcacctgt ttgagttggg tattcatact caaacacctc gtctgatttg aagagcaatg      480
gtgataaaaag aactgcggaa gactcactga aatttctgct gaaatggggt gagcggtttc      540
cggaatacaaa aggaaggagc ttttatatag taggggagag ctatgcagga cattacattc      600
ctcagcttga tgaagccatt taaaacata accaaggttc tgacaaaaac agtataaatc      660
tgaagggttga catgttagga aatgggctga tggacgattt ccatgacagg cttggtcttt      720
tccaatatat ttggtcgttg ggttttatat ctgacaaaac atacagctta ctgcaacttc      780
aatgcgggtt cgaatcggtt attcactctt ccaaacagtg taacaagatt ctggagatag      840
cggacaaaaga aataggtaac atagaccaat acagtgtctt caacccagct tgtgttgcca      900
atgcttcocca gtcaaatatg ttgtctaaaga aaagacctat gactagccgc gtgagcgaaac      960
agtatgatcc ttgtacggag aaacacacta cagttttatt caactctcca gaggtctcaa      1020
aagccctcca ttgtccaccca ggaacttgac catcaaaatg ggataactgc agtgatgtgc      1080
tgagtgtaaca ctggaatgac tctctctctc cggttctaaa catttaccac gaggttatag      1140
ctgctggggtc tcgtatctgg gtttctcagt gggagcgaga tgccgttgta ccaagtcaact      1200
caaccgggta cagtatcgat gcactaaacc ttgctctctt ggggtgcctat ggtccttggt      1260
acttagatgc acaggtggga ggggtggatc agcagtatgc tggctcgaac ttgttgacag      1320
tgagaggtgc aggcocatga gttctcttgc acagaccgga gcaagctctt gcgctctcca      1380
aggcttttat atctggaact ccattgtcca cacatgagaa cagcatcagc cgcgacattt      1440
ctgaactcgt tagtgactca taattgagtt tgatttgatg taatgtgtga ttgtattct      1500
caatcaaaaaa cttccacatc aggcggttga aataagaaga gggaaagaga ataatcaagt      1560
gttttaagtg atcaggttcaa tgcttctctc tctctctggt gtttgttgtt ttggataaac      1620
attgtcgtct ttgaattctaa taaaagaagt ttctaccatt tgcagccat tgcacccttg      1680
aataacaaca acatattctc gtgtaatgag aaagtgaagt ctgatctgtg atgtatagga      1740
ctgggtatta atctggtaac ggtataataa ctggggtaga aaatagaatt tagactagta      1800
```


ttgggggtct aaacgaatt atacagaagc attgggcttg acttggccca tgagacctaa 1860
gcccataattt taaagaatta ggggtttctt ctctctttgt ctgttcaaat tgaagaaaacc 1920
tggttttttt tatttc

(2) INFORMATION FOR SEQ ID NO:1112:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 486 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..486
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569026

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1112:

Ser	Ile	Val	Ser	Val	Thr	Thr	Met	Ala	Lys	Thr	Arg	Gly	Ser	Cys	Cys
1			5						10					15	
Leu	Val	Asn	Ala	Leu	Ile	Ala	Ile	Ala	Phe	Leu	Ala	Thr	Ala	His	Leu
			20					25					30		
Cys	Glu	Ala	Gly	Leu	Ser	Gln	Lys	Glu	Gln	Asp	Lys	Val	Ser	Lys	Leu
			35				40					45			
Pro	Gly	Gln	Asn	Phe	Asn	Val	Ser	Phe	Ala	His	Tyr	Ser	Gly	Phe	Val
			50			55					60				
Ala	Thr	Asn	Glu	Gln	Leu	Gly	Arg	Ala	Leu	Phe	Tyr	Trp	Leu	Phe	Glu
					70					75					80
Ala	Val	Glu	Asp	Ala	Lys	Ser	Lys	Pro	Leu	Val	Leu	Trp	Leu	Asn	Gly
					85					90				95	
Gly	Pro	Gly	Cys	Ser	Ser	Val	Ala	Tyr	Gly	Glu	Ala	Glu	Glu	Ile	Gly
						100			105				110		
Pro	Phe	His	Ile	Lys	Ala	Asp	Gly	Lys	Thr	Leu	Tyr	Leu	Asn	Gln	Tyr
						115			120			125			
Ser	Trp	Asn	Gln	Ala	Ala	Asn	Ile	Leu	Phe	Leu	Asp	Ala	Pro	Val	Gly
						130					140				
Val	Gly	Tyr	Ser	Tyr	Ser	Asn	Thr	Ser	Ser	Asp	Leu	Lys	Ser	Asn	Gly
						145				150		155			160
Asp	Lys	Arg	Thr	Ala	Glu	Asp	Ser	Leu	Lys	Phe	Leu	Leu	Lys	Trp	Val
					165					170				175	
Glu	Arg	Phe	Pro	Glu	Tyr	Lys	Gly	Arg	Asp	Phe	Tyr	Ile	Val	Gly	Glu
					180				185				190		
Ser	Tyr	Ala	Gly	His	Tyr	Ile	Pro	Gln	Leu	Ser	Glu	Ala	Ile	Val	Lys
					195				200			205			
His	Asn	Gln	Gly	Ser	Asp	Lys	Asn	Ser	Ile	Asn	Leu	Lys	Gly	Tyr	Met
						210						220			
Val	Gly	Asn	Gly	Leu	Met	Asp	Asp	Phe	His	Asp	Arg	Leu	Gly	Leu	Phe
						225				230					240
Gln	Tyr	Ile	Trp	Ser	Leu	Gly	Phe	Ile	Ser	Asp	Gln	Thr	Tyr	Ser	Leu
						245				250				255	
Leu	Gln	Leu	Gln	Cys	Gly	Phe	Glu	Ser	Phe	Ile	His	Ser	Ser	Lys	Gln
						260			265				270		
Cys	Asn	Lys	Ile	Leu	Glu	Ile	Ala	Asp	Lys	Glu	Ile	Gly	Asn	Ile	Asp
						275			280			285			
Gln	Tyr	Ser	Val	Phe	Thr	Pro	Ala	Cys	Val	Ala	Asn	Ala	Ser	Gln	Ser
						290					300				
Asn	Met	Leu	Leu	Lys	Lys	Arg	Pro	Met	Thr	Ser	Arg	Val	Ser	Glu	Gln
						305					315				320
Tyr	Asp	Pro	Cys	Thr	Glu	Lys	His	Thr	Thr	Val	Tyr	Phe	Asn	Leu	Pro
						325			330				335		
Glu	Val	Gln	Lys	Ala	Leu	His	Val	Pro	Pro	Gly	Leu	Ala	Pro	Ser	Lys
						340			345				350		
Trp	Asp	Thr	Cys	Ser	Asp	Val	Val	Ser	Glu	His	Trp	Asn	Asp	Ser	Pro
						355			360				365		

Ser Ser Val Leu Asn Ile Tyr His Glu Leu Ile Ala Ala Gly Leu Arg
370 375 380
Ile Trp Val Phe Ser Gly Asp Ala Asp Ala Val Val Pro Val Thr Ser
385 390 395 400
Thr Arg Tyr Ser Ile Asp Ala Leu Asn Leu Arg Pro Leu Gly Ala Tyr
405 410 415
Gly Pro Trp Tyr Leu Asp Gly Gln Val Gly Gly Trp Ser Gln Gln Tyr
420 425 430
Ala Gly Leu Asn Phe Val Thr Val Arg Gly Ala Gly His Glu Val Pro
435 440 445
Leu His Arg Pro Lys Gln Ala Leu Ala Leu Phe Lys Ala Phe Ile Ser
450 455 460
Gly Thr Pro Leu Ser Thr His Glu Asn Ser Ile Ser Arg Asp Met Ser
465 470 475 480
Glu Leu Val Ser Asp Ser
485

(2) INFORMATION FOR SEQ ID NO:1113:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 479 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..479
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569027

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1113:

Met Ala Lys Thr Arg Gly Ser Cys Cys Leu Val Asn Ala Leu Ile Ala
1 5 10 15
Ile Ala Phe Leu Ala Thr Ala His Leu Cys Glu Ala Gly Leu Ser Gln
20 25 30
Lys Glu Gln Asp Lys Val Ser Lys Leu Pro Gly Gln Asn Phe Asn Val
35 40 45
Ser Phe Ala His Tyr Ser Gly Phe Val Ala Thr Asn Glu Gln Leu Gly
50 55 60
Arg Ala Leu Phe Tyr Trp Leu Phe Glu Ala Val Glu Asp Ala Lys Ser
65 70 75 80
Lys Pro Leu Val Leu Trp Leu Asn Gly Gly Pro Gly Cys Ser Ser Val
85 90 95
Ala Tyr Gly Glu Ala Glu Glu Ile Gly Pro Phe His Ile Lys Ala Asp
100 105 110
Gly Lys Thr Leu Tyr Leu Asn Gln Tyr Ser Trp Asn Gln Ala Ala Asn
115 120 125
Ile Leu Phe Leu Asp Ala Pro Val Gly Val Gly Tyr Ser Tyr Ser Asn
130 135 140
Thr Ser Ser Asp Leu Lys Ser Asn Gly Asp Lys Arg Thr Ala Glu Asp
145 150 155 160
Ser Leu Lys Phe Leu Leu Lys Trp Val Glu Arg Phe Pro Glu Tyr Lys
165 170 175
Gly Arg Asp Phe Tyr Ile Val Gly Glu Ser Tyr Ala Gly His Tyr Ile
180 185 190
Pro Gln Leu Ser Glu Ala Ile Val Lys His Asn Gln Gly Ser Asp Lys
195 200 205
Asn Ser Ile Asn Leu Lys Gly Tyr Met Val Gly Asn Gly Leu Met Asp
210 215 220
Asp Phe His Asp Arg Leu Gly Leu Phe Gln Tyr Ile Trp Ser Leu Gly
225 230 235 240
Phe Ile Ser Asp Gln Thr Tyr Ser Leu Leu Gln Leu Gln Cys Gly Phe
245 250 255
Glu Ser Phe Ile His Ser Ser Lys Gln Cys Asn Lys Ile Leu Glu Ile

260 265 270
Ala Asp Lys Glu Ile Gly Asn Ile Asp Gln Tyr Ser Val Phe Thr Pro
275 280 285
Ala Cys Val Ala Asn Ala Ser Gln Ser Asn Met Leu Leu Lys Lys Arg
290 295 300
Pro Met Thr Ser Arg Val Ser Glu Gln Tyr Asp Pro Cys Thr Glu Lys
305 310 315
His Thr Thr Val Tyr Phe Asn Leu Pro Glu Val Gln Lys Ala Leu His
325 330 335
Val Pro Pro Gly Leu Ala Pro Ser Lys Trp Asp Thr Cys Ser Asp Val
340 345 350
Val Ser Glu His Trp Asn Asp Ser Pro Ser Ser Val Leu Asn Ile Tyr
355 360 365
His Glu Leu Ile Ala Ala Gly Leu Arg Ile Trp Val Phe Ser Gly Asp
370 375 380
Ala Asp Ala Val Val Pro Val Thr Ser Thr Arg Tyr Ser Ile Asp Ala
385 390 395
Leu Asn Leu Arg Pro Leu Gly Ala Tyr Gly Pro Trp Tyr Leu Asp Gly
405 410 415
Gln Val Gly Gly Trp Ser Gln Gln Tyr Ala Gly Leu Asn Phe Val Thr
420 425 430
Val Arg Gly Ala Gly His Glu Val Pro Leu His Arg Pro Lys Gln Ala
435 440 445
Leu Ala Leu Phe Lys Ala Phe Ile Ser Gly Thr Pro Leu Ser Thr His
450 455 460
Glu Asn Ser Ile Ser Arg Asp Met Ser Glu Leu Val Ser Asp Ser
465 470 475

(2) INFORMATION FOR SEQ ID NO:1114:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 263 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..263
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569028

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1114:

Met Val Gly Asn Gly Leu Met Asp Asp Phe His Asp Arg Leu Gly Leu
1 5 10 15
Phe Gln Tyr Ile Trp Ser Leu Gly Phe Ile Ser Asp Gln Thr Tyr Ser
20 25 30
Leu Leu Gln Leu Gln Cys Gly Phe Glu Ser Phe Ile His Ser Ser Lys
35 40 45
Gln Cys Asn Lys Ile Leu Glu Ile Ala Asp Lys Glu Ile Gly Asn Ile
50 55 60
Asp Gln Tyr Ser Val Phe Thr Pro Ala Cys Val Ala Asn Ala Ser Gln
65 70 75 80
Ser Asn Met Leu Leu Lys Lys Arg Pro Met Thr Ser Arg Val Ser Glu
85 90 95
Gln Tyr Asp Pro Cys Thr Glu Lys His Thr Thr Val Tyr Phe Asn Leu
100 105 110
Pro Glu Val Gln Lys Ala Leu His Val Pro Pro Gly Leu Ala Pro Ser
115 120 125
Lys Trp Asp Thr Cys Ser Asp Val Val Ser Glu His Trp Asn Asp Ser
130 135 140
Pro Ser Ser Val Leu Asn Ile Tyr His Glu Leu Ile Ala Ala Gly Leu
145 150 155 160
Arg Ile Trp Val Phe Ser Gly Asp Ala Val Val Pro Val Thr
165 170 175

Ser Thr Arg Tyr Ser Ile Asp Ala Leu Asn Leu Arg Pro Leu Gly Ala
180 185 190
Tyr Gly Pro Trp Tyr Leu Asp Gly Gln Val Gly Gly Trp Ser Gln Gln
195 200 205
Tyr Ala Gly Leu Asn Phe Val Thr Val Arg Gly Ala Gly His Glu Val
210 215 220
Pro Leu His Arg Pro Lys Gln Ala Leu Ala Leu Phe Lys Ala Phe Ile
225 230 235 240
Ser Gly Thr Pro Leu Ser Thr His Glu Asn Ser Ile Ser Arg Asp Met
245 250 255
Ser Glu Leu Val Ser Asp Ser
260

(2) INFORMATION FOR SEQ ID NO:1115:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1666 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1666
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569029

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1115:

ctgattacga	tccaatcctc	tccgatcggt	ggcctcctgt	ttccgtttta	ctcgacatcg	60
ttccgacgac	ttttgacctg	gaatcgacgc	agtgaattca	attcaactat	tcacattgggt	120
ttgttgga	tggaacaaag	agcacctcct	agtaattttg	tgaatgatgg	gtcatttcagt	180
gaaagattca	gacagcttca	acaggagaaa	gataaagaca	aggataagggt	tgccaagttt	240
gaggattcta	agcccggtgaa	gattatatca	aatcccaaac	ctgctgtcaa	taaaaattcc	300
attggattaa	agcccaatga	tgcccagaag	aaagggtggt	agcttgcttt	cagcttgaag	360
caaaagtcta	agctctttgc	acctcctgtg	aagcttggt	cagaagaaga	tgaggatgat	420
gaggatgtta	aacatgaaca	aggcttttga	tcogtaaaag	gtcaaaagt	agagcagaga	480
gacacacctg	taaagtcaag	aaaagtatcg	gatgttgac	cacctccgcc	cagtgatcgt	540
actgtgaaga	aagtgtctga	taaaactaga	agttttgtg	ctaaagcatg	aaggccattt	600
gagcacatta	cacggcaaaa	gaatcctggg	gatacaccat	ttaaatttct	ttttgacgag	660
aactgtgcgg	actacaagta	ctatgtattc	aggctggctg	aagaggaaaa	attaatttca	720
caaaccaagg	attctgggtg	acttcacagt	gggtgatgcg	gctcgcgacc	gtccacagca	780
gcaatccctt	tgcaaaagcc	agcttatcaa	caaacaggat	atcagatccc	tgctccagct	840
ctctatgata	ctcctgtgga	acctggagct	tcctctagat	ctgctcaggc	atcaattaga	900
agaccagcgc	acagtgactc	ctttagtggg	cagagggggt	cagaccctct	atcaatagct	960
gagcttttca	tgaagaaggg	tgcccagaag	gagaaatga	gagcttctag	cagctcaaaa	1020
gacgaaatgc	ctccaccagc	ttcccttcaa	ggcccatctg	aaacttcctc	cacagaccct	1080
ggaaagagag	gtcatcacat	gggtgattat	atcccacttg	AGgagctaga	taagttcctt	1140
tcaaaagtga	atgacgcagc	tgacacaaaa	gccacaaaag	aggctgctga	gaaagcggaag	1200
atccagcag	ataatgtttg	acataaactc	ttgtcaaaaa	tggtgtgaaa	agaaggtgaa	1260
gggtattgaa	gctccagaaa	gggtatggca	gacctataa	tgccaggcga	tgtaaagaca	1320
aacaaacttg	gagttgggtg	ttccgctcca	ggagaagtca	agcctgagga	tgatatatac	1380
gagcagta	agaagcggat	gatgctgggt	tacaaacaca	gacccaatcc	actcgggaat	1440
ccagggaagg	cgtattacta	aggatcaaat	caatgtgtta	tgcgcaatta	ttatctttgg	1500
ttcacctcag	cacgctctga	gctttgcttt	tctattataa	agaatgttga	agcttttaga	1560
ttactgat	attgaagtgt	tggtatgcat	tgaatttcgc	tttcagtggt	caaatagatc	1620
tccttgacag	acatatcagt	tgaaatacaa	tggattttgt	attggcc		

(2) INFORMATION FOR SEQ ID NO:1116:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 486 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide

(B) LOCATION: 1..486

(D) OTHER INFORMATION: / Ceres Seq. ID 1569030

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1116:

Leu	Ile	Thr	Ile	Gln	Ser	Ser	Pro	Ile	Val	Gly	Leu	Leu	Phe	Pro	Phe
1				5					10					15	
Tyr	Ser	Thr	Ser	Phe	Arg	Arg	Leu	Leu	Thr	Trp	Asn	Arg	Arg	Ser	Asp
			20					25					30		
Phe	Asn	Ser	Thr	Ile	Ala	Leu	Gly	Leu	Ala	Met	Asp	Lys	Gly	Ala	
			35				40				45				
Pro	Pro	Ser	Ile	Phe	Val	Asn	Asp	Gly	Ser	Phe	Met	Glu	Arg	Phe	Arg
			50			55					60				
Gln	Leu	Gln	Gln	Glu	Lys	Asp	Lys	Asp	Lys	Val	Val	Gln	Val		
65				70				75				80			
Glu	Asp	Ser	Lys	Pro	Val	Lys	Ile	Ile	Ser	Asn	Pro	Lys	Pro	Ala	Ala
			85					90				95			
Asn	Lys	Ile	Ser	Ile	Gly	Leu	Lys	Pro	Asn	Asp	Ala	Gln	Lys	Lys	Gly
			100				105					110			
Gly	Lys	Leu	Ala	Phe	Ser	Leu	Lys	Gln	Lys	Ser	Lys	Leu	Leu	Ala	Pro
			115				120					125			
Pro	Val	Lys	Leu	Gly	Thr	Glu	Glu	Asp	Glu	Asp	Asp	Glu	Asp	Val	Lys
			130			135					140				
His	Glu	Gln	Gly	Phe	Gly	Ser	Val	Lys	Arg	Gln	Lys	Leu	Glu	Gln	Arg
145				150						155					160
Asp	Thr	Pro	Val	Lys	Ser	Ala	Lys	Val	Ser	Asp	Val	Ala	Pro	Pro	Pro
			165						170				175		
Pro	Ser	Asp	Pro	Thr	Val	Lys	Lys	Val	Ala	Asp	Lys	Leu	Ala	Ser	Phe
			180				185					190			
Val	Ala	Lys	His	Gly	Arg	Pro	Phe	Glu	His	Ile	Thr	Arg	Gln	Lys	Asn
			195				200					205			
Pro	Gly	Asp	Thr	Pro	Phe	Lys	Phe	Leu	Phe	Asp	Glu	Asn	Cys	Ala	Asp
			210			215					220				
Tyr	Lys	Tyr	Tyr	Val	Phe	Arg	Leu	Ala	Glu	Glu	Glu	Lys	Leu	Ile	Ser
225				230					235					240	
Gln	Thr	Lys	Asp	Ser	Gly	Val	Leu	His	Ser	Gly	Asp	Ala	Gly	Ser	Arg
			245					250					255		
Thr	Ser	Thr	Ala	Ala	Ile	Pro	Leu	Gln	Lys	Pro	Ala	Tyr	Gln	Gln	Thr
			260				265						270		
Gly	Tyr	Gln	Ile	Pro	Ala	Ser	Ala	Leu	Tyr	Asp	Thr	Pro	Val	Glu	Pro
			275				280					285			
Gly	Ala	Ser	Ser	Arg	Ser	Ala	Gln	Ala	Ser	Ile	Thr	Arg	Pro	Ser	Asp
			290			295						300			
Ser	Asp	Ser	Phe	Ser	Gly	Pro	Arg	Gly	Ala	Asp	Pro	Leu	Ser	Met	Met
305				310					315						320
Glu	Phe	Tyr	Met	Lys	Lys	Ala	Ala	Gln	Glu	Glu	Lys	Met	Arg	Arg	Pro
			325					330				335			
Arg	Gln	Ser	Lys	Asp	Glu	Met	Pro	Pro	Pro	Ala	Ser	Leu	Gln	Gly	Pro
			340				345					350			
Ser	Glu	Thr	Ser	Ser	Thr	Asp	Pro	Gly	Lys	Arg	Gly	His	His	Met	Gly
			355				360					365			
Asp	Tyr	Ile	Pro	Leu	Glu	Glu	Leu	Asp	Lys	Phe	Leu	Ser	Lys	Cys	Asn
			370			375					380				
Asp	Ala	Ala	Ala	Gln	Lys	Ala	Thr	Lys	Glu	Ala	Ala	Glu	Lys	Ala	Lys
385				390					395						400
Ile	Gln	Ala	Asp	Asn	Val	Gly	His	Lys	Leu	Leu	Ser	Lys	Met	Gly	Trp
			405						410				415		
Lys	Glu	Gly	Glu	Gly	Ile	Gly	Ser	Ser	Arg	Lys	Gly	Met	Ala	Asp	Pro
			420				425					430			
Ile	Met	Ala	Gly	Asp	Val	Lys	Thr	Asn	Asn	Leu	Gly	Val	Gly	Ala	Ser
			435				440					445			
Ala	Pro	Gly	Glu	Val	Lys	Pro	Glu	Asp	Asp	Ile	Tyr	Glu	Gln	Tyr	Lys
			450			455						460			

Lys Arg Met Met Leu Gly Tyr Lys His Arg Pro Asn Pro Leu Gly Asn
465 470 475 480
Pro Arg Lys Ala Tyr Tyr
485

(2) INFORMATION FOR SEQ ID NO:1117:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 443 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..443
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569031

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1117:

Met	Asp	Lys	Gly	Ala	Pro	Pro	Ser	Ile	Phe	Val	Asn	Asp	Gly	Ser	Phe
1				5					10					15	
Met	Glu	Arg	Phe	Arg	Gln	Leu	Gln	Gln	Glu	Lys	Asp	Lys	Asp	Lys	Asp
			20					25					30		
Lys	Val	Val	Gln	Val	Glu	Asp	Ser	Lys	Pro	Val	Lys	Ile	Ile	Ser	Asn
		35					40					45			
Pro	Lys	Pro	Ala	Ala	Asn	Lys	Ile	Ser	Ile	Gly	Leu	Lys	Pro	Asn	Asp
		50				55					60				
Ala	Gln	Lys	Lys	Gly	Gly	Lys	Leu	Ala	Phe	Ser	Leu	Lys	Gln	Lys	Ser
65					70				75					80	
Lys	Leu	Leu	Ala	Pro	Pro	Val	Lys	Leu	Gly	Thr	Glu	Glu	Asp	Glu	Asp
			85						90				95		
Asp	Glu	Asp	Val	Lys	His	Glu	Gln	Gly	Phe	Gly	Ser	Val	Lys	Arg	Gln
			100					105					110		
Lys	Leu	Glu	Gln	Arg	Asp	Thr	Pro	Val	Lys	Ser	Ala	Lys	Val	Ser	Asp
		115					120					125			
Val	Ala	Pro	Pro	Pro	Pro	Ser	Asp	Pro	Thr	Val	Lys	Lys	Val	Ala	Asp
		130				135					140				
Lys	Leu	Ala	Ser	Phe	Val	Ala	Lys	His	Gly	Arg	Pro	Phe	Glu	His	Ile
145					150					155					160
Thr	Arg	Gln	Lys	Asn	Pro	Gly	Asp	Thr	Pro	Phe	Lys	Phe	Leu	Phe	Asp
			165						170					175	
Glu	Asn	Cys	Ala	Asp	Tyr	Lys	Tyr	Tyr	Val	Phe	Arg	Leu	Ala	Glu	Glu
			180					185					190		
Glu	Lys	Leu	Ile	Ser	Gln	Thr	Lys	Asp	Ser	Gly	Val	Leu	His	Ser	Gly
		195					200				205				
Asp	Ala	Gly	Ser	Arg	Thr	Ser	Thr	Ala	Ala	Ile	Pro	Leu	Gln	Lys	Pro
		210				215					220				
Ala	Tyr	Gln	Gln	Thr	Gly	Tyr	Gln	Ile	Pro	Ala	Ser	Ala	Leu	Tyr	Asp
225					230				235					240	
Thr	Pro	Val	Glu	Pro	Gly	Ala	Ser	Ser	Arg	Ser	Ala	Gln	Ala	Ser	Ile
			245						250					255	
Thr	Arg	Pro	Ser	Asp	Ser	Asp	Ser	Phe	Ser	Gly	Pro	Arg	Gly	Ala	Asp
			260					265					270		
Pro	Leu	Ser	Met	Met	Glu	Phe	Tyr	Met	Lys	Lys	Ala	Ala	Gln	Glu	Glu
		275					280					285			
Lys	Met	Arg	Arg	Pro	Arg	Gln	Ser	Lys	Asp	Glu	Met	Pro	Pro	Pro	Ala
		290				295					300				
Ser	Leu	Gln	Gly	Pro	Ser	Glu	Thr	Ser	Ser	Thr	Asp	Pro	Gly	Lys	Arg
305					310					315					320
Gly	His	His	Met	Gly	Asp	Tyr	Ile	Pro	Leu	Glu	Glu	Leu	Asp	Lys	Phe
			325						330					335	
Leu	Ser	Lys	Cys	Asn	Asp	Ala	Ala	Ala	Gln	Lys	Ala	Thr	Lys	Glu	Ala
			340					345					350		
Ala	Glu	Lys	Ala	Lys	Ile	Gln	Ala	Asp	Asn	Val	Gly	His	Lys	Leu	Leu

(2) INFORMATION FOR SEQ ID NO:1118:

(A) LENGTH: 427 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

MOLECULE TYPE: peptid

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..427

(D) OTHER INFORMATION: / Ceres Seq. ID 1569032

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1118:

Met	Glu	Arg	Phe	Arg	Gln	Leu	Gln	Gln	Glu	Lys	Asp	Lys	Asp	Lys	Asp
1				5					10					15	
Lys	Val	Val	Gln	Val	Glu	Asp	Ser	Lys	Pro	Val	Lys	Ile	Ile	Ser	Asn
			20					25					30		
Pro	Lys	Pro	Ala	Ala	Asn	Lys	Ile	Ser	Ile	Gly	Leu	Lys	Pro	Asn	Asp
		35					40					45			
Ala	Gln	Lys	Lys	Gly	Gly	Lys	Leu	Ala	Phe	Ser	Leu	Lys	Gln	Lys	Ser
	50					55					60				
Lys	Leu	Leu	Ala	Pro	Pro	Val	Lys	Leu	Gly	Thr	Glu	Glu	Asp	Glu	Asp
65				70						75				80	
Asp	Glu	Asp	Val	Lys	His	Glu	Gln	Gly	Phe	Gly	Ser	Val	Lys	Arg	Gln
				85					90					95	
Lys	Leu	Glu	Gln	Arg	Asp	Thr	Pro	Val	Lys	Ser	Ala	Lys	Val	Ser	Asp
		100						105					110		
Val	Ala	Pro	Pro	Pro	Pro	Ser	Asp	Pro	Thr	Val	Lys	Lys	Val	Ala	Asp
		115						120				125			
Lys	Leu	Ala	Ser	Phe	Val	Ala	Lys	His	Gly	Arg	Pro	Phe	Glu	His	Ile
	130					135					140				
Thr	Arg	Gln	Lys	Asn	Pro	Gly	Asp	Thr	Pro	Phe	Lys	Phe	Leu	Phe	Asp
145				150						155					160
Glu	Asn	Cys	Ala	Asp	Tyr	Lys	Tyr	Tyr	Val	Phe	Arg	Leu	Ala	Glu	Glu
				165					170					175	
Glu	Lys	Leu	Ile	Ser	Gln	Thr	Lys	Asp	Ser	Gly	Val	Leu	His	Ser	Gly
			180					185					190		
Asp	Ala	Gly	Ser	Arg	Thr	Ser	Thr	Ala	Ala	Ile	Pro	Leu	Gln	Lys	Pro
		195					200					205			
Ala	Tyr	Gln	Gln	Thr	Gly	Tyr	Gln	Ile	Pro	Ala	Ser	Ala	Leu	Tyr	Asp
	210					215					220				
Thr	Pro	Val	Glu	Pro	Gly	Ala	Ser	Ser	Arg	Ser	Ala	Gln	Ala	Ser	Ile
225					230					235				240	
Thr	Arg	Pro	Ser	Asp	Ser	Asp	Ser	Phe	Ser	Gly	Pro	Arg	Gly	Ala	Asp
			245					250					255		
Pro	Leu	Ser	Met	Met	Glu	Phe	Tyr	Met	Lys	Lys	Ala	Ala	Gln	Glu	Glu
		260						265					270		
Lys	Met	Arg	Arg	Pro	Arg	Gln	Ser	Lys	Asp	Glu	Met	Pro	Pro	Pro	Ala
		275					280					285			
Ser	Leu	Gln	Gly	Pro	Ser	Glu	Thr	Ser	Ser	Thr	Asp	Pro	Gly	Lys	Arg
	290					295					300				

Gly His His Met Gly Asp Tyr Ile Pro Leu Glu Glu Leu Asp Lys Phe
305 310 315 320
Leu Ser Lys Cys Asn Asp Ala Ala Ala Gln Lys Ala Thr Lys Glu Ala
325 330 335
Ala Glu Lys Ala Lys Ile Gln Ala Asp Asn Val Gly His Lys Leu Leu
340 345 350
Ser Lys Met Gly Trp Lys Glu Gly Glu Gly Ile Gly Ser Ser Arg Lys
355 360 365
Gly Met Ala Asp Pro Ile Met Ala Gly Asp Val Lys Thr Asn Asn Leu
370 375 380
Gly Val Gly Ala Ser Ala Pro Gly Glu Val Lys Pro Glu Asp Asp Ile
385 390 395 400
Tyr Glu Gln Tyr Lys Lys Arg Met Met Leu Gly Tyr Lys His Arg Pro
405 410 415
Asn Pro Leu Gly Asn Pro Arg Lys Ala Tyr Tyr
420 425

(2) INFORMATION FOR SEQ ID NO:1119:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1316 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1316
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569041

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1119:

aaaaaccaaa	attcgcgcaga	gagaaagtatg	tccgaagaCgc	tggtgcaacc	ggtagggcaa	60
aagaggttga	ctaattgtgc	agtggttcgt	ctcaaaaagc	aaggccaatcg	cttcgcagatc	120
gcttggtaca	agaataaagt	ccatttcacg	cggtctggcg	tggaagaagga	atagatagaa	180
gtgctacagt	cgataactgt	ttattcaaat	gtttcgaaag	gagttcttgc	aaaatcgaaa	240
gacttgatga	agtcgtttgg	atcagatgat	catcacgaaa	tatgcacga	tattttggag	300
aaaggagagc	ttcaagttgc	tggaaaagaa	agagaatcac	agttctcaag	ccaggtttcgg	360
gatatagcaa	cgattgttat	gcagaaaact	atcaaccctg	aaacacaaag	accattatacc	420
atcagcatgg	tagagcgctc	aatgcacgaa	attcattttg	ctgttgatcc	tcataagtaat	480
tccaagaagc	aggcacttga	tgtcatccgt	gagctgcaaa	agcacttccc	tataaagcgt	540
tctccaatga	gactgcgtct	tactgttcct	gttcaaaatt	tccctctcgt	tctggagaag	600
ctaaaagaat	gggatggtag	tgttgtctcc	aaagacgaat	ctggaacaca	gatgtccact	660
gtctgcgaga	tggaaacccgg	ccattatccga	gagtgatgat	cccattgtgag	gagtatccag	720
ggaagactag	aaataactgc	tgtatcagtt	catgcagaag	gtgacacaag	catggatcat	780
tacgatgaagc	atgatgatat	ggcattgcaa	accacaaagc	cgttgttacc	tgctgagact	840
gagactaagg	atttgaccga	tccctcgctt	gaacttagca	agaaaactgca	gaagcaagag	900
ataagtacta	catagatacac	aaagcaagaa	ggtggagaag	aaaagaaggg	gaccaagtgc	960
agcacttgca	acacgtttcg	ttggagagct	aagcaataca	gagagcactg	taagagtgtat	1020
tgccacaaca	acaacottaa	tcgtaaagact	cggaaactcc	ctcctattag	tgctgcagcaa	1080
tgcattctcg	agattgacat	ggaagactct	agagcagatt	tgaagaacta	ctctttctga	1140
aactacaatt	ttctctcttt	gtgcttttaa	ttttgtcaat	gtgttaaatc	tcgtagtcat	1200
atgtgagtat	gaatacacaa	aacttgtgga	atgaaatttt	gcgcacaaat	taagagtgaaa	1260
aacttgtgtt	taagagacaa	gcttggtgat	ttggtatttt	attaataaat	gtgacc	

(2) INFORMATION FOR SEQ ID NO:1120:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 379 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..379
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569042

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1120:

Lys	Asn	Gln	Asn	Ser	Arg	Glu	Arg	Ser	Met	Ser	Lys	Thr	Leu	Val	Gln
1			5					10					15		
Pro	Val	Gly	Gln	Lys	Arg	Leu	Thr	Asn	Val	Ala	Val	Val	Arg	Leu	Lys
			20					25					30		
Lys	Gln	Gly	Asn	Arg	Phe	Glu	Ile	Ala	Cys	Tyr	Lys	Asn	Lys	Val	Leu
			35				40					45			
Ser	Trp	Arg	Ser	Gly	Val	Glu	Lys	Asp	Ile	Asp	Glu	Val	Leu	Gln	Ser
			50			55					60				
His	Thr	Val	Tyr	Ser	Asn	Val	Ser	Lys	Gly	Val	Leu	Ala	Lys	Ser	Lys
			65		70				75					80	
Asp	Leu	Met	Lys	Ser	Phe	Gly	Ser	Asp	Asp	His	Thr	Lys	Ile	Cys	Ile
			85					90					95		
Asp	Ile	Leu	Glu	Lys	Gly	Glu	Leu	Gln	Val	Ala	Gly	Lys	Glu	Arg	Glu
			100					105					110		
Ser	Gln	Phe	Ser	Ser	Gln	Phe	Arg	Asp	Ile	Ala	Thr	Ile	Val	Met	Gln
			115				120					125			
Lys	Thr	Ile	Asn	Pro	Glu	Thr	Gln	Arg	Pro	Tyr	Thr	Ile	Ser	Met	Val
			130			135					140				
Glu	Arg	Leu	Met	His	Glu	Ile	His	Phe	Ala	Val	Asp	Pro	His	Ser	Asn
			145		150				155						160
Ser	Lys	Lys	Gln	Ala	Leu	Asp	Val	Ile	Arg	Glu	Leu	Gln	Lys	His	Phe
			165					170						175	
Pro	Ile	Lys	Arg	Ser	Pro	Met	Arg	Leu	Arg	Leu	Thr	Val	Pro	Val	Gln
			180				185						190		
Asn	Phe	Pro	Ser	Leu	Leu	Glu	Lys	Leu	Lys	Glu	Trp	Asp	Gly	Ser	Val
			195				200					205			
Val	Ser	Lys	Asp	Glu	Ser	Gly	Thr	Gln	Met	Ser	Thr	Val	Cys	Glu	Met
			210			215					220				
Glu	Pro	Gly	Leu	Phe	Arg	Glu	Cys	Asp	Ser	His	Val	Arg	Ser	Ile	Gln
			225		230				235					240	
Gly	Arg	Leu	Glu	Ile	Leu	Ala	Val	Ser	Val	His	Ala	Glu	Gly	Asp	Thr
			245					250					255		
Ser	Met	Asp	His	Tyr	Asp	Glu	His	Asp	Asp	Met	Ala	Leu	Gln	Thr	His
			260				265					270			
Lys	Pro	Leu	Leu	Pro	Ala	Glu	Thr	Glu	Thr	Lys	Asp	Leu	Thr	Asp	Pro
			275				280					285			
Val	Val	Glu	Leu	Ser	Lys	Lys	Leu	Gln	Lys	Gln	Glu	Ile	Ser	Thr	Thr
			290			295					300				
Asp	Asn	Thr	Lys	Gln	Glu	Gly	Gly	Glu	Glu	Lys	Lys	Gly	Thr	Lys	Cys
			305		310					315					320
Ser	Thr	Cys	Asn	Thr	Phe	Val	Gly	Glu	Ala	Lys	Gln	Tyr	Arg	Glu	His
			325					330						335	
Cys	Lys	Ser	Asp	Trp	His	Lys	His	Asn	Leu	Asn	Arg	Lys	Thr	Arg	Lys
			340				345					350			
Leu	Pro	Pro	Ile	Ser	Ala	Asp	Glu	Cys	Met	Ser	Glu	Ile	Asp	Met	Asp
			355			360						365			
Asp	Ser	Arg	Ala	Asp	Leu	Lys	Asp	Tyr	Ser	Phe					
			370			375									

(2) INFORMATION FOR SEQ ID NO:1121:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 370 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..370
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569043

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1121:

Met Ser Lys Thr Leu Val Gln Pro Val Gly Gln Lys Arg Leu Thr Asn
1 5 10 15
Val Ala Val Val Arg Leu Lys Lys Gln Gly Asn Arg Phe Glu Ile Ala
20 25 30
Cys Tyr Lys Asn Lys Val Leu Ser Trp Arg Ser Gly Val Glu Lys Asp
35 40 45
Ile Asp Glu Val Leu Gln Ser His Thr Val Tyr Ser Asn Val Ser Lys
50 55 60
Gly Val Leu Ala Lys Ser Lys Asp Leu Met Lys Ser Phe Gly Ser Asp
65 70 75 80
Asp His Thr Lys Ile Cys Ile Asp Ile Leu Glu Lys Gly Glu Leu Gln
85 90 95
Val Ala Gly Lys Glu Arg Glu Ser Gln Phe Ser Ser Gln Phe Arg Asp
100 105 110
Ile Ala Thr Ile Val Met Gln Lys Thr Ile Asn Pro Glu Thr Gln Arg
115 120 125
Pro Tyr Thr Ile Ser Met Val Glu Arg Leu Met His Glu Ile His Phe
130 135 140
Ala Val Asp Pro His Ser Asn Ser Lys Lys Gln Ala Leu Asp Val Ile
145 150 155 160
Arg Glu Leu Gln Lys His Phe Pro Ile Lys Arg Ser Pro Met Arg Leu
165 170 175
Arg Leu Thr Val Pro Val Gln Asn Phe Pro Ser Leu Leu Glu Lys Leu
180 185 190
Lys Glu Trp Asp Gly Ser Val Val Ser Lys Asp Glu Ser Gly Thr Gln
195 200 205
Met Ser Thr Val Cys Glu Met Glu Pro Gly Leu Phe Arg Glu Cys Asp
210 215 220
Ser His Val Arg Ser Ile Gln Gly Arg Leu Glu Ile Leu Ala Val Ser
225 230 235 240
Val His Ala Glu Gly Asp Thr Ser Met Asp His Tyr Asp Glu His Asp
245 250 255
Asp Met Ala Leu Gln Thr His Lys Pro Leu Leu Pro Ala Glu Thr Glu
260 265 270
Thr Lys Asp Leu Thr Asp Pro Val Val Glu Leu Ser Lys Lys Leu Gln
275 280 285
Lys Gln Glu Ile Ser Thr Thr Asp Asn Thr Lys Gln Glu Gly Gly Glu
290 295 300
Glu Lys Lys Gly Thr Lys Cys Ser Thr Cys Asn Thr Phe Val Gly Glu
305 310 315 320
Ala Lys Gln Tyr Arg Glu His Cys Lys Ser Asp Trp His Lys His Asn
325 330 335
Leu Asn Arg Lys Thr Arg Lys Leu Pro Pro Ile Ser Ala Asp Glu Cys
340 345 350
Met Ser Glu Ile Asp Met Asp Asp Ser Arg Ala Asp Leu Lys Asp Tyr
355 360 365
Ser Phe
370

(2) INFORMATION FOR SEQ ID NO:1122:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 297 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..297

(D) OTHER INFORMATION: / Ceres Seq. ID 1569044

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1122:

Met Lys Ser Phe Gly Ser Asp Asp His Thr Lys Ile Cys Ile Asp Ile

1	5	10	15
Leu Glu Lys Gly	Glu Leu Gln Val	Ala Gly Lys Glu Arg	Glu Ser Gln
20	25	30	
Phe Ser Ser Gln	Phe Arg Asp	Ile Ala Thr	Ile Val Met
35	40	45	
Ile Asn Pro Glu	Thr Gln Arg	Pro Tyr Thr	Ile Ser Met
50	55	60	
Leu Met His Glu	Ile His Phe	Ala Val Asp	Pro His Ser
65	70	75	
Lys Gln Ala Leu	Asp Val Ile	Arg Glu Leu	Gln Lys His
85	90	95	
Lys Arg Ser Pro	Met Arg Leu	Arg Leu Thr	Val Pro Val
100	105	110	
Pro Ser Leu Leu	Glu Lys Leu	Lys Glu Trp	Asp Gly Ser
115	120	125	
Lys Asp Glu Ser	Gly Thr Gln	Met Ser Thr	Val Cys Glu
130	135	140	
Gly Leu Phe Arg	Glu Cys Asp	Ser His Val	Arg Ser Ile
145	150	155	
Leu Glu Ile Leu	Ala Val Ser	Val His Ala	Glu Gly Asp
165	170	175	
Asp His Tyr Asp	Glu His Asp	Asp Met Ala	Leu Gln Thr
180	185	190	
Leu Leu Pro Ala	Glu Thr Glu	Thr Lys Asp	Leu Thr Asp
195	200	205	
Glu Leu Ser Lys	Lys Leu Gln	Lys Glu Ile	Ser Thr Thr
210	215	220	
Thr Lys Gln Glu	Gly Gly Glu	Lys Lys Gly	Thr Lys Cys
225	230	235	
Cys Asn Thr Phe	Val Gly Glu	Ala Lys Gln	Tyr Arg Glu
245	250	255	
Ser Asp Trp His	Lys His Asn	Leu Asn Arg	Lys Thr Arg
260	265	270	
Pro Ile Ser Ala	Asp Glu Cys	Met Ser Glu	Ile Asp Met
275	280	285	
Arg Ala Asp Leu	Lys Asp Tyr	Ser Phe	
290	295		

(2) INFORMATION FOR SEQ ID NO:1123:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1314 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1314

(D) OTHER INFORMATION: / Ceres Seq. ID 1569049

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1123:

aaaaaaagac	gtctcacaca	aaaaagctgc	tagaggaaga	agacgattca	cttctttTcc	60
cgccacatttc	actatcttct	ccggttggtga	gcaaaagatgt	tgtgggtcga	caagtacagg	120
ccgaaatacac	tcgacaagggt	catagtctcat	gaagatatcg	cccaaaaaact	caagaaatttg	180
gtttccgagc	aagattgtcc	acatttgcctc	ttttatgggc	cgtcagggttc	tggtaaagaaa	240
accctaatta	tgctcttctc	caagcagata	tatggggccca	gtgcagagaa	ggtgaaagtgt	300
gagaaacagg	catggaaagt	tgatgctggg	agtagaacta	ttgatctgga	gctcactaca	360
ttatcaagca	ccaatcatgt	ggaaacttact	ccaagtgtat	caggctttca	ggacagatat	420
attgttcagg	agataattaa	agaaattggcc	aagaacagac	caattgacac	gaaagaaaag	480
aagggatata	aggtgttgtt	attaaatgag	gttgacaagc	tctcacgaga	agctcaacat	540
tctctgcgga	gaacaatgga	gaaatacagc	tcactcttgc	gtctcatctt	atgtctcaac	600
agctcttcga	aggttaccca	agccattaag	tctcgtttgc	tcaatgtgcg	cataaatgca	660
ccttcgcagg	aagagatagt	gaaagtgttg	gagttcgttg	caagaaaaga	aagtctgcaa	720

ctgccccagg	gttttgctgc	tcgtattgct	gaaaaatcaa	atcgcgactct	aagaagagct	780
attttgtcac	ttgaaacttg	tcgtgtccaa	aactatccgt	tcacaggttaa	ccaagtgtata	840
tctccatgag	attgggaaga	gtatgttgct	gaaatagcaa	ctgacatgat	gaaagaacaa	900
agccctaaaa	agttatttca	ggtgcgtgga	aagggtgacg	aattactagt	taattgtatt	960
ccaccagaag	tcatttctaa	gagactctct	catgaattgc	tgaagaaact	ggactcagag	1020
ctaaagcttg	aagtcctgca	ctgggctgca	tattatgaac	atcggtatgag	attaggtcag	1080
aaagccatat	ttcacataga	agcatttggt	gccaaagtta	tgacatata	caaaacttc	1140
ctcatttcaa	cgtttgggta	gagaagagag	gcttcaaatc	gaggaaaaga	agatagactt	1200
gcactttgac	tgttattttt	atgcgtgac	cggtggttctg	aagttaaagt	ttctgtttag	1260
tggtctgctt	taacttttga	tgtttgaatt	tgtttccttc	aacttgactg	tctt	

(2) INFORMATION FOR SEQ ID NO:1124:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 354 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..354

(D) OTHER INFORMATION: / Ceres Seq. ID 1569050

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1124:

Met	Leu	Trp	Val	Asp	Lys	Tyr	Arg	Pro	Lys	Ser	Leu	Asp	Lys	Val	Ile
1				5					10					15	
Val	His	Glu	Asp	Ile	Ala	Gln	Lys	Leu	Lys	Lys	Leu	Val	Ser	Glu	Gln
				20					25					30	
Asp	Cys	Pro	His	Leu	Leu	Phe	Tyr	Gly	Pro	Ser	Gly	Ser	Gly	Lys	Lys
				35					40					45	
Thr	Leu	Ile	Met	Ala	Leu	Leu	Lys	Gln	Ile	Tyr	Gly	Ala	Ser	Ala	Glu
				50					55					60	
Lys	Val	Lys	Val	Glu	Asn	Arg	Ala	Trp	Lys	Val	Asp	Ala	Gly	Ser	Arg
				65					70					75	
Thr	Ile	Asp	Leu	Glu	Leu	Thr	Thr	Leu	Ser	Ser	Thr	Asn	His	Val	Glu
				85					90					95	
Leu	Thr	Pro	Ser	Asp	Ala	Gly	Phe	Gln	Asp	Arg	Tyr	Ile	Val	Gln	Glu
				100					105					110	
Ile	Ile	Lys	Glu	Met	Ala	Lys	Asn	Arg	Pro	Ile	Asp	Thr	Lys	Gly	Lys
				115					120					125	
Lys	Gly	Tyr	Lys	Val	Leu	Val	Leu	Asn	Glu	Val	Asp	Lys	Leu	Ser	Arg
				130					135					140	
Glu	Ala	Gln	His	Ser	Leu	Arg	Arg	Thr	Met	Glu	Lys	Tyr	Ser	Ser	Ser
				145					150					155	
Cys	Arg	Leu	Ile	Leu	Cys	Cys	Asn	Ser	Ser	Ser	Lys	Val	Thr	Glu	Ala
				165					170					175	
Ile	Lys	Ser	Arg	Cys	Leu	Asn	Val	Arg	Ile	Asn	Ala	Pro	Ser	Gln	Glu
				180					185					190	
Glu	Ile	Val	Lys	Val	Leu	Glu	Phe	Val	Ala	Lys	Lys	Glu	Ser	Leu	Gln
				195					200					205	
Leu	Pro	Gln	Gly	Phe	Ala	Ala	Arg	Ile	Ala	Glu	Lys	Ser	Asn	Arg	Ser
				210					215					220	
Leu	Arg	Arg	Ala	Ile	Leu	Ser	Leu	Glu	Thr	Cys	Arg	Val	Gln	Asn	Tyr
				225					230					235	
Pro	Phe	Thr	Gly	Asn	Gln	Val	Ile	Ser	Pro	Met	Asp	Trp	Glu	Glu	Tyr
				245					250					255	
Val	Ala	Glu	Ile	Ala	Thr	Asp	Met	Met	Lys	Glu	Gln	Ser	Pro	Lys	Lys
				260					265					270	
Leu	Phe	Gln	Val	Arg	Gly	Lys	Val	Tyr	Glu	Leu	Leu	Val	Asn	Cys	Ile
				275					280					285	
Pro	Pro	Glu	Val	Ile	Leu	Lys	Arg	Leu	Leu	His	Glu	Leu	Leu	Lys	Lys
				290					295					300	
Leu	Asp	Ser	Glu	Leu	Lys	Leu	Glu	Val	Cys	His	Trp	Ala	Ala	Tyr	Tyr

305 310 315 320
Glu His Arg Met Arg Leu Gly Gln Lys Ala Ile Phe His Ile Glu Ala
325 330 335
Phe Val Ala Lys Phe Met Ser Ile Tyr Lys Asn Phe Leu Ile Ser Thr
340 345 350
Phe Gly

(2) INFORMATION FOR SEQ ID NO:1125:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 303 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..303
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569051

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1125:

Met Ala Leu Leu Lys Gln Ile Tyr Gly Ala Ser Ala Glu Lys Val Lys
1 5 10 15
Val Glu Asn Arg Ala Trp Lys Val Asp Ala Gly Ser Arg Thr Ile Asp
20 25 30
Leu Glu Leu Thr Thr Leu Ser Ser Thr Asn His Val Glu Leu Thr Pro
35 40 45
Ser Asp Ala Gly Phe Gln Asp Arg Tyr Ile Val Gln Glu Ile Ile Lys
50 55 60
Glu Met Ala Lys Asn Arg Pro Ile Asp Thr Lys Gly Lys Lys Gly Tyr
65 70 75 80
Lys Val Leu Val Leu Asn Glu Val Asp Lys Leu Ser Arg Glu Ala Gln
85 90 95
His Ser Leu Arg Arg Thr Met Glu Lys Tyr Ser Ser Ser Cys Arg Leu
100 105 110
Ile Leu Cys Asn Ser Ser Ser Lys Val Thr Glu Ala Ile Lys Ser
115 120 125
Arg Cys Leu Asn Val Arg Ile Asn Ala Pro Ser Gln Glu Glu Ile Val
130 135 140
Lys Val Leu Glu Phe Val Ala Lys Lys Glu Ser Leu Gln Leu Pro Gln
145 150 155 160
Gly Phe Ala Ala Arg Ile Ala Glu Lys Ser Asn Arg Ser Leu Arg Arg
165 170 175
Ala Ile Leu Ser Leu Glu Thr Cys Arg Val Gln Asn Tyr Pro Phe Thr
180 185 190
Gly Asn Gln Val Ile Ser Pro Met Asp Trp Glu Glu Tyr Val Ala Glu
195 200 205
Ile Ala Thr Asp Met Met Lys Glu Gln Ser Pro Lys Lys Leu Phe Gln
210 215 220
Val Arg Gly Lys Val Tyr Glu Leu Leu Val Asn Cys Ile Pro Pro Glu
225 230 235 240
Val Ile Leu Lys Arg Leu Leu His Glu Leu Leu Lys Lys Leu Asp Ser
245 250 255
Glu Leu Lys Leu Glu Val Cys His Trp Ala Ala Tyr Tyr Glu His Arg
260 265 270
Met Arg Leu Gly Gln Lys Ala Ile Phe His Ile Glu Ala Phe Val Ala
275 280 285
Lys Phe Met Ser Ile Tyr Lys Asn Phe Leu Ile Ser Thr Phe Gly
290 295 300

(2) INFORMATION FOR SEQ ID NO:1126:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 238 amino acids
- (B) TYPE: amino acid

- (C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1..238

(D) OTHER INFORMATION: / Ceres Seq. ID 1569052

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1126:

Met	Ala	Lys	Asn	Arg	Pro	Ile	Asp	Thr	Lys	Gly	Lys	Lys	Gly	Thr	Lys
1			5						10				15		
Val	Leu	Val	Leu	Asn	Glu	Val	Asp	Lys	Leu	Ser	Arg	Glu	Ala	Gln	His
			20					25					30		
Ser	Leu	Arg	Arg	Thr	Met	Glu	Lys	Tyr	Ser	Ser	Ser	Cys	Arg	Leu	Ile
		35					40					45			
Leu	Cys	Cys	Asn	Ser	Ser	Ser	Lys	Val	Thr	Glu	Ala	Ile	Lys	Ser	Arg
		50					55				60				
Cys	Leu	Asn	Val	Arg	Ile	Asn	Ala	Pro	Ser	Gln	Glu	Glu	Ile	Val	Lys
		65			70					75				80	
Val	Leu	Glu	Phe	Val	Ala	Lys	Lys	Glu	Ser	Leu	Gln	Leu	Pro	Gln	Gly
			85						90				95		
Phe	Ala	Ala	Arg	Ile	Ala	Glu	Lys	Ser	Asn	Arg	Ser	Leu	Arg	Arg	Ala
			100					105					110		
Ile	Leu	Ser	Leu	Glu	Thr	Cys	Arg	Val	Gln	Asn	Tyr	Pro	Phe	Thr	Gly
		115					120					125			
Asn	Gln	Val	Ile	Ser	Pro	Met	Asp	Trp	Glu	Glu	Tyr	Val	Ala	Glu	Ile
		130					135					140			
Ala	Thr	Asp	Met	Met	Lys	Glu	Gln	Ser	Pro	Lys	Lys	Leu	Phe	Gln	Val
		145			150					155				160	
Arg	Gly	Lys	Val	Tyr	Glu	Leu	Leu	Val	Asn	Cys	Ile	Pro	Pro	Glu	Val
			165						170					175	
Ile	Leu	Lys	Arg	Leu	Leu	His	Glu	Leu	Leu	Lys	Lys	Leu	Asp	Ser	Glu
		180					185						190		
Leu	Lys	Leu	Glu	Val	Cys	His	Trp	Ala	Ala	Tyr	Tyr	Glu	His	Arg	Met
		195					200						205		
Arg	Leu	Gly	Gln	Lys	Ala	Ile	Phe	His	Ile	Glu	Ala	Phe	Val	Ala	Lys
		210					215					220			
Phe	Met	Ser	Ile	Tyr	Lys	Asn	Phe	Leu	Ile	Ser	Thr	Phe	Gly		
		225			230					235					

- (2) INFORMATION FOR SEQ ID NO:1127:

- (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1148 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)

- (ix) FEATURE:

(A) NAME/KEY: -
(B) LOCATION: 1..1148
(D) OTHER INFORMATION: / Ceres Seq. ID 1569061

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1127:

actatctatt	tcttctttca	tcatcatcat	catcatcatc	atcactctct	cttcttcttc	60
tctctattcc	aKggcttttag	tacgtgaacg	tcgtcagcta	aatctcgcgt	tctcttcttc	120
tccaatctcc	gaccgcgcgt	tctccacctc	ttctctctca	gccaccacca	ccaccgtcgc	180
tggtgttaac	ggaatctcgc	cttgtgatct	cgagaaactc	aacgtttctc	gatgcggaaa	240
cggtcggtgatt	gtttacaaag	tcgtcataaa	aaccacatcg	gagatctacg	ctttgaaaaa	300
agtttaacggc	gacatgggatc	cgattttcac	aagacagttg	atgcgagaga	tggagattct	360
ccgacgtatac	gattcacctg	acgtcgttaa	atgtcacgga	atcttcgaga	aacctgtcgt	420
cggtgaagta	tcgattctaa	tgagtatat	ggacggcgga	accctagaat	cactacgcgg	480
cggtgttaacg	gagcaaaaac	tcgcgggatt	cgctaaaacg	atctttaaag	gattaaagta	540
tttacacgct	cttaagatcg	ttcatcgtga	tataaaacc	gcgaatcttc	ttctcaattc	600
gaaaaacgaa	gttaaaatcg	cgcatttcgc	agtttagtaag	atattagtc	gatcattaga	660

ttcgtgtaat	tcgtatgttg	gtacttgtgc	ttatatgagt	cggagaggt	ttgattccgga	720
atctccgggt	ggaagctctg	atatctacgc	cggagatato	tggagttttg	gattgatgat	780
gcttgagett	tcgtttgttc	atcttccgtt	gcttccgcgc	ggacagagac	ctgattgggc	840
aacgttgatg	tcgcgggtgt	gttttgaga	accgcgcgca	gcgcggagg	gttgtctgta	900
agagtttagg	agcttctgtt	agtgttgtct	ccgttaaagat	tcgagtaagc	gatggacggc	960
gcgcgagott	cttgctcttc	ctttctccg	ggaagattct	tgattcgatt	ctttttgtaa	1020
cagaatctgg	aactctaaaa	gttggaatat	tagatttgaa	attatttttaa	tttttgtaga	1080
gtttcttgga	gatatattatg	atcgtgattt	ttgtacatac	tgtataatat	actccagaat	1140
gttagggc						

(2) INFORMATION FOR SEQ ID NO:1128:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 333 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..333

(D) OTHER INFORMATION: / Ceres Seq. ID 1569062

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1128:

Leu	Ser	Ile	Ser	Ser	Phe	Ile	Ile	Ile	Ile	Ile	Ile	Ile	Ile	Thr	Leu
1			5					10						15	
Ser	Ser	Ser	Ser	Leu	Tyr	Ser	Xaa	Ala	Leu	Val	Arg	Glu	Arg	Arg	Gln
			20					25					30		
Leu	Asn	Leu	Arg	Leu	Pro	Leu	Pro	Pro	Ile	Ser	Asp	Arg	Arg	Phe	Ser
			35				40					45			
Thr	Ser	Ser	Ser	Ser	Ala	Thr	Thr	Thr	Val	Ala	Gly	Cys	Asn	Gly	
			50				55				60				
Ile	Ser	Ala	Cys	Asp	Leu	Glu	Lys	Leu	Asn	Val	Leu	Gly	Cys	Gly	Asn
					70					75				80	
Gly	Gly	Ile	Val	Tyr	Lys	Val	Arg	His	Lys	Thr	Thr	Ser	Glu	Ile	Tyr
					85				90					95	
Ala	Leu	Lys	Thr	Val	Asn	Gly	Asp	Met	Asp	Pro	Ile	Phe	Thr	Arg	Gln
					100				105					110	
Leu	Met	Arg	Glu	Met	Glu	Ile	Leu	Arg	Arg	Thr	Asp	Ser	Ser	Pro	Tyr
					115				120					125	
Val	Lys	Cys	His	Gly	Ile	Phe	Glu	Lys	Pro	Val	Val	Gly	Glu	Val	Ser
					130				135					140	
Ile	Leu	Met	Glu	Tyr	Met	Asp	Gly	Gly	Thr	Leu	Glu	Ser	Leu	Arg	Gly
					145					150				155	
Gly	Val	Thr	Glu	Gln	Lys	Leu	Ala	Gly	Phe	Ala	Lys	Gln	Ile	Leu	Lys
					165					170				175	
Gly	Leu	Ser	Tyr	Leu	His	Ala	Leu	Lys	Ile	Val	His	Arg	Asp	Ile	Lys
					180					185				190	
Pro	Ala	Asn	Leu	Leu	Leu	Asn	Ser	Lys	Asn	Glu	Val	Lys	Ile	Ala	Asp
					195					200				205	
Phe	Gly	Val	Ser	Lys	Ile	Leu	Val	Arg	Ser	Leu	Asp	Ser	Cys	Asn	Ser
					210					215				220	
Tyr	Val	Gly	Thr	Cys	Ala	Tyr	Met	Ser	Pro	Glu	Arg	Phe	Asp	Ser	Glu
					225					230				235	
Ser	Ser	Gly	Gly	Ser	Ser	Asp	Ile	Tyr	Ala	Gly	Asp	Ile	Trp	Ser	Phe
					245					250				255	
Gly	Leu	Met	Met	Leu	Glu	Leu	Leu	Val	Gly	His	Phe	Pro	Leu	Leu	Pro
					260					265				270	
Pro	Gly	Gln	Arg	Pro	Asp	Trp	Ala	Thr	Leu	Met	Cys	Ala	Val	Cys	Phe
					275					280				285	
Gly	Glu	Pro	Pro	Arg	Ala	Pro	Glu	Gly	Cys	Ser	Glu	Glu	Phe	Arg	Ser
					290					295				300	
Phe	Val	Glu	Cys	Cys	Leu	Arg	Lys	Asp	Ser	Ser	Lys	Arg	Trp	Thr	Ala
					305					310				315	

Pro Gln Leu Leu Ala His Pro Phe Leu Arg Glu Asp Leu
325 330

(2) INFORMATION FOR SEQ ID NO:1129:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 229 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..229
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569063

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1129:

Met Asp Pro Ile Phe Thr Arg Gln Leu Met Arg Glu Met Glu Ile Leu
1 5 10 15
Arg Arg Thr Asp Ser Pro Tyr Val Val Lys Cys His Gly Ile Phe Glu
20 25 30
Lys Pro Val Val Gly Glu Val Ser Ile Leu Met Glu Tyr Met Asp Gly
35 40 45
Gly Thr Leu Glu Ser Leu Arg Gly Gly Val Thr Glu Gln Lys Leu Ala
50 55 60
Gly Phe Ala Lys Gln Ile Leu Lys Gly Leu Ser Tyr Leu His Ala Leu
65 70 75 80
Lys Ile Val His Arg Asp Ile Lys Pro Ala Asn Leu Leu Leu Asn Ser
85 90 95
Lys Asn Glu Val Lys Ile Ala Asp Phe Gly Val Ser Lys Ile Leu Val
100 105 110
Arg Ser Leu Asp Ser Cys Asn Ser Tyr Val Gly Thr Cys Ala Tyr Met
115 120 125
Ser Pro Glu Arg Phe Asp Ser Glu Ser Ser Gly Gly Ser Ser Asp Ile
130 135 140
Tyr Ala Gly Asp Ile Trp Ser Phe Gly Leu Met Met Leu Glu Leu Leu
145 150 155 160
Val Gly His Phe Pro Leu Leu Pro Pro Gly Gln Arg Pro Asp Trp Ala
165 170 175
Thr Leu Met Cys Ala Val Cys Phe Gly Glu Pro Pro Arg Ala Pro Glu
180 185 190
Gly Cys Ser Glu Glu Phe Arg Ser Phe Val Glu Cys Cys Leu Arg Lys
195 200 205
Asp Ser Ser Lys Arg Trp Thr Ala Pro Gln Leu Leu Ala His Pro Phe
210 215 220
Leu Arg Glu Asp Leu
225

(2) INFORMATION FOR SEQ ID NO:1130:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 220 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..220
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569064

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1130:

Met Arg Glu Met Glu Ile Leu Arg Arg Thr Asp Ser Pro Tyr Val Val
1 5 10 15
Lys Cys His Gly Ile Phe Glu Lys Pro Val Val Gly Glu Val Ser Ile
20 25 30
Leu Met Glu Tyr Met Asp Gly Gly Thr Leu Glu Ser Leu Arg Gly Gly

35	40	45
Val Thr Glu Gln Lys Leu Ala Gly Phe Ala Lys Gln Ile Leu Lys Gly		
50	55	60
Leu Ser Tyr Leu His Ala Leu Lys Ile Val His Arg Asp Ile Lys Pro		
65	70	75
Ala Asn Leu Leu Leu Asn Ser Lys Asn Glu Val Lys Ile Ala Asp Phe		
85	90	95
Gly Val Ser Lys Ile Leu Val Arg Ser Leu Asp Ser Cys Asn Ser Tyr		
100	105	110
Val Gly Thr Cys Ala Tyr Met Ser Pro Glu Arg Phe Asp Ser Glu Ser		
115	120	125
Ser Gly Gly Ser Ser Asp Ile Tyr Ala Gly Asp Ile Trp Ser Phe Gly		
130	135	140
Leu Met Met Leu Glu Leu Leu Val Gly His Phe Pro Leu Leu Pro Pro		
145	150	155
Gly Gln Arg Pro Asp Trp Ala Thr Leu Met Cys Ala Val Cys Phe Gly		
165	170	175
Glu Pro Pro Arg Ala Pro Glu Gly Cys Ser Glu Glu Phe Arg Ser Phe		
180	185	190
Val Glu Cys Cys Leu Arg Lys Asp Ser Ser Lys Arg Trp Thr Ala Pro		
195	200	205
Gln Leu Leu Ala His Pro Phe Leu Arg Glu Asp Leu		
210	215	220

(2) INFORMATION FOR SEQ ID NO:1131:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1591 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1591
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569065

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1131:

atgcacaatc attccacta atagtttaat aaagtgtata attttttttc aaattaaaaac	60
agctaaacac acacaaacc attcaaaaag gggttaaaga ttgaagaata ttctaagaaa	120
aattgtttct ctctttcaag aagtaaaagc gtctctctct ctcattaagc atcaaggag	180
ttctgttttt ctgtctttgc tgttacattc ttcaggaaaa agcggttacc ttactctct	240
ctgcacatcac gaggaagcgt gtagaacta aaggagctta atttgagaga tttttttttt	300
tgtttctggg ttgtttcaaa gatgcaaat tttagtgtct tTctgtctgt gaaaaggatt	360
tgtatcgcaa aagaagggtga aaacggagcc atctgtggag atcttttca ctaaggaaact	420
tcacgcagca acaaacagtt ttaattacga taacaagctc ggtgaaggca gatttggcag	480
tgtgtattgg ggtcagctat gggatggatc tcaaatgca gtcaagagat tgaaggcatc	540
gagtagcaga gaagagatag attttgtgtt agaagtcgag attctgtctc gtatcgtca	600
caagaatcta ttgagtgtag gaggttactg tgcagaagga caagaacgac tcatgtgata	660
tgattacatg ccaaatttga gcttggctct tcatcttcat gggtcaacatt catctgagtc	720
gcttcttgat tggactagcc ggaatgaat tctgtgtatc tctgtctacg cgattgccta	780
cttgcacatct ttgtcaaac ctagaatagt ccatggagat gtgagagcaa gcaatgtgct	840
gctagattcat gagtttgaag ctccgggttac agattttcgga tacgataagc tgaatgccaga	900
tgtatggagct aacaaagcga ccaaggggtaa taacattggg tatctctcac cagaatgtat	960
cgaatctgCa aaagaatcag acatgggaga tgtgtatagt tctcgtgttc ttttctgga	1020
gcttgttaact ggttaagagac ctacagagag ggtaaaacta acaacaaga ggggtattac	1080
cgaatggggt ttacctcttg tttacgaaa aaagtttggg gaaattgtgg atcaaaaggct	1140
gaatgggaag tatgtggaag aagagctgaa aaggatagtt ttggttggtc tcatgtgtgc	1200
tcagagggag tcagagaaga gaccaacaat gtctgaagtt gtggagatgc taatgattga	1260
atcaaaaggag aaaaatggctc agcttgaagc taatccactc ttcaatggaa acaatgatgg	1320
tgaagtata gatgaaagct cagagatcat ttctgaagtg agagatcatc aataacaaga	1380
acaagaatgt tatccaattt cagcatattc tgtttctctt tctgataatc tgggtttttg	1440
ttgtgctgtg ttttagaaga gtgtttgtgc ttgtttttag aatagcgaag ttggctttta	1500
aaagtttatt gtgtattttt ttccagctta agattggatt ttgatcattg atatttgagc	1560

ttgtaagaga gtgtagtgggt acatatattgg t

(2) INFORMATION FOR SEQ ID NO:1132:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 235 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..235
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569066

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1132:

Met	Pro	Asn	Leu	Ser	Leu	Val	Ser	His	Leu	His	Gly	Gln	His	Ser	Ser
1			5						10					15	
Glu	Ser	Leu	Leu	Asp	Trp	Thr	Arg	Arg	Met	Asn	Ile	Ala	Val	Ser	Ser
			20					25					30		
Ala	Gln	Ala	Ile	Ala	Tyr	Leu	His	His	Phe	Ala	Thr	Pro	Arg	Ile	Val
			35					40					45		
His	Gly	Asp	Val	Arg	Ala	Ser	Asn	Val	Leu	Leu	Asp	Ser	Glu	Phe	Glu
			50				55				60				
Ala	Arg	Val	Thr	Asp	Phe	Gly	Tyr	Asp	Lys	Leu	Met	Pro	Asp	Asp	Gly
65					70				75					80	
Ala	Asn	Lys	Ser	Thr	Lys	Gly	Asn	Asn	Ile	Gly	Tyr	Leu	Ser	Pro	Glu
					85				90				95		
Cys	Ile	Glu	Ser	Gly	Lys	Glu	Ser	Asp	Met	Gly	Asp	Val	Tyr	Ser	Phe
					100			105					110		
Gly	Val	Leu	Leu	Leu	Glu	Leu	Val	Thr	Gly	Lys	Arg	Pro	Thr	Glu	Arg
					115			120				125			
Val	Asn	Leu	Thr	Thr	Lys	Arg	Gly	Ile	Thr	Glu	Trp	Val	Leu	Pro	Leu
					130		135				140				
Val	Tyr	Glu	Arg	Lys	Phe	Gly	Glu	Ile	Val	Asp	Gln	Arg	Leu	Asn	Gly
145					150				155					160	
Lys	Tyr	Val	Glu	Glu	Glu	Leu	Lys	Arg	Ile	Val	Leu	Val	Gly	Leu	Met
					165				170					175	
Cys	Ala	Gln	Arg	Glu	Ser	Glu	Lys	Arg	Pro	Thr	Met	Ser	Glu	Val	Val
					180			185					190		
Glu	Met	Leu	Met	Ile	Glu	Ser	Lys	Glu	Lys	Met	Ala	Gln	Leu	Glu	Ala
					195			200				205			
Asn	Pro	Leu	Phe	Asn	Gly	Asn	Asn	Asp	Gly	Glu	Val	Ile	Asp	Glu	Ser
					210			215				220			
Ser	Glu	Ile	Ile	Ser	Glu	Val	Arg	Asp	His	Gln					
225					230					235					

(2) INFORMATION FOR SEQ ID NO:1133:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 210 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..210
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569067

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1133:

Met	Asn	Ile	Ala	Val	Ser	Ser	Ala	Gln	Ala	Ile	Ala	Tyr	Leu	His	His
1														15	
Phe	Ala	Thr	Pro	Arg	Ile	Val	His	Gly	Asp	Val	Arg	Ala	Ser	Asn	Val
								25					30		
Leu	Leu	Asp	Ser	Glu	Phe	Glu	Ala	Arg	Val	Thr	Asp	Phe	Gly	Tyr	Asp
					35			40					45		

Lys Leu Met Pro Asp Asp Gly Ala Asn Lys Ser Thr Lys Gly Asn Asn
50 55 60
Ile Gly Tyr Leu Ser Pro Glu Cys Ile Glu Ser Gly Lys Glu Ser Asp
65 70 75 80
Met Gly Asp Val Tyr Ser Phe Gly Val Leu Leu Glu Leu Val Thr
85 90 95
Gly Lys Arg Pro Thr Glu Arg Val Asn Leu Thr Thr Lys Arg Gly Ile
100 105 110
Thr Glu Trp Val Leu Pro Leu Val Tyr Glu Arg Lys Phe Gly Glu Ile
115 120 125
Val Asp Gln Arg Leu Asn Gly Lys Tyr Val Glu Glu Glu Leu Lys Arg
130 135 140
Ile Val Leu Val Gly Leu Met Cys Ala Gln Arg Glu Ser Glu Lys Arg
145 150 155 160
Pro Thr Met Ser Glu Val Val Glu Met Leu Met Ile Glu Ser Lys Glu
165 170 175
Lys Met Ala Gln Leu Glu Ala Asn Pro Leu Phe Asn Gly Asn Asn Asp
180 185 190
Gly Glu Val Ile Asp Glu Ser Ser Glu Ile Ile Ser Glu Val Arg Asp
195 200 205
His Gln
210

(2) INFORMATION FOR SEQ ID NO:1134:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 160 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..160
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569068

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1134:

Met Pro Asp Asp Gly Ala Asn Lys Ser Thr Lys Gly Asn Asn Ile Gly
1 5 10 15
Tyr Leu Ser Pro Glu Cys Ile Glu Ser Gly Lys Glu Ser Asp Met Gly
20 25 30
Asp Val Tyr Ser Phe Gly Val Leu Leu Leu Val Thr Gly Lys
35 40 45
Arg Pro Thr Glu Arg Val Asn Leu Thr Thr Lys Arg Gly Ile Thr Glu
50 55 60
Trp Val Leu Pro Leu Val Tyr Glu Arg Lys Phe Gly Glu Ile Val Asp
65 70 75 80
Gln Arg Leu Asn Gly Lys Tyr Val Glu Glu Leu Lys Arg Ile Val
85 90 95
Leu Val Gly Leu Met Cys Ala Gln Arg Glu Ser Glu Lys Arg Pro Thr
100 105 110
Met Ser Glu Val Val Glu Met Leu Met Ile Glu Ser Lys Glu Lys Met
115 120 125
Ala Gln Leu Glu Ala Asn Pro Leu Phe Asn Gly Asn Asn Asp Gly Glu
130 135 140
Val Ile Asp Glu Ser Ser Glu Ile Ile Ser Glu Val Arg Asp His Gln
145 150 155 160

(2) INFORMATION FOR SEQ ID NO:1135:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1227 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

- (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1227

(D) OTHER INFORMATION: / Ceres Seq. ID 1569097

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1135:

atatctcaaa	atatgaataa	tcaaaaatgg	agtataggtt	tcatatctct	cgtctttctc	60
ttcatcacct	cctcttcagc	tgagttcatc	attcaacagg	tcacaaaggg	cagaggaata	120
gagtacaaca	gttcttcacg	tctcgaggag	aattctggag	tgacaagaga	gttgagagaa	180
gagcgacatc	cagtaagatg	agtgaacaat	acaagcttct	ctgtgattaa	aggcagagaa	240
gaacctctatg	aatcctctgt	ttttgagcgc	tgctggttac	aaatggagat	tggttttgtt	300
cgtagaatggt	aataaaaaacg	acggtggaaa	tgatcatatt	tccttttacg	caaggatcga	360
agagKacaaa	ctctcttcca	gtaggatggg	aagtgaatgt	tgatctcaaa	ctctttgtcc	420
ataatgggaa	gctacacaaa	tatttgactg	ttacagatgg	cttagtgaag	cgatataaca	480
atgcgaaaaa	agaatgggggt	ttcggacaat	tgattttctg	atcaacattc	tacaacgcga	540
acgaaggtta	ccttgaccag	gacactgggt	cttttggtgc	tgagatcttt	attgtttaaac	600
cggtctcaaca	acaagagaaa	gttacattca	tatcaaaacc	tccaaaacat	gttttcacct	660
ggaagatact	tcgtytctct	acottggaag	ataaattcta	ttactccgat	gattttctcg	720
ttgaagaccg	atactggaga	ctaggattta	accggaagg	ggatggagga	ggaagaccac	780
atgcacttcc	aatcttccat	tttgctcaag	gccataaagg	aaacgcagtt	gttacaacaa	840
cttggggagc	ggtttaactc	cggttaaaga	atcaacgaag	tactaaccat	agacaaatat	900
attctgcagc	ttggtaccgc	attggaagcg	gttatggtgt	gggagtgaac	aatatcatat	960
tgttagctga	tttaaacgat	gcatacaaa	gatatttggt	gaatgatgcc	attatctttg	1020
aaagctgaaat	ggttaaagtc	tctataacca	acatcgcttc	cgcttaaaat	tctgcacttc	1080
tttgtctaat	atcaatcaac	cttatgaata	aagagatat	tgatgaattt	gtaataagaa	1140
aacgcttaatg	tttgtaatt	gtgaaattat	ttctgttctt	ctgagttttt	tattttcaatg	1200
aaaataaaac	tcttaccggt	ttaaatt				

- (2) INFORMATION FOR SEQ ID NO:1136:

- (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 253 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide

- (ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..253

(D) OTHER INFORMATION: / Ceres Seq. ID 1569098

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1136:

Met	Val	Ile	Lys	Thr	Thr	Val	Glu	Met	Ile	Ile	Phe	Pro	Phe	Thr	Gln
1			5						10					15	
Gly	Ser	Lys	Xaa	Thr	Asn	Ser	Leu	Pro	Val	Gly	Trp	Glu	Val	Asn	Val
			20					25					30		
Asp	Leu	Lys	Leu	Phe	Val	His	Asn	Gly	Lys	Leu	His	Lys	Tyr	Leu	Thr
			35				40				45				
Val	Thr	Asp	Gly	Leu	Val	Lys	Arg	Tyr	Asn	Asn	Ala	Lys	Lys	Glu	Trp
			50			55					60				
Gly	Phe	Gly	Gln	Leu	Ile	Ser	Arg	Ser	Thr	Phe	Tyr	Asn	Ala	Asn	Glu
65			70						75					80	
Gly	Tyr	Leu	Asp	Gln	Asp	Thr	Gly	Ser	Phe	Gly	Ala	Glu	Ile	Phe	Ile
			85					90					95		
Val	Lys	Pro	Ala	Gln	Gln	Gln	Glu	Lys	Val	Thr	Phe	Ile	Ser	Asn	Pro
			100				105						110		
Pro	Asn	Asn	Val	Phe	Thr	Trp	Lys	Ile	Leu	Arg	Xaa	Ser	Thr	Leu	Glu
			115				120					125			
Asp	Lys	Phe	Tyr	Tyr	Ser	Asp	Asp	Phe	Leu	Val	Glu	Asp	Arg	Tyr	Trp
			130			135					140				
Arg	Leu	Gly	Phe	Asn	Pro	Lys	Gly	Asp	Gly	Gly	Gly	Arg	Pro	His	Ala
145				150					155					160	
Leu	Pro	Ile	Phe	Leu	Phe	Ala	Gln	Gly	His	Lys	Ala	Asn	Ala	Val	Val

(2) INFORMATION FOR SEQ ID NO:1137:

(A) LENGTH: 245 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..245

(D) OTHER INFORMATION: / Ceres Seq. ID 1569099

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1137:

(2) INFORMATION FOR SEQ ID NO:1138:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1481 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1481

(D) OTHER INFORMATION: / Ceres Seq. ID 1569112

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1138:

```

cactgtgtctc  tcttcttcaa  tggaaacaaca  attaacctta  gtattgtctg  atagcccaaaa  60
aggcgccaaaa  tatgtagaaa  cctttgaaga  agccgttctt  tcttcttctt  ctctctcttc  120
ttctctctgtt  cctctcctga  ctgatcaccg  ccatcgaaac  ttctgtaaat  tcttctcttta  180
cttctctcttc  gtctgtcttg  ctctactatt  catcatctcc  agtctcgccg  tctctccaat  240
tcccccaaca  tccgcaatct  tctcccgtaa  acgtttcatc  agcaaatgtg  gatctttttc  300
cgggagattg  gataccagat  ccaacaggtc  ctctgtagac  aaatgtcact  tctctgcaca  360
ttcaagattt  tcagaactgc  ctattgaatg  gacgaccaga  tgtgaattat  ctcttctgga  420
gatggaagcc  tctgtattgt  gatcttctta  gggttagtcc  atcgcagttt  ctgtcttcag  480
tgaagaacaa  atgtgtgggt  tttatcgtgt  attccattgc  tctgaatcat  gtccagcttc  540
tcattctgat  tcttctctag  gtggaagaag  tggaggaaat  ctatcacgat  aaggagttca  600
gatccaagat  atggagattc  ccttctcaca  acttcacact  atcagtcatt  tggctctctt  660
tcttctctcaa  atccgaaaac  tctagcaact  cggatattca  gctttacctc  gaccagcttg  720
accacaaatg  gactgtccaa  taccgaaat  tctactactg  tgttatctct  ggaggcaaat  780
ggtttcttaa  aacaacaatt  ttccatgaaa  acaacgtagt  caccggctgt  cattactgcc  840
aagggaagaaa  caacctaaat  gatctcggtc  atgattactc  ctaccgcaaa  accctaaacc  900
ttctctgtga  ctctgtctta  aactcaaccc  acaaacgcgt  ggttctgttt  cgaacaacaa  960
cgcttgacca  ttctgaaac  ggagagtggg  acactgggtg  gtattgcac  agaacgatgc  1020
cgtttaaaga  aggcacaagc  aatatgaaaa  ctgtagatga  tgtgatgcgt  gatgttgagc  1080
ttagaggtgt  tcagaaattt  gggaaaggtt  ttggcttagg  ttccaacatc  aggtatttag  1140
acacagctgg  aatgtctctt  ctccgtccag  acgggcatcc  gggaccatac  cggcatccaa  1200
atcttcttgc  tggagttaag  aataagagca  atgttcagaa  tgattgtctg  cattggtgtc  1260
tacctgttcc  aattgattca  tggaaatgat  tgatggtgga  aaccacgctt  aaccgggaac  1320
gggaactata  cgatttaaac  ggtaaatgta  ccacgatatt  gcttgtagct  agttacagtc  1380
aatagccatt  ccaactgtca  atgtctcgta  tatgatagtt  ctatatatta  attttgtaat  1440
ggttctaaac  aagaataaac  gatgcaaat  ttgcagtggt  g
```

(2) INFORMATION FOR SEQ ID NO:1139:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 96 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..96

(D) OTHER INFORMATION: / Ceres Seq. ID 1569113

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1139:

```

Met Ser Ser Leu Ser Ser Ala Phe Ser Leu Arg Trp Lys Lys Trp Arg
1      5      10      15
Lys Ser Ile Thr Ile Arg Ser Ser Asp Pro Arg Tyr Gly Asp Ser Leu
20      25      30
Leu Thr Thr Ser His Tyr Gln Ser Phe Gly Leu Leu Ser Phe Ser Asn
35      40      45
Pro Lys His Leu Ala Thr Arg Ile Phe Ser Phe Thr Ser Thr Ser Leu
50      55      60
Thr Thr Asn Gly Leu Ser Asn Thr Arg Asn Ser Thr Thr Leu Leu Ser
65      70      75      80
Leu Glu Ala Asn Gly Phe Leu Lys Gln Gln Phe Ser Met Lys Thr Thr
85      90      95
```

(2) INFORMATION FOR SEQ ID NO:1140:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 109 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..109
(D) OTHER INFORMATION: / Ceres Seq. ID 1569114
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1140:
Met Pro Phe Lys Glu Gly Gln Ala Asn Met Lys Thr Val Asp Asp Val
1 5 10 15
Met Arg Asp Val Glu Leu Glu Val Phe Gln Lys Phe Gly Lys Gly Phe
20 25 30
Gly Leu Gly Ser Asn Ile Arg Leu Leu Asp Thr Thr Gly Met Ser Leu
35 40 45
Leu Arg Pro Asp Gly His Pro Gly Pro Tyr Arg His Pro Asn Pro Phe
50 55 60
Ala Gly Val Lys Asn Lys Ser Asn Val Gln Asn Asp Cys Leu His Trp
65 70 75 80
Cys Leu Pro Gly Pro Ile Asp Ser Trp Asn Asp Val Met Val Glu Thr
85 90 95
Thr Leu Asn Arg Glu Arg Glu Leu Tyr Asp Leu Thr Gly
100 105
(2) INFORMATION FOR SEQ ID NO:1141:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 100 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..100
(D) OTHER INFORMATION: / Ceres Seq. ID 1569115
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1141:
Met Lys Thr Val Asp Asp Val Met Arg Asp Val Glu Leu Glu Val Phe
1 5 10 15
Gln Lys Phe Gly Lys Gly Phe Gly Leu Gly Ser Asn Ile Arg Leu Leu
20 25 30
Asp Thr Thr Gly Met Ser Leu Leu Arg Pro Asp Gly His Pro Gly Pro
35 40 45
Tyr Arg His Pro Asn Pro Phe Ala Gly Val Lys Asn Lys Ser Asn Val
50 55 60
Gln Asn Asp Cys Leu His Trp Cys Leu Pro Gly Pro Ile Asp Ser Trp
65 70 75 80
Asn Asp Val Met Val Glu Thr Thr Leu Asn Arg Glu Arg Glu Leu Tyr
85 90 95
Asp Leu Thr Gly
100
(2) INFORMATION FOR SEQ ID NO:1142:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1794 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..1794
(D) OTHER INFORMATION: / Ceres Seq. ID 1569116
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1142:
attcttgctc cgacaatact ctcagaatac gatcttgaag agcaaagatt gttcctttat

tgtatgaattg	agtgcacaaag	agtgttatat	aatggctact	gcagctgttta	taggactcaa	120
actctggcaaa	agatttgttga	gttcatcggt	ttatcactca	gatgtttacag	agaagtttct	180
cactgttaatt	gatcatgttt	catcacagta	tcattattgt	tcaacgaaaa	ggcgataaac	240
tgcgaaaaagc	gcgtcgaaact	atagtcggag	ttttctctcg	tccaatcgctc	acacacaaact	300
tgctaaaagct	ttgaaaagaga	atgtagatgt	tgcttctact	gagaagccat	ggctacctcaa	360
tggaactgat	aaggaatttg	aagaagaatg	ttatgatgat	gatgatctaa	ttagtcatct	420
tggtgaggca	attttactgt	tacagaagtc	tatgttagag	aaaagttgga	atctttcatt	480
tgaaaaggcgg	gtgtcgagtg	agtatccggg	caagggggact	atacgggaaga	agaagattcc	540
gggttatcacc	tggttcaggga	tttcagctcg	tcaaaagaag	gttggtgcta	agaagaaaaac	600
taatatgatc	catgtttaaag	cagttttctga	tgttttctagt	ggaaagcaag	ttagagggtta	660
tggtaaaaggt	gtaataagtg	aagatgtgct	tagtcatgcg	gaagttgtgc	gcttgtctcaa	720
gaaaaatcaaa	tctggctcttc	gtcttgatga	tcataagta	agattacagg	atagattagg	780
ctgtgagocct	tctgatgaac	agcttgcagt	atctttgaag	atatctcggg	ccgagctcaa	840
ggcgctgttg	atggaaatgt	atctagctag	agagaagttg	gctatgagta	atgtgcgcttt	900
gggtatgtct	attgctcaag	gttatgataa	tttgggagca	gaaatgtctg	accottgttca	960
gggtggtctt	atcggaacttt	tgccggggaat	agagaaaattt	gattctttcca	aaggttttcag	1020
aatttcaact	tatgtatatt	ggtggattcg	acaggggtgtc	tcaagagcac	tagtggacaa	1080
ctcaagaacc	ttgaggtttac	ctactcaact	acatgaaaga	ctcggtttaa	tccgaaatgc	1140
aaagcttaga	cttcaagaga	aaggaatcac	accctccatt	gataggattg	cagagtctct	1200
aaacatgtcg	cagaagaaga	ttagaaatgc	aacagaggct	gtaagcaaat	tattttctct	1260
agacagagat	gcatttccct	ctttgaatgg	ttctccctgga	gaaactcatc	acagttacat	1320
tcgggataact	cggtttgaga	acaatccctg	gcacggggtat	gatgatttgg	cactcaagga	1380
ggaagtaagc	aagcttataa	gtgcaacact	cggagaacgg	gaaaaagaga	tcattogatt	1440
atactatggt	ctagacaaa	aatgtctcac	atggggaagac	attagtaaac	ggataggatt	1500
atcgagagag	aggggtgagc	aggttagggct	tggtggcactg	gagaaactaa	aacacgcagc	1560
gaggaagaga	aaaatggagg	caatgatcct	taagaattga	ttttgttttt	gtacattttg	1620
attacatcag	agccatagag	agcggtgtgt	aattgtgata	tatacaggac	aaaaaagggg	1680
gaagagtact	actctctttt	attttatttt	acccttctgt	ctctctttgt	aaactgagtt	1740
gagaacaag	agacagttat	gtaatatggo	ttcacgtaaa	cttcatcatt	cttc	

(2) INFORMATION FOR SEQ ID NO:1143:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 532 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..532

(D) OTHER INFORMATION: / Ceres Seq. ID 1569117

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1143:

Phe	Leu	Ser	Arg	Gln	Tyr	Ser	Gln	Asn	Thr	Ile	Leu	Lys	Ser	Lys	Asp
1			5				10						15		
Cys	Ser	Phe	Ile	Asp	Glu	Leu	Ser	Ala	Lys	Glu	Cys	Tyr	Ile	Met	Ala
			20				25						30		
Thr	Ala	Ala	Val	Ile	Gly	Leu	Asn	Thr	Gly	Lys	Arg	Leu	Leu	Ser	Ser
			35				40						45		
Ser	Phe	Tyr	His	Ser	Asp	Val	Thr	Glu	Lys	Phe	Leu	Ser	Val	Asn	Asp
			50				55				60				
His	Cys	Ser	Ser	Gln	Tyr	His	Ile	Ala	Ser	Thr	Lys	Ser	Gly	Ile	Thr
			65				70				75			80	
Ala	Lys	Lys	Ala	Ser	Asn	Tyr	Ser	Pro	Ser	Phe	Pro	Ser	Ser	Asn	Arg
			85				90						95		
His	Thr	Gln	Ser	Ala	Lys	Ala	Leu	Lys	Glu	Asn	Val	Asp	Val	Ala	Ser
			100				105						110		
Thr	Glu	Lys	Pro	Trp	Leu	Pro	Asn	Gly	Thr	Asp	Lys	Glu	Leu	Glu	Glu
			115				120					125			
Glu	Cys	Tyr	Asp	Asp	Asp	Asp	Leu	Ile	Ser	His	Ser	Val	Glu	Ala	Ile
			130				135					140			
Leu	Leu	Leu	Gln	Lys	Ser	Met	Leu	Glu	Lys	Ser	Trp	Asn	Leu	Ser	Phe
			145				150				155				160

Glu Lys Ala Val Ser Ser Glu Tyr Pro Gly Lys Gly Thr Ile Arg Lys
165 170 175
Lys Lys Ile Pro Val Ile Thr Cys Ser Gly Ile Ser Ala Arg Gln Arg
180 185 190
Arg Ile Gly Ala Lys Lys Lys Thr Asn Met Thr His Val Lys Ala Val
195 200 205
Ser Asp Val Ser Ser Gly Lys Gln Val Arg Gly Tyr Val Lys Gly Val
210 215 220
Ile Ser Glu Asp Val Leu Ser His Ala Glu Val Val Arg Leu Ser Lys
225 230 235 240
Lys Ile Lys Ser Gly Leu Arg Leu Asp Asp His Lys Ser Arg Leu Gln
245 250 255
Asp Arg Leu Gly Cys Glu Pro Ser Asp Glu Gln Leu Ala Val Ser Leu
260 265 270
Lys Ile Ser Arg Ala Glu Leu Gln Ala Trp Leu Met Glu Cys His Leu
275 280 285
Ala Arg Glu Lys Leu Ala Met Ser Asn Val Arg Leu Val Met Ser Ile
290 295 300
Ala Gln Arg Tyr Asp Asn Leu Gly Ala Glu Met Ser Asp Leu Val Gln
305 310 315 320
Gly Gly Leu Ile Gly Leu Leu Arg Gly Ile Glu Lys Phe Asp Ser Ser
325 330 335
Lys Gly Phe Arg Ile Ser Thr Tyr Val Tyr Trp Trp Ile Arg Gln Gly
340 345 350
Val Ser Arg Ala Leu Val Asp Asn Ser Arg Thr Leu Arg Leu Pro Thr
355 360 365
His Leu His Glu Arg Leu Gly Leu Ile Arg Asn Ala Lys Leu Arg Leu
370 375 380
Gln Glu Lys Gly Ile Thr Pro Ser Ile Asp Arg Ile Ala Glu Ser Leu
385 390 395 400
Asn Met Ser Gln Lys Lys Val Arg Asn Ala Thr Glu Ala Val Ser Lys
405 410 415
Val Phe Ser Leu Asp Arg Asp Ala Phe Pro Ser Leu Asn Gly Leu Pro
420 425 430
Gly Glu Thr His His Ser Tyr Ile Ala Asp Thr Arg Leu Glu Asn Asn
435 440 445
Pro Trp His Gly Tyr Asp Asp Leu Ala Leu Lys Glu Glu Val Ser Lys
450 455 460
Leu Ile Ser Ala Thr Leu Gly Glu Arg Glu Lys Glu Ile Ile Arg Leu
465 470 475 480
Tyr Tyr Gly Leu Asp Lys Glu Cys Leu Thr Trp Glu Asp Ile Ser Lys
485 490 495
Arg Ile Gly Leu Ser Arg Glu Arg Val Arg Gln Val Gly Leu Val Ala
500 505 510
Leu Glu Lys Leu Lys His Ala Ala Arg Lys Arg Lys Met Glu Ala Met
515 520 525
Ile Leu Lys Asn
530

(2) INFORMATION FOR SEQ ID NO:1144:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 502 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..502

(D) OTHER INFORMATION: / Ceres Seq. ID 1569118

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1144:

Met Ala Thr Ala Ala Val Ile Gly Leu Asn Thr Gly Lys Arg Leu Leu

1	5	10	15
Ser Ser Ser Phe Tyr His Ser Asp Val Thr Glu Lys Phe Leu Ser Val	20	25	30
Asn Asp His Cys Ser Ser Gln Tyr His Ile Ala Ser Thr Lys Ser Gly	35	40	45
Ile Thr Ala Lys Lys Ala Ser Asn Tyr Ser Pro Ser Phe Pro Ser Ser	50	55	60
Asn Arg His Thr Gln Ser Ala Lys Ala Leu Lys Glu Asn Val Asp Val	65	70	75
Ala Ser Thr Glu Lys Pro Trp Leu Pro Asn Gly Thr Asp Lys Glu Leu	85	90	95
Glu Glu Glu Cys Tyr Asp Asp Asp Asp Leu Ile Ser His Ser Val Glu	100	105	110
Ala Ile Leu Leu Leu Gln Lys Ser Met Leu Glu Lys Ser Trp Asn Leu	115	120	125
Ser Phe Glu Lys Ala Val Ser Ser Glu Tyr Pro Gly Lys Gly Thr Ile	130	135	140
Arg Lys Lys Lys Ile Pro Val Ile Thr Cys Ser Gly Ile Ser Ala Arg	145	150	155
Gln Arg Arg Ile Gly Ala Lys Lys Lys Thr Asn Met Thr His Val Lys	165	170	175
Ala Val Ser Asp Val Ser Ser Gly Lys Gln Val Arg Gly Tyr Val Lys	180	185	190
Gly Val Ile Ser Glu Asp Val Leu Ser His Ala Glu Val Val Arg Leu	195	200	205
Ser Lys Lys Ile Lys Ser Gly Leu Arg Leu Asp Asp His Lys Ser Arg	210	215	220
Leu Gln Asp Arg Leu Gly Cys Glu Pro Ser Asp Glu Gln Leu Ala Val	225	230	235
Ser Leu Lys Ile Ser Arg Ala Glu Leu Gln Ala Trp Leu Met Glu Cys	245	250	255
His Leu Ala Arg Glu Lys Leu Ala Met Ser Asn Val Arg Leu Val Met	260	265	270
Ser Ile Ala Gln Arg Tyr Asp Asn Leu Gly Ala Glu Met Ser Asp Leu	275	280	285
Val Gln Gly Gly Leu Ile Gly Leu Leu Arg Gly Ile Glu Lys Phe Asp	290	295	300
Ser Ser Lys Gly Phe Arg Ile Ser Thr Tyr Val Tyr Trp Trp Ile Arg	305	310	315
Gln Gly Val Ser Arg Ala Leu Val Asp Asn Ser Arg Thr Leu Arg Leu	325	330	335
Pro Thr His Leu His Glu Arg Leu Gly Leu Ile Arg Asn Ala Lys Leu	340	345	350
Arg Leu Gln Glu Lys Gly Ile Thr Pro Ser Ile Asp Arg Ile Ala Glu	355	360	365
Ser Leu Asn Met Ser Gln Lys Lys Val Arg Asn Ala Thr Glu Ala Val	370	375	380
Ser Lys Val Phe Ser Leu Asp Arg Asp Ala Phe Pro Ser Leu Asn Gly	385	390	395
Leu Pro Gly Glu Thr His His Ser Tyr Ile Ala Asp Thr Arg Leu Glu	405	410	415
Asn Asn Pro Trp His Gly Tyr Asp Asp Leu Ala Leu Lys Glu Glu Val	420	425	430
Ser Lys Leu Ile Ser Ala Thr Leu Gly Glu Arg Glu Lys Glu Ile Ile	435	440	445
Arg Leu Tyr Tyr Gly Leu Asp Lys Glu Cys Leu Thr Trp Glu Asp Ile	450	455	460
Ser Lys Arg Ile Gly Leu Ser Arg Glu Arg Val Arg Gln Val Gly Leu	465	470	475
Val Ala Leu Glu Lys Leu Lys His Ala Ala Arg Lys Arg Lys Met Glu	485	490	495

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Ala Met Ile Leu Lys Asn
500

(2) INFORMATION FOR SEQ ID NO:1145:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 382 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..382

(D) OTHER INFORMATION: / Ceres Seq. ID 1569119

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1145:

Met	Leu	Glu	Lys	Ser	Trp	Asn	Leu	Ser	Phe	Glu	Lys	Ala	Val	Ser	Ser
1			5					10			15				
Glu	Tyr	Pro	Gly	Lys	Gly	Thr	Ile	Arg	Lys	Lys	Lys	Ile	Pro	Val	Ile
			20					25					30		
Thr	Cys	Ser	Gly	Ile	Ser	Ala	Arg	Gln	Arg	Arg	Ile	Gly	Ala	Lys	Lys
			35				40				45				
Lys	Thr	Asn	Met	Thr	His	Val	Lys	Ala	Val	Ser	Asp	Val	Ser	Ser	Gly
			50				55				60				
Lys	Gln	Val	Arg	Gly	Tyr	Val	Lys	Gly	Val	Ile	Ser	Glu	Asp	Val	Leu
65					70					75					80
Ser	His	Ala	Glu	Val	Arg	Leu	Ser	Lys	Lys	Ile	Lys	Ser	Gly	Leu	
			85					90					95		
Arg	Leu	Asp	Asp	His	Lys	Ser	Arg	Leu	Gln	Asp	Arg	Leu	Gly	Cys	Glu
			100					105					110		
Pro	Ser	Asp	Glu	Gln	Leu	Ala	Val	Ser	Leu	Lys	Ile	Ser	Arg	Ala	Glu
			115					120					125		
Leu	Gln	Ala	Trp	Leu	Met	Glu	Cys	His	Leu	Ala	Arg	Glu	Lys	Leu	Ala
			130				135					140			
Met	Ser	Asn	Val	Arg	Leu	Val	Met	Ser	Ile	Ala	Gln	Arg	Tyr	Asp	Asn
145					150					155					160
Leu	Gly	Ala	Glu	Met	Ser	Asp	Leu	Val	Gln	Gly	Gly	Leu	Ile	Gly	Leu
			165						170					175	
Leu	Arg	Gly	Ile	Glu	Lys	Phe	Asp	Ser	Ser	Lys	Gly	Phe	Arg	Ile	Ser
			180					185					190		
Thr	Tyr	Val	Tyr	Trp	Trp	Ile	Arg	Gln	Gly	Val	Ser	Arg	Ala	Leu	Val
			195					200					205		
Asp	Asn	Ser	Arg	Thr	Leu	Arg	Gly	Pro	Thr	His	Leu	His	Glu	Arg	Leu
			210				215					220			
Gly	Leu	Ile	Arg	Asn	Ala	Lys	Leu	Arg	Leu	Gln	Glu	Lys	Gly	Ile	Thr
225					230					235					240
Pro	Ser	Ile	Asp	Arg	Ile	Ala	Glu	Ser	Leu	Asn	Met	Ser	Gln	Lys	Lys
			245						250					255	
Val	Arg	Asn	Ala	Thr	Glu	Ala	Val	Ser	Lys	Val	Phe	Ser	Leu	Asp	Arg
			260					265					270		
Asp	Ala	Phe	Pro	Ser	Leu	Asn	Gly	Leu	Pro	Gly	Glu	Thr	His	His	Ser
			275					280					285		
Tyr	Ile	Ala	Asp	Thr	Arg	Leu	Glu	Asn	Asn	Pro	Trp	His	Gly	Tyr	Asp
			290					295					300		
Asp	Leu	Ala	Leu	Lys	Glu	Glu	Val	Ser	Lys	Leu	Ile	Ser	Ala	Thr	Leu
305					310					315					320
Gly	Glu	Arg	Glu	Lys	Glu	Ile	Ile	Arg	Leu	Tyr	Tyr	Gly	Leu	Asp	Lys
			325						330					335	
Glu	Cys	Leu	Thr	Trp	Glu	Asp	Ile	Ser	Lys	Arg	Ile	Gly	Leu	Ser	Arg
			340					345						350	
Glu	Arg	Val	Arg	Gln	Val	Gly	Leu	Val	Ala	Leu	Glu	Lys	Leu	Lys	His
			355					360					365		
Ala	Ala	Arg	Lys	Arg	Lys	Met	Glu	Ala	Met	Ile	Leu	Lys	Asn		

370 375 380

(2) INFORMATION FOR SEQ ID NO:1146:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1352 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1352

(D) OTHER INFORMATION: / Ceres Seq. ID 1569144

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1146:

aaaaRoccc	tctctcttca	gtctctctct	ctctagacga	tctctatctt	gaataaaaa	60
ccgataatga	cctcaaccaa	tccgggtggtc	gcggaagtaa	taccggcgga	aacttctaca	120
gatgctacag	agacgaagat	tgcaacgaag	gaagctgggtg	aagcaccgga	gaagaaggtg	180
aggaagagc	atacaatcac	caagtctaga	gagagtggga	ctgaaggaga	acacgacaa	240
ttctcggaag	ctcttcaatt	gtttgatcgt	gactggaaaa	agatagaaga	ttttgtgtgt	300
tcaagagacg	ttattcagat	cagtagccat	gccccaaaa	actttctaaa	gggtccaaaa	360
aatgggactt	tagcacatgt	tccacccctc	aggcctaagc	gcaaaagtgc	tcattccat	420
cctcaaaagg	catcgaaaaa	tgctcaaatg	tcgcttcacg	tttccatgtc	ctttctact	480
caataaaaa	acctgctcgg	atatactcca	tggggatgat	atacatctgc	attgttaaac	540
attgctgtta	gtgggggttat	tccaccagaa	gatgaacttg	atactctttg	tgagacagaa	600
gttgatgttg	gatcaaatga	catgataagt	gaaactagtc	cttcagcatc	tggtatcgga	660
agctcaagca	gaacactatc	agattctaag	ggttttgagac	tgccgaaaca	agctccotca	720
atgcattggtc	ttctcgattt	tgctgaggtt	tataaacttca	ttgggaggtg	gttcgatcct	780
gacagcaaa	gcgcgatgaa	aaagctcaag	gaaatggatc	ctataaaatt	cgaaactgtt	840
ttgctgttga	tgagaaacct	cacagtgaac	ttgtcaaac	ctgactttga	acctacttct	900
gaatatgttg	atgctgcaga	ggaaggtcat	gaacacttaa	gctcttagct	gtttgtgcac	960
tcaacaagtt	atatacttct	ttgacgactt	cttgctcgca	acaaactctc	accagctatc	1020
aaatgcacatg	taaggttgtt	gtctgaggag	aacataactg	agtcgtctgc	acaaacagaa	1080
ggaacatag	cagtttcggt	cagaaccagt	cgtgtgaatg	gtagatatat	gtatgtgtgt	1140
gtagaaaatg	gtttaccaat	gtatcttctt	tttgataaatt	atttttccat	gcottttgtg	1200
atatgtaaat	ttctttacct	cgttctctga	ttggttattt	cttcgtttatc	tgtttaacca	1260
aaagctatgt	aaacacagtag	caaattgtta	cttaactcgg	aagttagata	cataactctg	1320
ttgtattgca	cttgatcaaa	gcgttaacgt	cc			

(2) INFORMATION FOR SEQ ID NO:1147:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 293 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..293

(D) OTHER INFORMATION: / Ceres Seq. ID 1569145

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1147:

Met	Thr	Ser	Thr	Asn	Pro	Val	Val	Ala	Glu	Val	Ile	Pro	Ala	Glu	Thr
1			5					10			15				
Ser	Thr	Asp	Ala	Thr	Glu	Thr	Thr	Ile	Ala	Thr	Thr	Glu	Ala	Gly	Glu
			20					25				30			
Ala	Pro	Glu	Lys	Lys	Val	Arg	Lys	Ala	Tyr	Thr	Ile	Thr	Lys	Ser	Arg
			35				40					45			
Glu	Ser	Trp	Thr	Glu	Gly	Glu	His	Asp	Lys	Phe	Leu	Glu	Ala	Leu	Gln
			50				55				60				
Leu	Phe	Asp	Arg	Asp	Trp	Lys	Lys	Ile	Glu	Asp	Phe	Val	Gly	Ser	Lys
			65				70			75				80	
Thr	Val	Ile	Gln	Ile	Ser	Ser	His	Ala	Gln	Lys	Tyr	Phe	Leu	Lys	Val
			85						90				95		
Gln	Lys	Asn	Gly	Thr	Leu	Ala	His	Val	Pro	Pro	Arg	Pro	Lys	Arg	

Lys	Ala	Ala	His	Pro	Tyr	Pro	Gln	Lys	Ala	Ser	Lys	Asn	Ala	Gln	Met
	115						120					125			
Ser	Leu	His	Val	Ser	Met	Ser	Phe	Pro	Thr	Gln	Ile	Asn	Asn	Leu	Pro
	130						135				140				
Gly	Tyr	Thr	Pro	Trp	Asp	Asp	Asp	Thr	Ser	Ala	Leu	Leu	Asn	Ile	Ala
	145						150				155				160
Val	Ser	Gly	Val	Ile	Pro	Pro	Glu	Asp	Glu	Leu	Asp	Thr	Leu	Cys	Gly
				165					170					175	
Ala	Glu	Val	Asp	Val	Gly	Ser	Asn	Asp	Met	Ile	Ser	Glu	Thr	Ser	Pro
			180						185					190	
Ser	Ala	Ser	Gly	Ile	Gly	Ser	Ser	Ser	Arg	Thr	Leu	Ser	Asp	Ser	Lys
			195					200					205		
Gly	Leu	Arg	Leu	Ala	Lys	Gln	Ala	Pro	Ser	Met	His	Gly	Leu	Pro	Asp
							215					220			
Phe	Ala	Glu	Val	Tyr	Asn	Phe	Ile	Gly	Ser	Val	Phe	Asp	Pro	Asp	Ser
	225						230					235			240
Lys	Gly	Arg	Met	Lys	Lys	Leu	Lys	Glu	Met	Asp	Pro	Ile	Asn	Phe	Glu
				245					250					255	
Thr	Val	Leu	Leu	Leu	Met	Arg	Asn	Leu	Thr	Val	Asn	Leu	Ser	Asn	Pro
				260					265					270	
Asp	Phe	Glu	Pro	Thr	Ser	Glu	Tyr	Val	Asp	Ala	Ala	Glu	Glu	Gly	His
				275			280							285	
Glu	His	Leu	Ser	Ser											
															290

(2) INFORMATION FOR SEQ ID NO:1148:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 166 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..166

(D) OTHER INFORMATION: / Ceres Seq. ID 1569146

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1148:

Met	Ser	Leu	His	Val	Ser	Met	Ser	Phe	Pro	Thr	Gln	Ile	Asn	Asn	Leu
1				5					10					15	
Pro	Gly	Tyr	Thr	Pro	Trp	Asp	Asp	Asp	Thr	Ser	Ala	Leu	Leu	Asn	Ile
				20				25					30		
Ala	Val	Ser	Gly	Val	Ile	Pro	Pro	Glu	Asp	Glu	Leu	Asp	Thr	Leu	Cys
				35				40				45			
Gly	Ala	Glu	Val	Asp	Val	Gly	Ser	Asn	Asp	Met	Ile	Ser	Glu	Thr	Ser
				50				55				60			
Pro	Ser	Ala	Ser	Gly	Ile	Gly	Ser	Ser	Ser	Arg	Thr	Leu	Ser	Asp	Ser
				65				70				75			80
Lys	Gly	Leu	Arg	Leu	Ala	Lys	Gln	Ala	Pro	Ser	Met	His	Gly	Leu	Pro
				85					90					95	
Asp	Phe	Ala	Glu	Val	Tyr	Asn	Phe	Ile	Gly	Ser	Val	Phe	Asp	Pro	Asp
				100				105					110		
Ser	Lys	Gly	Arg	Met	Lys	Lys	Leu	Lys	Glu	Met	Asp	Pro	Ile	Asn	Phe
				115				120				125			
Glu	Thr	Val	Leu	Leu	Met	Arg	Asn	Leu	Thr	Val	Asn	Leu	Ser	Asn	
				130				135				140			
Pro	Asp	Phe	Glu	Pro	Thr	Ser	Glu	Tyr	Val	Asp	Ala	Ala	Glu	Glu	Gly
				145						155					160
His	Glu	His	Leu	Ser	Ser										
															165

(2) INFORMATION FOR SEQ ID NO:1149:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 160 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..160
(D) OTHER INFORMATION: / Ceres Seq. ID 1569147

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1149:
Met Ser Phe Pro Thr Gln Ile Asn Asn Leu Pro Gly Tyr Thr Pro Trp
1 5 10 15
Asp Asp Asp Thr Ser Ala Leu Leu Asn Ile Ala Val Ser Gly Val Ile
20 25 30
Pro Pro Glu Asp Glu Leu Asp Thr Leu Cys Gly Ala Glu Val Asp Val
35 40 45
Gly Ser Asn Asp Met Ile Ser Glu Thr Ser Pro Ser Ala Ser Gly Ile
50 55 60
Gly Ser Ser Ser Arg Thr Leu Ser Asp Ser Lys Gly Leu Arg Leu Ala
65 70 75 80
Lys Gln Ala Pro Ser Met His Gly Leu Pro Asp Phe Ala Glu Val Tyr
85 90 95
Asn Phe Ile Gly Ser Val Phe Asp Pro Asp Ser Lys Gly Arg Met Lys
100 105 110
Lys Leu Lys Glu Met Asp Pro Ile Asn Phe Glu Thr Val Leu Leu Leu
115 120 125
Met Arg Asn Leu Thr Val Asn Leu Ser Asn Pro Asp Phe Glu Pro Thr
130 135 140
Ser Glu Tyr Val Asp Ala Ala Glu Glu Gly His Glu His Leu Ser Ser
145 150 155 160

(2) INFORMATION FOR SEQ ID NO:1150:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1198 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..1198
(D) OTHER INFORMATION: / Ceres Seq. ID 1569148

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1150:

aaaaacccac	aaatggggat	gagtgtccaa	agactgcact	ctctctctct	ccctctggctc	60
cggcgaaaaa	cccccttttg	atttcattga	taaaacgcga	atcgatctct	cggtgtggaag	120
aagaagaaga	acacgatggg	aacaatgggt	aaagcattct	acagcgtagg	attctggatc	180
cgtagaaactg	gtcaaagcact	tgatccggctc	ggttgtcgcg	tccaagggaa	aaatcatttc	240
cgagaaacagc	tatcaaggca	ccgcacactc	atgaatgttt	ttgacaaaa	ccctaagtgtg	300
gataaaggggg	ctttttgtggc	tctctaacgct	tctctctctg	gtgatgttca	tgtgggaaga	360
ggttcttccca	tttggtatgg	atgtgtctttg	agaggagatg	ctaacagcat	tagtgtttga	420
gctgggacga	atattcaagg	caacgctctt	gtccacgttg	ctaagaccac	cttaagtggg	480
aaggtctttac	ctactgtcat	tggagacaat	gtcaccattg	gtcatagtgc	tgttttaccat	540
ggctgcactg	tcgaggatga	ggcctatatt	ggtacaaagt	caactgtctt	ggatggagct	600
catgttgaaa	aacatgccat	ggttgcttct	ggagctcttg	ttaggcagaa	cactagaatt	660
Ccctctggcg	aggtttgggg	agggcaaccga	gctaattttc	tgagggaagt	gacagaaga	720
gaagaagtct	tcttctccag	tctggcgtgtg	gagtaactcca	acttagctca	agctcacgcc	780
acagagaacg	caagaacact	ggacgaggtg	gagttcaaga	agcttctaaa	caagaagaa	840
gctgcagata	cagaatatga	ttcagtaact	gatgatctga	cgctccctga	gaatgtacca	900
aaagcagctt	gaggcgttta	acctgtgcgc	cttgcgaat	cttgatttgt	ttggtattga	960
aaagtaaaaa	caaaGAAct	gatttccctgc	ttctcccaata	aagttttctt	gggcgtaaaa	1020

tccattggcc agtgcctact gggaaagttt tgggttataa ggcatcatt tctctgttaa 1080
agattgtgag gggttttgtt ctcttgtaac ttgagaaaga aaagttgtaa ccttttcttc 1140
ctttttatgt cgtctaataa attgttgatc agacagacat ttagggtgac ctttgccc

(2) INFORMATION FOR SEQ ID NO:1151:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 258 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..258

(D) OTHER INFORMATION: / Ceres Seq. ID 1569149

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1151:

Met Gly Thr Met Gly Lys Ala Phe Tyr Ser Val Gly Phe Trp Ile Arg
1 5 10 15
Glu Thr Gly Gln Ala Leu Asp Arg Leu Gly Cys Arg Leu Gln Gly Lys
20 25 30
Asn His Phe Arg Glu Gln Leu Ser Arg His Arg Thr Leu Met Asn Val
35 40 45
Phe Asp Lys Thr Pro Asn Val Asp Lys Gly Ala Phe Val Ala Pro Asn
50 55 60
Ala Ser Leu Ser Gly Asp Val His Val Gly Arg Gly Ser Ser Ile Trp
65 70 75 80
Tyr Gly Cys Val Leu Arg Gly Asp Ala Asn Ser Ile Ser Val Gly Ala
85 90 95
Gly Thr Asn Ile Gln Asp Asn Ala Leu Val His Val Ala Lys Thr Asn
100 105 110
Leu Ser Gly Lys Val Leu Pro Thr Val Ile Gly Asp Asn Val Thr Ile
115 120 125
Gly His Ser Ala Val Leu His Gly Cys Thr Val Glu Asp Glu Ala Tyr
130 135 140
Ile Gly Thr Ser Ala Thr Val Leu Asp Gly Ala His Val Glu Lys His
145 150 155 160
Ala Met Val Ala Ser Gly Ala Leu Val Arg Gln Asn Thr Arg Ile Pro
165 170 175
Ser Gly Glu Val Trp Gly Gly Asn Pro Ala Lys Phe Leu Arg Lys Val
180 185 190
Thr Glu Glu Glu Arg Val Phe Phe Ser Ser Ser Ala Val Glu Tyr Ser
195 200 205
Asn Leu Ala Gln Ala His Ala Thr Glu Asn Ala Lys Asn Leu Asp Glu
210 215 220
Ala Glu Phe Lys Lys Leu Leu Asn Lys Lys Asn Ala Arg Asp Thr Glu
225 230 235 240
Tyr Asp Ser Val Leu Asp Asp Leu Thr Leu Pro Glu Asn Val Pro Lys
245 250 255
Ala Ala

(2) INFORMATION FOR SEQ ID NO:1152:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 255 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..255

(D) OTHER INFORMATION: / Ceres Seq. ID 1569150

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1152:

Met Gly Lys Ala Phe Tyr Ser Val Gly Phe Trp Ile Arg Glu Thr Gly
1 5 10 15
Gln Ala Leu Asp Arg Leu Gly Cys Arg Leu Gln Gly Lys Asn His Phe
20 25 30
Arg Glu Gln Leu Ser Arg His Arg Thr Leu Met Asn Val Phe Asp Lys
35 40 45
Thr Pro Asn Val Asp Lys Gly Ala Phe Val Ala Pro Asn Ala Ser Leu
50 55 60
Ser Gly Asp Val His Val Gly Arg Gly Ser Ser Ile Trp Tyr Gly Cys
65 70 75 80
Val Leu Arg Gly Asp Ala Asn Ser Ile Ser Val Gly Ala Gly Thr Asn
85 90 95
Ile Gln Asp Asn Ala Leu Val His Val Ala Lys Thr Asn Leu Ser Gly
100 105 110
Lys Val Leu Pro Thr Val Ile Gly Asp Asn Val Thr Ile Gly His Ser
115 120 125
Ala Val Leu His Gly Cys Thr Val Glu Asp Glu Ala Tyr Ile Gly Thr
130 135 140
Ser Ala Thr Val Leu Asp Gly Ala His Val Glu Lys His Ala Met Val
145 150 155 160
Ala Ser Gly Ala Leu Val Arg Gln Asn Thr Arg Ile Pro Ser Gly Glu
165 170 175
Val Trp Gly Gly Asn Pro Ala Lys Phe Leu Arg Lys Val Thr Glu Glu
180 185 190
Glu Arg Val Phe Phe Ser Ser Ser Ala Val Glu Tyr Ser Asn Leu Ala
195 200 205
Gln Ala His Ala Thr Glu Asn Ala Lys Asn Leu Asp Glu Ala Glu Phe
210 215 220
Lys Lys Leu Leu Asn Lys Lys Asn Ala Arg Asp Thr Glu Tyr Asp Ser
225 230 235 240
Val Leu Asp Asp Leu Thr Leu Pro Glu Asn Val Pro Lys Ala Ala
245 250 255

(2) INFORMATION FOR SEQ ID NO:1153:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 213 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..213

(D) OTHER INFORMATION: / Ceres Seq. ID 1569151

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1153:

Met Asn Val Phe Asp Lys Thr Pro Asn Val Asp Lys Gly Ala Phe Val
1 5 10 15
Ala Pro Asn Ala Ser Leu Ser Gly Asp Val His Val Gly Arg Gly Ser
20 25 30
Ser Ile Trp Tyr Gly Cys Val Leu Arg Gly Asp Ala Asn Ser Ile Ser
35 40 45
Val Gly Ala Gly Thr Asn Ile Gln Asp Asn Ala Leu Val His Val Ala
50 55 60
Lys Thr Asn Leu Ser Gly Lys Val Leu Pro Thr Val Ile Gly Asp Asn
65 70 75 80
Val Thr Ile Gly His Ser Ala Val Leu His Gly Cys Thr Val Glu Asp
85 90 95
Glu Ala Tyr Ile Gly Thr Ser Ala Thr Val Leu Asp Gly Ala His Val
100 105 110
Glu Lys His Ala Met Val Ala Ser Gly Ala Leu Val Arg Gln Asn Thr
115 120 125
Arg Ile Pro Ser Gly Glu Val Trp Gly Gly Asn Pro Ala Lys Phe Leu

130	135	140	
Arg Lys Val Thr Glu Glu Arg Val Phe Phe Ser Ser Ser Ala Val			
145	150	155	160
Glu Tyr Ser Asn Leu Ala Gln Ala His Ala Thr Glu Asn Ala Lys Asn			
	165	170	175
Leu Asp Glu Ala Glu Phe Lys Lys Leu Leu Asn Lys Lys Asn Ala Arg			
	180	185	190
Asp Thr Glu Tyr Asp Ser Val Leu Asp Asp Leu Thr Leu Pro Glu Asn			
	195	200	205
Val Pro Lys Ala Ala			
210			

(2) INFORMATION FOR SEQ ID NO:1154:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1537 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1537
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569156

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1154:

atcgaaatta	ttgtggtggt	ttgtgaacag	aaaccaagca	ggattaaaga	tggttcaatc	60
ttgtttaatt	tctcgtaaca	agggtttggc	ggaGcaagat	ctaactaagc	ttgatgtaac	120
aaagttacat	cctctgtctc	ctgaagtcac	ttctgcgcaa	gcaaccataa	atatcggaac	180
cattggtcac	gtcgctcacg	gtaaatcgac	tatagtgaag	gctatctctg	gtgttcacag	240
ttgtgcgttt	aagaatgaat	tagagcgtaa	cattaccatt	aagcttgggt	atgcacaaatgc	300
aaagatttac	aagtgtagg	atgacaagtg	ccttagacca	atgtgtctaca	agtcacatagg	360
gagtggaaaa	gaagacaacc	caactttgtg	tgtccccgga	tttgacaatt	gcaagatgac	420
actactgaga	catgtctcat	gtgtcgattg	tccaggacac	gatattctta	tggcgacaatt	480
gtcctaagga	gcagcaatcg	tggatgggtg	tttacttcta	attgtgtgta	acgggagttg	540
tccacaacca	caaacccgtg	aacatcttgc	ttctgttgat	atgatgogcc	ttaagcatat	600
cataatcctt	cagaacaaga	ttgatctcat	taatgagaaa	gccgccactg	aacagcacga	660
ggctattccg	aaattttata	cgaacacgaa	tgctgaggat	gcacctatag	ttcctgtctc	720
agcacaaact	aaatacaaca	ttgatgttgt	gagtgataac	attgtcaaga	agattccaat	780
cctgtgaga	gactttgtgt	caccaccaaa	gatgattgtg	attcgttctt	tcatgtctca	840
taaacctggc	tcggcgggtc	atgaaatgaa	agggtgtgtt	gctgggtgga	gtatcctcca	900
gtgaacccaa	tgattgaaat	tagaccttgt	atcaactggc	aagatgagca	tggaaactca	960
aaatgcactc	caattttact	gcgtataact	tcactatacg	cggaacagaa	cgagctctcag	1020
tttgtgttac	cgggagggtct	aatcggagtt	ggaacaacca	tggaacctac	gtctaccggt	1080
gtgatgaagt	tggtttgtca	agtccttggt	gaaatgggta	ctctccctga	cgtcttttgtt	1140
gagcttgtag	taagttaaca	gctttctgac	gcctctcatt	gagtgaggac	aaaggaaaaa	1200
gagaagcaaa	tgaaggtgtc	aaagctaacc	aaagaagaga	tattgatggt	gaacatcggg	1260
tctatgtcta	cgggagctaa	ggtttattga	gtcaagaaaag	atatggtgaa	actccaactg	1320
acgtctccgg	tgtgtaccac	cataggagag	aaggttgctt	taagcccgag	tgtgtacagg	1380
catgtggctc	taattggtaa	gggtcagatt	atggctggaa	ccaccatcga	gtttctctct	1440
cctcctcttt	aatgaagtag	tgatgagttt	tttatattgt	ttgcattcaa	aaataattaa	1500
catgtgcctt	tgatgtgtta	atcactttct	ttcgact			

(2) INFORMATION FOR SEQ ID NO:1155:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 300 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..300
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569157

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1155:

```

Ser Lys Leu Leu Trp Cys Phe Val Asn Arg Asn Gln Ala Gly Leu Lys
1      5      10
Met Val Gln Ser Val Leu Ile Ser Arg Asn Lys Gly Leu Ala Glu Gln
20      25      30
Asp Leu Thr Lys Leu Asp Val Thr Lys Leu His Pro Leu Ser Pro Glu
35      40      45
Val Ile Ser Arg Gln Ala Thr Ile Asn Ile Gly Thr Ile Gly His Val
50      55      60
Ala His Gly Lys Ser Thr Ile Val Lys Ala Ile Ser Gly Val Gln Thr
65      70      75      80
Val Arg Phe Lys Asn Glu Leu Glu Arg Asn Ile Thr Ile Lys Leu Gly
85      90      95
Tyr Ala Asn Ala Lys Ile Tyr Lys Cys Glu Asp Asp Lys Cys Pro Arg
100      105      110
Pro Met Cys Tyr Lys Ser Tyr Gly Ser Gly Lys Glu Asp Asn Pro Thr
115      120      125
Cys Asp Val Pro Gly Phe Asp Asn Cys Lys Met Thr Leu Leu Arg His
130      135      140
Val Ser Cys Val Asp Cys Pro Gly His Asp Ile Leu Met Ala Thr Met
145      150      155      160
Leu Asn Gly Ala Ala Ile Val Asp Gly Ala Leu Leu Ile Ala Ala
165      170      175
Asn Gly Ser Cys Pro Gln Pro Gln Thr Ala Glu His Leu Ala Ser Val
180      185      190
Asp Met Met Arg Leu Lys His Ile Ile Ile Leu Gln Asn Lys Ile Asp
195      200      205
Leu Ile Asn Glu Lys Ala Ala Thr Glu Gln His Glu Ala Ile Gln Lys
210      215      220
Phe Ile Thr Asn Thr Asn Ala Glu Asp Ala Pro Ile Val Pro Val Ser
225      230      235      240
Ala Gln Leu Lys Tyr Asn Ile Asp Val Val Ser Glu Tyr Ile Val Lys
245      250      255
Lys Ile Pro Ile Pro Val Arg Asp Phe Val Ser Pro Pro Lys Met Ile
260      265      270
Val Ile Arg Ser Phe Asp Val Asn Lys Pro Gly Ser Ala Gly His Glu
275      280      285
Met Lys Gly Gly Val Ala Gly Gly Ser Ile Leu Gln
290      295      300

```

(2) INFORMATION FOR SEQ ID NO:1156:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 284 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..284

(D) OTHER INFORMATION: / Ceres Seq. ID 1569158

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1156:

```

Met Val Gln Ser Val Leu Ile Ser Arg Asn Lys Gly Leu Ala Glu Gln
1      5      10
Asp Leu Thr Lys Leu Asp Val Thr Lys Leu His Pro Leu Ser Pro Glu
20      25      30
Val Ile Ser Arg Gln Ala Thr Ile Asn Ile Gly Thr Ile Gly His Val
35      40      45
Ala His Gly Lys Ser Thr Ile Val Lys Ala Ile Ser Gly Val Gln Thr
50      55      60
Val Arg Phe Lys Asn Glu Leu Glu Arg Asn Ile Thr Ile Lys Leu Gly
65      70      75      80
Tyr Ala Asn Ala Lys Ile Tyr Lys Cys Glu Asp Asp Lys Cys Pro Arg

```


(2) INFORMATION FOR SEQ ID NO:1158:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1311 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -

- (B) LOCATION: 1..1311

- (D) OTHER INFORMATION: / Ceres Seq. ID 1569164

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1158:

```
aaggcgtgag ataataaaac cotttggcctt tctcatagag atttgcctgg tctcttgttc 60
ctctttctcc ttcttctact gttagactcc tcgaccaaac aactagctcc aatggcataa 120
tgagcattgt agtttggcaat ttcttcttcc gtgaagaaga agaagatggc ttgggagaaa 180
gagggaagaag cgtcacaaaa cgggtgcgtt ttgtctcttg atgggctcta ttgcgaggaa 240
gaaacgcgggt ttgtggagga cgaatcttga gacgatggag atttagattt tctcgagaaa 300
tctgatgaga gtgtgtgaaa gtttcagttt ttacctcttt tggatattgt cttatgggat 360
gacgatgaga ttctgagttt gatttcaaa gaaaacgaaa cgaatccatg ttttggggaa 420
caaatcttag atggcctttt gggttcttgt aggaagaggc ctttagattg gggtcttagg 480
gttaaatctc attatggggt tacttcattg acggctatac ttgctgtgaa ctacttcgat 540
aggtttatga caagtataaa gcttcagact gataagccat ggaatgtctc gcttgtgtgt 600
gtggctctct tgtcttttagc tgcataaagt gaagagattc aagttccatt gctcttagac 660
ctccaagtgg aagaagcaag atatctcttt gaagctaaga cgattcaaag aatggagcct 720
ttgattcttt ctactcttca atggagaatg caccctgtga tagactctg taggaagtgt 780
cacattatcc ggcgatttgg ctctaaatgg caccagcaat tcgaactctg taggaagtgt 840
gagcgtcttc tgactcttgt tattgtgatg acgaggttta tgaggtactt cctctctctc 900
ttagctactg caataatgat ccttgccttc gaggaaatga agccatgtga tgaagtgtga 960
taccaatctc aaataacgac tctactcaaa gtcaatcagg agaaaagtaa tgaatgtcat 1020
gaactgttgt tggagcacaa tcacaagcag aagaggatga tgaatttgtt tgatcaggac 1080
agtcacaagt gtgtattaga cttttagtgc agtctcaata gctcctggaa tgtctccact 1140
actgcttcag tgcctctcac atcttctgtt ccagagcctc tgctcaagag aagaagagtt 1200
caggagcagc aaatgagatt gccctcaata aaccgtatgt ttctcgatgt gcttagtagt 1260
cctcgctagt acctttcttt gatcaaatgt gtcaaaacat aaattcGat c
```

(2) INFORMATION FOR SEQ ID NO:1159:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 367 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide

- (B) LOCATION: 1..367

- (D) OTHER INFORMATION: / Ceres Seq. ID 1569165

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1159:

```
Met Ala Leu Glu Lys Glu Glu Glu Ala Ser Gln Asn Gly Ala Phe Cys
1 5 10 15
Val Leu Asp Gly Leu Tyr Cys Glu Glu Glu Thr Gly Phe Val Glu Asp
20 25 30
Asp Leu Asp Asp Asp Gly Asp Leu Asp Phe Leu Glu Lys Ser Asp Glu
35 40 45
Ser Val Val Lys Phe Gln Phe Leu Pro Leu Leu Asp Met Phe Leu Trp
50 55 60
Asp Asp Asp Glu Ile Leu Ser Leu Ile Ser Lys Glu Asn Glu Thr Asn
65 70 75 80
Pro Cys Phe Gly Glu Gln Ile Leu Asp Gly Phe Leu Val Ser Cys Arg
85 90 95
Lys Glu Ala Leu Asp Trp Val Leu Arg Val Lys Ser His Tyr Gly Phe
100 105 110
Thr Ser Leu Thr Ala Ile Leu Ala Val Asn Tyr Phe Asp Arg Phe Met
```

Met	Phe	Leu	Trp	Asp	Asp	Glu	Ile	Leu	Ser	Leu	Ile	Ser	Lys	Glu
1			5				10					15		
Asn	Glu	Thr	Asn	Pro	Cys	Phe	Gly	Glu	Gln	Ile	Leu	Asp	Gly	Phe
		20					25					30		
Val	Ser	Cys	Arg	Lys	Glu	Ala	Leu	Asp	Trp	Val	Leu	Arg	Val	Lys
		35					40					45		
His	Tyr	Gly	Phe	Thr	Ser	Leu	Thr	Ala	Ile	Leu	Ala	Val	Asn	Tyr
	50					55					60			
Asp	Arg	Phe	Met	Thr	Ser	Ile	Lys	Leu	Gln	Thr	Asp	Lys	Pro	Trp
65					70					75				80
Ser	Gln	Leu	Val	Ala	Val	Ala	Ser	Leu	Ser	Leu	Ala	Ala	Lys	Val
					85				90					95
Glu	Ile	Gln	Val	Pro	Leu	Leu	Leu	Asp	Leu	Gln	Val	Glu	Glu	Ala
			100					105				110		
Tyr	Leu	Phe	Glu	Ala	Lys	Thr	Ile	Gln	Arg	Met	Glu	Leu	Leu	Ile
		115					120					125		
Ser	Thr	Ser	Gln	Trp	Arg	Met	His	Pro	Val	Thr	Pro	Ile	Ser	Phe
	130					135					140			

Asp His Ile Ile Arg Arg Phe Gly Ser Lys Trp His Gln Gln Leu Asp
145 150 155 160
Phe Cys Arg Lys Cys Glu Arg Leu Leu Ile Ser Val Ile Ala Asp Thr
165 170 175
Arg Phe Met Arg Tyr Phe Pro Ser Val Leu Ala Thr Ala Ile Met Ile
180 185 190
Leu Val Phe Glu Glu Leu Lys Pro Cys Asp Glu Val Glu Tyr Gln Ser
195 200 205
Gln Ile Thr Thr Leu Leu Lys Val Asn Gln Glu Lys Val Asn Glu Cys
210 215 220
Tyr Glu Leu Leu Leu Glu His Asn Pro Ser Lys Lys Arg Met Met Asn
225 230 235 240
Leu Val Asp Gln Asp Ser Pro Ser Gly Val Leu Asp Phe Asp Asp Ser
245 250 255
Ser Asn Ser Ser Trp Asn Val Ser Thr Thr Ala Ser Val Ser Ser Ser
260 265 270
Ser Ser Ser Pro Glu Pro Leu Leu Lys Arg Arg Arg Val Gln Glu Gln
275 280 285
Gln Met Arg Leu Pro Ser Ile Asn Arg Met Phe Leu Asp Val Leu Ser
290 295 300
Ser Pro Arg
305

(2) INFORMATION FOR SEQ ID NO:1161:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 240 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..240

(D) OTHER INFORMATION: / Ceres Seq. ID 1569167

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1161:

Met Thr Ser Ile Lys Leu Gln Thr Asp Lys Pro Trp Met Ser Gln Leu
1 5 10 15
Val Ala Val Ala Ser Leu Ser Leu Ala Ala Lys Val Glu Glu Ile Gln
20 25 30
Val Pro Leu Leu Leu Asp Leu Gln Val Glu Glu Ala Arg Tyr Leu Phe
35 40 45
Glu Ala Lys Thr Ile Gln Arg Met Glu Leu Leu Ile Leu Ser Thr Leu
50 55 60
Gln Trp Arg Met His Pro Val Thr Pro Ile Ser Phe Phe Asp His Ile
65 70 75 80
Ile Arg Arg Phe Gly Ser Lys Trp His Gln Gln Leu Asp Phe Cys Arg
85 90 95
Lys Cys Glu Arg Leu Leu Ile Ser Val Ile Ala Asp Thr Arg Phe Met
100 105 110
Arg Tyr Phe Pro Ser Val Leu Ala Thr Ala Ile Met Ile Leu Val Phe
115 120 125
Glu Glu Leu Lys Pro Cys Asp Glu Val Glu Tyr Gln Ser Gln Ile Thr
130 135 140
Thr Leu Leu Lys Val Asn Gln Glu Lys Val Asn Glu Cys Tyr Glu Leu
145 150 155 160
Leu Leu Glu His Asn Pro Ser Lys Lys Arg Met Met Asn Leu Val Asp
165 170 175
Gln Asp Ser Pro Ser Gly Val Leu Asp Phe Asp Asp Ser Ser Asn Ser
180 185 190
Ser Trp Asn Val Ser Thr Thr Ala Ser Val Ser Ser Ser Ser Ser Ser
195 200 205
Pro Glu Pro Leu Leu Lys Arg Arg Val Gln Glu Gln Met Arg

210	215	220
Leu Pro Ser Ile Asn Arg	Met Phe Leu Asp Val	Leu Ser Ser Pro Arg
225	230	235
		240

(2) INFORMATION FOR SEQ ID NO:1162:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1386 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1386

(D) OTHER INFORMATION: / Ceres Seq. ID 1569168

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1162:

attttctcta	cttgtccact	tttctcacgc	cgcacatcac	ttctcccttg	tgcgataatc	60
tttgcgtgag	atttgtctga	aaagttagcta	accatgggta	aagagaagtt	tcacatcaac	120
atttgggtca	tgggccacgt	cgattctgga	aagtcgacaa	ccactgggac	cttgatctac	180
aagttgggtg	gtattgacaa	cggtgtgac	gagaggttcg	agaaggaggc	tgctgagatg	240
aacaagaagg	ccttcaagta	cgcattgggtg	ttggacaaac	tttaaggctga	gcgtgagcgt	300
ggtatcacca	tgcacattgc	ttcttggaa	ttcggagacca	ccaagtacta	ctgcactgtc	360
attgatgctc	ctgtgtcatc	tgatttcatc	aagaacatga	tcactgtgtac	ctcccaggct	420
gattgtgctc	tccttatcat	cgactccacc	actgggtgGtt	ttgaggctgg	tatctccaag	480
gatggtcaga	cccgtagaga	cgcttcctct	gctttcacc	ttgggtgcaa	gcagatgatc	540
tgctgtgtga	acaagatgga	tgccactacc	cccaagtact	ccaaggccag	gtacgatgaa	600
atcatcaagg	agggtgtctc	ctacttgaag	aagggtgggt	acaaccccca	caaaatccca	660
tttctgcccc	ttcttggttc	tgagggtgac	aacatgattg	agaggtccac	caactctgac	720
tggtacaagg	gaccaactct	ccttgaggct	cttgaccaga	tcaacgagcc	caagaggccg	780
tcagacaagg	cccttcgtct	cccacttcag	gatgtctaca	agattgtgtg	tattggaacg	840
gtgcatttgg	gacgtgttga	gactgtgtat	atcaagcctg	gtatgtgtgt	gacottttgt	900
cccacaggat	tgaccaactga	ggtcaagctc	gttgagatgc	accacgagtc	tcctttgtgag	960
gcacttccag	gtgacaaagt	tggtttcaat	gttaagaatg	ttgccgtgaa	ggatctttaa	1020
agagggtacg	tgcatcccaa	ctccaaggat	gacctgccca	agggtgtgac	taacttcaac	1080
tcacagggtca	tcactcatgaa	ccaccctggt	cagattggta	acgggttaac	ccagctttgt	1140
gattgcccaca	ctcttcacat	tgacgtcaag	ttctctgaga	tcctgaccaa	gattgacagg	1200
cgttcttggt	aggagattga	gaaggagccc	aaattcttga	agaatgggtga	tgctgggtatg	1260
gtgaagatga	ctccaaacca	gcccatgggt	gtggagacct	ttcttgagta	cccaccactt	1320
ggacgttttcg	ctgttaggga	catgaggcag	actgttgcag	tcggtgttat	caagagtgtt	1380
gacaag						

(2) INFORMATION FOR SEQ ID NO:1163:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 431 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..431

(D) OTHER INFORMATION: / Ceres Seq. ID 1569169

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1163:

Met	Gly	Lys	Glu	Lys	Phe	His	Ile	Asn	Ile	Val	Val	Ile	Gly	His	Val
1						5				10				15	
Asp	Ser	Gly	Lys	Ser	Thr	Thr	Thr	Gly	His	Leu	Ile	Tyr	Lys	Leu	Gly
					20				25					30	
Gly	Ile	Asp	Lys	Arg	Val	Ile	Glu	Arg	Phe	Glu	Lys	Glu	Ala	Ala	Glu
					35				40				45		
Met	Asn	Lys	Arg	Ser	Phe	Lys	Tyr	Ala	Trp	Val	Leu	Asp	Lys	Leu	Lys
	50						55							60	

Ala	Glu	Arg	Glu	Arg	Gly	Ile	Thr	Ile	Asp	Ile	Ala	Leu	Trp	Lys	Phe	
65					70				75						80	
Glu	Thr	Thr	Lys	Tyr	Tyr	Cys	Thr	Val	Ile	Asp	Ala	Pro	Gly	His	Arg	
			85					90						95		
Asp	Phe	Ile	Lys	Asn	Met	Ile	Thr	Gly	Thr	Ser	Gln	Ala	Asp	Cys	Ala	
			100					105						110		
Val	Leu	Ile	Ile	Asp	Ser	Thr	Thr	Gly	Gly	Phe	Glu	Ala	Gly	Ile	Ser	
			115					120					125			
Lys	Asp	Gly	Gln	Thr	Arg	Glu	His	Ala	Leu	Leu	Ala	Phe	Thr	Leu	Gly	
			130				135				140					
Val	Lys	Gln	Met	Ile	Cys	Cys	Cys	Asn	Lys	Met	Asp	Ala	Thr	Thr	Pro	
			145				150			155					160	
Lys	Tyr	Ser	Lys	Ala	Arg	Tyr	Asp	Glu	Ile	Ile	Lys	Glu	Val	Ser	Ser	
			165					170						175		
Tyr	Leu	Lys	Lys	Val	Gly	Tyr	Asn	Pro	Asp	Lys	Ile	Pro	Phe	Val	Pro	
			180					185						190		
Ile	Ser	Gly	Phe	Glu	Gly	Asp	Asn	Met	Ile	Glu	Arg	Ser	Thr	Asn	Leu	
			195				200					205				
Asp	Trp	Tyr	Lys	Gly	Pro	Thr	Leu	Leu	Glu	Ala	Leu	Asp	Gln	Ile	Asn	
			210			215					220					
Glu	Pro	Lys	Arg	Pro	Ser	Asp	Lys	Pro	Leu	Arg	Leu	Pro	Leu	Gln	Asp	
			225			230				235					240	
Val	Tyr	Lys	Ile	Gly	Gly	Ile	Gly	Thr	Val	Pro	Leu	Gly	Arg	Val	Glu	
			245						250					255		
Thr	Gly	Met	Ile	Lys	Pro	Gly	Met	Val	Val	Thr	Phe	Ala	Pro	Thr	Gly	
			260				265							270		
Leu	Thr	Thr	Glu	Val	Lys	Ser	Val	Glu	Met	His	His	Glu	Ser	Leu	Leu	
			275				280					285				
Glu	Ala	Leu	Pro	Gly	Asp	Asn	Val	Gly	Phe	Asn	Val	Lys	Asn	Val	Ala	
			290			295					300					
Val	Lys	Asp	Leu	Lys	Arg	Gly	Tyr	Val	Ala	Ser	Asn	Ser	Lys	Asp	Asp	
			305			310				315					320	
Pro	Ala	Lys	Gly	Ala	Ala	Asn	Phe	Thr	Ser	Gln	Val	Ile	Ile	Met	Asn	
			325						330					335		
His	Pro	Gly	Gln	Ile	Gly	Asn	Gly	Tyr	Ala	Pro	Val	Leu	Asp	Cys	His	
			340				345						350			
Thr	Ser	His	Ile	Ala	Val	Lys	Phe	Ser	Glu	Ile	Leu	Thr	Lys	Ile	Asp	
			355				360					365				
Arg	Arg	Ser	Gly	Lys	Glu	Ile	Glu	Lys	Glu	Pro	Lys	Phe	Leu	Lys	Asn	
			370			375					380					
Gly	Asp	Ala	Gly	Met	Val	Lys	Met	Thr	Pro	Thr	Lys	Pro	Met	Val	Val	
			385			390				395					400	
Glu	Thr	Phe	Ser	Glu	Tyr	Pro	Pro	Leu	Gly	Arg	Phe	Ala	Val	Arg	Asp	
			405					410						415		
Met	Arg	Gln	Thr	Val	Ala	Val	Gly	Val	Ile	Lys	Ser	Val	Asp	Lys		
			420				425						430			

(2) INFORMATION FOR SEQ ID NO:1164:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 383 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..383

(D) OTHER INFORMATION: / Ceres Seq. ID 1569170

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1164:

Met	Asn	Lys	Arg	Ser	Phe	Lys	Tyr	Ala	Trp	Val	Leu	Asp	Lys	Leu	Lys	
1		5						10					15			
Ala	Glu	Arg	Glu	Arg	Gly	Ile	Thr	Ile	Asp	Ile	Ala	Leu	Trp	Lys	Phe	

Met Ile Thr Gly Thr Ser Gln Ala Asp Cys Ala Val Leu Ile Ile Asp
1 5 10 15
Ser Thr Thr Gly Phe Glu Ala Gly Ile Ser Lys Asp Gly Gln Thr
20 25 30

(2) INFORMATION FOR SEQ ID NO:1166:

(A) LENGTH: 1227 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..1227
(D) OTHER INFORMATION

ctcgaagact	attaaagga	tatccgcgaaa	gaagaaaaaa	aaaacttttt	tttggtaaaag	60
gactaaactt	tttgtttgca	ctgcgcattc	ctaacctctac	gattgtgtgt	tttgtgtttg	120
agcgaaacc	tagaatcgg	cttaacccat	ttagcgcag	atgctgcgag	tagacggaag	180
gaggtctttt	tttgtttcgc	agagatcttc	gaacggtgacc	tctctcgtcc	tttcccgtag	240
ctacatacct	tcctgattgg	gcgaactcct	ttccgctttc	agactgtctc	cctctcgaga	300
ttctctcatt	ttcaattctt	accacccggg	cggtataaga	ggttttgtct	ctcaagttat	360
ctcagcagga	aatgagatag	gttttgtgtc	gggaagctcca	ccgacagtct	aagctgtcaa	420
aaacactaac	ctaaagattg	ttctatgaca	ctataacacct	gacggttacc	cactcgtgta	480
ccctagacga	cggcgattcg	ccatttttgt	cttgtcgggt	ggaagatttc	AtHWWGctg	540
tttgtctcgc	ccctcgttgt	ctggaactga	gtgtgagcat	ctgcgcaagt	aaagatgtcc	600
cttgcctctc	atccctgtgt	gttgacacta	ggagcataga	accggaagct	accgtgacag	660

tcaagtggcg	tggaagagccc	gtcttcatca	ggcgaagaac	agaagatgac	atcaagctgg	720
ccaatagtgt	ggatgttga	tccttgaggg	accacacaaga	agactcgggt	agagtcaaga	780
atccagaatg	gttgatcggt	gttgagatg	gcactcattt	gggtgcatc	cccttgcccta	840
atgctggtga	ttaatgggtg	tggtttttgtc	cgtgtcacgg	atcaccattac	gatatactgt	900
gaagaattag	gaaaggtcct	gcaccataca	acctggaagt	accgacctac	agctttcttgg	960
aagagaataa	attactcaat	ggttaatgaa	taaaagcaca	cagtccgagt	gtcatgggtct	1020
ggatgatctt	aaatctgttt	ttgtttttat	attttccggc	atttttagctg	gcaagttcgc	1080
tttctcaaca	ctttgggctc	agcaaaaatt	ggcttgtttt	gctgaataat	acaaacttgt	1140
catgtatga	cttagtatct	gtctcatctg	gtgaaaaatac	attgttcata	cttcatagtc	1200
tctgtttatt	attgaaaag	agttttg				

(2) INFORMATION FOR SEQ ID NO:1167:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 143 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..143

(D) OTHER INFORMATION: / Ceres Seq. ID 1569180

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1167:

Met	Leu	Arg	Val	Ala	Gly	Arg	Arg	Leu	Phe	Ser	Val	Ser	Gln	Arg	Ser	
1				5				10					15			
Ser	Thr	Val	Thr	Ser	Phe	Val	Leu	Ser	Arg	Asp	His	Thr	Leu	Ser	Asp	
			20					25					30			
Gly	Gly	Asn	Ser	Ser	Ser	Ala	Ser	Arg	Ser	Val	Pro	Ser	Ala	Asp	Leu	
			35					40					45			
Ser	Ser	Phe	Asn	Ser	Tyr	His	Arg	Ser	Val	Ile	Arg	Gly	Phe	Ala	Ser	
			50				55					60				
Gln	Val	Ile	Thr	Gln	Gly	Asn	Glu	Ile	Gly	Phe	Gly	Ser	Glu	Val	Pro	
			65			70			75				80			
Ala	Thr	Val	Glu	Ala	Val	Lys	Thr	Pro	Asn	Ser	Lys	Ile	Val	Tyr	Asp	
			85						90				95			
Asp	His	Asn	His	Glu	Arg	Tyr	Pro	Pro	Gly	Asp	Pro	Ser	Lys	Arg	Ala	
			100					105					110			
Phe	Ala	Tyr	Phe	Val	Leu	Ser	Gly	Gly	Arg	Phe	Asp	Xaa	Xaa	Leu	Cys	
			115				120					125				
Ser	Pro	Pro	Ala	Cys	Ser	Glu	Ala	Tyr	Cys	Glu	His	Val	Cys	Lys		
			130				135					140				

(2) INFORMATION FOR SEQ ID NO:1168:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 180 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..180

(D) OTHER INFORMATION: / Ceres Seq. ID 1569181

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1168:

Met	Thr	Thr	Ile	Thr	Met	Ser	Val	Thr	His	Leu	Val	Thr	Leu	Ala	Ser	
1			5					10					15			
Gly	His	Ser	Pro	Ile	Leu	Ser	Cys	Arg	Val	Glu	Gly	Leu	Xaa	Xaa	Ala	
			20					25					30			
Ser	Val	Leu	Arg	Leu	Leu	Val	Leu	Lys	Leu	Ile	Val	Ser	Met	Ser	Ala	
			35					40					45			
Ser	Lys	Asp	Val	Leu	Ala	Leu	Ala	Ser	Leu	Glu	Val	Asp	Leu	Gly	Ser	
			50				55					60				
Ile	Glu	Pro	Gly	Thr	Thr	Val	Thr	Val	Lys	Trp	Arg	Gly	Lys	Pro	Val	

65				70				75					80
Phe	Ile	Arg	Arg	Thr	Glu	Asp	Asp	Ile	Lys	Leu	Ala	Asn	Ser
				85				90					95
Asp	Val	Gly	Ser	Leu	Arg	Asp	Pro	Gln	Glu	Asp	Ser	Val	Arg
				100				105					110
Asn	Pro	Glu	Trp	Leu	Ile	Val	Val	Gly	Val	Cys	Thr	His	Leu
				115				120					125
Ile	Pro	Leu	Pro	Asn	Ala	Gly	Asp	Tyr	Gly	Gly	Trp	Phe	Cys
				130				135					140
His	Gly	Ser	His	Tyr	Asp	Ile	Ser	Gly	Arg	Ile	Arg	Lys	Gly
				145				150					155
Pro	Tyr	Asn	Leu	Glu	Val	Pro	Thr	Tyr	Ser	Phe	Leu	Glu	Glu
				165				170					175
Leu	Leu	Ile	Gly										
			180										

(2) INFORMATION FOR SEQ ID NO:1169:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 175 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..175

(D) OTHER INFORMATION: / Ceres Seq. ID 1569182

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1169:

Met	Ser	Val	Thr	His	Leu	Val	Thr	Leu	Ala	Ser	Gly	His	Ser	Pro	Ile
1				5				10						15	
Leu	Ser	Cys	Arg	Val	Glu	Gly	Leu	Xaa	Xaa	Ala	Ser	Val	Leu	Arg	Leu
				20				25					30		
Leu	Val	Leu	Lys	Leu	Ile	Val	Ser	Met	Ser	Ala	Ser	Lys	Asp	Val	Leu
				35				40					45		
Ala	Leu	Ala	Ser	Leu	Glu	Val	Asp	Leu	Gly	Ser	Ile	Glu	Pro	Gly	Thr
				50				55				60			
Thr	Val	Thr	Val	Lys	Trp	Arg	Gly	Lys	Pro	Val	Phe	Ile	Arg	Arg	Arg
				65				70					75		80
Thr	Glu	Asp	Asp	Ile	Lys	Leu	Ala	Asn	Ser	Val	Asp	Val	Gly	Ser	Leu
				85				90					95		
Arg	Asp	Pro	Gln	Glu	Asp	Ser	Val	Arg	Val	Lys	Asn	Pro	Glu	Trp	Leu
				100				105					110		
Ile	Val	Val	Gly	Val	Cys	Thr	His	Leu	Gly	Cys	Ile	Pro	Leu	Pro	Asn
				115				120					125		
Ala	Gly	Asp	Tyr	Gly	Gly	Trp	Phe	Cys	Pro	Cys	His	Gly	Ser	His	Tyr
				130				135					140		
Asp	Ile	Ser	Gly	Arg	Ile	Arg	Lys	Gly	Pro	Ala	Pro	Tyr	Asn	Leu	Glu
				145				150					155		160
Val	Pro	Thr	Tyr	Ser	Phe	Leu	Glu	Glu	Asn	Lys	Leu	Leu	Ile	Gly	
				165				170						175	

(2) INFORMATION FOR SEQ ID NO:1170:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1507 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1507

(D) OTHER INFORMATION: / Ceres Seq. ID 1569183

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1170:

```

acctgaatat tgactacgca ttataagagg tttgtttttt gggttttttc ttcttcacat    60
atcatttttt tgatttctccc acgaagatga accacctcgt tcgtaaaaagc tccgtcggtt    120
actccgcctt gagtgcggtt tegtacctcc gtcaactctgc cgttacctct ccacctccga    180
tttttccgcg cgcgcgttca accgttgcgc agttcacttc cgcgcggtat ccttccaaca    240
gttttcaatt gagccgcgcg acgaattggg gaatccggag aggaagcggt    300
ttgtgattga gcgattcggt aaatacgcta cgacgttgcc gtccggggatt catttctcta    360
ttccgttcgt ggatcgattt gcttatgttc attctctcaa ggaagaagct atcccgattc    420
cgaatcacag tcgattactt aaagacaacg ttagtatcca catcgatggt gtctctacg    480
ttaagattgt ggatcctaag ttatgcttctt atggcggtga gagtccctatc tatgtctgtt    540
tacagcttgc tcagaccaca atgcgttagt agcttggtta gatcaactct gataagacct    600
ttgaggaaac agacactctc acgagaaga tagtggaagc catcaatggt gctgcaaaaag    660
actggggtct tcaagtgcctt cgttatgaga taagggatat tatgccccct catggagtgc    720
gagctgctat ggaaatgcaa gctgaagctg agcgtaaaaa gagagcccgag attcttgagt    780
ctgaaggaga aaggcaatcc catatcaaca ttgctgatgg taagaaaagt tctgtaact    840
tggaactctg agcagcaaac atggaccagg tgaatcgagc acaaggtgag gcagaaacaa    900
tactagctag agcacaagca actgcgaaa gcttggtctt gttatctcag tccctcaagg    960
aaactggggg agtagagggc gcgagtttga gagtgcaga gcaataactt acagctctcg   1020
gtaacattgc caaggagggt acgataatgt tgcctccaag ttgtgcttca aatcctgcta   1080
gcattgattg tcaagcttta acaatgtaca aaagccttgt catcaatggt ccaagcaaaag   1140
atcaccaaag aacacaagca cttgatgaaa cagatttgga agagtttgaa gacatgggtg   1200
agaaacatat atcagaagcg tctaataacc gatcaggctc aatatcattt gacacagaga   1260
aaccagggtc caccgggtga ccacgatttt ctcttcagaa ccgcaacaag gatccgcagt   1320
agggcagcca accgggggatg agataaaatt ttgggcttg agaaaaactg aaacattttt   1380
tcattcttca aatatgagcg agtaaccatc ttttccgttt gaatagctag aatatcatca   1440
ctttgcatat agaaacgaat ctgaacatct gttctccgat aagaattttc ctactggatt   1500
tggttatg

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(2) INFORMATION FOR SEQ ID NO:1171:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 411 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..411

(D) OTHER INFORMATION: / Ceres Seq. ID 1569184

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1171:

```

Met Asn His Leu Val Arg Lys Ser Ser Val Gly Tyr Ser Ala Leu Arg
1          5          10          15
Ser Val Ser Tyr Leu Arg Gln Ser Ala Val Thr Ser Pro Pro Pro Ile
20          25          30
Phe Ser Ala Ala Ala Ser Thr Val Arg Gln Phe Thr Ser Ala Gly Tyr
35          40          45
Pro Ser Asn Ser Phe Gln Leu Thr Pro Pro Thr Asn Trp Gly Ile Arg
50          55          60
Ile Val Pro Glu Arg Lys Ala Phe Val Ile Glu Arg Phe Gly Lys Tyr
65          70          75          80
Ala Thr Thr Leu Pro Ser Gly Ile His Phe Leu Ile Pro Phe Val Asp
85          90          95
Arg Ile Ala Tyr Val His Ser Leu Lys Glu Glu Ala Ile Pro Ile Pro
100         105         110
Asn Gln Thr Ala Ile Thr Lys Asp Asn Val Ser Ile His Ile Asp Gly
115         120         125
Val Leu Tyr Val Lys Ile Val Asp Pro Lys Leu Ala Ser Tyr Gly Val
130         135         140
Glu Ser Pro Ile Tyr Ala Val Val Gln Leu Ala Gln Thr Thr Met Arg
145         150         155         160
Ser Glu Leu Gly Lys Ile Thr Leu Asp Lys Thr Phe Glu Glu Arg Asp
165         170         175
Thr Leu Asn Glu Lys Ile Val Glu Ala Ile Asn Val Ala Ala Lys Asp

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Trp	Gly	Leu	Gln	Cys	Leu	Arg	Tyr	Glu	Ile	Arg	Asp	Ile	Met	Pro	Pro
		195					200					205			
His	Gly	Val	Arg	Ala	Ala	Met	Glu	Met	Gln	Ala	Glu	Ala	Glu	Arg	Lys
		210					215				220				
Lys	Arg	Ala	Gln	Ile	Leu	Glu	Ser	Glu	Gly	Glu	Arg	Gln	Ser	His	Ile
		225					230				235				240
Asn	Ile	Ala	Asp	Gly	Lys	Lys	Ser	Ser	Val	Ile	Leu	Ala	Ser	Glu	Ala
							245				250				255
Ala	Lys	Met	Asp	Gln	Val	Asn	Arg	Ala	Gln	Gly	Glu	Ala	Glu	Ala	Ile
							260				265				270
Leu	Ala	Arg	Ala	Gln	Ala	Thr	Ala	Lys	Gly	Leu	Val	Leu	Leu	Ser	Gln
							275								285
Ser	Leu	Lys	Glu	Thr	Gly	Gly	Val	Glu	Ala	Ala	Ser	Leu	Arg	Val	Ala
							280								290
Glu	Gln	Tyr	Ile	Thr	Ala	Phe	Gly	Asn	Ile	Ala	Lys	Glu	Gly	Thr	Ile
							295				300				305
Met	Leu	Leu	Pro	Ser	Gly	Ala	Ser	Asn	Pro	Ala	Ser	Met	Ile	Ala	Gln
							310				315				320
							325				330				335
Ala	Leu	Thr	Met	Tyr	Lys	Ser	Leu	Val	Ile	Asn	Gly	Pro	Ser	Lys	Asp
							340				345				350
His	Gln	Glu	Thr	Gln	Ala	Leu	Asp	Glu	Thr	Asp	Leu	Glu	Glu	Leu	Glu
							355				360				365
Asp	Met	Gly	Glu	Lys	His	Ile	Ser	Glu	Gly	Ser	Asn	Asn	Arg	Ser	Gly
							370				375				380
Ser	Ile	Ser	Phe	Asp	Thr	Glu	Lys	Pro	Gly	His	Thr	Gly	Glu	Pro	Arg
							385				390				400
Phe	Ser	Leu	Gln	Asn	Arg	Asn	Lys	Asp	Pro	Gln					
							405				410				

(2) INFORMATION FOR SEQ ID NO:1172:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 253 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..253

(D) OTHER INFORMATION: / Ceres Seq. ID 1569185

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1172:

Met	Arg	Ser	Glu	Leu	Gly	Lys	Ile	Thr	Leu	Asp	Lys	Thr	Phe	Glu	Glu
1			5						10					15	
Arg	Asp	Thr	Leu	Asn	Glu	Lys	Ile	Val	Glu	Ala	Ile	Asn	Val	Ala	Ala
			20					25					30		
Lys	Asp	Trp	Gly	Leu	Gln	Cys	Leu	Arg	Tyr	Glu	Ile	Arg	Asp	Ile	Met
			35					40				45			
Pro	Pro	His	Gly	Val	Arg	Ala	Ala	Met	Glu	Met	Gln	Ala	Glu	Ala	Glu
			50				55				60				
Arg	Lys	Lys	Arg	Ala	Gln	Ile	Leu	Glu	Ser	Glu	Gly	Glu	Arg	Gln	Ser
			65				70				75			80	
His	Ile	Asn	Ile	Ala	Asp	Gly	Lys	Lys	Ser	Ser	Val	Ile	Leu	Ala	Ser
			85					90					95		
Glu	Ala	Ala	Lys	Met	Asp	Gln	Val	Asn	Arg	Ala	Gln	Gly	Glu	Ala	Glu
			100					105					110		
Ala	Ile	Leu	Ala	Arg	Ala	Gln	Ala	Thr	Ala	Lys	Gly	Leu	Val	Leu	Leu
			115				120					125			
Ser	Gln	Ser	Leu	Lys	Glu	Thr	Gly	Gly	Val	Glu	Ala	Ala	Ser	Leu	Arg
			130				135				140				
Val	Ala	Glu	Gln	Tyr	Ile	Thr	Ala	Phe	Gly	Asn	Ile	Ala	Lys	Glu	Gly
			145				150				155			160	

Thr Ile Met Leu Leu Pro Ser Gly Ala Ser Asn Pro Ala Ser Met Ile
165 170 175
Ala Gln Ala Leu Thr Met Tyr Lys Ser Leu Val Ile Asn Gly Pro Ser
180 185 190
Lys Asp His Gln Glu Thr Gln Ala Leu Asp Glu Thr Asp Leu Glu Glu
195 200 205
Leu Glu Asp Met Gly Glu Lys His Ile Ser Glu Gly Ser Asn Asn Arg
210 215 220
Ser Gly Ser Ile Ser Phe Asp Thr Glu Lys Pro Gly His Thr Gly Glu
225 230 235 240
Pro Arg Phe Ser Leu Gln Asn Arg Asn Lys Asp Pro Gln
245 250

(2) INFORMATION FOR SEQ ID NO:1173:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 206 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..206
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569186

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1173:

Met Pro Pro His Gly Val Arg Ala Ala Met Glu Met Gln Ala Glu Ala
1 5 10 15
Glu Arg Lys Lys Arg Ala Gln Ile Leu Glu Ser Glu Gly Glu Arg Gln
20 25 30
Ser His Ile Asn Ile Ala Asp Gly Lys Lys Ser Ser Val Ile Leu Ala
35 40 45
Ser Glu Ala Ala Lys Met Asp Gln Val Asn Arg Ala Gln Gly Glu Ala
50 55 60
Glu Ala Ile Leu Ala Arg Ala Gln Ala Thr Ala Lys Gly Leu Val Leu
65 70 75 80
Leu Ser Gln Ser Leu Lys Glu Thr Gly Gly Val Glu Ala Ala Ser Leu
85 90 95
Arg Val Ala Glu Gln Tyr Ile Thr Ala Phe Gly Asn Ile Ala Lys Glu
100 105 110
Gly Thr Ile Met Leu Leu Pro Ser Gly Ala Ser Asn Pro Ala Ser Met
115 120 125
Ile Ala Gln Ala Leu Thr Met Tyr Lys Ser Leu Val Ile Asn Gly Pro
130 135 140
Ser Lys Asp His Gln Glu Thr Gln Ala Leu Asp Glu Thr Asp Leu Glu
145 150 155 160
Glu Leu Glu Asp Met Gly Glu Lys His Ile Ser Glu Gly Ser Asn Asn
165 170 175
Arg Ser Gly Ser Ile Ser Phe Asp Thr Glu Lys Pro Gly His Thr Gly
180 185 190
Glu Pro Arg Phe Ser Leu Gln Asn Arg Asn Lys Asp Pro Gln
195 200 205

(2) INFORMATION FOR SEQ ID NO:1174:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1646 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1646
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569187

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1174:

atcaactcaa	tctgtttgtc	tattttctct	cccttgact	gttttttgtt	ttttaccaa	60
gcacacogt	tcacaaacat	gatcgocgca	cggatctggc	gaagccacgc	gtttctcgc	120
ccatcagct	cgtctatctg	tgtctctccg	cgtttccggg	taccggagta	tctttctcag	180
tctgtctctc	ctccggcgct	gcgcccattc	tttgttcacc	ctcccacttt	gatgaaatgg	240
ggtggagaaa	gtagaagctg	gttttcgaac	gaagccatgg	ccactgattc	aaattcaggg	300
tttaattgtg	tgccactagc	tcaaacctgg	gaaggtattg	ctgaatgtga	gcttctcaag	360
tgtgtttgca	aagaggagga	tctgtgtgaa	gagtttcagc	cactctgtga	agttcagagc	420
gataaagcaa	ctatagagat	cacaagctgt	tttaaaagga	aagtggctct	gatttcacat	480
tctccaggtg	acattattaa	ggttggagag	actctgggta	ggttgccggt	tgaagactcg	540
caggattcgc	tcttaaccac	tgatagtcca	gaaattgtaa	ctctggggag	tccaaagcag	600
ggaacagaaa	atcttcttgg	agctctctca	acgcctgcgc	tctgtaacct	tgcaaaagac	660
cttggcatag	atatcaatgt	tataactgga	actggtaaa	atggtagagt	tttgaaaagag	720
gatgttctcc	ggttttagtg	ccagaaaagga	tttgaacag	atcaggtttc	tctctgacat	780
gctgttatag	gaggagactc	ggtttccact	aaagctagta	gtaactttga	agataaaaaca	840
gttctctcaa	ggggattcag	ccgagcaatg	gtcaagacaa	tgactatggc	tacaagtgtga	900
ccgcattttc	attttgttga	agagataaac	tgcgactcac	ttgtggagct	caagcagttc	960
ttcaaaagaa	acaatacaga	tccaccactc	aaacacactt	ttcttctact	tttaatacaag	1020
tctctgtcaa	tggctctaac	caaatatccc	ttcgtgaata	gttgcttcaa	cgcggaaattc	1080
ctcgagatca	tcttcaaaag	ttcacataat	attggagttg	caatggccac	tgaacatggc	1140
cttgcgtctc	caaatataaa	gaatgttccg	tcatattctc	tgctagagat	aaccaaaagag	1200
ctgtcccggt	tacaacattt	ggcagcaaac	aacaaactta	accccgagga	tgtgactggg	1260
ggaaccataa	ctctgagtga	cattggagca	attggtggta	aattcggaatc	ccctcttttta	1320
aacttaccgg	caagttgcaat	catcgctctt	ggaagaatcg	agaaagtctc	aaaattctcca	1380
aaagaagaaa	tgtctatctc	tcgcatcgata	atgatgggta	acattgctgc	ggaatcataga	1440
gttctagatg	gggcaacggg	agctcgggtt	tgctgccagt	ggaagaagta	tgtcgagaaa	1500
ccggagctgc	tgatgcttca	aatgagataa	gaaggaaggg	ttcatgttta	tttgtgaact	1560
attatgtatg	aaacctctat	gttcgaataa	gatcaagaac	tgagctagca	gttgtaaaact	1620
aaacaaSvaa	agtaaaagtc	atatct				

(2) INFORMATION FOR SEQ ID NO:1175:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 509 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..509
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569188

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1175:

Ile	Asn	Ser	Ile	Cys	Leu	Ser	Ile	Ser	Ser	Pro	Leu	Tyr	Cys	Phe	Leu
1			5						10				15		
Phe	Phe	Thr	Lys	Asp	Gln	Pro	Phe	Thr	Thr	Met	Ile	Ala	Arg	Arg	Ile
			20					25					30		
Trp	Arg	Ser	His	Arg	Phe	Leu	Arg	Pro	Phe	Ser	Ser	Ser	Ser	Val	Cys
			35				40					45			
Ser	Pro	Pro	Phe	Arg	Val	Pro	Glu	Tyr	Leu	Ser	Gln	Ser	Ser	Ser	Ser
			50				55				60				
Pro	Ala	Ser	Arg	Pro	Phe	Phe	Val	His	Pro	Pro	Thr	Leu	Met	Lys	Trp
			70							75				80	
Gly	Gly	Gly	Ser	Arg	Ser	Trp	Phe	Ser	Asn	Glu	Ala	Met	Ala	Thr	Asp
			85						90				95		
Ser	Asn	Ser	Gly	Leu	Ile	Asp	Val	Pro	Leu	Ala	Gln	Thr	Gly	Gly	Gly
			100				105					110			
Ile	Ala	Glu	Cys	Glu	Leu	Leu	Lys	Trp	Phe	Val	Lys	Glu	Gly	Asp	Ser
			115				120				125				
Val	Glu	Glu	Phe	Gln	Pro	Leu	Cys	Glu	Val	Gln	Ser	Asp	Lys	Ala	Thr
			130				135				140				
Ile	Glu	Ile	Thr	Ser	Arg	Phe	Lys	Gly	Lys	Val	Ala	Leu	Ile	Ser	His
			145				150			155					160

THE FULL SEQUENCE

Ser Pro Gly Asp Ile Ile Lys Val Gly Glu Thr Leu Val Arg Leu Ala
165 170 175
Val Glu Asp Ser Gln Asp Ser Leu Leu Thr Thr Asp Ser Ser Glu Ile
180 185 190
Val Thr Leu Gly Gly Ser Lys Gln Gly Thr Glu Asn Leu Leu Gly Ala
195 200 205
Leu Ser Thr Pro Ala Val Arg Asn Leu Ala Lys Asp Leu Gly Ile Asp
210 215 220
Ile Asn Val Ile Thr Gly Thr Gly Lys Asp Gly Arg Val Leu Lys Glu
225 230 235
Asp Val Leu Arg Phe Ser Asp Gln Lys Gly Phe Val Thr Asp Ser Val
245 250 255
Ser Ser Glu His Ala Val Ile Gly Gly Asp Ser Val Ser Thr Lys Ala
260 265 270
Ser Ser Asn Phe Glu Asp Lys Thr Val Pro Leu Arg Gly Phe Ser Arg
275 280 285
Ala Met Val Lys Thr Met Thr Met Ala Thr Ser Val Pro His Phe His
290 295 300
Phe Val Glu Glu Ile Asn Cys Asp Ser Leu Val Glu Leu Lys Gln Phe
305 310 315
Phe Lys Glu Asn Asn Thr Asp Ser Thr Ile Lys His Thr Phe Leu Pro
325 330 335
Thr Leu Ile Lys Ser Leu Ser Met Ala Leu Thr Lys Tyr Pro Phe Val
340 345 350
Asn Ser Cys Phe Asn Ala Glu Ser Leu Glu Ile Ile Leu Lys Gly Ser
355 360 365
His Asn Ile Gly Val Ala Met Ala Thr Glu His Gly Leu Val Val Pro
370 375 380
Asn Ile Lys Asn Val Gln Ser Leu Ser Leu Leu Glu Ile Thr Lys Glu
385 390 395
Leu Ser Arg Leu Gln His Leu Ala Ala Asn Asn Lys Leu Asn Pro Glu
405 410 415
Asp Val Thr Gly Gly Thr Ile Thr Leu Ser Asn Ile Gly Ala Ile Gly
420 425 430
Gly Lys Phe Gly Ser Pro Leu Leu Asn Leu Pro Glu Val Ala Ile Ile
435 440 445
Ala Leu Gly Arg Ile Glu Lys Val Pro Lys Phe Ser Lys Glu Gly Thr
450 455 460
Val Tyr Pro Ala Ser Ile Met Met Val Asn Ile Ala Ala Asp His Arg
465 470 475
Val Leu Asp Gly Ala Thr Val Ala Arg Phe Cys Cys Gln Trp Lys Glu
485 490 495
Tyr Val Glu Lys Pro Glu Leu Leu Met Leu Gln Met Arg
500 505

(2) INFORMATION FOR SEQ ID NO:1176:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 483 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..483
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569189

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1176:

Met Ile Ala Arg Arg Ile Trp Arg Ser His Arg Phe Leu Arg Pro Phe
1 5 10 15
Ser Ser Ser Ser Val Cys Ser Pro Pro Phe Arg Val Pro Glu Tyr Leu
20 25 30
Ser Gln Ser Ser Ser Ser Pro Ala Ser Arg Pro Phe Phe Val His Pro

(2) INFORMATION FOR SEQ ID NO:1177:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 432 amino acids
 (B) TYPE: amino acid

1	Met	Lys	Trp	Gly	Gly	Gly	Ser	Arg	Ser	Trp	Phe	Ser	Asn	Glu	Ala	Met
Ala	Thr	Asp	Ser	Asn	Ser	Gly	Leu	Ile	Asp	Val	Pro	Leu	Ala	Gln	Thr	
Gly	Glu	Gly	Ile	Ala	Glu	Cys	Glu	Leu	Leu	Lys	Trp	Phe	Val	Lys	Glu	
Gly	Asp	Ser	Val	Glu	Glu	Phe	Glu	Pro	Leu	Cys	Glu	Val	Gln	Ser	Asp	
Lys	Ala	Thr	Ile	Glu	Ile	Thr	Ser	Arg	Phe	Lys	Lys	Val	Val	Ala	Leu	
65	Ile	Ser	His	Ser	Pro	Gly	Asp	Ile	Ile	Lys	Val	Gly	Glu	Thr	Leu	
Arg	Leu	Ala	Val	Glu	Asp	Ser	Gln	Asp	Ser	Leu	Leu	Thr	Thr	Asp	Ser	
Ser	Glu	Ile	Val	Thr	Leu	Gly	Gly	Ser	Lys	Gln	Gly	Thr	Glu	Asn	Leu	
Leu	Gly	Ala	Leu	Ser	Thr	Pro	Ala	Val	Arg	Asn	Leu	Ala	Lys	Asp	Leu	
Gly	Ile	Asp	Ile	Asn	Val	Ile	Thr	Gly	Thr	Gly	Lys	Asp	Gly	Arg	Val	
145	Leu	Lys	Glu	Asp	Val	Leu	Arg	Phe	Ser	Asp	Gln	Lys	Gly	Phe	Val	
Asp	Ser	Val	Ser	Ser	Glu	His	Ala	Val	Ile	Gly	Gly	Asp	Ser	Val	Ser	
Thr	Lys	Ala	Ser	Ser	Asn	Phe	Glu	Asp	Lys	Thr	Val	Pro	Leu	Arg	Gly	
Phe	Ser	Arg	Ala	Met	Val	Lys	Thr	Met	Thr	Met	Ala	Thr	Ser	Val	Pro	
225	His	Phe	His	Phe	Val	Glu	Glu	Ile	Asn	Cys	Asp	Ser	Leu	Val	Glu	
Lys	Gln	Phe	Phe	Lys	Glu	Asn	Asn	Thr	Asp	Ser	Thr	Ile	Lys	His	Thr	
Phe	Leu	Pro	Thr	Leu	Ile	Lys	Ser	Leu	Ser	Met	Ala	Leu	Thr	Lys	Tyr	
Pro	Phe	Val	Asn	Ser	Cys	Phe	Asn	Ala	Glu	Ser	Leu	Glu	Ile	Ile	Leu	
Lys	Gly	Ser	His	Asn	Ile	Gly	Val	Ala	Met	Ala	Thr	Glu	His	Gly	Leu	
Val	Val	Pro	Asn	Ile	Lys	Asn	Val	Gln	Ser	Leu	Ser	Leu	Leu	Glu	Ile	
305	Thr	Lys	Glu	Leu	Ser	Arg	Leu	Gln	His	Leu	Ala	Ala	Asn	Asn	Lys	
Asn	Pro	Glu	Asp	Val	Thr	Gly	Gly	Thr	Ile	Thr	Leu	Ser	Asn	Ile	Gly	
Ala	Ile	Gly	Gly	Lys	Phe	Gly	Ser	Pro	Leu	Leu	Asn	Leu	Pro	Glu	Val	
Ala	Ile	Ile	Ala	Leu	Gly	Arg	Ile	Glu	Lys	Val	Pro	Lys	Phe	Ser	Lys	
Glu	Gly	Thr	Val	Tyr	Pro	Ala	Ser	Ile	Met	Met	Val	Asn	Ile	Ala	Ala	
385	Asp	His	Arg	Val	Leu	Asp	Gly	Ala	Thr	Val	Ala	Arg	Phe	Cys	Cys	
Trp	Lys	Glu	Tyr	Val	Glu	Lys	Pro	Glu	Leu	Leu	Met	Leu	Gln	Met	Arg	

420

425

430

(2) INFORMATION FOR SEQ ID NO:1178:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1211 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1211

(D) OTHER INFORMATION: / Ceres Seq. ID 1569230

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1178:

attcatattt	gctcacotca	aactctctct	ttctctctct	ctctgggtcc	ctagaatttg	60
agcaaaattt	ctaccataat	tgctaattat	taaaaggaaa	cataagtaat	cggtgcttcg	120
atccctttgt	acatggatgg	atccctgaaca	ggaatctcca	aacgagactt	tggaacctat	180
attggtaagt	tcaacaaaaa	gaagcaataa	taacAaataa	gaaaatggaa	gaagaaatga	240
agaagaaagt	atcaagagga	gaattaggag	gtgaagctca	aaattgtcca	agatgtgaat	300
ctccaacac	aaagttttgt	tactacaaca	actatagtct	ctcacaacct	cgttacttct	360
gcaaatcttg	toggagatat	tggaactaaa	gcgggtactct	tcgtaacggt	cccgctcggtg	420
gtgggtgccc	togaacacaaa	cgatcctctt	cctcagcttt	ctccaagaac	aacaacaata	480
agtcatttaa	ttctcatact	gatccacttc	agaacccctt	aattacggga	atgccaccat	540
catctttttg	ttatgatcac	tccattgato	tcaacctctgc	tttcgctact	ctccaaaagc	600
atcattttat	ctctcaagct	actactcctt	cttttgggtt	tggaagtgat	ctttctattt	660
atggaaacct	aacgaatgat	gtagggatct	tcggagggga	aaacggtact	tataacaata	720
gtttgtgtta	tgggtttgtg	tccggaaaatg	gtaataataa	tcaaaaatgaa	atcaagatgg	780
ctcttcacatt	ggggatgtct	ttggaaggaa	acgagagaaa	gcaagagaat	gtgaacaata	840
acaataataa	ctcagagaat	cctagcaagg	tgttctgggg	gtttccatgg	cagatgacgg	900
gagattccgc	cggagtgtga	ccggagattg	atcccggaa	ggaaagctgg	aatgggatgg	960
tttcatcttg	gaataatgtg	ttaactcaaca	ctccttttgt	ctagcagatc	atataataat	1020
aaataataaa	tatattacta	tatatataag	Kttatgtcat	cacatgtttg	tacaccactt	1080
tcactataat	gggggatggt	tggtttttat	aattcttagg	gtttctatct	ttttttagtt	1140
tcaccaattt	tctgtttgag	acgaagactt	ataagagttc	ttctatgaaa	actatagaaa	1200
aaagtttctc	c					

(2) INFORMATION FOR SEQ ID NO:1179:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 259 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..259

(D) OTHER INFORMATION: / Ceres Seq. ID 1569231

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1179:

Met	Glu	Glu	Glu	Met	Lys	Lys	Lys	Val	Ser	Arg	Gly	Glu	Leu	Gly	Gly
1				5				10					15		
Glu	Ala	Gln	Asn	Cys	Pro	Arg	Cys	Glu	Ser	Pro	Asn	Thr	Lys	Phe	Cys
				20				25					30		
Tyr	Tyr	Asn	Asn	Tyr	Ser	Leu	Ser	Gln	Pro	Arg	Tyr	Phe	Cys	Lys	Ser
				35				40					45		
Cys	Arg	Arg	Tyr	Trp	Thr	Lys	Gly	Gly	Thr	Leu	Arg	Asn	Val	Pro	Val
				50				55					60		
Gly	Gly	Gly	Cys	Arg	Arg	Asn	Lys	Arg	Ser	Ser	Ser	Ala	Phe	Ser	
				65				70					75		
Lys	Asn	Asn	Asn	Asn	Lys	Ser	Ile	Asn	Phe	His	Thr	Asp	Pro	Leu	Gln
				85				90					95		
Asn	Pro	Leu	Ile	Thr	Gly	Met	Pro	Pro	Ser	Ser	Phe	Gly	Tyr	Asp	His

	100		105		110
Ser Ile Asp	Leu Asn	Leu Ala	Phe Ala	Thr Leu	Gln Lys
	115		120		125
Ser Ser Gln	Ala Thr	Thr Pro	Ser Phe	Gly Phe	Gly Gly
	130		135		140
Ile Tyr Gly	Asn Ser	Thr Asn	Asp Val	Gly Ile	Phe Gly
	145		150		155
Gly Thr Tyr	Asn Asn	Ser Leu	Cys Tyr	Gly Phe	Val Ser
	165		170		175
Asn Asn Asn	Gln Asn	Glu Ile	Lys Met	Ala Ser	Thr Leu
	180		185		190
Leu Glu Gly	Asn Glu	Arg Lys	Gln Glu	Asn Val	Asn Asn
	195		200		205
Asn Ser Glu	Asn Pro	Ser Lys	Val Phe	Trp Gly	Phe Pro
	210		215		220
Thr Gly Asp	Ser Ala	Gly Val	Val Pro	Glu Ile	Asp Pro
	225		230		235
Ser Trp Asn	Gly Met	Val Ser	Ser Trp	Asn Asn	Gly Leu
	245		250		255
Pro Leu Val					

(2) INFORMATION FOR SEQ ID NO:1180:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 255 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..255
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569232
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1180:

Met Lys Lys	Lys Val	Ser Arg	Gly Glu	Leu Gly	Gly Glu	Ala Gln	Asn
1	5		10			15	
Cys Pro Arg	Cys Glu	Ser Pro	Asn Thr	Lys Phe	Cys Tyr	Tyr Asn	Asn
	20		25			30	
Tyr Ser Leu	Ser Gln	Pro Arg	Tyr Phe	Cys Lys	Ser Cys	Arg Arg	Tyr
	35		40			45	
Trp Thr Lys	Gly Gly	Thr Leu	Arg Asn	Val Pro	Val Gly	Gly Gly	Cys
	50		55			60	
Arg Arg Asn	Lys Arg	Ser Ser	Ser Ser	Ala Phe	Ser Lys	Asn Asn	Asn
65	70			75		80	
Asn Lys Ser	Ile Asn	Phe His	Thr Asp	Pro Leu	Gln Asn	Pro Leu	Ile
	85		90			95	
Thr Gly Met	Pro Pro	Ser Ser	Phe Gly	Tyr Asp	His Ser	Ile Asp	Leu
	100		105			110	
Asn Leu Ala	Phe Ala	Thr Leu	Gln Lys	His His	Leu Ser	Ser Gln	Ala
	115		120			125	
Thr Thr Pro	Ser Phe	Gly Phe	Gly Gly	Asp Leu	Ser Ile	Tyr Gly	Asn
	130		135			140	
Ser Thr Asn	Asp Val	Gly Ile	Phe Gly	Gly Gln	Asn Gly	Thr Tyr	Asn
	145		150			155	
Asn Ser Leu	Cys Tyr	Gly Phe	Val Ser	Gly Asn	Gly Asn	Asn Gln	
	165		170			175	
Asn Glu Ile	Lys Met	Ala Ser	Thr Leu	Gly Met	Ser Leu	Glu Gly	Asn
	180		185			190	
Glu Arg Lys	Gln Glu	Asn Val	Asn Asn	Asn Asn	Asn Ser	Glu Asn	
	195		200			205	
Pro Ser Lys	Val Phe	Trp Gly	Phe Pro	Trp Gln	Met Thr	Gly Asp	Ser
	210		215			220	

Ala Gly Val Val Pro Glu Ile Asp Pro Gly Arg Glu Ser Trp Asn Gly
225 230 235 240
Met Val Ser Ser Trp Asn Asn Gly Leu Leu Asn Thr Pro Leu Val
245 250 255

(2) INFORMATION FOR SEQ ID NO:1181:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 157 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..157

(D) OTHER INFORMATION: / Ceres Seq. ID 1569233

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1181:

Met	Pro	Pro	Ser	Ser	Phe	Gly	Tyr	Asp	His	Ser	Ile	Asp	Leu	Asn	Leu
1			5						10					15	
Ala	Phe	Ala	Thr	Leu	Gln	Lys	His	His	Leu	Ser	Ser	Gln	Ala	Thr	Thr
			20					25					30		
Pro	Ser	Phe	Gly	Phe	Gly	Gly	Asp	Leu	Ser	Ile	Tyr	Gly	Asn	Ser	Thr
		35					40					45			
Asn	Asp	Val	Gly	Ile	Phe	Gly	Gly	Gln	Asn	Gly	Thr	Tyr	Asn	Asn	Ser
		50				55						60			
Leu	Cys	Tyr	Gly	Phe	Val	Ser	Gly	Asn	Gly	Asn	Asn	Gln	Asn	Glu	
		65			70				75					80	
Ile	Lys	Met	Ala	Ser	Thr	Leu	Gly	Met	Ser	Leu	Glu	Gly	Asn	Glu	Arg
			85					90						95	
Lys	Gln	Glu	Asn	Val	Asn	Asn	Asn	Asn	Asn	Ser	Glu	Asn	Pro	Ser	
			100					105					110		
Lys	Val	Phe	Trp	Gly	Phe	Pro	Trp	Gln	Met	Thr	Gly	Asp	Ser	Ala	Gly
			115				120					125			
Val	Val	Pro	Glu	Ile	Asp	Pro	Gly	Arg	Glu	Ser	Trp	Asn	Gly	Met	Val
		130					135					140			
Ser	Ser	Trp	Asn	Asn	Gly	Leu	Leu	Asn	Thr	Pro	Leu	Val			
		145			150					155					

(2) INFORMATION FOR SEQ ID NO:1182:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1125 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1125

(D) OTHER INFORMATION: / Ceres Seq. ID 1569234

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1182:

gactccatta	ttatccctct	ctctacaaaa	aaaaacagta	gagagagata	tagagagcat	60
caatggcgctc	gtcgtaaga	ctttgcgatt	cgtgcaaatc	gacggcgacga	actctattct	120
gcgcgcgaga	cgccgcgttt	ctctgcggca	actgcgcagg	taagatccac	acagctaaca	180
aactgcagtc	acgtcacgaa	cgagtttgcc	tatgtgaagt	atgcgaacaa	gcaccagcac	240
acgtcacgtc	caaagctgac	gcgcctgcgt	tatgcgtcac	gtgcgacggt	gatattccact	300
cagctaatcc	actctctcgc	cgccacgagc	gcgtaccaat	cactccttct	tacgacgctg	360
ttggtccagc	aaaatccgct	tctctctccg	tcaatttcgt	agatgaagat	ggcggtagacg	420
tcactgcctc	gtgggtttta	gctaaagaag	gaatcgaaat	cactaatttg	ttttccgattc	480
ttgattatcc	gaagattgag	gtcactgcgg	aggagaatag	ctccggtaac	gacggagttg	540
ttctctgtga	gaataagttg	ttcttcaatt	aagattactt	caatttcgat	ctctctgctt	600
ccaaaatttc	tcaacaagga	ttcaatttca	tcaaccaaac	tggtttcgacg	agaacgatag	660
atgtaccggt	ggtgcctgaa	agtgaggagg	tgcagcgagg	gatgacgaac	acgggagacg	720
cagctgtgca	gttatccagc	gcggagaggg	aagcaagggt	tttgaggtat	agagagaaga	780

ggaagaatcg gaaatttgag aagacgatta ggtatgcgtc gcgtaaaagCt tacgctgaga 840
tgaggccgag aatcaaaagga cgttttgcta agagaacaga ttcgagagag aatgatgggtg 900
gagacgtcgg agtttatgcg ggattcgggtg ttgttcgcgag tttctgatat ttcccggtta 960
aagaacaatg gtagtagtat atcgggttaat agcagattaa ggataattaa aactaaaaatg 1020
tttcttgatt taatcagggg ctaagttatt gttagaagat tggtgttttt tgaattaatt 1080
ctcacaaattg tatectaaat tatatatgtt acttaagtgtt gaact

(2) INFORMATION FOR SEQ ID NO:1183:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 294 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..294
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569235

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1183:

Met	Ala	Ser	Ser	Ser	Arg	Leu	Cys	Asp	Ser	Cys	Lys	Ser	Thr	Ala	Ala
1															
Thr	Leu	Phe	Cys	Arg	Ala	Asp	Ala	Ala	Phe	Leu	Cys	Gly	Asn	Cys	Asp
Gly	Lys	Ile	His	Thr	Ala	Asn	Lys	Leu	Ala	Ser	Arg	His	Glu	Arg	Val
Trp	Leu	Cys	Glu	Val	Cys	Glu	Gln	Ala	Pro	Ala	His	Val	Thr	Cys	Lys
Ala	Asp	Ala	Ala	Ala	Leu	Cys	Val	Thr	Cys	Asp	Arg	Asp	Ile	His	Ser
Ala	Asn	Pro	Leu	Ser	Arg	Arg	His	Glu	Arg	Val	Pro	Ile	Thr	Pro	Phe
Tyr	Asp	Ala	Val	Gly	Pro	Ala	Lys	Ser	Ala	Ser	Ser	Ser	Val	Asn	Phe
Val	Asp	Glu	Asp	Gly	Gly	Asp	Val	Thr	Ala	Ser	Trp	Leu	Leu	Ala	Lys
Glu	Gly	Ile	Glu	Ile	Thr	Asn	Leu	Phe	Ser	Asp	Leu	Asp	Tyr	Pro	Lys
Ile	Glu	Val	Thr	Ser	Glu	Glu	Asn	Ser	Ser	Gly	Asn	Asp	Gly	Val	Val
Pro	Val	Gln	Asn	Lys	Leu	Phe	Leu	Asn	Glu	Asp	Tyr	Phe	Asn	Phe	Asp
Leu	Ser	Ala	Ser	Lys	Ile	Ser	Gln	Gln	Gly	Phe	Asn	Phe	Ile	Asn	Gln
Thr	Val	Ser	Thr	Arg	Thr	Ile	Asp	Val	Pro	Leu	Val	Pro	Glu	Ser	Gly
Gly	Val	Thr	Ala	Glu	Met	Thr	Asn	Thr	Glu	Thr	Pro	Ala	Val	Gln	Leu
Ser	Pro	Ala	Glu	Arg	Glu	Ala	Arg	Val	Leu	Arg	Tyr	Arg	Glu	Lys	Arg
Lys	Asn	Arg	Lys	Phe	Glu	Lys	Thr	Ile	Arg	Tyr	Ala	Ser	Arg	Lys	Ala
Tyr	Ala	Glu	Met	Arg	Pro	Arg	Ile	Lys	Gly	Arg	Phe	Ala	Lys	Arg	Thr
Asp	Ser	Arg	Glu	Asn	Asp	Gly	Gly	Asp	Val	Gly	Val	Tyr	Cys	Gly	Phe
Gly	Val	Val	Pro	Ser	Phe										

(2) INFORMATION FOR SEQ ID NO:1184:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1515 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:

(A) NAME/KEY: -
(B) LOCATION: 1..1515
(D) OTHER INFORMATION: / Ceres Seq. ID 1569255

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1184:

aagttcagct	tcgtacctga	gccaaagagt	gtttcaggat	ggagctaagg	tcgagaatgc	60
tcaaagactg	tctcttggaa	gattccaact	catgttcctc	aaacgggttc	aaatcgattc	120
ccagacggca	tcctctcaac	cctttcccaa	tgataccaaa	gaggaacaaa	tccaatgcac	180
tcgacgctgt	gattaacgac	atcaagaacc	tccattccaa	caccatccaa	tcgcgtccat	240
cggggatctt	accaaggagc	ctttctcgcc	ggttagcaac	caagaacaaa	gcagaaaacc	300
aagcaagcat	caccgttatt	cgggtcaaa	acatcgtgcg	atggcactcg	tctaaggacc	360
tgcatagaga	catatcacat	tttgaacctc	atcagtcac	aaaccaagac	acgacaacaa	420
ccacaggatc	ctccaccaMc	agcggcacat	cctgcagcag	ttggtctgac	ttggatttta	480
catcgagatt	tttaccatca	tcatggggaa	gtaacgttga	ggagtgcggt	gaaaaacaga	540
gtgttaaaaa	caacttacac	tgcgtcgccg	aagattcttg	cacagcagta	atactagccg	600
acactgaagt	gggacctgag	gagaacttac	agtgtagaaa	ggagcacaac	agccctgtct	660
cagtggttga	gattcaacat	gaggaatatg	acgaacatc	agactcttct	ttcagtcaat	720
gccttgacaa	tgtgaaagaa	accaaacaac	agctcatgca	aacgattcag	cgggtttgag	780
ctttgtccaa	cattagtccct	ttcaatttgg	atgaatgggg	ctcaatggat	gaagcatcct	840
gcagtgaaag	aggacaagag	acagatacca	agtatgatga	tgatgagaa	tgtgatactg	900
ttgatagaga	aagtgaagat	gaatacaatg	atgaggttga	agagaaggca	gcacagctat	960
ggaaccgagt	caaagaaaga	cacgccattt	ggatccacga	agaacatctg	ataatggact	1020
attccagaga	tgaattgatg	caaaaggacaa	actcattcca	cgaaactcAa	acactttgag	1080
aaccatttgg	tatgcgaggg	aaaaggatgg	ttgcagggaa	agagagaatc	agagcttgaa	1140
cgcggaacaa	gtgagcagag	gagacaagca	tgctgtagag	aaatcgaaag	acgagactgg	1200
aatgagaaac	agatagagga	ggagcacgaa	gtgggtggta	ccacagattga	ggaagaactc	1260
ttcagcctgt	tattggacga	aactttaaca	acgctctcta	ccaaaactga	ttccagtcga	1320
cctgaacatc	acaaaacagt	aacatcaatg	cttaagcttt	agaatattaga	aagcaaaaac	1380
atttttgaat	aaggctttga	cttaaaagot	caggtttttt	tagctctact	tttgtaagaa	1440
tgaagcaaac	gaataataca	atgtatatgt	acctctaaaa	ccatatatat	atatatgcct	1500
aattcatatt	tcctgc					

(2) INFORMATION FOR SEQ ID NO:1185:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 346 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..346
(D) OTHER INFORMATION: / Ceres Seq. ID 1569256

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1185:

Met	Glu	Leu	Arg	Ser	Arg	Met	Leu	Lys	Asp	Cys	Leu	Leu	Glu	Asp	Ser
1				5					10					15	
Asn	Ser	Cys	Ser	Ser	Asn	Gly	Phe	Lys	Ser	Ile	Pro	Arg	Arg	His	Pro
				20				25						30	
Leu	Asn	Pro	Phe	Pro	Met	Ile	Pro	Lys	Arg	Lys	Gln	Ser	Asn	Ala	Leu
				35				40					45		
Gln	Ala	Val	Ile	Asn	Ala	Ile	Lys	Asn	Leu	His	Ser	Asn	Thr	Ile	Lys
				50			55				60				
Ser	Ala	Pro	Ser	Gly	Ile	Leu	Pro	Arg	Ser	Leu	Ser	Arg	Arg	Leu	Ala
65				70				75						80	
Thr	Lys	Asn	Lys	Ala	Glu	Asn	Gln	Ala	Ser	Ile	Thr	Val	Ile	Arg	Val
				85				90						95	
Lys	Asp	Ile	Val	Arg	Trp	His	Ser	Ser	Lys	Asp	Leu	His	Glu	Asp	Ile
				100			105						110		
Ser	His	Phe	Glu	Pro	His	Gln	Tyr	Thr	Thr	Lys	Asn	Thr	Thr	Thr	Thr
				115			120						125		

Thr Gly Ser Ser Thr Xaa Ser Gly Thr Ser Cys Ser Ser Trp Ser Asp
130 135 140
Leu Asp Phe Thr Ser Glu Phe Leu Pro Ser Ser Trp Gly Ser Asn Val
145 150 155 160
Glu Glu Cys Gly Glu Lys Gln Ser Val Lys Asn Asn Leu His Cys Val
165 170 175
Gly Glu Asp Ser Cys Thr Ala Val Ile Leu Ala Asp Thr Glu Val Gly
180 185 190
Pro Glu Glu Asn Leu Gln Cys Glu Lys Glu His Asn Ser Pro Val Ser
195 200 205
Val Phe Glu Ile Gln His Glu Glu Tyr Asp Glu Thr Ser Asp Ser Ser
210 215 220
Phe Ser Gln Cys Leu Asp Asn Val Glu Arg Thr Lys Gln Lys Leu Met
225 230 235 240
Gln Thr Ile Gln Arg Phe Glu Ser Leu Ala Asn Ile Ser Pro Phe Asn
245 255
Leu Asp Glu Trp Gly Ser Met Asp Glu Ala Ser Cys Met Glu Gly Gly
260 265 270
Gln Glu Thr Asp Thr Lys Tyr Asp Asp Asp Glu Asn Cys Asp Thr Val
275 280 285
Asp Arg Glu Ser Glu Asp Glu Tyr Asn Asp Glu Val Glu Glu Lys Ala
290 295 300
Ala Gln Leu Trp Asn Arg Val Lys Glu Arg His Ala Ile Trp Ile His
305 310 315 320
Glu Glu His Leu Ile Met Asp Tyr Phe Arg Asp Glu Leu Met Gln Arg
325 330 335
Thr Asn Ser Phe His Glu Thr Gln Thr Leu
340 345

(2) INFORMATION FOR SEQ ID NO:1186:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 340 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..340

(D) OTHER INFORMATION: / Ceres Seq. ID 1569257

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1186:

Met Leu Lys Asp Cys Leu Leu Glu Asp Ser Asn Ser Cys Ser Ser Asn
1 5 10 15
Gly Phe Lys Ser Ile Pro Arg Arg His Pro Leu Asn Pro Phe Pro Met
20 25 30
Ile Pro Lys Arg Lys Gln Ser Asn Ala Leu Gln Ala Val Ile Asn Ala
35 40 45
Ile Lys Asn Leu His Ser Asn Thr Ile Lys Ser Ala Pro Ser Gly Ile
50 55 60
Leu Pro Arg Ser Leu Ser Arg Arg Leu Ala Thr Lys Asn Lys Ala Glu
65 70 75 80
Asn Gln Ala Ser Ile Thr Val Ile Arg Val Lys Asp Ile Val Arg Trp
85 90 95
His Ser Ser Lys Asp Leu His Glu Asp Ile Ser His Phe Glu Pro His
100 105 110
Gln Tyr Thr Thr Lys Asn Thr Thr Thr Thr Gly Ser Ser Thr Xaa
115 120 125
Ser Gly Thr Ser Cys Ser Ser Trp Ser Asp Leu Asp Phe Thr Ser Glu
130 135 140
Phe Leu Pro Ser Ser Trp Gly Ser Asn Val Glu Glu Cys Gly Glu Lys
145 150 155 160
Gln Ser Val Lys Asn Asn Leu His Cys Val Gly Glu Asp Ser Cys Thr

Met	Ile	Pro	Lys	Arg	Lys	Gln	Ser	Asn	Ala	Leu	Gln	Ala	Val	Ile	Asn
1			5					10						15	
Ala	Ile	Lys	Asn	Leu	His	Ser	Asn	Thr	Ile	Lys	Ser	Ala	Pro	Ser	Gly
			20					25					30		
Ile	Leu	Pro	Arg	Ser	Leu	Ser	Arg	Arg	Leu	Ala	Thr	Lys	Asn	Lys	Ala
			35				40					45			
Glu	Asn	Gln	Ala	Ser	Ile	Thr	Val	Ile	Arg	Val	Lys	Asp	Ile	Val	Arg
			50			55					60				
Trp	His	Ser	Ser	Lys	Asp	Leu	His	Glu	Asp	Ile	Ser	His	Phe	Glu	Pro
65				70					75					80	
His	Gln	Tyr	Thr	Thr	Lys	Asn	Thr	Thr	Thr	Thr	Thr	Gly	Ser	Ser	Thr
				85				90					95		
Xaa	Ser	Gly	Thr	Ser	Cys	Ser	Ser	Trp	Ser	Asp	Leu	Asp	Phe	Thr	Ser
			100					105					110		
Glu	Phe	Leu	Pro	Ser	Ser	Trp	Gly	Ser	Asn	Val	Glu	Glu	Cys	Gly	Glu
			115				120					125			
Lys	Gln	Ser	Val	Lys	Asn	Asn	Leu	His	Cys	Val	Gly	Glu	Asp	Ser	Cys
			130			135				140					
Thr	Ala	Val	Ile	Leu	Ala	Asp	Thr	Glu	Val	Gly	Pro	Glu	Glu	Asn	Leu
145				150					155					160	
Gln	Cys	Glu	Lys	Glu	His	Asn	Ser	Pro	Val	Ser	Val	Phe	Glu	Ile	Gln
				165				170					175		
His	Glu	Glu	Tyr	Asp	Glu	Thr	Ser	Asp	Ser	Ser	Phe	Ser	Gln	Cys	Leu
			180					185				190			
Asp	Asn	Val	Glu	Arg	Thr	Lys	Gln	Lys	Leu	Met	Gln	Thr	Ile	Gln	Arg
			195			200						205			

Phe Glu Ser Leu Ala Asn Ile Ser Pro Phe Asn Leu Asp Glu Trp Gly
210 215 220
Ser Met Asp Glu Ala Ser Cys Met Glu Gly Glu Glu Thr Asp Thr
225 230 235 240
Lys Tyr Asp Asp Asp Glu Asn Cys Asp Thr Val Asp Arg Glu Ser Glu
245 250 255
Asp Glu Tyr Asn Asp Glu Val Glu Glu Lys Ala Ala Gln Leu Trp Asn
260 265 270
Arg Val Lys Glu Arg His Ala Ile Trp Ile His Glu Glu His Leu Ile
275 280 285
Met Asp Tyr Phe Arg Asp Glu Leu Met Gln Arg Thr Asn Ser Phe His
290 295 300
Glu Thr Gln Thr Leu
305

(2) INFORMATION FOR SEQ ID NO:1188:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1198 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1198

(D) OTHER INFORMATION: / Ceres Seq. ID 1569277

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1188:

actccctatt	cttcagtaatt	gactaatatt	agaactctct	atactactag	ctaaaactaa	60
aaattgaaga	aaaaacatga	gtctcaccac	cgacgaaatc	gaagtgaag	atttcgtggt	120
gaaccaaaag	aatggagatga	aaggactcgt	cgactttcta	acctaaca	cactctcttc	180
tcatacatt	caactctctc	aagaacgctt	cacttcogac	aagatcctcc	tcggatcacc	240
tgctccgggtc	attgacgtgt	ccaattggaa	tgaaccgcac	gtggctagag	agatctgcc	300
tgacgcgtca	aagctcgggt	tgtttcagat	agtgaaccac	gggatagctc	cggtcgtgatt	360
caagggtgtg	attgctgcgg	cgctgggtt	tttcgagttg	ccggcgagg	agagaagaag	420
gtattggaga	gggagttcag	tgctggagac	ggcgtggttg	accacaagtt	tcaatccttg	480
catagaaagt	gttttgaat	ggagagattt	cctcaagttt	gagtatcttc	ctcaacgaca	540
tgacttcgct	gccacgtggc	cttctgtctg	caaggaaaca	gtgatagacc	atttcaaaag	600
gatcaaacca	atcacagaga	ggatcttaaa	catactctac	aacaatctaa	acacaatcat	660
cgatgagtc	aataaaagaa	cctaattggg	aacaatgaga	atgaacttca	actactatcc	720
gaaatgtctc	gagccaagcc	tggccatagg	aactgggtgc	cactcagaca	tcaacactct	780
cactctctc	ctacaagaag	atggtgtatt	aagcagtcct	tacgcccag	ccactgagga	840
tggagacaaa	tggattcatg	tcctccaatt	tccgggagct	attgtctga	atatcggaag	900
tgattatacag	atattgagca	atgatatgta	taggagcgtg	gagcatttgt	tggtggtcaa	960
taagtattgt	agccgggttt	cattccggtt	ttctgcgga	ccggttcaatg	attcggttat	1020
tgagccgtta	ccggaggtgt	tagataagaa	caatgagatg	gctcgtgata	gaagaattgt	1080
gtattcggac	tacttgaagt	tttttttttg	aagacctcat	gatggaaaga	agactattga	1140
gtcgataaaa	ttaccatgat	atgattttacg	aagcttaaat	catcattatc	tacggscc	

(2) INFORMATION FOR SEQ ID NO:1189:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 360 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..360

(D) OTHER INFORMATION: / Ceres Seq. ID 1569278

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1189:

Met	Ser	Leu	Thr	Thr	Asp	Glu	Ile	Glu	Val	Arg	Asp	Phe	Val	Val	Asn
1		5					10						15		
Gln	Lys	Asn	Gly	Val	Lys	Gly	Leu	Val	Asp	Phe	Leu	Thr	Leu	Thr	Thr

20 25 30
Leu Pro Ser Pro Tyr Ile Gln Pro Pro Gln Glu Arg Phe Thr Ser Asp
35 40 45
Lys Ile Leu Leu Gly Ser Pro Val Pro Val Ile Asp Val Ser Asn Trp
50 55 60
Asn Glu Pro His Val Ala Arg Glu Ile Cys His Ala Ala Ser Lys Leu
65 70 75 80
Gly Leu Phe Gln Ile Val Asn His Gly Ile Ala Pro Ala Glu Phe Lys
85 90 95
Gly Val Ile Ala Ala Ala Arg Gly Phe Phe Glu Leu Pro Ala Glu Glu
100 105 110
Arg Arg Arg Tyr Trp Arg Gly Ser Ser Val Ser Glu Thr Ala Trp Leu
115 120 125
Thr Thr Ser Phe Asn Pro Cys Ile Glu Ser Val Leu Glu Trp Arg Asp
130 135 140
Phe Leu Lys Phe Glu Tyr Leu Pro Gln Arg His Asp Phe Ala Ala Thr
145 150 155 160
Trp Pro Ser Val Cys Lys Glu Gln Val Ile Asp His Phe Lys Arg Ile
165 170 175
Lys Pro Ile Thr Glu Arg Ile Leu Asn Ile Leu Ile Asn Asn Leu Asn
180 185 190
Thr Ile Ile Asp Glu Ser Asn Lys Glu Thr Leu Met Gly Thr Met Arg
195 200 205
Met Asn Phe Asn Tyr Tyr Pro Lys Cys Pro Glu Pro Ser Leu Ala Ile
210 215 220
Gly Thr Gly Arg His Ser Asp Ile Asn Thr Leu Thr Leu Leu Gln
225 230 235 240
Glu Asp Gly Val Leu Ser Ser Leu Tyr Ala Arg Ala Thr Glu Asp Gly
245 250 255
Asp Lys Trp Ile His Val Pro Pro Ile Pro Gly Ala Ile Val Val Asn
260 265 270
Ile Gly Asp Val Leu Gln Ile Leu Ser Asn Asp Arg Tyr Arg Ser Val
275 280 285
Glu His Cys Val Val Val Asn Lys Tyr Cys Ser Arg Val Ser Ile Pro
290 295 300
Val Phe Cys Gly Pro Val His Asp Ser Val Ile Glu Pro Leu Pro Glu
305 310 315 320
Val Leu Asp Lys Asn Asn Glu Met Ala Arg Tyr Arg Lys Ile Val Tyr
325 330 335
Ser Asp Tyr Leu Lys Phe Phe Phe Gly Arg Pro His Asp Gly Lys Lys
340 345 350
Thr Ile Glu Ser Ile Lys Leu Pro
355 360

(2) INFORMATION FOR SEQ ID NO:1190:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1308 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1308
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569286

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1190:

attattatttc	cactctctct	ctctagactc	tgaattagct	cattcttgcc	tccaaacaaa	60
tattctctgac	agaccagacc	actcgtgaaga	cagaccacaaac	cctaaactaa	aagcatccac	120
gttcttttgtt	ttgtatttga	tggctctgac	tcatatccat	ggagatggag	aatcaccgcc	180
cggcgagttt	caactacatg	ggccgcgaat	tcagcgattt	aagctctcaac	gatgactcct	240
ctgcttttcag	cgattgtaac	agcgacagat	cggcggaatt	ccccactgct	tcctcccgag	300
ggcgtctgct	ctctctctct	tcgcctcttg	agaattccga	tgatctcatt	aatcatctct	360

(2) INFORMATION FOR SEQ ID NO:1191:

(17) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 355 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..355
(D) OTHER INFORMATION

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1191:

Met	Glu	Met	Glu	Asn	His	Arg	Pro	Gly	Ser	Phe	Thr	Tyr	Met	Gly	Arg
1				5				10						15	
Lys	Phe	Ser	Asp	Leu	Ser	Leu	Asn	Asp	Asp	Ser	Ser	Ala	Phe	Ser	Asp
			20					25					30		
Cys	Asn	Ser	Asp	Arg	Ser	Gly	Glu	Phe	Pro	Thr	Ala	Ser	Ser	Glu	Ser
			35			40						45			
Arg	Arg	Leu	Leu	Leu	Ser	Cys	Ala	Ser	Glu	Asn	Ser	Asp	Asp	Leu	Ile
			50			55					60				
Asn	His	Leu	Val	Ser	His	Leu	Asp	Ser	Ser	Tyr	Ser	Ile	Asp	Glu	Gln
65					70					75				80	
Lys	Gln	Ala	Ala	Met	Glu	Ile	Arg	Leu	Leu	Ser	Lys	Asn	Lys	Pro	Glu
				85				90					95		
Asn	Arg	Ile	Lys	Ile	Ala	Lys	Ala	Gly	Ala	Ile	Lys	Pro	Leu	Ile	Ser
			100					105					110		
Leu	Ile	Ser	Ser	Ser	Asp	Leu	Gln	Leu	Gln	Glu	Tyr	Gly	Val	Thr	Xaa
			115				120					125			
Ile	Leu	Asn	Leu	Ser	Leu	Cys	Asp	Glu	Asn	Lys	Glu	Ser	Ile	Ala	Ser
			130			135					140				
Ser	Gly	Ala	Ile	Lys	Pro	Leu	Val	Arg	Ala	Leu	Lys	Met	Gly	Thr	Pro
145					150					155				160	
Thr	Ala	Lys	Asp	Asn	Ala	Ala	Cys	Ala	Leu	Leu	Arg	Leu	Ser	Gln	Ile
				165					170					175	
Glu	Glu	Asn	Lys	Val	Ala	Ile	Gly	Arg	Ser	Gly	Ala	Ile	Pro	Leu	Leu
				180				185					190		
Val	Asn	Leu	Leu	Glu	Thr	Gly	Gly	Phe	Arg	Ala	Lys	Lys	Asp	Ala	Ser
			195				200					205			
Thr	Ala	Leu	Tyr	Ser	Leu	Cys	Ser	Ala	Lys	Glu	Asn	Lys	Ile	Arg	Ala
				210		215					220				
Val	Gln	Ser	Gly	Ile	Met	Lys	Pro	Leu	Val	Glu	Leu	Met	Ala	Asp	Phe
225					230					235				240	
Gly	Ser	Asn	Met	Val	Asp	Lys	Ser	Ala	Phe	Val	Met	Ser	Leu	Leu	Met
				245					250				255		
Ser	Val	Pro	Glu	Ser	Lys	Pro	Ala	Ile	Val	Glu	Glu	Gly	Gly	Val	Pro

260 265 270
Val Leu Val Glu Ile Val Glu Val Gly Thr Gln Arg Gln Lys Glu Met
275 280 285
Ala Val Ser Ile Leu Leu Gln Leu Cys Glu Glu Ser Val Val Tyr Arg
290 295 300
Thr Met Val Ala Arg Glu Gly Ala Ile Pro Pro Leu Val Ala Leu Ser
305 310 315 320
Gln Ala Gly Thr Ser Arg Ala Lys Gln Lys Ala Glu Ala Leu Ile Glu
325 330 335
Leu Leu Arg Gln Pro Arg Ser Ile Ser Asn Gly Gly Ala Arg Ser Ser
340 345 350
Ser Gln Leu
355

(2) INFORMATION FOR SEQ ID NO:1192:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 353 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..353

(D) OTHER INFORMATION: / Ceres Seq. ID 1569288

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1192:

Met Glu Asn His Arg Pro Gly Ser Phe Thr Tyr Met Gly Arg Lys Phe
1 5 10 15
Ser Asp Leu Ser Leu Asn Asp Asp Ser Ser Ala Phe Ser Asp Cys Asn
20 25 30
Ser Asp Arg Ser Gly Glu Phe Pro Thr Ala Ser Ser Glu Ser Arg Arg
35 40 45
Leu Leu Leu Ser Cys Ala Ser Glu Asn Ser Asp Asp Leu Ile Asn His
50 55 60
Leu Val Ser His Leu Asp Ser Ser Tyr Ser Ile Asp Glu Gln Lys Gln
65 70 75 80
Ala Ala Met Glu Ile Arg Leu Leu Ser Lys Asn Lys Pro Glu Asn Arg
85 90 95
Ile Lys Ile Ala Lys Ala Gly Ala Ile Lys Pro Leu Ile Ser Leu Ile
100 105 110
Ser Ser Ser Asp Leu Gln Leu Gln Glu Tyr Gly Val Thr Xaa Ile Leu
115 120 125
Asn Leu Ser Leu Cys Asp Glu Asn Lys Glu Ser Ile Ala Ser Ser Gly
130 135 140
Ala Ile Lys Pro Leu Val Arg Ala Leu Lys Met Gly Thr Pro Thr Ala
145 150 155 160
Lys Asp Asn Ala Ala Cys Ala Leu Leu Arg Leu Ser Gln Ile Glu Glu
165 170 175
Asn Lys Val Ala Ile Gly Arg Ser Gly Ala Ile Pro Leu Leu Val Asn
180 185 190
Leu Leu Glu Thr Gly Gly Phe Arg Ala Lys Lys Asp Ala Ser Thr Ala
195 200 205
Leu Tyr Ser Leu Cys Ser Ala Lys Glu Asn Lys Ile Arg Ala Val Gln
210 215 220
Ser Gly Ile Met Lys Pro Leu Val Glu Leu Met Ala Asp Phe Gly Ser
225 230 235 240
Asn Met Val Asp Lys Ser Ala Phe Val Met Ser Leu Leu Met Ser Val
245 250 255
Pro Glu Ser Lys Pro Ala Ile Val Glu Glu Gly Gly Val Pro Val Leu
260 265 270
Val Glu Ile Val Glu Val Gly Thr Gln Arg Gln Lys Glu Met Ala Val
275 280 285

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Ser Ile Leu Leu Gln Leu Cys Glu Glu Ser Val Val Tyr Arg Thr Met
290 295 300
Val Ala Arg Glu Gly Ala Ile Pro Pro Leu Val Ala Leu Ser Gln Ala
305 310 315 320
Gly Thr Ser Arg Ala Lys Gln Lys Ala Glu Ala Leu Ile Glu Leu Leu
325 330 335
Arg Gln Pro Arg Ser Ile Ser Asn Gly Gly Ala Arg Ser Ser Ser Gln
340 345 350
Leu

(2) INFORMATION FOR SEQ ID NO:1193:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 342 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..342

(D) OTHER INFORMATION: / Ceres Seq. ID 1569289

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1193:

Met Gly Arg Lys Phe Ser Asp Leu Ser Leu Asn Asp Asp Ser Ser Ala
1 5 10 15
Phe Ser Asp Cys Asn Ser Asp Arg Ser Gly Glu Phe Pro Thr Ala Ser
20 25 30
Ser Glu Ser Arg Arg Leu Leu Ser Cys Ala Ser Glu Asn Ser Asp
35 40 45
Asp Leu Ile Asn His Leu Val Ser His Leu Asp Ser Ser Tyr Ser Ile
50 55 60
Asp Glu Gln Lys Gln Ala Ala Met Glu Ile Arg Leu Leu Ser Lys Asn
65 70 75 80
Lys Pro Glu Asn Arg Ile Lys Ile Ala Lys Ala Gly Ala Ile Lys Pro
85 90 95
Leu Ile Ser Leu Ile Ser Ser Ser Asp Leu Gln Leu Gln Glu Tyr Gly
100 105 110
Val Thr Xaa Ile Leu Asn Leu Ser Leu Cys Asp Glu Asn Lys Glu Ser
115 120 125
Ile Ala Ser Ser Gly Ala Ile Lys Pro Leu Val Arg Ala Leu Lys Met
130 135 140
Gly Thr Pro Thr Ala Lys Asp Asn Ala Ala Cys Ala Leu Leu Arg Leu
145 150 155 160
Ser Gln Ile Glu Glu Asn Lys Val Ala Ile Gly Arg Ser Gly Ala Ile
165 170 175
Pro Leu Leu Val Asn Leu Leu Glu Thr Gly Gly Phe Arg Ala Lys Lys
180 185 190
Asp Ala Ser Thr Ala Leu Tyr Ser Leu Cys Ser Ala Lys Glu Asn Lys
195 200 205
Ile Arg Ala Val Gln Ser Gly Ile Met Lys Pro Leu Val Glu Leu Met
210 215 220
Ala Asp Phe Gly Ser Asn Met Val Asp Lys Ser Ala Phe Val Met Ser
225 230 235 240
Leu Leu Met Ser Val Pro Glu Ser Lys Pro Ala Ile Val Glu Glu Gly
245 250 255
Gly Val Pro Val Leu Val Glu Ile Val Glu Val Gly Thr Gln Arg Gln
260 265 270
Lys Glu Met Ala Val Ser Ile Leu Leu Gln Leu Cys Glu Glu Ser Val
275 280 285
Val Tyr Arg Thr Met Val Ala Arg Glu Gly Ala Ile Pro Pro Leu Val
290 295 300
Ala Leu Ser Gln Ala Gly Thr Ser Arg Ala Lys Gln Lys Ala Glu Ala

305 310 315 320
Leu Ile Glu Leu Leu Arg Gln Pro Arg Ser Ile Ser Asn Gly Gly Ala
325 330 335
Arg Ser Ser Ser Gln Leu
340

(2) INFORMATION FOR SEQ ID NO:1194:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1204 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1204
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569294

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1194:

```
acactagct tctctgtatt caattcttca caaagtttct aaaagctttt ctcttgttat 60
tcaacaactt ggcaccgagc ttcgtaacgc cgtgtgtgtg ttctacttga ttctccGgag 120
ctcttgatgc tgttgaggat gacacaagcg taccagtggg catcaaatgtt ccaattcttga 180
tagcttttcca cagtcatata taacgatggtg actggcattt ttcatgtggtt acaaaagagt 240
ataaacttctt aatggaccaa tttcaccatg tttctgcagc ttttctgaaa ctgaaaaaag 300
gggtatcaaga ggctattgaa gatataacta aaagaatggg tgcaggaatg gccaaagtta 360
tttgcaaggga tgtgagaaca attgatgact atgatgaata ctgccattat gctgcaggagc 420
ttgttggttt aggtttgtca aaaactctca ttgtcttcgga attagaaata ctgactccag 480
attggaagca gatttcaaat tctacagggtt tattttctgc gaaaacaac attatcaaaag 540
attatcttga agacattaat gagagaccac agtcgcgcac gttttggcct cgtgagattt 600
gggaaaaata tgttgacaaa cttgaggact tcaaaaatga ggagaaagctt acaaaagcac 660
tgcaagtgtt gaagtgaatg gtcactaatg cattgaaatc tgttgaagat tgtttgaaat 720
ccttggcNtt cActgcgtga tctctgcaata tttcagtctt gcgccatccc tcagatcgctg 780
gcgatttgaa cacttacatt atgctataac aatgtacaag tgtttagagg cgtcgtgaga 840
atgagacgag gctctaatagc taaagtcatt gatcgacaca agacaatgga tgatgtctat 900
ggtcgcttct atgatttttc ttgcatgcta caaacaaaag ttgacataaa cgatccaaat 960
gctatgaaaa cattaaatcg actcgaaaac atcaagaaag ttgcagaga aatggagta 1020
cttcacaaaa gaaaacttca tgttaacgat gaaacacaa ccaaggctat ctttgttga 1080
atgtttgtgc ttactctggc tatagtcgtt gtatatctca aagcaaacca acgtaagtga 1140
ctctgattgt gaagcatca tgaacataat tctagctttt ttgaaatgt ttgatcaaat 1200
cttg
```

(2) INFORMATION FOR SEQ ID NO:1195:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 162 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..162
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569295

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1195:

```
Met Asp Gln Phe His His Val Ser Ala Ala Phe Leu Lys Leu Glu Lys
1 5 10 15
Gly Tyr Gln Glu Ala Ile Glu Asp Ile Thr Lys Arg Met Gly Ala Gly
20 25 30
Met Ala Lys Phe Ile Cys Lys Glu Val Glu Thr Ile Asp Asp Tyr Asp
35 40 45
Glu Tyr Cys His Tyr Ala Ala Gly Leu Val Gly Leu Gly Leu Ser Lys
50 55 60
Ile Phe Ile Ala Ser Glu Leu Glu Ile Leu Thr Pro Asp Trp Lys Gln
65 70 75 80
Ile Ser Asn Ser Thr Gly Leu Phe Leu Gln Lys Thr Asn Ile Ile Lys
```


85 90 95
Asp Tyr Leu Glu Asp Ile Asn Glu Arg Pro Lys Ser Arg Met Phe Trp
100 105 110
Pro Arg Glu Ile Trp Gly Lys Tyr Val Asp Lys Leu Glu Asp Phe Lys
115 120 125
Asn Glu Glu Lys Ala Thr Lys Ala Val Gln Cys Leu Asn Glu Met Val
130 135 140
Thr Asn Ala Leu Asn His Val Glu Asp Cys Leu Lys Ser Leu Xaa Phe
145 150 155 160
Thr Ala

(2) INFORMATION FOR SEQ ID NO:1196:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 134 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..134
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569296

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1196:

Met Gly Ala Gly Met Ala Lys Phe Ile Cys Lys Glu Val Glu Thr Ile
1 5 10 15
Asp Asp Tyr Asp Glu Tyr Cys His Tyr Ala Ala Gly Leu Val Gly Leu
20 25 30
Gly Leu Ser Lys Ile Phe Ile Ala Ser Glu Leu Glu Ile Leu Thr Pro
35 40 45
Asp Trp Lys Gln Ile Ser Asn Ser Thr Gly Leu Phe Leu Gln Lys Thr
50 55 60
Asn Ile Ile Lys Asp Tyr Leu Glu Asp Ile Asn Glu Arg Pro Lys Ser
65 70 75 80
Arg Met Phe Trp Pro Arg Glu Ile Trp Gly Lys Tyr Val Asp Lys Leu
85 90 95
Glu Asp Phe Lys Asn Glu Glu Lys Ala Thr Lys Ala Val Gln Cys Leu
100 105 110
Asn Glu Met Val Thr Asn Ala Leu Asn His Val Glu Asp Cys Leu Lys
115 120 125
Ser Leu Xaa Phe Thr Ala
130

(2) INFORMATION FOR SEQ ID NO:1197:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 130 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..130
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569297

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1197:

Met Ala Lys Phe Ile Cys Lys Glu Val Glu Thr Ile Asp Asp Tyr Asp
1 5 10 15
Glu Tyr Cys His Tyr Ala Ala Gly Leu Val Gly Leu Gly Leu Ser Lys
20 25 30
Ile Phe Ile Ala Ser Glu Leu Glu Ile Leu Thr Pro Asp Trp Lys Gln
35 40 45
Ile Ser Asn Ser Thr Gly Leu Phe Leu Gln Lys Thr Asn Ile Ile Lys
50 55 60

Asp Tyr Leu Glu Asp Ile Asn Glu Arg Pro Lys Ser Arg Met Phe Trp
65 70 75 80
Pro Arg Glu Ile Trp Gly Lys Tyr Val Asp Lys Leu Glu Asp Phe Lys
85 90 95
Asn Glu Glu Lys Ala Thr Lys Ala Val Gln Cys Leu Asn Glu Met Val
100 105 110
Thr Asn Ala Leu Asn His Val Glu Asp Cys Leu Lys Ser Leu Xaa Phe
115 120 125
Thr Ala
130

(2) INFORMATION FOR SEQ ID NO:1198:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1156 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1156

(D) OTHER INFORMATION: / Ceres Seq. ID 1569298

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1198:

atactctctt	ttttctcgg	acaagaaggc	tacagaaaga	tatgtcgtg	tctgtctacc	60
tcagcccgac	gcgccttcta	taaggctacc	tccgcccgtg	tctcaggcgc	gcaggactga	120
cgtcgcagAc	gctttccata	gactctgaaa	caaccatcca	cttctggggc	ccaccactc	180
tagaccaccg	gagcgacgat	gacagaccgg	ttatgcttct	cctccacggc	ttcgggtccg	240
cgtccatgtg	gcagtgggcg	cgacagatgc	aagccttctc	tcctcccgct	ttcagggggt	300
attctccgca	tcttctcttc	tccggcgact	ctaccctctc	ctccaccaat	cgcaccgaag	360
cttccacggc	ggaatgatg	gcaaaagctaa	tggcgaaaat	aggaataggg	aagtataatg	420
tggctggaac	aagctacggg	gggtttgttg	cgtaccacat	ggccaaaatg	tggccggaag	480
aagtggagaa	agtggtgat	gcaagctccg	gcatacaat	gcgaaagtgt	gacggtgaaa	540
gtttattgca	aagatccaat	tgtgagtgc	tcgagaaggt	tatgttacca	tccactgcga	600
ctgagtttgc	cacacttatg	gctttggcat	cttcattgct	gttatgtctg	atgtttctcg	660
atgctctctg	gaacgacgta	atcaataatt	tgtataaaaa	aaatagaaaa	gagaagatag	720
aattgttgaa	gggagtgact	tccggccgga	gcgaaaaatt	aaacatcgat	tctcttcttc	780
aggaggtcct	aattgtatgg	ggagacaaa	atcagatatt	tctgtggaag	atggcttacg	840
aattaaaaga	gattcttgga	gacaaaacga	aactagaaat	cattgacaac	acttcacatg	900
ttctccagat	tgaatgtgct	caagagtcca	acaatattgt	tttgagattt	ttgaagggtt	960
cttaagagcc	gtaattttat	tccatgctac	atgattcttc	agtttttttt	aagtgttaaa	1020
ctattggtta	cgtaattttt	cgactttact	tgccatgctt	tctcattttt	catgtaagaa	1080
ctttatccat	tactgtcatt	gtagagaact	ctatttatag	caaaaagtga	tactaatatg	1140
caacttaatt	ttcgtc					

(2) INFORMATION FOR SEQ ID NO:1199:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 250 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..250

(D) OTHER INFORMATION: / Ceres Seq. ID 1569299

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1199:

Met Leu Leu Leu His Gly Phe Gly Pro Ser Ser Met Trp Gln Trp Arg
1 5 10 15
Arg Gln Met Gln Ala Phe Ser Pro Ser Ala Phe Arg Val Tyr Ser Pro
20 25 30
Asp Leu Val Phe Phe Gly Asp Ser Thr Ser Ser Ser Thr Asn Arg Thr
35 40 45
Glu Val Phe Gln Ala Glu Cys Met Ala Lys Leu Met Ala Lys Ile Gly

50	55	60
Ile Gly Lys Tyr Asn Val Ala Gly Thr Ser Tyr Gly Gly Phe Val Ala		
65	70	75
Tyr His Met Ala Lys Met Trp Pro Glu Lys Val Glu Lys Val Val Ile		80
	85	90
Ala Ser Ser Gly Ile Asn Met Arg Lys Cys Asp Gly Glu Ser Leu Leu		95
	100	105
Gln Arg Ser Asn Cys Glu Cys Ile Glu Lys Val Met Leu Pro Ser Thr		110
	115	120
Ala Thr Glu Phe Arg Thr Leu Met Ala Leu Ala Ser Ser Trp Arg Leu		125
	130	135
Val Arg Met Phe Pro Asp Ala Leu Trp Asn Asp Val Ile Asn Asn Leu		140
	145	150
Tyr Lys Lys Asn Arg Lys Glu Lys Ile Glu Leu Lys Gly Val Thr		155
	160	165
Phe Gly Arg Ser Glu Asn Leu Asn Ile Asp Ser Leu Ser Gln Glu Val		170
	175	180
Leu Ile Val Trp Gly Asp Lys Asp Gln Ile Phe Pro Val Lys Met Ala		185
	190	195
Tyr Glu Leu Lys Glu Ile Leu Gly Asp Lys Thr Lys Leu Glu Ile Ile		200
	205	210
Asp Asn Thr Ser His Val Pro Gln Ile Glu Cys Ala Gln Glu Phe Asn		215
	220	225
Asn Ile Val Leu Arg Phe Leu Lys Gly Ser		230
	235	240
	245	250

(2) INFORMATION FOR SEQ ID NO:1200:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 239 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..239

(D) OTHER INFORMATION: / Ceres Seq. ID 1569300

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1200:

Met Trp Gln Trp Arg Arg Gln Met Gln Ala Phe Ser Pro Ser Ala Phe		
1	5	10
Arg Val Tyr Ser Pro Asp Leu Val Phe Phe Gly Asp Ser Thr Ser Ser		15
	20	25
Ser Thr Asn Arg Thr Glu Val Phe Gln Ala Glu Cys Met Ala Lys Leu		30
	35	40
Met Ala Lys Ile Gly Ile Gly Lys Tyr Asn Val Ala Gly Thr Ser Tyr		45
	50	55
Gly Gly Phe Val Ala Tyr His Met Ala Lys Met Trp Pro Glu Lys Val		60
	65	70
Glu Lys Val Val Ile Ala Ser Ser Gly Ile Asn Met Arg Lys Cys Asp		75
	80	85
Gly Glu Ser Leu Gln Arg Ser Asn Cys Glu Cys Ile Glu Lys Val		90
	95	100
Met Leu Pro Ser Thr Ala Thr Glu Phe Arg Thr Leu Met Ala Leu Ala		105
	110	115
Ser Ser Trp Arg Leu Val Arg Met Phe Pro Asp Ala Leu Trp Asn Asp		120
	125	130
Val Ile Asn Asn Leu Tyr Lys Lys Asn Arg Lys Glu Lys Ile Glu Leu		135
	140	145
Leu Lys Gly Val Thr Phe Gly Arg Ser Glu Asn Leu Asn Ile Asp Ser		150
	155	160
Leu Ser Gln Glu Val Leu Ile Val Trp Gly Asp Lys Asp Gln Ile Phe		165
	170	175
	180	185
	190	

Pro Val Lys Met Ala Tyr Glu Leu Lys Glu Ile Leu Gly Asp Lys Thr
195 200 205
Lys Leu Glu Ile Ile Asp Asn Thr Ser His Val Pro Gln Ile Glu Cys
210 215 220
Ala Gln Glu Phe Asn Asn Ile Val Leu Arg Phe Leu Lys Gly Ser
225 230 235

(2) INFORMATION FOR SEQ ID NO:1201:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 232 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..232
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569301

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1201:

Met Gln Ala Phe Ser Pro Ser Ala Phe Arg Val Tyr Ser Pro Asp Leu
1 5 10 15
Val Phe Phe Gly Asp Ser Thr Ser Ser Thr Thr Asn Arg Thr Glu Val
20 25 30
Phe Gln Ala Glu Cys Met Ala Lys Leu Met Ala Lys Ile Gly Ile Gly
35 40 45
Lys Tyr Asn Val Ala Gly Thr Ser Tyr Gly Gly Phe Val Ala Tyr His
50 55 60
Met Ala Lys Met Trp Pro Glu Lys Val Glu Lys Val Val Ile Ala Ser
65 70 75 80
Ser Gly Ile Asn Met Arg Lys Cys Asp Gly Glu Ser Leu Leu Gln Arg
85 90 95
Ser Asn Cys Glu Cys Ile Glu Lys Val Met Leu Pro Ser Thr Ala Thr
100 105 110
Glu Phe Arg Thr Leu Met Ala Leu Ala Ser Ser Trp Arg Leu Val Arg
115 120 125
Met Phe Pro Asp Ala Leu Trp Asn Asp Val Ile Asn Asn Leu Tyr Lys
130 135 140
Lys Asn Arg Lys Glu Lys Ile Glu Leu Leu Lys Gly Val Thr Phe Gly
145 150 155 160
Arg Ser Glu Asn Leu Asn Ile Asp Ser Leu Ser Gln Glu Val Leu Ile
165 170 175
Val Trp Gly Asp Lys Asp Gln Ile Phe Pro Val Lys Met Ala Tyr Glu
180 185 190
Leu Lys Glu Ile Leu Gly Asp Lys Thr Lys Leu Glu Ile Ile Asp Asn
195 200 205
Thr Ser His Val Pro Gln Ile Glu Cys Ala Gln Glu Phe Asn Asn Ile
210 215 220
Val Leu Arg Phe Leu Lys Gly Ser
225 230

(2) INFORMATION FOR SEQ ID NO:1202:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1431 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1431
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569306

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1202:

attttatttt ctggaatctt ctctctcttc ctgatttcca ggcagcttaac aacaacaaca

acaacatatt	ctctgctg	tattagattc	gaatttctct	ttttgtgac	agaaatggat	120
cgagctccgg	tgaccacagg	accgttggat	atgccgatta	tgccagcacg	tgatcgatat	180
gaacttcgtta	aggatatggg	ttctggtaat	ttcgggtgtg	ctcgtcttat	gagagataaa	240
ctcactaaag	agcttgttgc	tgccaagtag	atcgagagag	gagacaagat	tgatgaaaaa	300
gttccaaagg	agatcattaa	ccacaggcca	ctaaggcatc	ctaattattg	cagattttaa	360
gaggtcattt	tgacgccgac	tcactctggt	atcataatgg	aatatgcttc	tgccggtgaa	420
ctttacagag	ggatttgc	tgccaggacg	tttagtgaag	atgaggtcgt	gttcttcttt	480
cagcagcttc	tatctggagt	cagttatgtg	catgcatgac	aaatttgcca	tcgtgacctg	540
aagctagaga	atacatttgt	ggatggaagt	ccctgctctc	gattaaaaat	ttgtgatttt	600
ggatatccaa	agtcctctgt	ttctcattca	caaccaaaat	caactgttgg	tactcctgca	660
tacatctctc	cagaggttct	gcttcgtcag	gaatatgatg	gcaagattgc	agatgtatgg	720
tcagtgtgtg	tgacccttata	cgctcatgtt	gttgagcggt	atccgttcga	agatccagaa	780
gagccaagag	actatcggaa	aacaatacag	agaatcctta	gcgttaaaat	ctcaatccct	840
gatgacatac	ggatatccac	tgaatcgtgt	catcttattt	caagaatctt	cgtggtgatg	900
ccctgtacca	gaataagcat	accagagatc	aaaacccata	gttggttctt	gaagaatctc	960
cctgctgatt	taattgaacg	gagcaacaca	ggaagccagt	tccaggagcc	tgacaacca	1020
atgcacagcc	ttgacacaat	catgcaaatc	attcttgaag	ccacaattcc	cgctgttgca	1080
aaccgttgcc	tagacgattt	catgactgac	aatcttgatc	ttgacgatga	catggatgac	1140
tttgactctg	aatctgaaat	cgacattgac	atagcggagg	agatagttta	cgctctctaa	1200
taaaaagcct	tttttaacaa	ccaaaacact	ttcttatctg	ttctaagacc	agtagtgctc	1260
tgatctctct	gtttcaaat	ctaccaattt	ttgtattgtc	ttctgtttgt	ttctgttttc	1320
ttcatgcaca	catatatcat	atagttaatg	taaaatatca	ttctgttata	tatatccaa	1380
gttcacacaa	aagcaratta	gcaGttaaaa	cagttgaagc	aagttgaggt	c	

(2) INFORMATION FOR SEQ ID NO:1203:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 361 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..361

(D) OTHER INFORMATION: / Ceres Seq. ID 1569307

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1203:

Met	Asp	Arg	Ala	Pro	Val	Thr	Thr	Gly	Pro	Leu	Asp	Met	Pro	Ile	Met
1				5				10						15	
His	Asp	Ser	Asp	Arg	Tyr	Asp	Phe	Val	Lys	Asp	Ile	Gly	Ser	Gly	Asn
				20				25						30	
Phe	Gly	Val	Ala	Arg	Leu	Met	Arg	Asp	Lys	Leu	Thr	Lys	Glu	Leu	Val
				35				40						45	
Ala	Val	Lys	Tyr	Ile	Glu	Arg	Gly	Asp	Lys	Ile	Asp	Glu	Asn	Val	Gln
				50				55						60	
Arg	Glu	Ile	Ile	Asn	His	Arg	Ser	Leu	Arg	His	Pro	Asn	Ile	Val	Arg
				65				70						75	
Phe	Lys	Glu	Val	Ile	Leu	Thr	Pro	Thr	His	Leu	Ala	Ile	Ile	Met	Glu
				85				90						95	
Tyr	Ala	Ser	Gly	Gly	Glu	Leu	Tyr	Glu	Arg	Ile	Cys	Asn	Ala	Gly	Arg
				100				105						110	
Phe	Ser	Glu	Asp	Glu	Ala	Arg	Phe	Phe	Gln	Gln	Leu	Leu	Ser	Gly	
				115				120						125	
Val	Ser	Tyr	Cys	His	Ala	Met	Gln	Ile	Cys	His	Arg	Asp	Leu	Lys	Leu
				130				135						140	
Glu	Asn	Thr	Leu	Leu	Asp	Gly	Ser	Pro	Ala	Pro	Arg	Leu	Lys	Ile	Cys
				145				150						155	
Asp	Phe	Gly	Tyr	Ser	Lys	Ser	Ser	Val	Leu	His	Ser	Gln	Pro	Lys	Ser
				165				170						175	
Thr	Val	Gly	Thr	Pro	Ala	Tyr	Ile	Ala	Pro	Glu	Val	Leu	Leu	Arg	Gln
				180				185						190	
Glu	Tyr	Asp	Gly	Lys	Ile	Ala	Asp	Val	Trp	Ser	Cys	Gly	Val	Thr	Leu
				195				200						205	

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Tyr Val Met Leu Val Gly Ala Tyr Pro Phe Glu Asp Pro Glu Glu Pro
210 215 220
Arg Asp Tyr Arg Lys Thr Ile Gln Arg Ile Leu Ser Val Lys Tyr Ser
225 230 235 240
Ile Pro Asp Asp Ile Arg Ile Ser Pro Glu Cys Cys His Leu Ile Ser
245 250 255
Arg Ile Phe Val Ala Asp Pro Ala Thr Arg Ile Ser Ile Pro Glu Ile
260 265 270
Lys Thr His Ser Trp Phe Leu Lys Asn Leu Pro Ala Asp Leu Met Asn
275 280 285
Glu Ser Asn Thr Gly Ser Gln Phe Gln Glu Pro Glu Gln Pro Met Gln
290 295 300
Ser Leu Asp Thr Ile Met Gln Ile Ile Ser Glu Ala Thr Ile Pro Ala
305 310 315 320
Val Arg Asn Arg Cys Leu Asp Asp Phe Met Thr Asp Asn Leu Asp Leu
325 330 335
Asp Asp Asp Met Asp Asp Phe Asp Ser Glu Ser Glu Ile Asp Ile Asp
340 345 350
Ser Ser Gly Glu Ile Val Tyr Ala Leu
355 360

(2) INFORMATION FOR SEQ ID NO:1204:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 349 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..349

(D) OTHER INFORMATION: / Ceres Seq. ID 1569308

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1204:

Met Pro Ile Met His Asp Ser Asp Arg Tyr Asp Phe Val Lys Asp Ile
1 5 10 15
Gly Ser Gly Asn Phe Gly Val Ala Arg Leu Met Arg Asp Lys Leu Thr
20 25 30
Lys Glu Leu Val Ala Val Lys Tyr Ile Glu Arg Gly Asp Lys Ile Asp
35 40 45
Glu Asn Val Gln Arg Glu Ile Ile Asn His Arg Ser Leu Arg His Pro
50 55 60
Asn Ile Val Arg Phe Lys Glu Val Ile Leu Thr Pro Thr His Leu Ala
65 70 75 80
Ile Ile Met Glu Tyr Ala Ser Gly Gly Glu Leu Tyr Glu Arg Ile Cys
85 90 95
Asn Ala Gly Arg Phe Ser Glu Asp Glu Ala Arg Phe Phe Phe Gln Gln
100 105 110
Leu Leu Ser Gly Val Ser Tyr Cys His Ala Met Gln Ile Cys His Arg
115 120 125
Asp Leu Lys Leu Glu Asn Thr Leu Leu Asp Gly Ser Pro Ala Pro Arg
130 135 140
Leu Lys Ile Cys Asp Phe Gly Tyr Ser Lys Ser Ser Val Leu His Ser
145 150 155 160
Gln Pro Lys Ser Thr Val Gly Thr Pro Ala Tyr Ile Ala Pro Glu Val
165 170 175
Leu Leu Arg Gln Glu Tyr Asp Gly Lys Ile Ala Asp Val Trp Ser Cys
180 185 190
Gly Val Thr Leu Tyr Val Met Leu Val Gly Ala Tyr Pro Phe Glu Asp
195 200 205
Pro Glu Glu Pro Arg Asp Tyr Arg Lys Thr Ile Gln Arg Ile Leu Ser
210 215 220
Val Lys Tyr Ser Ile Pro Asp Asp Ile Arg Ile Ser Pro Glu Cys Cys

225 230 235 240
His Leu Ile Ser Arg Ile Phe Val Ala Asp Pro Ala Thr Arg Ile Ser
245 250 255
Ile Pro Glu Ile Lys Thr His Ser Trp Phe Leu Lys Asn Leu Pro Ala
260 265 270
Asp Leu Met Asn Glu Ser Asn Thr Gly Ser Gln Phe Gln Glu Pro Glu
275 280 285
Gln Pro Met Gln Ser Leu Asp Thr Ile Met Gln Ile Ile Ser Glu Ala
290 295 300
Thr Ile Pro Ala Val Arg Asn Arg Cys Leu Asp Asp Phe Met Thr Asp
305 310 315 320
Asn Leu Asp Leu Asp Asp Asp Met Asp Asp Phe Asp Ser Glu Ser Glu
325 330 335
Ile Asp Ile Asp Ser Ser Gly Glu Ile Val Tyr Ala Leu
340 345

(2) INFORMATION FOR SEQ ID NO:1205:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 346 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..346

(D) OTHER INFORMATION: / Ceres Seq. ID 1569309

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1205:

Met His Asp Ser Asp Arg Tyr Asp Phe Val Lys Asp Ile Gly Ser Gly
1 5 10 15
Asn Phe Gly Val Ala Arg Leu Met Arg Asp Lys Leu Thr Lys Glu Leu
20 25 30
Val Ala Val Lys Tyr Ile Glu Arg Gly Asp Lys Ile Asp Glu Asn Val
35 40 45
Gln Arg Glu Ile Ile Asn His Arg Ser Leu Arg His Pro Asn Ile Val
50 55 60
Arg Phe Lys Glu Val Ile Leu Thr Pro Thr His Leu Ala Ile Ile Met
65 70 75 80
Glu Tyr Ala Ser Gly Gly Glu Leu Tyr Glu Arg Ile Cys Asn Ala Gly
85 90 95
Arg Phe Ser Glu Asp Glu Ala Arg Phe Phe Gln Gln Leu Leu Ser
100 105 110
Gly Val Ser Tyr Cys His Ala Met Gln Ile Cys His Arg Asp Leu Lys
115 120 125
Leu Glu Asn Thr Leu Leu Asp Gly Ser Pro Ala Pro Arg Leu Lys Ile
130 135 140
Cys Asp Phe Gly Tyr Ser Lys Ser Ser Val Leu His Ser Gln Pro Lys
145 150 155 160
Ser Thr Val Gly Thr Pro Ala Tyr Ile Ala Pro Glu Val Leu Leu Arg
165 170 175
Gln Glu Tyr Asp Gly Lys Ile Ala Asp Val Trp Ser Cys Gly Val Thr
180 185 190
Leu Tyr Val Met Leu Val Gly Ala Tyr Pro Phe Glu Asp Pro Glu Glu
195 200 205
Pro Arg Asp Tyr Arg Lys Thr Ile Gln Arg Ile Leu Ser Val Lys Tyr
210 215 220
Ser Ile Pro Asp Asp Ile Arg Ile Ser Pro Glu Cys Cys His Leu Ile
225 230 235 240
Ser Arg Ile Phe Val Ala Asp Pro Ala Thr Arg Ile Ser Ile Pro Glu
245 250 255
Ile Lys Thr His Ser Trp Phe Leu Lys Asn Leu Pro Ala Asp Leu Met
260 265 270

Asn Glu Ser Asn Thr Gly Ser Gln Phe Gln Glu Pro Glu Gln Pro Met
275 280 285
Gln Ser Leu Asp Thr Ile Met Gln Ile Ile Ser Glu Ala Thr Ile Pro
290 295 300
Ala Val Arg Asn Arg Cys Leu Asp Asp Phe Met Thr Asp Asn Leu Asp
305 310 315 320
Leu Asp Asp Asp Met Asp Asp Phe Asp Ser Glu Ser Glu Ile Asp Ile
325 330 335
Asp Ser Ser Gly Glu Ile Val Tyr Ala Leu
340 345

(2) INFORMATION FOR SEQ ID NO:1206:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1533 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1533
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569310

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1206:

ctgatttttt	gacgttaaga	gatagaacca	gggagagata	gagagataga	gttatggcgt	60
tggcgatgat	gatccgaac	gcagcttcga	agcgaggaa	gactccgac	tccggtgatt	120
tgggtggttt	gagatctatg	tcttcatggt	ggaagagcgt	tgagcctgct	cttaagatc	180
cgatccctcgg	agttaccgaa	gcttttctcg	ctgatctctag	tcttgaaaaa	gttaattgtt	240
gtgtgggagc	atatactgat	gataatggga	agcctgttgt	cttggaatgt	gtcagagaa	300
ctgagaaaag	gcttgcgtgg	agcaactttca	tggagtacct	tcttatggga	ggaagtgcga	360
aaatggtgga	cctaaccatta	agcttgccta	cggggacaat	agtgaattta	tcaagataa	420
aagaattgct	gcagttcaga	ctctgtcttg	cactggagcc	tgccggctct	ttgcagactt	480
ccagaaacgt	ttttctctcg	gttcacagat	ctacattcct	gttccaacct	gggtccacca	540
ccacaacatc	tggaaaagatg	cacaagtcct	tcaaaagaca	tatcattact	atcatccaga	600
aaccaagggc	tgggatttct	cagcattgat	ggatgatgtg	aagaatgctc	cggaagggtc	660
attcttcctt	cttcatgctt	gtgctcataa	tctactgcca	gtagacccta	cagaggaaca	720
atggagagag	atatcacagc	tattcaaggc	taaaagcat	ttcgctattc	tcatatggc	780
ttaccaaggt	tttgctagtg	gagatccagc	gagagatgcc	aagtcctatc	ggatctttct	840
tgaagatggt	catcatattg	gaatttctca	gtcttatgca	aaaaacatgg	gactctacgg	900
ccagaggggt	ggatgtctca	gtgtgctttg	tgaagatccg	aagcaagccg	tggctgtgaa	960
aagtcaattg	cagcagctag	ctagaccaat	gtacagcaac	ccacctttgc	attggtgtca	1020
gctggtctca	accattcttg	aagaccaga	gttaaagagt	ctgtggctta	aagaagttaa	1080
ggtcatggct	gataggatca	tccgcatgag	aactactttg	cgagaaagcc	ttgagaagtt	1140
aggaatcgct	ttgtcatggg	agcacgttac	caaacagatt	ggaatgtctt	gtcacagtgg	1200
gttaaacaga	gaacaggttg	accgcttaac	aagcgaatat	acacatctata	tgacccgtaa	1260
cggcgcgtatc	agtatggctg	gtgttaCaac	aggaaacctg	ggataccttg	cgaatgctat	1320
acatgaagtc	accaagtcac	cttaaatcat	ttacttacat	gtttcagcca	aacatcacaaa	1380
ttttgtttga	agagtcaata	agacaggagg	ctagatttgt	acttctgcga	ttggttttgt	1440
gagaactgaa	agtttaacca	taaacagtaa	ttttattagc	cattttttctg	ttagctgggc	1500
aataaaaagca	aagcctaacc	gatggatttt	tgg			

(2) INFORMATION FOR SEQ ID NO:1207:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 191 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..191
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569311

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1207:

Met Ala Leu Ala Met Met Ile Arg Asn Ala Ala Ser Lys Arg Gly Met

1 5 10 15
Thr Pro Ile Ser Gly Asp Phe Gly Gly Leu Arg Ser Met Ser Ser Trp
20 25 30
Trp Lys Ser Val Glu Pro Ala Pro Lys Asp Pro Ile Leu Gly Val Thr
35 40 45
Glu Ala Phe Leu Ala Asp Pro Ser Pro Glu Lys Val Asn Val Gly Val
50 55 60
Gly Ala Tyr Arg Asp Asp Asn Gly Lys Pro Val Val Leu Glu Cys Val
65 70 75 80
Arg Glu Ala Glu Lys Arg Leu Ala Gly Ser Thr Phe Met Glu Tyr Leu
85 90 95
Pro Met Gly Gly Ser Ala Lys Met Val Asp Leu Thr Leu Ser Leu Pro
100 105 110
Thr Gly Thr Ile Val Asn Leu Ser Lys Ile Lys Glu Leu Leu Gln Phe
115 120 125
Arg Leu Cys Leu Ala Leu Glu Pro Ala Gly Ser Leu Gln Thr Ser Arg
130 135 140
Asn Val Phe Leu Leu Val His Arg Ser Thr Phe Leu Phe Gln Pro Gly
145 150 155 160
Pro Thr Thr Thr Thr Ser Gly Lys Met His Lys Ser Leu Lys Arg His
165 170 175
Ile Ile Thr Ile Ile Gln Lys Pro Arg Ala Trp Ile Ser Gln His
180 185 190

(2) INFORMATION FOR SEQ ID NO:1208:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 238 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..238
(D) OTHER INFORMATION: / Ceres Seq. ID 1569312
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1208:
Met Asp Asp Val Lys Asn Ala Pro Glu Gly Ser Phe Phe Leu Leu His
1 5 10 15
Ala Cys Ala His Asn Pro Thr Gly Val Asp Pro Thr Glu Glu Gln Trp
20 25 30
Arg Glu Ile Ser Gln Leu Phe Lys Ala Lys Lys His Phe Ala Phe Phe
35 40 45
Asp Met Ala Tyr Gln Gly Phe Ala Ser Gly Asp Pro Ala Arg Asp Ala
50 55 60
Lys Ser Ile Arg Ile Phe Leu Glu Asp Gly His His Ile Gly Ile Ser
65 70 75 80
Gln Ser Tyr Ala Lys Asn Met Gly Leu Tyr Gly Gln Arg Val Gly Cys
85 90 95
Leu Ser Val Leu Cys Glu Asp Pro Lys Gln Ala Val Ala Val Lys Ser
100 105 110
Gln Leu Gln Gln Leu Ala Arg Pro Met Tyr Ser Asn Pro Pro Leu His
115 120 125
Gly Ala Gln Leu Val Ser Thr Ile Leu Glu Asp Pro Glu Leu Lys Ser
130 135 140
Leu Trp Leu Lys Glu Val Lys Val Met Ala Asp Arg Ile Ile Gly Met
145 150 155 160
Arg Thr Thr Leu Arg Glu Ser Leu Glu Lys Leu Gly Ser Pro Leu Ser
165 170 175
Trp Glu His Val Thr Lys Gln Ile Gly Met Phe Cys Tyr Ser Gly Leu
180 185 190
Thr Pro Glu Gln Val Asp Arg Leu Thr Ser Glu Tyr His Ile Tyr Met
195 200 205

Thr Arg Asn Gly Arg Ile Ser Met Ala Gly Val Thr Thr Gly Asn Val
210 215 220
Gly Tyr Leu Ala Asn Ala Ile His Glu Val Thr Lys Ser Ser
225 230 235

(2) INFORMATION FOR SEQ ID NO:1209:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 189 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..189
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569313

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1209:

Met Ala Tyr Gln Gly Phe Ala Ser Gly Asp Pro Ala Arg Asp Ala Lys
1 5 10 15
Ser Ile Arg Ile Phe Leu Glu Asp Gly His His Ile Gly Ile Ser Gln
20 25 30
Ser Tyr Ala Lys Asn Met Gly Leu Tyr Gly Gln Arg Val Gly Cys Leu
35 40 45
Ser Val Leu Cys Glu Asp Pro Lys Gln Ala Val Ala Lys Ser Gln
50 55 60
Leu Gln Gln Leu Ala Arg Pro Met Tyr Ser Asn Pro Pro Leu His Gly
65 70 75 80
Ala Gln Leu Val Ser Thr Ile Leu Glu Asp Pro Glu Leu Lys Ser Leu
85 90 95
Trp Leu Lys Glu Val Lys Val Met Ala Asp Arg Ile Ile Gly Met Arg
100 105 110
Thr Thr Leu Arg Glu Ser Leu Glu Lys Leu Gly Ser Pro Leu Ser Trp
115 120 125
Glu His Val Thr Lys Gln Ile Gly Met Phe Cys Tyr Ser Gly Leu Thr
130 135 140
Pro Glu Gln Val Asp Arg Leu Thr Ser Glu Tyr His Ile Tyr Met Thr
145 150 155 160
Arg Asn Gly Arg Ile Ser Met Ala Gly Val Thr Thr Gly Asn Val Gly
165 170 175
Tyr Leu Ala Asn Ala Ile His Glu Val Thr Lys Ser Ser
180 185

(2) INFORMATION FOR SEQ ID NO:1210:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1326 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1326
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569326

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1210:

cttctcgcat cttatatgaa acacattcac tctccaaaat aatctatact ttctctacat 60
attctottga cgatcatgag actcatttcg tgaaaaatc gtcattatat caaattagaa 120
gttgatggaa aacatggggg attcgagcat agggccgggc catccgcac tcctcccg 180
gtttcggtt caccgcagct atgaggaact agtagttcat tactcaaga agaaagcagc 240
ttctgttcca cttccagttc caatcatcgc agagattgat ctttacaagt ttgatccttg 300
ggagcttcca agcaaggcga gttttggaga gcacgagtg tactttttaa gtccctcgga 360
tcggaagtat ccaaatgggg ttaggcctaa cgggcagca acttcgggtt attggaaagc 420
aacgggaacc gataaaccca tatttactgt caatagtcac aagggttggt tcaagaaagc 480
gcttgttttt tacggtggaa agcctcctaa agggataaaa acagattgga tcatgcata 540

atatacgcctc	actgatggta	accttagcac	tgccggctaag	cgcgcctgact	taaccacgac	600
aaggaaaaaac	tcactacgag	tagacgattg	ggttctatgt	aggatctata	agaagaatag	660
ttcacaagaag	S accaCacaat	ggagagagta	ttagagagga	tctaattggaa	ggcatgctct	720
caaaaatcatc	tgctaatctt	tcttctacat	cagtactaga	caacaacgac	aacaataatr	780
acaataacaaa	agaacacctt	ttcgacggta	tggtcgtttc	ttcagacaaa	cgttccctgt	840
gtggtcaata	ccgaatgggc	gacgaggcct	caggatcatc	ttcattcgga	tctttcttat	900
cgagcaagag	gtttcatcat	acagggtgatc	tcaacaatga	taactacaat	gtctcttttg	960
tttcgatgct	tagtgagatt	cctcagagtt	cggggtttca	tgcaaatggt	ggtatggata	1020
cgagctgctc	tctagctgat	catgggggttt	taagacaggc	gtttcagctt	cctaacatga	1080
actggcactc	ataatctata	tagatatata	tgtagtgatc	atatatgtat	ctatgcaggc	1140
ctaataatag	ttacacataa	atcatctggg	aatatatata	tacaagtacg	cgtgtctaca	1200
aatgtatacg	tattctgttta	attacgtcaa	gaaaaagtgt	atacgtttct	ttttactcaa	1260
tggtctcaaa	gatgtgtact	aataacagaa	gctgattaat	aaaaataata	aaagtatat	1320
ttttcc						

(2) INFORMATION FOR SEQ ID NO:1211:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 189 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..189
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569327

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1211:

Met	Glu	Asn	Met	Gly	Asp	Ser	Ser	Ile	Gly	Pro	Gly	His	Pro	His	Leu
1			5					10						15	
Pro	Pro	Gly	Phe	Arg	Phe	His	Pro	Thr	Asp	Glu	Glu	Leu	Val	Val	His
			20					25					30		
Tyr	Leu	Lys	Lys	Lys	Ala	Ala	Ser	Val	Pro	Leu	Pro	Val	Ser	Ile	Ile
		35					40					45			
Ala	Glu	Ile	Asp	Leu	Tyr	Lys	Phe	Asp	Pro	Trp	Glu	Leu	Pro	Ser	Lys
		50				55					60				
Ala	Ser	Phe	Gly	Glu	His	Glu	Trp	Tyr	Phe	Phe	Ser	Pro	Arg	Asp	Arg
		65			70				75					80	
Lys	Tyr	Pro	Asn	Gly	Val	Arg	Pro	Asn	Arg	Ala	Ala	Thr	Ser	Gly	Tyr
			85					90						95	
Trp	Lys	Ala	Thr	Gly	Thr	Asp	Lys	Pro	Ile	Phe	Thr	Cys	Asn	Ser	His
			100				105					110			
Lys	Val	Gly	Val	Lys	Lys	Ala	Leu	Val	Phe	Tyr	Gly	Gly	Lys	Pro	Pro
		115				120					125				
Lys	Gly	Ile	Lys	Thr	Asp	Trp	Ile	Met	His	Glu	Tyr	Arg	Leu	Thr	Asp
		130			135					140					
Gly	Asn	Leu	Ser	Thr	Ala	Ala	Lys	Pro	Pro	Asp	Leu	Thr	Thr	Thr	Arg
			145		150					155					160
Lys	Asn	Ser	Leu	Arg	Leu	Asp	Asp	Trp	Val	Leu	Cys	Arg	Ile	Tyr	Lys
			165					170						175	
Lys	Asn	Ser	Ser	Gln	Xaa	Thr	Thr	Gln	Trp	Arg	Glu	Tyr			
			180					185							

(2) INFORMATION FOR SEQ ID NO:1212:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 186 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..186
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569328

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1212:

Met	Gly	Asp	Ser	Ser	Ile	Gly	Pro	Gly	His	Pro	His	Leu	Pro	Pro	Gly
1			5					10						15	
Phe	Arg	Phe	His	Pro	Thr	Asp	Glu	Glu	Leu	Val	Val	His	Tyr	Leu	Lys
			20					25					30		
Lys	Lys	Ala	Ala	Ser	Val	Pro	Leu	Pro	Val	Ser	Ile	Ile	Ala	Glu	Ile
		35					40					45			
Asp	Leu	Trp	Lys	Phe	Asp	Pro	Trp	Glu	Leu	Pro	Ser	Lys	Ala	Ser	Phe
	50					55					60				
Gly	Glu	His	Glu	Trp	Tyr	Phe	Phe	Ser	Pro	Arg	Asp	Arg	Lys	Tyr	Pro
	65			70					75					80	
Asn	Gly	Val	Arg	Pro	Asn	Arg	Ala	Ala	Thr	Ser	Gly	Tyr	Trp	Lys	Ala
			85					90						95	
Thr	Gly	Thr	Asp	Lys	Pro	Ile	Phe	Thr	Cys	Asn	Ser	His	Lys	Val	Gly
			100					105					110		
Val	Lys	Lys	Ala	Leu	Val	Phe	Tyr	Gly	Gly	Lys	Pro	Pro	Lys	Gly	Ile
		115					120					125			
Lys	Thr	Asp	Trp	Ile	Met	His	Glu	Tyr	Arg	Leu	Thr	Asp	Gly	Asn	Leu
	130					135					140				
Ser	Thr	Ala	Ala	Lys	Pro	Pro	Asp	Leu	Thr	Thr	Thr	Arg	Lys	Asn	Ser
	145				150					155				160	
Leu	Arg	Leu	Asp	Asp	Trp	Val	Leu	Cys	Arg	Ile	Tyr	Lys	Lys	Asn	Ser
			165					170						175	
Ser	Gln	Xaa	Thr	Thr	Gln	Trp	Arg	Glu	Tyr						
			180					185							

(2) INFORMATION FOR SEQ ID NO:1213:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..129
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569329

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1213:

Met	Glu	Gly	Met	Leu	Ser	Lys	Ser	Ser	Ala	Asn	Ser	Ser	Ser	Thr	Ser
1			5						10					15	
Val	Leu	Asp	Asn	Asn	Asp	Asn	Asn	Xaa	Asn	Asn	Lys	Glu	His	Phe	
		20					25					30			
Phe	Asp	Gly	Met	Val	Val	Ser	Ser	Asp	Lys	Arg	Ser	Leu	Cys	Gly	Gln
		35					40				45				
Tyr	Arg	Met	Gly	Asp	Glu	Ala	Ser	Gly	Ser	Ser	Ser	Phe	Gly	Ser	Phe
		50				55					60				
Leu	Ser	Ser	Lys	Arg	Phe	His	His	Thr	Gly	Asp	Leu	Asn	Asn	Asp	Asn
		65			70				75					80	
Tyr	Asn	Val	Ser	Phe	Val	Ser	Met	Leu	Ser	Glu	Ile	Pro	Gln	Ser	Ser
			85					90						95	
Gly	Phe	His	Ala	Asn	Gly	Val	Met	Asp	Thr	Thr	Ser	Ser	Leu	Ala	Asp
		100					105						110		
His	Gly	Val	Leu	Arg	Gln	Ala	Phe	Gln	Leu	Pro	Asn	Met	Asn	Trp	His
		115					120					125			
Ser															

(2) INFORMATION FOR SEQ ID NO:1214:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 718 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..718

(D) OTHER INFORMATION: / Ceres Seq. ID 1569338

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1214:

aattgaaaga	cggtgggggg	tttctcacta	ccagaaaatt	atcatcatcc	acagagaaaac	60
ccaaaagaga	ttgaagaaga	tgcattacat	gggtttgttt	agtagagctg	gaaacatatt	120
taggcagcct	agagcgtttg	aggcctcaaa	cgctatgtta	cagggcaatc	tttcatat	180
tccatccaaa	atctttgttg	gaggtctctc	accatctact	gatgtggagc	tcttgaaaga	240
agcttttggc	agttttggaa	aaattgttga	tgcggtagtg	gttttggacc	gtgaaagtgg	300
tttatcaagg	ggctttgggt	tcgtaacata	tgattcgatc	gaagttgcta	ataacgcaat	360
cgaaagctatg	caaaaataagg	agcttgatgg	gcgaataatt	ggagtgcatc	cagctgattc	420
agghgtgtgt	nggsggyvgt	ggtgggtttg	caagaagggg	aggttatggt	ggtggtcggt	480
ggggatagtc	tcgtgggtga	tttggtcgcg	gtggatttgg	tgggtggtgc	tatggcttgg	540
ttcgttaact	ggacatccag	atatgtctac	gcgcaagatt	gattagctctg	tggtttaatt	600
ttctcttcac	aaagaccact	attttgttat	aacaacgctc	ttatgcttga	acaaacatat	660
caagcggtga	aagttggcaa	aaacatttgt	tgattcaatt	ggtattttgat	acaaattc	

(2) INFORMATION FOR SEQ ID NO:1215:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 194 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..194

(D) OTHER INFORMATION: / Ceres Seq. ID 1569339

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1215:

Ile	Glu	Arg	Arg	Trp	Gly	Val	Ser	His	Tyr	Pro	Glu	Ile	Ile	Ile	Ile	
1			5						10				15			
His	Arg	Glu	Thr	Gln	Lys	Arg	Leu	Lys	Lys	Met	His	Tyr	Met	Gly	Leu	
			20						25				30			
Phe	Ser	Arg	Ala	Gly	Asn	Ile	Phe	Arg	Gln	Pro	Arg	Ala	Leu	Gln	Ala	
			35						40				45			
Ser	Asn	Ala	Met	Leu	Gln	Gly	Asn	Leu	Ser	Leu	Thr	Pro	Ser	Lys	Ile	
			50						55				60			
Phe	Val	Gly	Gly	Leu	Ser	Pro	Ser	Thr	Asp	Val	Glu	Leu	Leu	Lys	Glu	
			65						70				75		80	
Ala	Phe	Gly	Ser	Phe	Gly	Lys	Ile	Val	Asp	Ala	Val	Val	Val	Leu	Asp	
			85						90				95			
Arg	Glu	Ser	Gly	Leu	Ser	Arg	Gly	Phe	Gly	Phe	Val	Thr	Tyr	Asp	Ser	
			100						105				110			
Ile	Glu	Val	Ala	Asn	Asn	Ala	Met	Gln	Ala	Met	Gln	Asn	Lys	Glu	Leu	
			115						120				125			
Asp	Gly	Arg	Ile	Ile	Gly	Val	His	Pro	Ala	Asp	Ser	Xaa	Xaa	Gly	Xaa	
			130						135				140			
Xaa	Xaa	Trp	Trp	Phe	Cys	Lys	Lys	Gly	Arg	Leu	Trp	Trp	Trp	Ser	Trp	
			145						150				155		160	
Gly	Ile	Cys	Ser	Trp	Trp	Ile	Trp	Ser	Arg	Trp	Ile	Trp	Trp	Trp	Trp	
			165						170				175			
Leu	Trp	Leu	Cys	Ser	Leu	Thr	Gly	His	Pro	Asp	Met	Ser	Thr	Ala	Lys	
			180						185				190			
Ile	Asp															

(2) INFORMATION FOR SEQ ID NO:1216:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 168 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..168
 (D) OTHER INFORMATION: / Ceres Seq. ID 1569340
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1216:
Met His Tyr Met Gly Leu Phe Ser Arg Ala Gly Asn Ile Phe Arg Gln
1 5 10 15
Pro Arg Ala Leu Gln Ala Ser Asn Ala Met Leu Gln Gly Asn Leu Ser
 20 25 30
Leu Thr Pro Ser Lys Ile Phe Val Gly Gly Leu Ser Pro Ser Thr Asp
 35 40 45
Val Glu Leu Leu Lys Glu Ala Phe Gly Ser Phe Gly Lys Ile Val Asp
50 55 60
Ala Val Val Val Leu Asp Arg Glu Ser Gly Leu Ser Arg Gly Phe Gly
65 70 75 80
Phe Val Thr Tyr Asp Ser Ile Glu Val Ala Asn Asn Ala Met Gln Ala
 85 90 95
Met Gln Asn Lys Glu Leu Asp Gly Arg Ile Ile Gly Val His Pro Ala
 100 105 110
Asp Ser Xaa Xaa Gly Xaa Xaa Xaa Trp Trp Phe Cys Lys Lys Gly Arg
 115 120 125
Leu Trp Trp Trp Ser Trp Gly Ile Cys Ser Trp Trp Ile Trp Ser Arg
130 135 140
Trp Ile Trp Trp Trp Trp Leu Trp Leu Cys Ser Leu Thr Gly His Pro
145 150 155 160
Asp Met Ser Thr Ala Lys Ile Asp
 165
(2) INFORMATION FOR SEQ ID NO:1217:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 165 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..165
 (D) OTHER INFORMATION: / Ceres Seq. ID 1569341
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1217:
Met Gly Leu Phe Ser Arg Ala Gly Asn Ile Phe Arg Gln Pro Arg Ala
1 5 10 15
Leu Gln Ala Ser Asn Ala Met Leu Gln Gly Asn Leu Ser Leu Thr Pro
 20 25 30
Ser Lys Ile Phe Val Gly Gly Leu Ser Pro Ser Thr Asp Val Glu Leu
 35 40 45
Leu Lys Glu Ala Phe Gly Ser Phe Gly Lys Ile Val Asp Ala Val Val
50 55 60
Val Leu Asp Arg Glu Ser Gly Leu Ser Arg Gly Phe Gly Phe Val Thr
65 70 75 80
Tyr Asp Ser Ile Glu Val Ala Asn Asn Ala Met Gln Ala Met Gln Asn
 85 90 95
Lys Glu Leu Asp Gly Arg Ile Ile Gly Val His Pro Ala Asp Ser Xaa
 100 105 110
Xaa Gly Xaa Xaa Xaa Trp Trp Phe Cys Lys Lys Gly Arg Leu Trp Trp
 115 120 125
Trp Ser Trp Gly Ile Cys Ser Trp Trp Ile Trp Ser Arg Trp Ile Trp
130 135 140
Trp Trp Trp Leu Trp Leu Cys Ser Leu Thr Gly His Pro Asp Met Ser
145 150 155 160

Thr Ala Lys Ile Asp
165

(2) INFORMATION FOR SEQ ID NO:1218:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1242 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1242

(D) OTHER INFORMATION: / Ceres Seq. ID 1569354

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1218:

gactacgaaa	tagaatcaag	ttgtgttctc	tgtgatggac	attgtgttag	tggtaataca	60
atccgggtgaa	aatggagcgg	gGccgagtg	ccagagaagc	accgaccgga	accggatgcc	120
tgcttctgttc	actctctgcg	atggttgacg	agtcagttac	gtttccgatt	gatctcacia	180
agactagaat	cgagctccat	gggtcgggat	ccgcttctgg	tgcgcgatcg	attggcgctt	240
tcggagtcgt	atcgagagatt	gcgagaaaag	aaggagtgat	tggtctctac	aaaggctcat	300
ctccggcgat	tatcagacac	ctgttctaca	cgcttatcag	aatcattgga	tacgagaatt	360
tgaaaggact	catcgtcaga	tctgaaacta	acaatagcga	gtctcttctc	ctcgccacaa	420
aggctctcgt	cggaggattt	tctggtgtta	tagctcagaa	atgcaggtag	tggctagtcc	480
agctgatttg	gtcaaaagtga	gaatgcgaag	agatggtaga	ttggtgagcc	aaggcctgaa	540
accgaggtac	tcggggaccaa	tcgaggtctt	tacccaaaatc	ctacaatcag	aaggagtaaa	600
agggttatgg	aaaggtgttc	ttccaaaacat	ccagagagca	tttctagtga	atatggggaga	660
actagcttgc	tatgatcaac	ccaaaacactt	tgctcatgat	aagaagattg	ctgaggataa	720
catttttgcg	cacactcttg	cttctataat	gtccggtctt	gcttcgacaa	gtttgagttg	780
tcacagctgt	gtggtgaaga	cgaggatgat	gaaccagggt	gaaaatgctg	gtacacagaa	840
ttcttaacag	tgtttggtga	agacggttaa	gtttgaagga	ataagagctt	tgtggaaagg	900
ttcttccccc	acatggggcaa	ggcttggaac	gtggcagttc	gtgttttggg	tctctatga	960
gaagtttaga	ctgctggcag	gaatctcttc	cttctagacc	tgagaaacctg	gaagaagcaaa	1020
tttgagattt	gtgtttctta	gttcttaact	gtttagtgtt	acacattttg	taagaacctt	1080
gagaaagtac	atcagttttc	gattaaacgcg	agaagagtta	tataaaattg	ggcccaaaaag	1140
tgtagggcca	tagattttac	attttttttt	tggttgattaa	attagattgg	acatcctaag	1200
caaaaaaata	ttttaaaaag	taagagatta	ataaaatatt	cc		

(2) INFORMATION FOR SEQ ID NO:1219:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 132 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..132

(D) OTHER INFORMATION: / Ceres Seq. ID 1569355

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1219:

Met	Glu	Arg	Ser	Arg	Val	Thr	Arg	Glu	Ala	Pro	Thr	Gly	Thr	Arg	Ile	
1					5				10					15		
Leu	Leu	Ala	Ser	Leu	Ser	Ala	Met	Val	Ala	Glu	Ser	Val	Thr	Phe	Pro	
		20						25					30			
Ile	Asp	Leu	Thr	Lys	Thr	Arg	Met	Gln	Leu	His	Gly	Ser	Gly	Ser	Ala	
		35					40					45				
Ser	Gly	Ala	His	Arg	Ile	Gly	Ala	Phe	Gly	Val	Val	Ser	Glu	Ile	Ala	
		50				55				60						
Arg	Lys	Glu	Gly	Val	Ile	Gly	Leu	Tyr	Lys	Gly	Leu	Ser	Pro	Ala	Ile	
		65			70				75					80		
Ile	Arg	His	Leu	Phe	Tyr	Thr	Pro	Ile	Arg	Ile	Ile	Gly	Tyr	Glu	Asn	
			85					90						95		
Leu	Lys	Gly	Leu	Ile	Val	Arg	Ser	Glu	Thr	Asn	Asn	Ser	Glu	Ser	Leu	
			100					105						110		

Pro Leu Ala Thr Lys Ala Leu Val Gly Gly Phe Ser Gly Val Ile Ala
115 120 125
Gln Lys Cys Arg
130

(2) INFORMATION FOR SEQ ID NO:1220:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 178 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..178
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569356

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1220:

Met	Gln	Val	Val	Ala	Ser	Pro	Ala	Asp	Leu	Val	Lys	Val	Arg	Met	Gln	
1					5						10			15		
Ala	Asp	Gly	Arg	Gly	Leu	Val	Ser	Gln	Gly	Leu	Lys	Pro	Arg	Tyr	Ser	Gly
					20				25					30		
Pro	Ile	Glu	Ala	Phe	Thr	Lys	Ile	Leu	Gln	Ser	Glu	Gly	Val	Lys	Gly	
		35					40						45			
Leu	Trp	Lys	Gly	Val	Leu	Pro	Asn	Ile	Gln	Arg	Ala	Phe	Leu	Val	Asn	
	50					55					60					
Met	Gly	Glu	Leu	Ala	Cys	Tyr	Asp	His	Ala	Lys	His	Phe	Val	Ile	Asp	
65					70					75				80		
Lys	Lys	Ile	Ala	Glu	Asp	Asn	Ile	Phe	Ala	His	Thr	Leu	Ala	Ser	Ile	
				85					90					95		
Met	Ser	Gly	Leu	Ala	Ser	Thr	Ser	Leu	Ser	Cys	Pro	Ala	Asp	Val	Val	
			100					105					110			
Lys	Thr	Arg	Met	Met	Asn	Gln	Gly	Glu	Asn	Ala	Val	Tyr	Arg	Asn	Ser	
		115				120						125				
Tyr	Asp	Cys	Leu	Val	Lys	Thr	Val	Lys	Phe	Glu	Gly	Ile	Arg	Ala	Leu	
	130					135					140					
Trp	Lys	Gly	Phe	Phe	Pro	Thr	Trp	Ala	Arg	Leu	Gly	Pro	Trp	Gln	Phe	
145					150					155				160		
Val	Phe	Trp	Val	Ser	Tyr	Glu	Lys	Phe	Arg	Leu	Leu	Ala	Gly	Ile	Ser	
				165					170					175		

Ser Phe

(2) INFORMATION FOR SEQ ID NO:1221:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 164 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..164
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569357

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1221:

Met	Gln	Ala	Asp	Gly	Arg	Leu	Val	Ser	Gln	Gly	Leu	Lys	Pro	Arg	Tyr	
1					5				10					15		
Ser	Gly	Pro	Ile	Glu	Ala	Phe	Thr	Lys	Ile	Leu	Gln	Ser	Glu	Gly	Val	
				20				25					30			
Lys	Gly	Leu	Trp	Lys	Gly	Val	Leu	Pro	Asn	Ile	Gln	Arg	Ala	Phe	Leu	
		35				40						45				
Val	Asn	Met	Gly	Glu	Leu	Ala	Cys	Tyr	Asp	His	Ala	Lys	His	Phe	Val	
	50					55				60						
Ile	Asp	Lys	Lys	Ile	Ala	Glu	Asp	Asn	Ile	Phe	Ala	His	Thr	Leu	Ala	

65	70	75	80
Ser Ile Met Ser Gly Leu Ala Ser Thr Ser Leu Ser Cys Pro Ala Asp			
	85	90	95
Val Val Lys Thr Arg Met Met Asn Gln Gly Glu Asn Ala Val Tyr Arg			
	100	105	110
Asn Ser Tyr Asp Cys Leu Val Lys Thr Val Lys Phe Glu Gly Ile Arg			
	115	120	125
Ala Leu Trp Lys Gly Phe Phe Pro Thr Trp Ala Arg Leu Gly Pro Trp			
	130	135	140
Gln Phe Val Phe Trp Val Ser Tyr Glu Lys Phe Arg Leu Leu Ala Gly			
	145	150	155
Ile Ser Ser Phe			160

(2) INFORMATION FOR SEQ ID NO:1222:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1595 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1595
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569358

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1222:

acaagagcca	tttgcaatta	ggcataatat	atgtcctaac	tcaccaaccc	octcaaaatt	60
gccaccaact	tcaaatcttc	ctccctttaa	cccttctcaa	tcattcttct	tctgcttgg	120
aatcctgac	atggcgctct	ctccacttc	caaatccatt	ctcggatcca	ccaaaccogg	180
ttctctctct	cttccctcgg	agctccgtcg	tctttcttct	cccgccgttc	agatctctct	240
ccgtacccaa	accaggaaga	acttccagat	acaagctact	ggaagtctat	atggggactca	300
ttttgagtt	tcaacttttg	gagaatcaca	tggaggagga	gttggttgta	tcattgatgg	360
ttgtctctct	cgtattccac	ttaactgaat	tgatttgcaa	ttcgatctcg	atagaaggag	420
acctggtcac	agcaggatga	caactcctag	aaaggagact	gatacttgcc	ggatactctc	480
tgaggtctcc	gaaggaaatg	cgacaggaac	acctatccat	gtgtttgtgc	ctaacacaga	540
tcagagagga	cttgattaca	gtgaaatgtc	ggttgccat	agaccatgc	atgctgatgc	600
aacttatgac	atgaagtatg	gtgtcagatc	agtgcagggt	ggaggaaagt	cttcagctag	660
agagaccatt	ggaagagtgt	ctcctggagc	tttggccaa	aaaaatttga	agcaatttgc	720
aggaactgag	attcttgctc	atgtctcgca	agttcaccat	gttgtaacttc	cagaagaatt	780
ggtagaccac	gagaatttaa	cactcgaaac	gatagaaaa	aacattgtca	gagccctaa	840
tcccagatgt	cgggaaaaga	tgatagctgc	gattgatgct	gtcaggacaa	aagggaactc	900
tggttggtgt	gtttgtacct	cgattgttgc	gaatgctcca	ctcgggcttg	gtacaccgct	960
tttcgataaa	cttgaagcag	aactggtcaa	agcttgtatg	tcgttaacctg	caacaagggtg	1020
atttgagttt	ggaagcggct	tttcaggtac	ctttttgact	gtgtctgaac	acaatgatga	1080
gttctatacc	gcagaaatgt	gaagaataac	taccagaaca	aaccgatctg	gtggaaattca	1140
gggagggatc	tcaaatgggtg	aaataataaa	catgagagta	gccttcaagc	caacatcaac	1200
aattggaagg	aagcagaata	cgttaaccag	agacaaggta	gaaacccgaa	tgattgcgctg	1260
tggtgtcatc	gatccttggt	tgttctctcg	agctgtgcca	atggttgaat	caatggtggc	1320
tttagttctt	gtggatcaat	tgtatggcca	atacgacaaa	tgccatttgt	ttccaataaa	1380
tcacagtggt	caggaaacctc	tcacagatga	gcagccccaa	aatgctactg	cttttgtaag	1440
aaaactcgag	aagataaagag	tcagagacag	taaggYttcg	ctttgtgtgt	gtgattatta	1500
ttatgaataa	aaaaaatggt	aattttgtac	ccaccagaga	aacaaaaaac	atgatttttt	1560
tgtaacagga	tttgtactcta	tatcattatt	cagct			

(2) INFORMATION FOR SEQ ID NO:1223:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 478 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide

(D) OTHER INFORMATION: / Ceres Seq. ID 1569359

Protein	Sequence Block															Protein
	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	
Gln	Pro	Lys	Leu	Pro	Pro	Thr	Ser	Asn	Phe	Ser	Pro	Leu	Asn	Ser	Leu	Thr
1	20	35	50	65	80	95	110	125	140	155	170	185	200	215	230	245
Gln	Ser	Ser	Phe	Phe	Cys	Leu	Gly	Ile	Leu	Ile	Met	Ala	Ser	Ser	Ser	Leu
1	20	35	50	65	80	95	110	125	140	155	170	185	200	215	230	245
Thr	Ser	Lys	Ser	Ile	Leu	Gly	Ser	Thr	Lys	Pro	Gly	Val	Gln	Ile	Ser	Leu
1	20	35	50	65	80	95	110	125	140	155	170	185	200	215	230	245
Pro	Ser	Glu	Leu	Arg	Arg	Leu	Ser	Ser	Pro	Ala	Val	Gln	Ile	Ser	Leu	Thr
1	20	35	50	65	80	95	110	125	140	155	170	185	200	215	230	245
Arg	Thr	Gln	Thr	Arg	Lys	Asn	Phe	Gln	Ile	Gln	Ala	Thr	Gly	Ser	Ser	Leu
1	20	35	50	65	80	95	110	125	140	155	170	185	200	215	230	245
Tyr	Gly	Thr	His	Phe	Arg	Val	Ser	Thr	Phe	Gly	Glu	Ser	His	Gly	Gly	Thr
1	20	35	50	65	80	95	110	125	140	155	170	185	200	215	230	245
Gly	Val	Gly	Cys	Ile	Ile	Asp	Gly	Cys	Pro	Pro	Arg	Ile	Pro	Leu	Thr	Thr
1	20	35	50	65	80	95	110	125	140	155	170	185	200	215	230	245
Glu	Ser	Asp	Leu	Gln	Phe	Asp	Leu	Asp	Arg	Arg	Arg	Pro	Gly	Gln	Ser	Thr
1	20	35	50	65	80	95	110	125	140	155	170	185	200	215	230	245
Arg	Ile	Thr	Thr	Pro	Arg	Lys	Glu	Thr	Asp	Thr	Cys	Arg	Ile	Ser	Ser	Thr
1	20	35	50	65	80	95	110	125	140	155	170	185	200	215	230	245
Gly	Val	Ser	Glu	Gly	Met	Thr	Thr	Gly	Thr	Pro	Ile	His	Val	Phe	Val	Thr
1	20	35	50	65	80	95	110	125	140	155	170	185	200	215	230	245
Pro	Asn	Thr	Asp	Gln	Arg	Gly	Leu	Asp	Tyr	Ser	Glu	Met	Ser	Val	Ala	Thr
1	20	35	50	65	80	95	110	125	140	155	170	185	200	215	230	245
Tyr	Arg	Pro	Ser	His	Ala	Asp	Ala	Thr	Tyr	Asp	Met	Lys	Tyr	Gly	Val	Thr
1	20	35	50	65	80	95	110	125	140	155	170	185	200	215	230	245
Arg	Ser	Val	Gln	Ser	Gly	Gly	Gly	Arg	Ser	Ser	Ala	Arg	Glu	Thr	Ile	Gly
1	20	35	50	65	80	95	110	125	140	155	170	185	200	215	230	245
Arg	Val	Ala	Pro	Gly	Ala	Leu	Ala	Lys	Lys	Ile	Leu	Lys	Gln	Phe	Ala	Thr
1	20	35	50	65	80	95	110	125	140	155	170	185	200	215	230	245
Gly	Thr	Glu	Ile	Leu	Ala	Tyr	Val	Ser	Gln	Val	His	His	Val	Val	Leu	Thr
1	20	35	50	65	80	95	110	125	140	155	170	185	200	215	230	245
Pro	Glu	Glu	Leu	Val	Asp	His	Glu	Asn	Leu	Thr	Leu	Glu	Gln	Ile	Glu	Thr
1	20	35	50	65	80	95	110	125	140	155						

Glu Pro Leu Gln Ile Glu Gln Pro Gln Asn Ala Thr Ala Leu
465 470 475

(2) INFORMATION FOR SEQ ID NO:1224:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 435 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..435

(D) OTHER INFORMATION: / Ceres Seq. ID 1569360

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1224:

Met	Ala	Ser	Ser	Leu	Thr	Ser	Lys	Ser	Ile	Leu	Gly	Ser	Thr	Lys	Pro
1			5						10					15	
Gly	Ser	Ser	Ser	Leu	Pro	Ser	Glu	Leu	Arg	Arg	Leu	Ser	Ser	Pro	Ala
			20					25					30		
Val	Gln	Ile	Ser	Leu	Arg	Thr	Gln	Thr	Arg	Lys	Asn	Phe	Gln	Ile	Gln
			35				40					45			
Ala	Thr	Gly	Ser	Ser	Tyr	Gly	Thr	His	Phe	Arg	Val	Ser	Thr	Phe	Gly
			50			55					60				
Glu	Ser	His	Gly	Gly	Gly	Val	Gly	Cys	Ile	Ile	Asp	Gly	Cys	Pro	Pro
					70					75				80	
Arg	Ile	Pro	Leu	Thr	Glu	Ser	Asp	Leu	Gln	Phe	Asp	Leu	Asp	Arg	Arg
				85				90						95	
Arg	Pro	Gly	Gln	Ser	Arg	Ile	Thr	Thr	Pro	Arg	Lys	Glu	Thr	Asp	Thr
				100				105						110	
Cys	Arg	Ile	Ser	Ser	Gly	Val	Ser	Glu	Gly	Met	Thr	Thr	Gly	Thr	Pro
				115			120						125		
Ile	His	Val	Phe	Val	Pro	Asn	Thr	Asp	Gln	Arg	Gly	Leu	Asp	Tyr	Ser
				130			135				140				
Glu	Met	Ser	Val	Ala	Tyr	Arg	Pro	Ser	His	Ala	Asp	Ala	Thr	Tyr	Asp
					145					155					160
Met	Lys	Tyr	Gly	Val	Arg	Ser	Val	Gln	Gly	Gly	Gly	Arg	Ser	Ser	Ala
				165					170					175	
Arg	Glu	Thr	Ile	Gly	Arg	Val	Ala	Pro	Gly	Ala	Leu	Ala	Lys	Lys	Ile
				180				185					190		
Leu	Lys	Gln	Phe	Ala	Gly	Thr	Glu	Ile	Leu	Ala	Tyr	Val	Ser	Gln	Val
				195			200					205			
His	His	Val	Val	Leu	Pro	Glu	Glu	Leu	Val	Asp	His	Glu	Asn	Leu	Thr
				210			215				220				
Leu	Glu	Gln	Ile	Glu	Asn	Asn	Ile	Val	Arg	Cys	Pro	Asn	Pro	Glu	Tyr
					225					235					240
Ala	Glu	Lys	Met	Ile	Ala	Ala	Ile	Asp	Ala	Val	Arg	Thr	Lys	Gly	Asn
				245				250						255	
Ser	Val	Gly	Gly	Val	Val	Thr	Cys	Ile	Val	Arg	Asn	Ala	Pro	Arg	Gly
				260			265						270		
Leu	Gly	Thr	Pro	Val	Phe	Asp	Lys	Leu	Glu	Ala	Glu	Leu	Ala	Lys	Ala
				275			280					285			
Cys	Met	Ser	Leu	Pro	Ala	Thr	Lys	Gly	Phe	Glu	Phe	Gly	Ser	Gly	Phe
				290			295				300				
Ala	Gly	Thr	Phe	Leu	Thr	Gly	Leu	Glu	His	Asn	Asp	Glu	Phe	Tyr	Thr
					305					315					320
Asp	Glu	Asn	Gly	Arg	Ile	Arg	Thr	Arg	Thr	Asn	Arg	Ser	Gly	Gly	Ile
				325					330					335	
Gln	Gly	Gly	Ile	Ser	Asn	Gly	Glu	Ile	Ile	Asn	Met	Arg	Val	Ala	Phe
				340				345					350		
Lys	Pro	Thr	Ser	Thr	Ile	Gly	Arg	Lys	Gln	Asn	Thr	Val	Thr	Arg	Asp
				355			360					365			
Lys	Val	Glu	Thr	Glu	Met	Ile	Ala	Arg	Gly	Arg	His	Asp	Pro	Cys	Val

370	375	380	
Val Pro Arg Ala Val	Pro Met Val Glu Ser Met Val Ala Leu Val Leu		
385	390	395	400
Val Asp Gln Leu Met	Ala Gln Tyr Ala Gln Cys His Leu Phe Pro Ile		
	405	410	415
Asn Pro Glu Leu Gln	Glu Pro Leu Gln Ile Glu Gln Pro Gln Asn Ala		
	420	425	430
Thr Ala Leu			
435			

(2) INFORMATION FOR SEQ ID NO:1225:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 313 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..313

(D) OTHER INFORMATION: / Ceres Seq. ID 1569361

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1225:

Met Thr Thr Gly Thr Pro Ile His Val Phe Val Pro Asn Thr Asp Gln	
1	5
Arg Gly Leu Asp Tyr Ser Glu Met Ser Val Ala Tyr Arg Pro Ser His	
	20
Ala Asp Ala Thr Tyr Asp Met Lys Tyr Gly Val Arg Ser Val Gln Gly	
	35
Gly Gly Arg Ser Ser Ala Arg Glu Thr Ile Gly Arg Val Ala Pro Gly	
	50
Ala Leu Ala Lys Lys Ile Leu Lys Gln Phe Ala Gly Thr Glu Ile Leu	
65	70
Ala Tyr Val Ser Gln Val His His Val Val Leu Pro Glu Glu Leu Val	
	85
Asp His Glu Asn Leu Thr Leu Glu Gln Ile Glu Asn Asn Ile Val Arg	
	100
Cys Pro Asn Pro Glu Tyr Ala Glu Lys Met Ile Ala Ala Ile Asp Ala	
	115
Val Arg Thr Lys Gly Asn Ser Val Gly Gly Val Val Thr Cys Ile Val	
	130
Arg Asn Ala Pro Arg Gly Leu Gly Thr Pro Val Phe Asp Lys Leu Glu	
145	150
Ala Glu Leu Ala Lys Ala Cys Met Ser Leu Pro Ala Thr Lys Gly Phe	
	165
Glu Phe Gly Ser Gly Phe Ala Gly Thr Phe Leu Thr Gly Leu Glu His	
	180
Asn Asp Glu Phe Tyr Thr Asp Glu Asn Gly Arg Ile Arg Thr Arg Thr	
	195
Asn Arg Ser Gly Gly Ile Gln Gly Gly Ile Ser Asn Gly Glu Ile Ile	
	210
Asn Met Arg Val Ala Phe Lys Pro Thr Ser Thr Ile Gly Arg Lys Gln	
225	230
Asn Thr Val Thr Arg Asp Lys Val Glu Thr Glu Met Ile Ala Arg Gly	
	245
Arg His Asp Pro Cys Val Val Pro Arg Ala Val Pro Met Val Glu Ser	
	260
Met Val Ala Leu Val Leu Val Asp Gln Leu Met Ala Gln Tyr Ala Gln	
	275
Cys His Leu Phe Pro Ile Asn Pro Glu Leu Gln Glu Pro Leu Gln Ile	
	290
Glu Gln Pro Gln Asn Ala Thr Ala Leu	
305	310

(2) INFORMATION FOR SEQ ID NO:1226:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 925 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..925
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569370

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1226:

acaacacaaa	acaagaacaa	cagacacata	gagatgagcc	gctgcggctc	tottgggctc	60
tatgccccaa	atgctttgcc	atctctctcc	ttgaagccac	gcagtttcaa	atctccttcc	120
tgtattacat	ctcacaccaa	accccaacac	actcttcttc	ataatgttaa	caagatgaga	180
gcaaaaggcc	gtgatatact	tggagcaaa	aagacaatct	tggcagctca	actcggggca	240
gttcttgcca	cgattgacca	tccagcctta	gcaataacag	gagttaacaa	ccagcaggaa	300
ttgagcagtg	ttgtgctcga	tatcgggatc	atatccgttt	ggatcttcc	agtaatgcca	360
ccaatcatca	tgaactggct	aagagtaaga	tggtagacaa	ggaagattag	aacttgcaaa	420
aaatggcttc	caaggctttg	attctgttag	gtctcttctc	agttcttctc	gtcgtctccg	480
aagtgtctgc	cgcaaggCaa	Wtcgggcatg	gtgaagcCag	agagtGagg	aaactgtgca	540
Acctgaagtg	tatgtcgggtR	GScCacggag	gacatggtgg	tcacggaggg	ggaggaggcc	600
acggacatgg	aggacacaac	ggaggagggg	gccacggact	tgacggatac	ggaggagggtg	660
gaggacacta	tggaggaggt	ggaggacact	acggaggagg	tggaggacac	tacggaggag	720
gtggaggaca	ctacggagga	ggtggtggag	gacacggagg	tggaggacac	tacggagggtg	780
gtggaggagg	atacggaggt	ggaggaggac	accacggagg	aggaggccac	gggctaaacg	840
aacctgttca	gactaagcgg	ggtgtttaa	actatataat	atcttcta	ccatgcatga	900
ttgcataat	atatatacgs	ttatg				

(2) INFORMATION FOR SEQ ID NO:1227:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 146 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..146
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569371

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1227:

Thr	Thr	Lys	Asn	Lys	Asn	Asn	Arg	His	Ile	Glu	Met	Ser	Arg	Cys	Gly
1			5						10					15	
Ser	Leu	Gly	Leu	Tyr	Ala	Pro	Asn	Ala	Leu	Pro	Ser	Leu	Ser	Leu	Lys
			20					25					30		
Pro	Arg	Ser	Phe	Lys	Ser	Pro	Phe	Cys	Ile	Thr	Ser	His	Thr	Lys	Pro
			35				40					45			
Asn	Asp	Thr	Leu	Leu	His	Asn	Val	Asn	Lys	Met	Arg	Ala	Lys	Ala	Cys
	50					55					60				
Asp	Ile	Leu	Gly	Ala	Lys	Lys	Thr	Ile	Leu	Ala	Ala	Gln	Leu	Gly	Ala
65				70					75					80	
Val	Leu	Ala	Thr	Ile	Asp	His	Pro	Ala	Leu	Ala	Ile	Thr	Gly	Val	Asn
			85						90					95	
Asn	Gln	Gln	Glu	Leu	Ser	Ser	Val	Val	Leu	Asp	Ile	Gly	Ile	Ile	Ser
			100					105					110		
Val	Trp	Tyr	Phe	Leu	Val	Met	Pro	Pro	Ile	Ile	Met	Asn	Trp	Leu	Arg
		115						120				125			
Val	Arg	Trp	Tyr	Arg	Arg	Lys	Ile	Arg	Thr	Cys	Lys	Lys	Trp	Leu	Pro
	130					135					140				
Arg	Leu														
145															

(2) INFORMATION FOR SEQ ID NO:1228:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 135 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..135
(D) OTHER INFORMATION: / Ceres Seq. ID 1569372
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1228:
Met Ser Arg Cys Gly Ser Leu Gly Leu Tyr Ala Pro Asn Ala Leu Pro
1 5 10 15
Ser Leu Ser Leu Lys Pro Arg Ser Phe Lys Ser Pro Phe Cys Ile Thr
20 25 30
Ser His Thr Lys Pro Asn Asp Thr Leu Leu His Asn Val Asn Lys Met
35 40 45
Arg Ala Lys Ala Cys Asp Ile Leu Gly Ala Lys Lys Thr Ile Leu Ala
50 55 60
Ala Gln Leu Gly Ala Val Leu Ala Thr Ile Asp His Pro Ala Leu Ala
65 70 75 80
Ile Thr Gly Val Asn Asn Gln Gln Glu Leu Ser Ser Val Val Leu Asp
85 90 95
Ile Gly Ile Ile Ser Val Trp Tyr Phe Leu Val Met Pro Pro Ile Ile
100 105 110
Met Asn Trp Leu Arg Val Arg Trp Tyr Arg Arg Lys Ile Arg Thr Cys
115 120 125
Lys Lys Trp Leu Pro Arg Leu
130 135
(2) INFORMATION FOR SEQ ID NO:1229:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 148 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..148
(D) OTHER INFORMATION: / Ceres Seq. ID 1569373
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1229:
Met Ala Ser Lys Ala Leu Ile Leu Leu Gly Leu Phe Ser Val Leu Leu
1 5 10 15
Val Val Ser Glu Val Ser Ala Ala Arg Gln Xaa Gly His Gly Glu Ala
20 25 30
Arg Glu Trp Arg Lys Leu Cys Asn Leu Lys Val Met Ala Xaa Xaa His
35 40 45
Gly Gly His Gly Gly His Gly Gly Gly Gly His Gly His Gly Gly
50 55 60
His Asn Gly Gly Gly Gly His Gly Leu Asp Gly Tyr Gly Gly Gly Gly
65 70 75 80
Gly His Tyr Gly Gly Gly Gly His Tyr Gly Gly Gly Gly Gly His
85 90 95
Tyr Gly Gly Gly Gly His Tyr Gly Gly Gly Gly Gly His Gly
100 105 110
Gly Gly Gly His Tyr Gly Gly Gly Gly Tyr Gly Gly Gly Gly
115 120 125
Gly His His Gly Gly Gly His Gly Leu Asn Glu Pro Val Gln Thr
130 135 140
Lys Pro Gly Val
145

(2) INFORMATION FOR SEQ ID NO:1230:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 810 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..810
(D) OTHER INFORMATION: / Ceres Seq. ID 1569378

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1230:

agaacaaaac	aaacaaaaag	tcattgtctc	gacgacgaca	tcgttacgat	ccctaagcgt	60
ctcgcgtttac	gctctcttcta	attctactcc	gatttctaca	ccaattgagg	cccgacagtt	120
actgagttca	tgcagtagat	tctacggctc	gtctctcttc	agctctcttc	cctccctcac	180
tacttcatct	ttgatcgga	atcttgtttt	ctcatcaagg	aatcagttct	tctcgttaaa	240
gggtccaaagc	ttatgtctga	aacogaacag	ccaaaatggt	gggagaggaa	agcaggggcca	300
aacatgattg	acattacctc	agctgagcag	tttctcaacg	cgtttaaaga	tgcggggagat	360
agattagtta	tctgtagattt	ttacggaaat	tgggtgtggt	cttgccgtgc	aatgttccca	420
aagctctgca	aaacggcgaa	agaacaccc	gacatcttgt	tctctaaagt	aaactttgac	480
gagaacaagt	ctctctgcaa	aagcttaaac	gtcaagggtg	taccgtattt	ccacttctac	540
cgcggtgctg	atggccaagt	ogaatccttc	tcattgtctc	ttgccaaagt	ccagaaactg	600
agagagcgca	tagagagaca	caatgtagga	agtatcagta	acatctcttc	ttcagctctc	660
gagaaagtgt	aagattcaag	tgaataatca	atgctcgtgt	cagattgatc	acagattatt	720
tgtttaaatc	gcttccctgt	atatatgttg	atcgtatttt	ccatgtgggt	catcataatt	780
ttgtacata	aataaatgag	tctgacttgc				

(2) INFORMATION FOR SEQ ID NO:1231:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 101 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..101
(D) OTHER INFORMATION: / Ceres Seq. ID 1569379

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1231:

Glu	Gln	Asn	Lys	Gln	Lys	Val	Met	Ser	Pro	Thr	Thr	Ser	Leu	Arg
1				5					10				15	
Ser	Leu	Ser	Phe	Ser	Leu	Tyr	Ala	Ser	Ser	Asn	Ser	Thr	Pro	Ile
				20					25				30	Ser
Thr	Pro	Ile	Glu	Ala	Arg	Gln	Leu	Leu	Ser	Ser	Cys	Ser	Arg	Phe
				35					40				45	Tyr
Gly	Leu	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Leu	Thr	Thr	Ser	Ser	Leu
									55				60	
Ile	Gly	Asn	Leu	Val	Phe	Ser	Ser	Arg	Asn	Gln	Ser	Leu	Ser	Val
									70				75	Lys
Val	Gln	Ala	Leu	Xaa	Leu	Lys	Pro	Asn	Ser	Gln	Asn	Gly	Gly	Arg
									85				90	Gly
Lys	Gln	Gly	Gln	Thr										
														100

(2) INFORMATION FOR SEQ ID NO:1232:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 94 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide

(B) LOCATION: 1..94

(D) OTHER INFORMATION: / Ceres Seq. ID 1569380

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1232:

Met	Ser	Pro	Thr	Thr	Thr	Ser	Leu	Arg	Ser	Leu	Ser	Phe	Ser	Leu	Tyr
1			5					10						15	
Ala	Ser	Ser	Asn	Ser	Thr	Pro	Ile	Ser	Thr	Pro	Ile	Glu	Ala	Arg	Gln
			20					25						30	
Leu	Leu	Ser	Ser	Cys	Ser	Arg	Phe	Tyr	Gly	Leu	Ser	Ser	Ser	Ser	Ser
			35					40						45	
Ser	Ser	Ser	Leu	Thr	Thr	Ser	Ser	Leu	Ile	Gly	Asn	Leu	Val	Phe	Ser
			50					55						60	
Ser	Arg	Asn	Gln	Ser	Leu	Ser	Val	Lys	Val	Gln	Ala	Leu	Xaa	Leu	Lys
			65					70						75	
Pro	Asn	Ser	Gln	Asn	Gly	Gly	Arg	Gly	Lys	Gln	Gly	Gln	Thr		80
			85						90						

(2) INFORMATION FOR SEQ ID NO:1233:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 127 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..127

(D) OTHER INFORMATION: / Ceres Seq. ID 1569381

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1233:

Met	Ile	Asp	Ile	Thr	Ser	Ala	Glu	Gln	Phe	Leu	Asn	Ala	Leu	Lys	Asp
1				5					10					15	
Ala	Gly	Asp	Arg	Leu	Val	Ile	Val	Asp	Phe	Tyr	Gly	Thr	Trp	Cys	Gly
			20					25						30	
Ser	Cys	Arg	Ala	Met	Phe	Pro	Lys	Leu	Cys	Lys	Thr	Ala	Lys	Glu	His
			35					40						45	
Pro	Asp	Ile	Leu	Phe	Leu	Lys	Val	Asn	Phe	Asp	Glu	Asn	Lys	Ser	Leu
			50					55						60	
Cys	Lys	Ser	Leu	Asn	Val	Lys	Val	Leu	Pro	Tyr	Phe	His	Phe	Tyr	Arg
			65					70						75	
Gly	Ala	Asp	Gly	Gln	Val	Glu	Ser	Phe	Ser	Cys	Ser	Leu	Ala	Lys	Phe
			85					90						95	
Gln	Lys	Leu	Arg	Glu	Ala	Ile	Glu	Arg	His	Asn	Val	Gly	Ser	Ile	Ser
			100					105						110	
Asn	Ile	Ser	Ser	Ser	Ala	Ser	Glu	Lys	Val	Glu	Asp	Ser	Ser	Glu	
			115					120						125	

(2) INFORMATION FOR SEQ ID NO:1234:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1854 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1854

(D) OTHER INFORMATION: / Ceres Seq. ID 1569385

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1234:

atatactttc	tctgtttaca	ttctgttttc	cgaggagaaa	agtctgcgac	ttctgtgatct	60
ggggttttgt	ttgggtttggg	gttgactcgg	ttttgactcg	ggacaaagtcg	tctcgtgaga	120
tgatgtcttc	tcgttttatta	gtatctcttt	gagagtcgtg	ctttctgggt	tcaatagatt	180
cttatagttt	cgcttagaaa	cacgcacaaa	aagatgtcgt	tgaagcatca	tcacagagga	240
ttagagctct	ctgtcttgaa	gagttttgtc	tcaaagaagt	ggactttatt	tctctgtatc	300
ggtttcttct	gcgcaggaat	tctcttcttc	gacagaatgt	ggccagagcc	tgaatccaat	360

gttgatcaaa	gggacacagt	agcatcagat	gaacggctgc	ggttagagtc	tgaggactgt	420
gattcatcaa	aaaagggttt	taaagcgtga	atcgaaagac	atccttggag	atgtttacaa	480
gagtcacagt	gcaattcaaa	cgcttgataa	aacgatttca	aagctggaaa	cagaactggc	540
cgatgcgaag	gctgcgcaag	aattctatcat	gaatgggtca	ccagtttctg	atgactttaa	600
gctccctgaa	actgtcaacta	aaagaaaagta	tctgatgggt	gttgggtgta	atactgcgtt	660
tagcagcaga	aagcgcaggg	attcagtcgg	tgctacttgg	atgcctcccg	gtgaggagag	720
aaagaagctc	gaggaagaga	aagggatcgt	galgcgggtt	gtgataggcc	atagttctac	780
tcccgttgga	attcttgata	gagcgattca	ggctgaagaa	agataaacatg	gagacttctt	840
gaggtcgatg	catgttgaag	gttatctcga	gctgtcagca	aagactaaaa	cttactttac	900
cacggctttt	gcaatgtggg	atcgagactt	ctacgtcaaa	gtcgatgatg	atgtgcgatg	960
aaatatagcc	acgcttggag	cagaattagc	aagataccgg	atgaagcccc	gagtgatcat	1020
tggttgcatg	aaatctggac	ctgtttcttg	tcagaaaagga	gtgagatatt	atgaaccoga	1080
atactgtgaaa	tttggagaag	agggtaacaa	atacttcocg	catgccacag	gtcagctcta	1140
tgcaataatc	agggagttgg	cgctttacat	atcgataaac	caaaaactac	ttcacaaaata	1200
tgatgaatga	gatgtctctt	taggatcatg	gtttcttgga	ttagatgtgg	agcatgtaga	1260
tgaccgtagg	ctatgtttgtg	gtacacagaa	ttgtgagttg	aaggcgcagg	cgggcaacat	1320
ctgtgttgcc	tggttcgatt	ggagctgcag	tggtgattgt	agatcagcgg	ataggatgaa	1380
ggatgttcat	cgtaggtgtg	gagaaggtga	aaaggccott	ctggctgcac	ctttctgaaA	1440
cacaataact	aaagaaacac	attgaggaag	aagagtacag	agacaaaatcc	gctgcacagt	1500
ctacacttgg	tagtatagac	acacagtcac	actctctcta	tatatgtatg	tatgtatgta	1560
tgtagtcttc	ttgtgaactg	agatgagaag	ggtgcttttt	ggcctccctt	cttgtttctt	1620
tatgcttttc	tcaattctct	gaaggtctgg	agttctttgc	acacagaaaa	tcgagatttt	1680
agctgcaaaag	gcggactcca	tgagtgaccc	ttcagagtcca	tttcattgat	gcgtttcttc	1740
tgccctttga	gcttttcttc	ttcatttctt	tttgattttt	gcctattttg	ttcatttttt	1800
cccttgccat	gattgtgggt	aaacatgggt	tgtttatgtg	tgtacttgaa	acgc	

(2) INFORMATION FOR SEQ ID NO:1235:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 289 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..289

(D) OTHER INFORMATION: / Ceres Seq. ID 1569386

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1235:

Met	Asn	Gly	Ser	Pro	Val	Ser	Asp	Asp	Phe	Lys	Leu	Pro	Glu	Thr	Val
1			5						10					15	
Thr	Lys	Arg	Lys	Tyr	Leu	Met	Val	Val	Gly	Val	Asn	Thr	Ala	Phe	Ser
			20						25				30		
Ser	Arg	Lys	Lys	Arg	Arg	Asp	Ser	Val	Arg	Ala	Thr	Trp	Met	Pro	Gly
			35						40				45		
Glu	Glu	Arg	Lys	Lys	Leu	Glu	Glu	Glu	Lys	Gly	Ile	Val	Met	Arg	Phe
			50						55				60		
Val	Ile	Gly	His	Ser	Ser	Thr	Pro	Gly	Gly	Ile	Leu	Asp	Arg	Ala	Ile
			65						70				75		
Gln	Ala	Glu	Glu	Ser	Lys	His	Gly	Asp	Phe	Leu	Arg	Leu	Asp	His	Val
			85						90				95		
Glu	Gly	Tyr	Leu	Glu	Leu	Ser	Ala	Lys	Thr	Lys	Thr	Tyr	Phe	Thr	Thr
			100						105				110		
Ala	Phe	Ala	Met	Trp	Asp	Ala	Asp	Phe	Thr	Val	Lys	Val	Asp	Asp	Asp
			115						120				125		
Val	His	Val	Asn	Ile	Ala	Thr	Leu	Gly	Ala	Glu	Leu	Ala	Arg	Tyr	Arg
			130						135				140		
Met	Lys	Pro	Arg	Val	Tyr	Ile	Gly	Cys	Met	Lys	Ser	Gly	Pro	Val	Leu
			145						150				155		
Ala	Gln	Lys	Gly	Val	Arg	Tyr	His	Glu	Pro	Glu	Tyr	Trp	Lys	Phe	Gly
			165						170				175		
Glu	Glu	Gly	Asn	Lys	Tyr	Phe	Arg	His	Ala	Thr	Gly	Gln	Leu	Tyr	Ala
			180						185				190		

Ile	Ser	Arg	Glu	Leu	Ala	Ser	Tyr	Ile	Ser	Ile	Asn	Gln	Asn	Val	Leu	
	195						200				205					
His	Lys	Tyr	Val	Asn	Glu	Asp	Val	Ser	Leu	Gly	Ser	Trp	Phe	Leu	Gly	
	210					215					220					
Leu	Asp	Val	Glu	His	Val	Asp	Asp	Arg	Arg	Leu	Cys	Cys	Gly	Thr	Thr	
	225				230					235					240	
Asp	Cys	Glu	Trp	Lys	Ala	Gln	Ala	Gly	Asn	Ile	Cys	Val	Ala	Ser	Phe	
			245						250					255		
Asp	Trp	Ser	Cys	Ser	Gly	Ile	Cys	Arg	Ser	Ala	Asp	Arg	Met	Lys	Asp	
		260					265						270			
Val	His	Arg	Arg	Cys	Gly	Glu	Gly	Glu	Lys	Ala	Leu	Leu	Ala	Ala	Ser	
		275					280					285				
Phe																

(2) INFORMATION FOR SEQ ID NO:1236:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 267 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..267

(D) OTHER INFORMATION: / Ceres Seq. ID 1569387

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1236:

Met	Val	Val	Gly	Val	Asn	Thr	Ala	Phe	Ser	Ser	Arg	Lys	Arg	Arg	Asp	
1			5						10					15		
Ser	Val	Arg	Ala	Thr	Trp	Met	Pro	Pro	Gly	Glu	Glu	Arg	Lys	Lys	Leu	
			20					25					30			
Glu	Glu	Glu	Lys	Gly	Ile	Val	Met	Arg	Phe	Val	Ile	Gly	His	Ser	Ser	
		35				40						45				
Thr	Pro	Gly	Gly	Ile	Leu	Asp	Arg	Ala	Ile	Gln	Ala	Glu	Glu	Ser	Lys	
	50				55					60						
His	Gly	Asp	Phe	Leu	Arg	Leu	Asp	His	Val	Glu	Gly	Tyr	Leu	Glu	Leu	
	65				70					75				80		
Ser	Ala	Lys	Thr	Lys	Thr	Tyr	Phe	Thr	Thr	Ala	Phe	Ala	Met	Trp	Asp	
			85						90					95		
Ala	Asp	Phe	Tyr	Val	Lys	Val	Asp	Asp	Asp	Val	His	Val	Asn	Ile	Ala	
		100					105						110			
Thr	Leu	Gly	Ala	Glu	Leu	Ala	Arg	Tyr	Arg	Met	Lys	Pro	Arg	Val	Tyr	
		115				120					125					
Ile	Gly	Cys	Met	Lys	Ser	Gly	Pro	Val	Leu	Ala	Gln	Lys	Gly	Val	Arg	
	130					135					140					
Tyr	His	Glu	Pro	Glu	Tyr	Trp	Lys	Phe	Gly	Glu	Gly	Asn	Lys	Tyr		
			145		150					155				160		
Phe	Arg	His	Ala	Thr	Gly	Gln	Leu	Tyr	Ala	Ile	Ser	Arg	Glu	Leu	Ala	
			165					170						175		
Ser	Tyr	Ile	Ser	Ile	Asn	Gln	Asn	Val	Leu	His	Lys	Tyr	Val	Asn	Glu	
		180					185						190			
Asp	Val	Ser	Leu	Gly	Ser	Trp	Phe	Leu	Gly	Leu	Asp	Val	Glu	His	Val	
		195					200					205				
Asp	Asp	Arg	Arg	Leu	Cys	Cys	Gly	Thr	Thr	Asp	Cys	Glu	Trp	Lys	Ala	
	210					215					220					
Gln	Ala	Gly	Asn	Ile	Cys	Val	Ala	Ser	Phe	Asp	Trp	Ser	Cys	Ser	Gly	
	225				230					235					240	
Ile	Cys	Arg	Ser	Ala	Asp	Arg	Met	Lys	Asp	Val	His	Arg	Arg	Cys	Gly	
			245						250					255		
Glu	Gly	Glu	Lys	Ala	Leu	Leu	Ala	Ala	Ser	Phe						
		260					265									

(2) INFORMATION FOR SEQ ID NO:1237:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 245 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..245
(D) OTHER INFORMATION: / Ceres Seq. ID 1569388
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1237:

Met	Pro	Pro	Gly	Glu	Glu	Arg	Lys	Lys	Leu	Glu	Glu	Lys	Gly	Ile
1			5					10					15	
Val	Met	Arg	Phe	Val	Ile	Gly	His	Ser	Ser	Thr	Pro	Gly	Gly	Ile
			20				25						30	Leu
Asp	Arg	Ala	Ile	Gln	Ala	Glu	Glu	Ser	Lys	His	Gly	Asp	Phe	Leu
			35				40					45		Arg
Leu	Asp	His	Val	Glu	Gly	Tyr	Leu	Glu	Leu	Ser	Ala	Lys	Thr	Lys
			50			55					60			Thr
Tyr	Phe	Thr	Thr	Ala	Phe	Ala	Met	Trp	Asp	Ala	Asp	Phe	Tyr	Val
			65		70				75					Lys
Val	Asp	Asp	Asp	Val	His	Val	Asn	Ile	Ala	Thr	Leu	Gly	Ala	Glu
			85						90				95	Leu
Ala	Arg	Tyr	Arg	Met	Lys	Pro	Arg	Val	Tyr	Ile	Gly	Cys	Met	Lys
			100				105					110		Ser
Gly	Pro	Val	Leu	Ala	Gln	Lys	Gly	Val	Arg	Tyr	His	Glu	Pro	Glu
			115				120					125		Tyr
Trp	Lys	Phe	Gly	Glu	Glu	Gly	Asn	Lys	Tyr	Phe	Arg	His	Ala	Thr
			130			135					140			Gly
Gln	Leu	Tyr	Ala	Ile	Ser	Arg	Glu	Leu	Ala	Ser	Tyr	Ile	Ser	Ile
			145		150				155					Asn
Gln	Asn	Val	Leu	His	Lys	Tyr	Val	Asn	Glu	Asp	Val	Ser	Leu	Gly
			165				170						175	Ser
Trp	Phe	Leu	Gly	Leu	Asp	Val	Glu	His	Val	Asp	Asp	Arg	Arg	Leu
			180				185					190		Cys
Cys	Gly	Thr	Thr	Asp	Cys	Glu	Trp	Lys	Ala	Gln	Ala	Gly	Asn	Ile
			195				200					205		Cys
Val	Ala	Ser	Phe	Asp	Trp	Ser	Cys	Ser	Gly	Ile	Cys	Arg	Ser	Ala
			210			215					220			Asp
Arg	Met	Lys	Asp	Val	His	Arg	Arg	Cys	Gly	Glu	Gly	Glu	Lys	Ala
			225		230				235					Leu
Leu	Ala	Ala	Ser	Phe										
			245											

(2) INFORMATION FOR SEQ ID NO:1238:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 889 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:

(A) NAME/KEY: -
(B) LOCATION: 1..889
(D) OTHER INFORMATION: / Ceres Seq. ID 1569392
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1238:

aaaggttctct	tctgtttcca	gacaaagaaa	acacaaattc	attccctctc	cctcttcac	60
tcttttgcag	atatggatgg	tattatttct	ctgtctccca	tctctgtctc	ccaccggatt	120
aaagattctc	tccatttgcg	cgtctctgcc	cttctogcca	acctcttctc	cgctctcttc	180
accttctctc	tgccttttag	ggctttgatc	ggccaagaaa	cagagagcgg	tttcatcaga	240
ggagcgcgcg	ttggtgtcat	ctcaggcgcc	gtcttctcca	tgaagtctct	tgaatcttcc	300
ctctctcttt	ggcaatccga	tgaagtctga	attggatgcc	ttctctactt	gccttttgag	360

cgggaggcgtt gttcgtgagc gtatcgggtcc tgcaatgcta agtgccgtcc agagtcagat 420
gggagctgtg gaggccagct tccaagatca tacagacatc tttagacactg ccattttcaaa 480
gggtctcaact ggggactctc tcaacaggat ccctaaggct cgaatcacag acacctctcc 540
ggagattgtc tcttgcctctg tctgccttca ggaactttcag gtggggagaga cagttagaag 600
tttgccgcac tgccatcata tgttccacct accatgcacg gacaaaaggC ttgcgaggca 660
tgcttcttgt cctttgtgca gaagacatct ttgaattgat tttagaactct tctttctctt 720
cttctttgtg catgaggtat aggcatacac acacacacat atatacacac tagtagtctt 780
ccttgatttt ttttagatta cacgttacac agattttgat gcaccaatca ttgtaacttc 840
actcatctct tggagatcct gtttatttat gctacttatt cttggtctcc

(2) INFORMATION FOR SEQ ID NO:1239:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..125
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569393

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1239:

Lys	Gly	Ser	Phe	Cys	Phe	Gln	Thr	Lys	Lys	Thr	Gln	Ile	His	Ser	Leu
1		5						10					15		
Leu	Leu	Phe	Ile	Ser	Phe	Ala	Asp	Met	Asp	Gly	Tyr	Tyr	Ser	Leu	Ser
		20						25					30		
Pro	Ile	Ser	Val	Leu	His	Arg	Ile	Lys	Asp	Ser	Phe	His	Phe	Ala	Val
		35					40					45			
Ser	Ala	Leu	Leu	Ala	Asn	Leu	Phe	Ser	Ala	Leu	Phe	Thr	Phe	Phe	Phe
	50				55						60				
Ala	Leu	Gly	Ala	Leu	Ile	Gly	Gln	Glu	Thr	Glu	Ser	Gly	Phe	Ile	Arg
	65			70				75					80		
Gly	Ala	Ala	Val	Gly	Ala	Ile	Ser	Gly	Ala	Val	Phe	Ser	Ile	Glu	Val
		85						90					95		
Phe	Glu	Ser	Ser	Leu	Leu	Leu	Trp	Gln	Ser	Asp	Glu	Ser	Gly	Ile	Gly
		100						105					110		
Cys	Leu	Leu	Tyr	Leu	Pro	Phe	Glu	Arg	Glu	Ala	Cys	Ser			
	115					120						125			

(2) INFORMATION FOR SEQ ID NO:1240:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 101 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..101
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569394

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1240:

Met	Asp	Gly	Tyr	Tyr	Ser	Leu	Ser	Pro	Ile	Ser	Val	Leu	His	Arg	Ile
1		5						10					15		
Lys	Asp	Ser	Phe	His	Phe	Ala	Val	Ser	Ala	Leu	Leu	Ala	Asn	Leu	Phe
		20						25					30		
Ser	Ala	Leu	Phe	Thr	Phe	Phe	Phe	Ala	Leu	Gly	Ala	Leu	Ile	Gly	Gln
		35					40				45				
Glu	Thr	Glu	Ser	Gly	Phe	Ile	Arg	Gly	Ala	Ala	Val	Gly	Ala	Ile	Ser
	50				55						60				
Gly	Ala	Val	Phe	Ser	Ile	Glu	Val	Phe	Glu	Ser	Ser	Leu	Leu	Leu	Trp
	65			70				75					80		
Gln	Ser	Asp	Glu	Ser	Gly	Ile	Gly	Cys	Leu	Leu	Tyr	Leu	Pro	Phe	Glu
		85						90					95		

Arg Glu Ala Cys Ser
100

(2) INFORMATION FOR SEQ ID NO:1241:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 124 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..124
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569395

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1241:

Met	Ser	Leu	Glu	Leu	Asp	Ala	Phe	Ser	Thr	Cys	Leu	Leu	Ser	Gly	Arg
1			5						10					15	
Leu	Val	Arg	Glu	Arg	Ile	Gly	Pro	Ala	Met	Leu	Ser	Ala	Val	Gln	Ser
			20					25					30		
Gln	Met	Gly	Ala	Val	Glu	Ser	Gln	Phe	Gln	Asp	His	Thr	Asp	Ile	Phe
			35					40					45		
Asp	Thr	Ala	Ile	Ser	Lys	Gly	Leu	Thr	Gly	Asp	Ser	Leu	Asn	Arg	Ile
			50			55				60					
Pro	Lys	Val	Arg	Ile	Thr	Asp	Thr	Ser	Pro	Glu	Ile	Val	Ser	Cys	Ser
			65			70				75				80	
Val	Cys	Leu	Gln	Asp	Phe	Gln	Val	Gly	Glu	Thr	Val	Arg	Ser	Leu	Pro
			85					90						95	
His	Cys	His	His	Met	Phe	His	Leu	Pro	Cys	Ile	Asp	Lys	Trp	Leu	Arg
			100					105						110	
Arg	His	Ala	Ser	Cys	Pro	Leu	Cys	Arg	Arg	His	Leu				
			115					120							

(2) INFORMATION FOR SEQ ID NO:1242:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1580 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1580
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569403

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1242:

aatagggttca	gtgtttctga	catattgttc	cctctctgaa	tgaacctctc	ccaaatagag	60
aatggccctaa	ccacctatcc	aaccgcatca	aggcacttgg	tttcatcccc	ttgatttttc	120
tcctttttttc	ttttctctac	gcaggatttt	gtgttcttgg	tttgaatatg	aaatgtttcgt	180
cgatgtgttg	tttgatcttc	ttggcccttt	ctctctctac	cgctctcact	cttgctttctt	240
cgtcaaatgg	tatatagtgga	cctttctacg	actctactgc	ctacacagag	tgtagagccg	300
aagcagagaaa	gccactatata	aatggaggaaa	tgtctgaagg	ccaaaaggct	tccgtcccca	360
cgaaagactc	ttctcacaggc	attgggtgct	gttacacacc	aacttacata	tgtcacatac	420
taactgcca	acactcttat	tgtcttctca	tatgggtgaa	gatagagggt	ggtgctgcgt	480
cagctcatgt	aagagcaagg	ctgagagcag	acaacgcccac	attaaactgc	gtcgtgttct	540
taactgcca	acatggttgc	tgtctcttcc	tcaaaggagg	attctctctt	gattctctct	600
gtaaacatc	catctctctc	tttgagacat	cagaggacga	tgttaaatgc	caattacaag	660
tgacgagtgc	ctctctctac	ccattccacg	aggagcaatg	gagggaacac	caagattact	720
tcataaatac	cgccagaaaa	cgagcagtg	caattcacgt	gtcaaaaaga	aacggagaga	780
cggttgcaag	agcagaggtg	acagtagagc	agatctctaa	agactctctc	attggtttctg	840
ccattctcaa	aactatcctt	ggaaacattc	cttaccaca	atggttctgc	aagagattcg	900
acggccacggt	attcgagaa	gagctgaaat	ggtacgcgac	ggagcccgat	caaggcaaac	960
tcaactacac	attggctgat	aagatgatga	atttcgtctg	agccaacaga	atcatcgctc	1020
gcggtcacaa	catattctcg	gaggatccca	aatacaatcc	cgattggggt	cgtaattctaa	1080
ccggcggaaga	ttctccggtc	gcggttaacc	ggcgaatcaa	gagctctgat	atcgcgtaca	1140

gaggagaggtt cgtgcatttg gacgtgagca acgagatgct tcactttgac ttctacagaga 1200
ctcgactggg gaagaacgcg tcgtacggat tcttcgcccg ggctcgtgag attgactcat 1260
tggcgactct gttcttcaat gatttcaacg tgggtggagac ttgcagcgac gagaagtcaa 1320
cggttgacga atacatcgcg aggggtgaggg aactccaacg gtacgacggcg gtaaggatgg 1380
acggaatagg tctcggagggt cacttcaaga cgccaaacgt agcgctgatg agagccatcc 1440
tcgataaacT cgcKtacgct ccagctccca atctgggtca cagagattga tatcagcagc 1500
agcctcgacc accgctctca ggcgatttat ttggagcaag tggtacgtga aggattctcg 1560
caccatcgcg taacgggtat

(2) INFORMATION FOR SEQ ID NO:1243:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 440 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..440
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569404

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1243:

Met	Lys	Cys	Ser	Ser	Met	Cys	Cys	Leu	Ile	Leu	Leu	Ala	Leu	Ser	Leu
1			5					10						15	
Leu	Thr	Ala	Phe	Thr	Leu	Ala	Ser	Ser	Asn	Gly	Ile	Asp	Gly	Pro	
			20					25					30		
Phe	Tyr	Asp	Ser	Thr	Ala	Tyr	Thr	Glu	Cys	Arg	Ala	Glu	Ala	Glu	Lys
			35					40					45		
Pro	Leu	Tyr	Asn	Gly	Gly	Met	Leu	Lys	Asp	Gln	Lys	Pro	Ser	Val	Pro
			50				55				60				
Gly	Lys	Asp	Ser	Leu	Thr	Gly	Ile	Gly	Ala	Arg	Tyr	Thr	Pro	Thr	Tyr
			65				70				75				80
Ile	Leu	His	Asn	Leu	Thr	Gln	Asn	Thr	Ile	Tyr	Cys	Phe	Ser	Ile	Trp
			85					90						95	
Val	Lys	Ile	Glu	Ala	Gly	Ala	Ala	Ser	Ala	His	Val	Arg	Ala	Arg	Leu
			100					105					110		
Arg	Ala	Asp	Asn	Ala	Thr	Leu	Asn	Cys	Val	Gly	Ser	Val	Thr	Ala	Lys
			115				120					125			
His	Gly	Cys	Trp	Ser	Phe	Leu	Lys	Gly	Gly	Phe	Leu	Leu	Asp	Ser	Pro
			130				135					140			
Cys	Lys	Gln	Ser	Ile	Leu	Phe	Phe	Glu	Thr	Ser	Glu	Asp	Asp	Gly	Lys
					150					155				160	
Ile	Gln	Leu	Gln	Val	Thr	Ser	Ala	Ser	Leu	Gln	Pro	Phe	Thr	Gln	Glu
			165						170					175	
Gln	Trp	Arg	Asn	Asn	Gln	Asp	Tyr	Phe	Ile	Asn	Thr	Ala	Arg	Lys	Arg
			180					185					190		
Ala	Val	Thr	Ile	His	Val	Ser	Lys	Glu	Asn	Gly	Glu	Ser	Val	Glu	Gly
			195				200					205			
Ala	Glu	Val	Thr	Val	Glu	Gln	Ile	Ser	Lys	Asp	Phe	Ser	Ile	Gly	Ser
			210				215					220			
Ala	Ile	Ser	Lys	Thr	Ile	Leu	Gly	Asn	Ile	Pro	Tyr	Gln	Glu	Trp	Phe
			225				230				235			240	
Val	Lys	Arg	Phe	Asp	Ala	Thr	Val	Phe	Glu	Asn	Glu	Leu	Lys	Trp	Tyr
			245					250					255		
Ala	Thr	Glu	Pro	Asp	Gln	Gly	Lys	Leu	Asn	Tyr	Thr	Leu	Ala	Asp	Lys
			260					265				270			
Met	Met	Asn	Phe	Val	Arg	Ala	Asn	Arg	Ile	Ile	Ala	Arg	Gly	His	Asn
			275				280					285			
Ile	Phe	Trp	Glu	Asp	Pro	Lys	Tyr	Asn	Pro	Asp	Trp	Val	Arg	Asn	Leu
			290				295				300				
Thr	Gly	Glu	Asp	Leu	Arg	Ser	Ala	Val	Asn	Arg	Arg	Ile	Lys	Ser	Leu
			305				310				315			320	
Met	Thr	Arg	Tyr	Arg	Gly	Glu	Phe	Val	His	Trp	Asp	Val	Ser	Asn	Glu

1	Met	Cys	Cys	Leu	Ile	Leu	Leu	Ala	Leu	Ser	Leu	Leu	Thr	Ala	Phe	Thr
				5					10						15	
Leu	Ala	Ser	Ser	Ser	Asn	Gly	Ile	Asp	Gly	Pro	Phe	Tyr	Asp	Ser	Thr	
			20					25					30			
Ala	Met	Thr	Glu	Cys	Arg	Ala	Glu	Ala	Glu	Lys	Pro	Leu	Tyr	Asn	Gly	
		35					40					45				
Gly	Met	Leu	Lys	Asp	Gln	Lys	Pro	Ser	Val	Pro	Gly	Lys	Asp	Ser	Leu	
	50					55					60					
Thr	Gly	Ile	Gly	Ala	Arg	Tyr	Thr	Pro	Thr	Tyr	Ile	Leu	His	Asn	Leu	
	65				70					75				80		
Thr	Gln	Asn	Thr	Ile	Tyr	Cys	Phe	Ser	Ile	Trp	Val	Lys	Ile	Glu	Ala	
				85					90				95			
Gly	Ala	Ala	Ser	Ala	His	Val	Arg	Ala	Arg	Leu	Arg	Ala	Asp	Asn	Ala	
			100					105					110			
Thr	Leu	Asn	Cys	Val	Gly	Ser	Val	Thr	Ala	Lys	His	Gly	Cys	Trp	Ser	
		115					120					125				
Phe	Leu	Lys	Gly	Gly	Phe	Leu	Leu	Asp	Ser	Pro	Cys	Lys	Gln	Ser	Ile	
	130					135					140					
Leu	Phe	Phe	Glu	Thr	Ser	Glu	Asp	Asp	Gly	Lys	Ile	Gln	Leu	Gln	Val	
	145				150					155				160		
Thr	Ser	Ala	Ser	Leu	Gln	Pro	Phe	Thr	Gln	Glu	Gln	Trp	Arg	Asn	Asn	
			165						170					175		
Gln	Asp	Tyr	Phe	Ile	Asn	Thr	Ala	Arg	Lys	Arg	Ala	Val	Thr	Ile	His	
		180						185					190			
Val	Ser	Lys	Glu	Asn	Gly	Glu	Ser	Val	Glu	Gly	Ala	Glu	Val	Thr	Val	
		195					200					205				
Glu	Gln	Ile	Ser	Lys	Asp	Phe	Ser	Ile	Gly	Ser	Ala	Ile	Ser	Lys	Thr	
	210					215					220					
Ile	Leu	Gly	Asn	Ile	Pro	Tyr	Gln	Glu	Trp	Phe	Val	Lys	Arg	Phe	Asp	
	225				230					235				240		
Ala	Thr	Val	Phe	Glu	Asn	Glu	Leu	Lys	Trp	Tyr	Ala	Thr	Glu	Pro	Asp	
				245					250					255		
Gln	Gly	Lys	Leu	Asn	Tyr	Thr	Leu	Ala	Asp	Lys	Met	Met	Asn	Phe	Val	
			260					265					270			

Arg Ala Asn Arg Ile Ile Ala Arg Gly His Asn Ile Phe Trp Glu Asp
275 280 285
Pro Lys Tyr Asn Pro Asp Trp Val Arg Asn Leu Thr Gly Glu Asp Leu
290 295 300
Arg Ser Ala Val Asn Arg Arg Ile Lys Ser Leu Met Thr Arg Tyr Arg
305 310 315
Gly Glu Phe Val His Trp Asp Val Ser Asn Glu Met Leu His Phe Asp
325 330 335
Phe Tyr Glu Thr Arg Leu Gly Lys Asn Ala Ser Tyr Gly Phe Phe Ala
340 345 350
Ala Ala Arg Glu Ile Asp Ser Leu Ala Thr Leu Phe Phe Asn Asp Phe
355 360 365
Asn Val Val Glu Thr Cys Ser Asp Glu Lys Ser Thr Val Asp Glu Tyr
370 375 380
Ile Ala Arg Val Arg Glu Leu Gln Arg Tyr Asp Gly Val Arg Met Asp
385 390 395
Gly Ile Gly Leu Glu Gly His Phe Thr Thr Pro Asn Val Ala Leu Met
405 410 415
Arg Ala Ile Leu Asp Lys Leu Xaa Tyr Ala Pro Ala Pro Asn Leu Ala
420 425 430
His Arg Asp
435

(2) INFORMATION FOR SEQ ID NO:1245:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 386 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..386
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569406

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1245:

Met Leu Lys Asp Gln Lys Pro Ser Val Pro Gly Lys Asp Ser Leu Thr
1 5 10 15
Gly Ile Gly Ala Arg Tyr Thr Pro Thr Tyr Ile Leu His Asn Leu Thr
20 25 30
Gln Asn Thr Ile Tyr Cys Phe Ser Ile Trp Val Lys Ile Glu Ala Gly
35 40 45
Ala Ala Ser Ala His Val Arg Ala Arg Leu Arg Ala Asp Asn Ala Thr
50 55 60
Leu Asn Cys Val Gly Ser Val Thr Ala Lys His Gly Cys Trp Ser Phe
65 70 75 80
Leu Lys Gly Gly Phe Leu Leu Asp Ser Pro Cys Lys Gln Ser Ile Leu
85 90 95
Phe Phe Glu Thr Ser Glu Asp Asp Gly Lys Ile Gln Leu Gln Val Thr
100 105 110
Ser Ala Ser Leu Gln Pro Phe Thr Gln Glu Gln Trp Arg Asn Asn Gln
115 120 125
Asp Tyr Phe Ile Asn Thr Ala Arg Lys Arg Ala Val Thr Ile His Val
130 135 140
Ser Lys Glu Asn Gly Glu Ser Val Glu Gly Ala Glu Val Thr Val Glu
145 150 155 160
Gln Ile Ser Lys Asp Phe Ser Ile Gly Ser Ala Ile Ser Lys Thr Ile
165 170 175
Leu Gly Asn Ile Pro Tyr Gln Glu Trp Phe Val Lys Arg Phe Asp Ala
180 185 190
Thr Val Phe Glu Asn Glu Leu Lys Trp Tyr Ala Thr Glu Pro Asp Gln
195 200 205
Gly Lys Leu Asn Tyr Thr Leu Ala Asp Lys Met Met Asn Phe Val Arg

210	215	220
Ala Asn Arg Ile Ile Ala Arg Gly His Asn Ile Phe Trp Glu Asp Pro		
225	230	235
Lys Tyr Asn Pro Asp Trp Val Arg Asn Leu Thr Gly Glu Asp Leu Arg		
	245	250
Ser Ala Val Asn Arg Arg Ile Lys Ser Leu Met Thr Arg Tyr Arg Gly		
	260	265
Glu Phe Val His Trp Asp Val Ser Asn Glu Met Leu His Phe Asp Phe		
	275	280
Tyr Glu Thr Arg Leu Gly Lys Asn Ala Ser Tyr Gly Phe Phe Ala Ala		
	290	295
Ala Arg Glu Ile Asp Ser Leu Ala Thr Leu Phe Phe Asn Asp Phe Asn		
305	310	315
Val Val Glu Thr Cys Ser Asp Glu Lys Ser Thr Val Asp Glu Tyr Ile		
	325	330
Ala Arg Val Arg Glu Leu Gln Arg Tyr Asp Gly Val Arg Met Asp Gly		
	340	345
Ile Gly Leu Glu Gly His Phe Thr Thr Pro Asn Val Ala Leu Met Arg		
	355	360
Ala Ile Leu Asp Lys Leu Xaa Tyr Ala Pro Ala Pro Asn Leu Ala His		
	370	375
Arg Asp		380
385		

(2) INFORMATION FOR SEQ ID NO:1246:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1362 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1362
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569407

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1246:

aatttcattc	gtctctttatc	aacaacacac	tctctctctt	ctatcaaac	ttcttttcac	60
ctctgcgcgg	aaaaaacccat	aaccacaaca	atggccaccg	aaacccaaat	cgaatcggga	120
gtaatggggt	gcgcgcgat	cgctcgaaaa	gtctctcgag	caatccacct	cgctcccaac	180
gccacaatct	ccggcgtaGc	aagccgggtc	ttagaaaaag	ccaaagcctt	tgccaccgcc	240
aataactacc	cagaatcaac	caaaatccac	ggctcttacg	aatctctctt	cgaagatcca	300
gagatcgatg	cgctctatgt	tctctctccc	actagtcctc	acgttgagtg	ggctattaaa	360
cgagctgaga	aagggaaca	tatccttttg	gagaagcctg	ttgctatgaa	cgtaactgag	420
tttgataaga	ttgttgatgc	ttgtgaagct	aatgggtgtc	agattatgga	tggtactatg	480
tgggttcaat	atctagaac	tgctttgctt	aaagagtttc	tttctgattc	tgaacgtttt	540
ggtcagctta	aaactgtaca	gagttgtttc	tcatttgcgt	gagatgaaga	ttttcttaaa	600
aacgataacc	gtgtgaaacc	tggtcttgac	gggcttggtg	cgctaggaga	tgccgggtgg	660
tacgcgatca	gagcaactct	tttagctaat	aaatttgagc	ttccgaaaac	ttgtaactgt	720
ttcccgcgtg	ctgtgttgaa	tgaagcagga	ttgatacttt	ccgtgtggag	atctttgagt	780
tgggaagtat	gacgaactgc	aactatata	ttgtctattc	tggttaacct	aaacaaggag	840
ataactgcc	ttggaacgaa	aggcacaact	cggtgtacac	acttcattat	cccgataaag	900
gagactgagg	cgctgtttac	cacgagcact	aaagcttggt	tcaatgaact	tgtagctggc	960
tggtgttagc	ccccgagtga	gcatacgggt	aagacagagc	ttccacaaga	ggcatgtatg	1020
gtgagagagt	ttgtctgatt	ggttggagaa	atcaagaaca	atggtgcmaa	gcctgatggg	1080
tactggccta	gtattagccg	aaagacgcag	ctagtgtgtg	atgctgttaa	agagctctgt	1140
gataaaaact	atcaacagat	tagtctctct	ggctcgttga	ggaaggagct	cagactataa	1200
atgtgtgtgt	gtgtctctct	ctctctctgt	ctctatgttc	aaactctgat	caaccgttta	1260
agtgcttggt	accacttacc	aatatgttct	gtctctctgt	gtgtccgcct	gtatgtatgt	1320
taattgtttt	agactccaat	tactagcctt	caattactaa	gc		

(2) INFORMATION FOR SEQ ID NO:1247:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 392 amino acids

(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1..392
(D) OTHER INFORMATION: / Ceres Seq. ID 1569408

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1247:

Asn	Phe	Ile	Arg	Ser	Leu	Ser	Thr	Thr	Leu	Ser	Leu	Phe	Ser	Ile	Asn
1					5				10					15	
Thr	Phe	Phe	His	Leu	Ser	Pro	Glu	Lys	Pro	Ile	Thr	Thr	Thr	Met	Ala
			20					25					30		
Thr	Glu	Thr	Gln	Ile	Arg	Ile	Gly	Val	Met	Gly	Cys	Ala	Asp	Ile	Ala
			35				40					45			
Arg	Lys	Val	Ser	Arg	Ala	Ile	His	Leu	Ala	Pro	Asn	Ala	Thr	Ile	Ser
	50					55				60					
Gly	Val	Ala	Ser	Arg	Ser	Leu	Glu	Lys	Ala	Lys	Ala	Phe	Ala	Thr	Ala
65					70				75					80	
Asn	Asn	Tyr	Pro	Glu	Ser	Thr	Lys	Ile	His	Gly	Ser	Tyr	Glu	Ser	Leu
			85					90					95		
Leu	Glu	Asp	Pro	Glu	Ile	Asp	Ala	Leu	Tyr	Val	Pro	Leu	Pro	Thr	Ser
			100				105					110			
Leu	His	Val	Glu	Trp	Ala	Ile	Lys	Ala	Ala	Glu	Lys	Gly	Lys	His	Ile
	115						120					125			
Leu	Leu	Glu	Lys	Pro	Val	Ala	Met	Asn	Val	Thr	Glu	Phe	Asp	Lys	Ile
	130					135					140				
Val	Asp	Ala	Cys	Glu	Ala	Asn	Gly	Val	Gln	Ile	Met	Asp	Gly	Thr	Met
145					150					155				160	
Trp	Val	His	Asn	Pro	Arg	Thr	Ala	Leu	Leu	Lys	Glu	Phe	Leu	Ser	Asp
			165				170						175		
Ser	Glu	Arg	Phe	Gly	Gln	Leu	Lys	Thr	Val	Gln	Ser	Cys	Phe	Ser	Phe
	180					185						190			
Ala	Gly	Asp	Glu	Asp	Phe	Leu	Lys	Asn	Asp	Ile	Arg	Val	Lys	Pro	Gly
	195					200					205				
Leu	Asp	Gly	Leu	Gly	Ala	Leu	Gly	Asp	Ala	Gly	Trp	Tyr	Ala	Ile	Arg
	210					215					220				
Ala	Thr	Leu	Leu	Ala	Asn	Asn	Phe	Glu	Leu	Pro	Lys	Thr	Val	Thr	Ala
225					230					235				240	
Phe	Pro	Gly	Ala	Val	Leu	Asn	Glu	Ala	Gly	Leu	Ile	Leu	Ser	Cys	Gly
			245						250					255	
Ala	Ser	Leu	Ser	Trp	Glu	Asp	Gly	Arg	Thr	Ala	Thr	Ile	Tyr	Cys	Ser
		260					265					270			
Phe	Leu	Ala	Asn	Leu	Thr	Met	Glu	Ile	Thr	Ala	Ile	Gly	Thr	Lys	Gly
	275						280					285			
Thr	Leu	Arg	Val	His	Asp	Phe	Ile	Ile	Pro	Tyr	Lys	Glu	Thr	Glu	Ala
	290					295					300				
Ser	Phe	Thr	Thr	Ser	Thr	Lys	Ala	Trp	Phe	Asn	Asp	Leu	Val	Thr	Ala
305					310					315				320	
Trp	Val	Ser	Pro	Pro	Ser	Glu	His	Thr	Val	Lys	Thr	Glu	Leu	Pro	Gln
			325						330				335		
Glu	Ala	Cys	Met	Val	Arg	Glu	Phe	Ala	Arg	Leu	Val	Gly	Glu	Ile	Lys
		340					345					350			
Asn	Asn	Gly	Ala	Lys	Pro	Asp	Gly	Tyr	Trp	Pro	Ser	Ile	Ser	Arg	Lys
	355					360						365			
Thr	Gln	Leu	Val	Val	Asp	Ala	Val	Lys	Glu	Ser	Val	Asp	Lys	Asn	Tyr
	370				375						380				
Gln	Gln	Ile	Ser	Leu	Ser	Gly	Arg								
385				390											

(2) INFORMATION FOR SEQ ID NO:1248:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 362 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..362
(D) OTHER INFORMATION: / Ceres Seq. ID 1569409
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1248:
Met Ala Thr Glu Thr Gln Ile Arg Ile Gly Val Met Gly Cys Ala Asp
1 5 10 15
Ile Ala Arg Lys Val Ser Arg Ala Ile His Leu Ala Pro Asn Ala Thr
20 25 30
Ile Ser Gly Val Ala Ser Arg Ser Leu Glu Lys Ala Lys Ala Phe Ala
35 40 45
Thr Ala Asn Asn Tyr Pro Glu Ser Thr Lys Ile His Gly Ser Tyr Glu
50 55 60
Ser Leu Leu Glu Asp Pro Glu Ile Asp Ala Leu Tyr Val Pro Leu Pro
65 70 75 80
Thr Ser Leu His Val Glu Trp Ala Ile Lys Ala Ala Glu Lys Gly Lys
85 90 95
His Ile Leu Leu Glu Lys Pro Val Ala Met Asn Val Thr Glu Phe Asp
100 105 110
Lys Ile Val Asp Ala Cys Glu Ala Asn Gly Val Gln Ile Met Asp Gly
115 120 125
Thr Met Trp Val His Asn Pro Arg Thr Ala Leu Leu Lys Glu Phe Leu
130 135 140
Ser Asp Ser Glu Arg Phe Gly Gln Leu Lys Thr Val Gln Ser Cys Phe
145 150 155 160
Ser Phe Ala Gly Asp Glu Asp Phe Leu Lys Asn Asp Ile Arg Val Lys
165 170 175
Pro Gly Leu Asp Gly Leu Gly Ala Leu Gly Asp Ala Gly Trp Tyr Ala
180 185 190
Ile Arg Ala Thr Leu Leu Ala Asn Asn Phe Glu Leu Pro Lys Thr Val
195 200 205
Thr Ala Phe Pro Gly Ala Val Leu Asn Glu Ala Gly Leu Ile Leu Ser
210 215 220
Cys Gly Ala Ser Leu Ser Trp Glu Asp Gly Arg Thr Ala Thr Ile Tyr
225 230 235 240
Cys Ser Phe Leu Ala Asn Leu Thr Met Glu Ile Thr Ala Ile Gly Thr
245 250 255
Lys Gly Thr Leu Arg Val His Asp Phe Ile Ile Pro Tyr Lys Glu Thr
260 265 270
Glu Ala Ser Phe Thr Thr Ser Thr Lys Ala Trp Phe Asn Asp Leu Val
275 280 285
Thr Ala Trp Val Ser Pro Pro Ser Glu His Thr Val Lys Thr Glu Leu
290 295 300
Pro Gln Glu Ala Cys Met Val Arg Glu Phe Ala Arg Leu Val Gly Glu
305 310 315 320
Ile Lys Asn Asn Gly Ala Lys Pro Asp Gly Tyr Trp Pro Ser Ile Ser
325 330 335
Arg Lys Thr Gln Leu Val Val Asp Ala Val Lys Glu Ser Val Asp Lys
340 345 350
Asn Tyr Gln Gln Ile Ser Leu Ser Gly Arg
355 360
(2) INFORMATION FOR SEQ ID NO:1249:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 351 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:

- (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..351
(D) OTHER INFORMATION: / Ceres Seq. ID 1569410

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1249:
Met Gly Cys Ala Asp Ile Ala Arg Lys Val Ser Arg Ala Ile His Leu
1 5 10 15
Ala Pro Asn Ala Thr Ile Ser Gly Val Ala Ser Arg Ser Leu Glu Lys
 20 25 30
Ala Lys Ala Phe Ala Thr Ala Asn Asn Tyr Pro Glu Ser Thr Lys Ile
 35 40 45
His Gly Ser Tyr Glu Ser Leu Leu Glu Asp Pro Glu Ile Asp Ala Leu
 50 55 60
Tyr Val Pro Leu Pro Thr Ser Leu His Val Glu Trp Ala Ile Lys Ala
65 70 75 80
Ala Glu Lys Gly Lys His Ile Leu Leu Glu Lys Pro Val Ala Met Asn
 85 90 95
Val Thr Glu Phe Asp Lys Ile Val Asp Ala Cys Glu Ala Asn Gly Val
 100 105 110
Gln Ile Met Asp Gly Thr Met Trp Val His Asn Pro Arg Thr Ala Leu
 115 120 125
Leu Lys Glu Phe Leu Ser Asp Ser Glu Arg Phe Gly Gln Leu Lys Thr
 130 135 140
Val Gln Ser Cys Phe Ser Phe Ala Gly Asp Glu Asp Phe Leu Lys Asn
145 150 155 160
Asp Ile Arg Val Lys Pro Gly Leu Asp Gly Leu Gly Ala Leu Gly Asp
 165 170 175
Ala Gly Trp Tyr Ala Ile Arg Ala Thr Leu Leu Ala Asn Asn Phe Glu
 180 185 190
Leu Pro Lys Thr Val Thr Ala Phe Pro Gly Ala Val Leu Asn Glu Ala
 195 200 205
Gly Leu Ile Leu Ser Cys Gly Ala Ser Leu Ser Trp Glu Asp Gly Arg
210 215 220
Thr Ala Thr Ile Tyr Cys Ser Phe Leu Ala Asn Leu Thr Met Glu Ile
225 230 235 240
Thr Ala Ile Gly Thr Lys Gly Thr Leu Arg Val His Asp Phe Ile Ile
 245 250 255
Pro Tyr Lys Glu Thr Glu Ala Ser Phe Thr Thr Ser Thr Lys Ala Trp
 260 265 270
Phe Asn Asp Leu Val Thr Ala Trp Val Ser Pro Pro Ser Glu His Thr
 275 280 285
Val Lys Thr Glu Leu Pro Gln Glu Ala Cys Met Val Arg Glu Phe Ala
290 295 300
Arg Leu Val Gly Glu Ile Lys Asn Asn Gly Ala Lys Pro Asp Gly Tyr
305 310 315 320
Trp Pro Ser Ile Ser Arg Lys Thr Gln Leu Val Val Asp Ala Val Lys
 325 330 335
Glu Ser Val Asp Lys Asn Tyr Gln Gln Ile Ser Leu Ser Gly Arg
 340 345 350

- (2) INFORMATION FOR SEQ ID NO:1250:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1202 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
 (A) NAME/KEY: -
 (B) LOCATION: 1..1202

(D) OTHER INFORMATION: / Ceres Seq. ID 1569411
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1250:

aacgcagatt	gccatccagg	agaggggaga	agaagaattt	gtattctcaa	gtgtgcgata	60
tgagagagat	gaagtccaga	acacgtttgt	gagagaacag	cttttagatg	tgattgtgga	120
tcagattctc	aaagactttt	cgcgaaagat	ctctgatcct	taaatcgctt	ctctctcgct	180
tgacctcatt	tcgtctgtga	aatcagatcc	gtgtgaaaaa	gccgaaacag	gatatggaga	240
agatggagct	tcgttaagaac	ttccgttaag	tttggcatac	cgattctacc	cacagtatcc	300
agaacgatac	tccttatgtg	tgcttcgctg	ttgtgtgtgc	cccttggtga	tcatacttgc	360
ttcgcaagcg	tgccgctttc	gatgatattg	caaggtacgt	ctgtctgtgc	ggttacatgc	420
cttgtagtgt	taggtgtgga	gaagccaaat	gtcctcaact	ttgtcttgcc	actgaggtct	480
ctctgtgctt	tgcaaacctc	gtggccctca	ctcgttttct	cttgcgaagt	gagttccaaa	540
ttcagacgac	aaaatgtgac	aactgcatac	ttgttttcat	ggtttgcttc	agccaagtgg	600
cttgcataatt	ctccatagtt	gcattgtatt	tcggtatgga	tgagctttca	gaagcttttc	660
agatactcac	atgtgtcctt	gacatgggtg	actgcacggt	ttgcgcatgt	atgcagacac	720
aacacaagat	ggaaatggac	aagagggagc	gtaagtctgg	gccacagcca	atggcagtgG	780
ctccggctca	gcataatgtc	cggtttgatc	aagccacccc	acccgcagtc	ggttatcttc	840
cacaacaagg	ttatccacct	ttctggttacc	ctcaacaccc	tcacaagggt	tatccacctt	900
ctggctatcc	tcaaaaaccc	ctccctcag	cttattctca	ataccctctc	ggggcttacc	960
ctcctctccc	cgcttaccoc	aagtgtatcc	cttttgccctg	ttttctctcc	cgattggaaa	1020
attttttttc	atcttttttt	aattgctgtc	tgttacgggt	caagaattga	acgttctgctg	1080
attgtttttg	ggctgtttgt	tgatgatgat	tttgacctca	catgtgtgtg	ttttctgaaa	1140
cgctcctctt	ggactaagag	atttcatgac	tttttctctt	cttttttaaa	ttctcttttt	1200

tc

(2) INFORMATION FOR SEQ ID NO:1251:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 255 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..255

(D) OTHER INFORMATION: / Ceres Seq. ID 1569412

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1251:

Met	Pro	Lys	Gln	Asp	Met	Glu	Lys	Met	Glu	Leu	Arg	Lys	Asn	Phe	Arg
1			5					10					15		
Asn	Val	Trp	His	Thr	Asp	Leu	Thr	His	Ser	Ile	Gln	Asn	Asp	Thr	Pro
			20					25					30		
Tyr	Cys	Cys	Phe	Ala	Leu	Trp	Cys	Ala	Pro	Cys	Ala	Ser	Tyr	Leu	Leu
		35					40					45			
Arg	Lys	Arg	Ala	Leu	Tyr	Asp	Asp	Met	Ser	Arg	Tyr	Val	Cys	Cys	Ala
	50					55					60				
Gly	Tyr	Met	Pro	Cys	Ser	Gly	Arg	Cys	Gly	Gly	Ala	Lys	Cys	Pro	Gln
65					70				75					80	
Leu	Cys	Leu	Ala	Thr	Glu	Val	Phe	Cys	Cys	Phe	Ala	Asn	Ser	Val	Ala
			85						90				95		
Ser	Thr	Arg	Phe	Leu	Leu	Gln	Asp	Glu	Phe	Gln	Ile	Gln	Thr	Thr	Lys
			100					105					110		
Cys	Asp	Asn	Cys	Ile	Ile	Gly	Phe	Met	Val	Cys	Leu	Ser	Glu	Val	Ala
		115				120						125			
Cys	Ile	Phe	Ser	Ile	Val	Ala	Cys	Ile	Val	Gly	Met	Asp	Glu	Leu	Ser
	130					135				140					
Glu	Ala	Ser	Gln	Ile	Leu	Thr	Cys	Cys	Ser	Asp	Met	Val	Tyr	Cys	Thr
145					150				155					160	
Val	Cys	Ala	Cys	Met	Gln	Thr	Gln	His	Lys	Met	Glu	Met	Asp	Lys	Arg
			165					170					175		
Asp	Gly	Lys	Phe	Gly	Pro	Gln	Pro	Met	Ala	Val	Pro	Pro	Ala	Gln	Gln
			180					185					190		
Met	Ser	Arg	Phe	Asp	Gln	Ala	Thr	Pro	Pro	Ala	Val	Gly	Tyr	Pro	Pro
	195					200					205				

Gln Gln Gly Tyr Pro Pro Ser Gly Tyr Pro Gln His Pro Pro Gln Gly
210 215 220
Tyr Pro Pro Ser Gly Tyr Pro Gln Asn Pro Pro Pro Ser Ala Tyr Ser
225 230 235 240
Gln Tyr Pro Pro Gly Ala Tyr Pro Pro Pro Pro Ala Tyr Pro Lys
245 250 255

(2) INFORMATION FOR SEQ ID NO:1252:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 250 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..250

(D) OTHER INFORMATION: / Ceres Seq. ID 1569413

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1252:

Met Glu Lys Met Glu Leu Arg Lys Asn Phe Arg Asn Val Trp His Thr
1 5 10 15
Asp Leu Thr His Ser Ile Gln Asn Asp Thr Pro Tyr Cys Cys Phe Ala
20 25 30
Leu Trp Cys Ala Pro Cys Ala Ser Tyr Leu Leu Arg Lys Arg Ala Leu
35 40 45
Tyr Asp Asp Met Ser Arg Tyr Val Cys Cys Ala Gly Tyr Met Pro Cys
50 55 60
Ser Gly Arg Cys Gly Glu Ala Lys Cys Pro Gln Leu Cys Leu Ala Thr
65 70 75 80
Glu Val Phe Cys Cys Phe Ala Asn Ser Val Ala Ser Thr Arg Phe Leu
85 90 95
Leu Gln Asp Glu Phe Gln Ile Gln Thr Thr Lys Cys Asp Asn Cys Ile
100 105 110
Ile Gly Phe Met Val Cys Leu Ser Gln Val Ala Cys Ile Phe Ser Ile
115 120 125
Val Ala Cys Ile Val Gly Met Asp Glu Leu Ser Glu Ala Ser Gln Ile
130 135 140
Leu Thr Cys Cys Ser Asp Met Val Tyr Cys Thr Val Cys Ala Cys Met
145 150 155 160
Gln Thr Gln His Lys Met Glu Met Asp Lys Arg Asp Gly Lys Phe Gly
165 170 175
Pro Gln Pro Met Ala Val Pro Pro Ala Gln Gln Met Ser Arg Phe Asp
180 185 190
Gln Ala Thr Pro Pro Ala Val Gly Tyr Pro Pro Gln Gln Gly Tyr Pro
195 200 205
Pro Ser Gly Tyr Pro Gln His Pro Pro Gln Gly Tyr Pro Pro Ser Gly
210 215 220
Tyr Pro Gln Asn Pro Pro Pro Ser Ala Tyr Ser Gln Tyr Pro Pro Gly
225 230 235 240
Ala Tyr Pro Pro Pro Pro Ala Tyr Pro Lys
245 250

(2) INFORMATION FOR SEQ ID NO:1253:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 247 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..247

(D) OTHER INFORMATION: / Ceres Seq. ID 1569414

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1253:

```

Met Glu Leu Arg Lys Asn Phe Arg Asn Val Trp His Thr Asp Leu Thr
1      5      10      15
His Ser Ile Gln Asn Asp Thr Pro Tyr Cys Cys Phe Ala Leu Trp Cys
20     25     30     35
Ala Pro Cys Ala Ser Tyr Leu Leu Arg Lys Arg Ala Leu Tyr Asp Asp
40     45     50     55
Met Ser Arg Tyr Val Cys Cys Ala Gly Tyr Met Pro Cys Ser Gly Arg
60     65     70     75
Cys Gly Glu Ala Lys Cys Pro Gln Leu Cys Leu Ala Thr Glu Val Phe
80     85     90     95
Cys Cys Phe Ala Asn Ser Val Ala Ser Thr Arg Phe Leu Leu Gln Asp
100    105   110   115
Glu Phe Gln Ile Gln Thr Thr Lys Cys Asp Asn Cys Ile Ile Gly Phe
120    125   130   135
Met Val Cys Leu Ser Gln Val Ala Cys Ile Phe Ser Ile Val Ala Cys
140    145   150   155
Ile Val Gly Met Asp Glu Leu Ser Glu Ala Ser Gln Ile Leu Thr Cys
160    165   170   175
Cys Ser Asp Met Val Tyr Cys Thr Val Cys Ala Cys Met Gln Thr Gln
180    185   190   195
His Lys Met Glu Met Asp Lys Arg Asp Gly Lys Phe Gly Pro Gln Pro
200    205   210   215
Met Ala Val Pro Pro Ala Gln Gln Met Ser Arg Phe Asp Gln Ala Thr
220    225   230   235
Pro Pro Ala Val Gly Tyr Pro Pro Gln Gln Gly Tyr Pro Pro Ser Gly
240    245   250   255
Tyr Pro Gln His Pro Pro Gln Gly Tyr Pro Pro Ser Gly Tyr Pro Gln
260    265   270   275
Asn Pro Pro Pro Ser Ala Tyr Ser Gln Tyr Pro Pro Gly Ala Tyr Pro
280    285   290   295
Pro Pro Pro Ala Tyr Pro Lys
300    305   310   315

```

(2) INFORMATION FOR SEQ ID NO:1254:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1348 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1348
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569427

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1254:

```

aaaaactcgaa aaaaagatgg cggcggtttt gcaaaactaac atccgtctgg agatcatacc 60
gggaagatcac agttctctca cccatcataa gtttcgtcgg ccgtatcgaa ttagtgcgc 120
cgccgcttca cccgtgaaaa aacggtataa catcactctg ctccccggcg atgggtatcgg 180
tccagaagtt atatctgttg ctaagaatgt gcttcagaaa gctggatttc tccaaggact 240
agagtttgat ttccaggaga tgccctttcg cggaGcagct ttggattttg tcggagttcc 300
attgcggagg gaaacttcca ctgctgctaa acagtctgat gccattctc ttggagctat 360
cggagggttac aaatgggaca agaattgaga acatctgaga cctgagatgg gctctgcttaa 420
cattcgaaga gatctcaatg tctttgctaa ttgagacct gctacagttt taccacagct 480
agttgatcgt tccacactga agaaagaagt agcacaggt gttgatata tgatttgtaag 540
ggagctcact ggaggtatatt accttgagg gccaagaggc attacgatca acgaaaatgg 600
cgaagaagtc ggttttaata cagagatcta cgctgctcac agatttgaca gaattgctcg 660
tgttgcattc gagactgcga ggaaggcg tgccaagctg tgttctgttg acaaaagccaa 720
tgctttggat gcatcaatat tctggaggaa aagagtaaca gctttagctt ctgaatatcc 780
agatgttgaa ctatcacata tgtatgtoga taatgStgcg atccagcttg tccgtgaccc 840
gaacagttt gacacaatcg tcaccaataa catttttgg gatataattg ctgatgaagc 900
ttcaatgatc actggttagca ttgggatgct tccatctgca agtcttggg aatcggggacc 960

```

tggactcttt gaacctatac atgggttcagc accagatata gctggacaag acaaggcaaa 1020
cccattggcc accattctca gtgcggcgat gcttctcaag tatggacttg gagaagaaaa 1080
ggctgcaaaag atgattgaag acgcggctgt ggatgctctg aacaaagggt tcagaaccgg 1140
agacatctac tcccccgaa ataaactggt gggatgcaag gaaatgggtg agggagttct 1200
caaatcagtg gactccaaag ttctgttta aaaaaagtgt gtacgccttg gttttactgt 1260
tactttttg ctaatacatg tattagaaac tgtattcttg tagcttttat aataataaaa 1320
tatttgggat cgattctgca attcaaa

(2) INFORMATION FOR SEQ ID NO:1255:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 409 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..409

(D) OTHER INFORMATION: / Ceres Seq. ID 1569428

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1255:

Lys Leu Glu Lys Lys Met Ala Ala Phe Leu Gln Thr Asn Ile Arg Leu
1 5 10 15
Glu Ile Ile Pro Gly Arg Tyr Ser Ser Leu Thr Asp His Lys Phe Arg
20 25 30
Ala Pro Tyr Arg Ile Arg Cys Ala Ala Ser Pro Val Lys Lys Arg
35 40 45
Tyr Asn Ile Thr Leu Leu Pro Gly Asp Gly Ile Gly Pro Glu Val Ile
50 55 60
Ser Val Ala Lys Asn Val Leu Gln Lys Ala Gly Phe Leu Gln Gly Leu
65 70 75 80
Glu Phe Asp Phe Gln Glu Met Pro Phe Gly Gly Ala Ala Leu Asp Leu
85 90 95
Val Gly Val Pro Leu Pro Glu Glu Thr Ser Thr Ala Ala Lys Gln Ser
100 105 110
Asp Ala Ile Leu Leu Gly Ala Ile Gly Gly Tyr Lys Trp Asp Lys Asn
115 120 125
Glu Lys His Leu Arg Pro Glu Met Gly Leu Leu Asn Ile Arg Arg Asp
130 135 140
Leu Asn Val Phe Ala Asn Leu Arg Pro Ala Thr Val Leu Pro Gln Leu
145 150 155
Val Asp Ala Ser Thr Leu Lys Lys Glu Val Ala Gln Gly Val Asp Met
160 165 170 175
Met Ile Val Arg Glu Leu Thr Gly Gly Ile Tyr Phe Gly Glu Pro Arg
180 185 190
Gly Ile Thr Ile Asn Glu Asn Gly Glu Glu Val Gly Phe Asn Thr Glu
195 200 205
Ile Tyr Ala Ala His Glu Ile Asp Arg Ile Ala Arg Val Ala Phe Glu
210 215 220
Thr Ala Arg Lys Arg Arg Gly Lys Leu Cys Ser Val Asp Lys Ala Asn
225 230 235 240
Val Leu Asp Ala Ser Ile Leu Trp Arg Lys Arg Val Thr Ala Leu Ala
245 250 255
Ser Glu Tyr Pro Asp Val Glu Leu Ser His Met Tyr Val Asp Asn Xaa
260 265 270
Ala Met Gln Leu Val Arg Asp Pro Lys Gln Phe Asp Thr Ile Val Thr
275 280 285
Asn Asn Ile Phe Gly Asp Ile Leu Ser Asp Glu Ala Ser Met Ile Thr
290 295 300
Gly Ser Ile Gly Met Leu Pro Ser Ala Ser Leu Gly Glu Ser Gly Pro
305 310 315 320
Gly Leu Phe Glu Pro Ile His Gly Ser Ala Pro Asp Ile Ala Gly Gln
325 330 335

Asp Lys Ala Asn Pro Leu Ala Thr Ile Leu Ser Ala Ala Met Leu Leu
340 345 350
Lys Tyr Gly Leu Gly Glu Glu Lys Ala Ala Lys Met Ile Glu Asp Ala
355 360 365
Val Val Asp Ala Leu Asn Lys Gly Phe Arg Thr Gly Asp Ile Tyr Ser
370 375 380
Pro Gly Asn Lys Leu Val Gly Cys Lys Glu Met Gly Glu Glu Val Leu
385 390 395 400
Lys Ser Val Asp Ser Lys Val Pro Val
405

(2) INFORMATION FOR SEQ ID NO:1256:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 404 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..404

(D) OTHER INFORMATION: / Ceres Seq. ID 1569429

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1256:

Met Ala Ala Phe Leu Gln Thr Asn Ile Arg Leu Glu Ile Ile Pro Gly
1 5 10 15
Arg Tyr Ser Ser Leu Thr Asp His Lys Phe Arg Ala Pro Tyr Arg Ile
20 25 30
Arg Cys Ala Ala Ala Ser Pro Val Lys Lys Arg Tyr Asn Ile Thr Leu
35 40 45
Leu Pro Gly Asp Gly Ile Gly Pro Glu Val Ile Ser Val Ala Lys Asn
50 55 60
Val Leu Gln Lys Ala Gly Phe Leu Gln Gly Leu Glu Phe Asp Phe Gln
65 70 75 80
Glu Met Pro Phe Gly Gly Ala Ala Leu Asp Leu Val Gly Val Pro Leu
85 90 95
Pro Glu Glu Thr Ser Thr Ala Ala Lys Gln Ser Asp Ala Ile Leu Leu
100 105 110
Gly Ala Ile Gly Gly Tyr Lys Trp Asp Lys Asn Glu Lys His Leu Arg
115 120 125
Pro Glu Met Gly Leu Leu Asn Ile Arg Arg Asp Leu Asn Val Phe Ala
130 135 140
Asn Leu Arg Pro Ala Thr Val Leu Pro Gln Leu Val Asp Ala Ser Thr
145 150 155 160
Leu Lys Lys Glu Val Ala Gln Gly Val Asp Met Met Ile Val Arg Glu
165 170 175
Leu Thr Gly Gly Ile Tyr Phe Gly Glu Pro Arg Gly Ile Thr Ile Asn
180 185 190
Glu Asn Gly Glu Glu Val Gly Phe Asn Thr Glu Ile Tyr Ala Ala His
195 200 205
Glu Ile Asp Arg Ile Ala Arg Val Ala Phe Glu Thr Ala Arg Lys Arg
210 215 220
Arg Gly Lys Leu Cys Ser Val Asp Lys Ala Asn Val Leu Asp Ala Ser
225 230 235 240
Ile Leu Trp Arg Lys Arg Val Thr Ala Leu Ala Ser Glu Tyr Pro Asp
245 250 255
Val Glu Leu Ser His Met Tyr Val Asp Asn Xaa Ala Met Gln Leu Val
260 265 270
Arg Asp Pro Lys Gln Phe Asp Thr Ile Val Thr Asn Asn Ile Phe Gly
275 280 285
Asp Ile Leu Ser Asp Glu Ala Ser Met Ile Thr Gly Ser Ile Gly Met
290 295 300
Leu Pro Ser Ala Ser Leu Gly Glu Ser Gly Pro Gly Leu Phe Glu Pro

305	310	315	320
Ile His Gly Ser Ala Pro Asp Ile Ala Gly Gln Asp Lys Ala Asn Pro			
	325	330	335
Leu Ala Thr Ile Leu Ser Ala Ala Met Leu Leu Lys Tyr Gly Leu Gly			
	340	345	350
Glu Glu Lys Ala Ala Lys Met Ile Glu Asp Ala Val Val Asp Ala Leu			
	355	360	365
Asn Lys Gly Phe Arg Thr Gly Asp Ile Tyr Ser Pro Gly Asn Lys Leu			
	370	375	380
Val Gly Cys Lys Glu Met Gly Glu Glu Val Leu Lys Ser Val Asp Ser			
	385	390	400
Lys Val Pro Val			

(2) INFORMATION FOR SEQ ID NO:1257:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 323 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..323
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569430

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1257:

Met Pro Phe Gly Gly Ala Ala Leu Asp Leu Val Gly Val Pro Leu Pro			
1	5	10	15
Glu Glu Thr Ser Thr Ala Ala Lys Gln Ser Asp Ala Ile Leu Leu Gly			
	20	25	30
Ala Ile Gly Gly Tyr Lys Trp Asp Lys Asn Glu Lys His Leu Arg Pro			
	35	40	45
Glu Met Gly Leu Leu Asn Ile Arg Arg Asp Leu Asn Val Phe Ala Asn			
	50	55	60
Leu Arg Pro Ala Thr Val Leu Pro Gln Leu Val Asp Ala Ser Thr Leu			
	65	70	75
Lys Lys Glu Val Ala Gln Gly Val Asp Met Met Ile Val Arg Glu Leu			
	85	90	95
Thr Gly Gly Ile Tyr Phe Gly Glu Pro Arg Gly Ile Thr Ile Asn Glu			
	100	105	110
Asn Gly Glu Glu Val Gly Phe Asn Thr Glu Ile Tyr Ala Ala His Glu			
	115	120	125
Ile Asp Arg Ile Ala Arg Val Ala Phe Glu Thr Ala Arg Lys Arg Arg			
	130	135	140
Gly Lys Leu Cys Ser Val Asp Lys Ala Asn Val Leu Asp Ala Ser Ile			
	145	150	155
Leu Trp Arg Lys Arg Val Thr Ala Leu Ala Ser Glu Tyr Pro Asp Val			
	165	170	175
Glu Leu Ser His Met Tyr Val Asp Asn Xaa Ala Met Gln Leu Val Arg			
	180	185	190
Asp Pro Lys Gln Phe Asp Thr Ile Val Thr Asn Asn Ile Phe Gly Asp			
	195	200	205
Ile Leu Ser Asp Glu Ala Ser Met Ile Thr Gly Ser Ile Gly Met Leu			
	210	215	220
Pro Ser Ala Ser Leu Glu Ser Gly Pro Gly Leu Phe Glu Pro Ile			
	225	230	235
His Gly Ser Ala Pro Asp Ile Ala Gly Gln Asp Lys Ala Asn Pro Leu			
	245	250	255
Ala Thr Ile Leu Ser Ala Ala Met Leu Leu Lys Tyr Gly Leu Gly Glu			
	260	265	270
Glu Lys Ala Ala Lys Met Ile Glu Asp Ala Val Val Asp Ala Leu Asn			
	275	280	285

Lys Gly Phe Arg Thr Gly Asp Ile Tyr Ser Pro Gly Asn Lys Leu Val
290 295 300
Gly Cys Lys Glu Met Gly Glu Glu Val Leu Lys Ser Val Asp Ser Lys
305 310 315 320
Val Pro Val

(2) INFORMATION FOR SEQ ID NO:1258:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1475 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1475
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569435

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1258:

gtgatctatc	tttgaatctc	aaaagcatac	ttgagagaga	tctgtttcga	taatttgctt	60
caatcacgct	gtttaatggc	gccgtagGag	tggaggcgag	acctcctgtg	acagcgatgg	120
aggaaacctg	caacgtttaa	ggagcggcgg	cgaaacaagg	agaagggtct	aacaagtact	180
acctccagca	ctctgatgag	ctccagcgcc	tgcaacgcga	aaagtctgat	aaccttaatc	240
gtcttgaagc	tcagaggaat	gaactcaatt	ctcgagtacg	aatgctcaga	gaagagttac	300
agctcctcca	agaaacctgg	tcctatgtgg	gtgaagtgtg	aaaagtgtat	ggaaaaaaca	360
aggtcttggt	taaggttcat	ccagagggga	agtatgttgt	cgatattgac	aaaagtatag	420
acataacgaa	actcactcca	tcaacgagag	tgctctctcg	taatgatagc	tatgttctcc	480
acctgtgtct	gccaaagtaa	gtagatccct	tggttaacct	tatgaaagt	gagaagggtc	540
cagactccac	atatgacatg	attggtggct	ttgaccagca	aatcaaggaa	ataaaggagg	600
tcattgaact	gccaatcaag	catcctgaat	tgtttgagtc	tcttggaatt	gcgcagccaa	660
agggtgtgtt	gtttgacggt	ccacctggaa	ctgggaagac	actattggct	cgggctgtgg	720
cacatcacac	tgaactgtact	ttcatcagag	tttctggttc	tgagctggtc	cagaaataca	780
tttgagaagg	ttctagaatg	gtcagagaaac	tttttgtgat	ggcaaggagg	catgcaccat	840
caatcatctt	catggatgaa	atcgatagta	tcgggtctgc	tcgtatggaa	tcgtgttagtg	900
gaaatggtga	cagtgaggtg	caaaggacta	tgcttgagct	tctcaatcaa	cttgaccgat	960
tcgagggcgt	aaacaaaatc	aaggttttga	tggctacaaa	tcgtattgat	attctggatc	1020
aagctcttct	ccggcctgga	aggattgata	ggaaaaattg	atttctaat	octaatgaag	1080
agtcacgttt	tgatatcttg	aagatacact	caaggaaaaa	gaatttgatg	cgtggaatcg	1140
atctgaaaaa	gattgcagag	aagatgaatg	gtgcttcagg	tgctgagctg	aaggctgtat	1200
gcacggaggc	gggcatgttt	gcacttcgtg	agaggagagt	acatgtgact	caggaagact	1260
ttgagatggc	tgtagcgaag	gtaatgaaga	aagacacaga	gaagaacatg	tctctgcgta	1320
agctctggaa	gtaggaaatt	cagagtcaca	gattaatttc	tcttacttgt	tctctactgt	1380
ctgtggttct	ttctgaaacc	ttttcggtca	gcgctttaa	cttttctaaa	caatgtttgt	1440
acactagttt	ctattcattc	aattggttgt	tcagc			

(2) INFORMATION FOR SEQ ID NO:1259:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 419 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..419
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569436

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1259:

Met	Ala	Ala	Val	Gly	Val	Glu	Ala	Arg	Pro	Val	Thr	Ala	Met	Glu
1			5						10				15	
Glu	Thr	Cys	Asn	Val	Lys	Gly	Ala	Ala	Lys	Gln	Gly	Glu	Gly	Leu
			20					25				30		
Asn	Lys	Tyr	Tyr	Leu	Gln	His	Leu	Asp	Glu	Leu	Gln	Arg	Leu	Arg
			35				40					45		

Glu	Lys	Ser	Tyr	Asn	Leu	Asn	Arg	Leu	Glu	Ala	Gln	Arg	Asn	Glu	Leu
50						55					60				
Asn	Ser	Arg	Val	Arg	Met	Leu	Arg	Glu	Glu	Leu	Gln	Leu	Leu	Gln	Glu
65					70					75				80	
Pro	Gly	Ser	Tyr	Val	Gly	Glu	Val	Val	Lys	Val	Met	Gly	Lys	Asn	Lys
				85					90					95	
Val	Leu	Val	Lys	Val	His	Pro	Glu	Gly	Lys	Tyr	Val	Val	Asp	Ile	Asp
				100					105				110		
Lys	Ser	Ile	Asp	Ile	Thr	Lys	Leu	Thr	Pro	Ser	Thr	Arg	Val	Ala	Leu
				115					120				125		
Arg	Asn	Asp	Ser	Tyr	Val	Leu	His	Leu	Val	Leu	Pro	Ser	Lys	Val	Asp
				130				135			140				
Pro	Leu	Val	Asn	Leu	Met	Lys	Val	Glu	Lys	Val	Pro	Asp	Ser	Thr	Tyr
				145				150			155				160
Asp	Met	Ile	Gly	Gly	Leu	Asp	Gln	Gln	Ile	Lys	Glu	Ile	Lys	Glu	Val
				165					170					175	
Ile	Glu	Leu	Pro	Ile	Lys	His	Pro	Glu	Leu	Phe	Glu	Ser	Leu	Gly	Ile
				180					185					190	
Ala	Gln	Pro	Lys	Gly	Val	Leu	Leu	Tyr	Gly	Pro	Pro	Gly	Thr	Gly	Lys
				195				200					205		
Thr	Leu	Leu	Ala	Arg	Ala	Val	Ala	His	His	Thr	Asp	Cys	Thr	Phe	Ile
				210				215				220			
Arg	Val	Ser	Gly	Ser	Glu	Leu	Val	Gln	Lys	Tyr	Ile	Gly	Glu	Gly	Ser
				225				230			235				240
Arg	Met	Val	Arg	Glu	Leu	Phe	Val	Met	Ala	Arg	Glu	His	Ala	Pro	Ser
				245					250					255	
Ile	Ile	Phe	Met	Asp	Glu	Ile	Asp	Ser	Ile	Gly	Ser	Ala	Arg	Met	Glu
				260					265					270	
Ser	Gly	Ser	Gly	Asn	Gly	Asp	Ser	Glu	Val	Gln	Arg	Thr	Met	Leu	Glu
				275				280					285		
Leu	Leu	Asn	Gln	Leu	Asp	Gly	Phe	Glu	Ala	Ser	Asn	Lys	Ile	Lys	Val
				290				295				300			
Leu	Met	Ala	Thr	Asn	Arg	Ile	Asp	Ile	Leu	Asp	Gln	Ala	Leu	Leu	Arg
				305				310				315			320
Pro	Gly	Arg	Ile	Asp	Arg	Lys	Ile	Glu	Phe	Pro	Asn	Pro	Asn	Glu	Glu
				325					330					335	
Ser	Arg	Phe	Asp	Ile	Leu	Lys	Ile	His	Ser	Arg	Lys	Met	Asn	Leu	Met
				340					345				350		
Arg	Gly	Ile	Asp	Leu	Lys	Lys	Ile	Ala	Glu	Lys	Met	Asn	Gly	Ala	Ser
				355					360				365		
Gly	Ala	Glu	Leu	Lys	Ala	Val	Cys	Thr	Glu	Ala	Gly	Met	Phe	Ala	Leu
				370			375				380				
Arg	Glu	Arg	Arg	Val	His	Val	Thr	Gln	Glu	Asp	Phe	Glu	Met	Ala	Val
				385			390			395					400
Ala	Lys	Val	Met	Lys	Lys	Asp	Thr	Glu	Lys	Asn	Met	Ser	Leu	Arg	Lys
				405					410					415	

(2) INFORMATION FOR SEQ ID NO:1260:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 405 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..405

(D) OTHER INFORMATION: / Ceres Seq. ID 1569437

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1260:

Met Glu Glu Thr Cys Asn Val Lys Gly Ala Ala Ala Lys Gln Gly Glu

1 5 10 15
Gly Leu Asn Lys Tyr Tyr Leu Gln His Leu Asp Glu Leu Gln Arg Leu
20 25 30
Gln Arg Glu Lys Ser Tyr Asn Leu Asn Arg Leu Glu Ala Gln Arg Asn
35 40 45
Glu Leu Asn Ser Arg Val Arg Met Leu Arg Glu Glu Leu Gln Leu Leu
50 55 60
Gln Glu Pro Gly Ser Tyr Val Gly Glu Val Val Lys Val Met Gly Lys
65 70 75 80
Asn Lys Val Leu Val Lys Val His Pro Glu Gly Lys Tyr Val Val Asp
85 90 95
Ile Asp Lys Ser Ile Asp Ile Thr Lys Leu Thr Pro Ser Thr Arg Val
100 105 110
Ala Leu Arg Asn Asp Ser Tyr Val Leu His Leu Val Leu Pro Ser Lys
115 120 125
Val Asp Pro Leu Val Asn Leu Met Lys Val Glu Lys Val Pro Asp Ser
130 135 140
Thr Tyr Asp Met Ile Gly Gly Leu Asp Gln Gln Ile Lys Glu Ile Lys
145 150 155 160
Glu Val Ile Glu Leu Pro Ile Lys His Pro Glu Leu Phe Glu Ser Leu
165 170 175
Gly Ile Ala Gln Pro Lys Gly Val Leu Leu Tyr Gly Pro Pro Gly Thr
180 185 190
Gly Lys Thr Leu Leu Ala Arg Ala Val Ala His His Thr Asp Cys Thr
195 200 205
Phe Ile Arg Val Ser Gly Ser Glu Leu Val Gln Lys Tyr Ile Gly Glu
210 215 220
Gly Ser Arg Met Val Arg Glu Leu Phe Val Met Ala Arg Glu His Ala
225 230 235 240
Pro Ser Ile Ile Phe Met Asp Glu Ile Asp Ser Ile Gly Ser Ala Arg
245 250 255
Met Glu Ser Gly Ser Gly Asn Gly Asp Ser Glu Val Gln Arg Thr Met
260 265 270
Leu Glu Leu Leu Asn Gln Leu Asp Gly Phe Glu Ala Ser Asn Lys Ile
275 280 285
Lys Val Leu Met Ala Thr Asn Arg Ile Asp Ile Leu Asp Gln Ala Leu
290 295 300
Leu Arg Pro Gly Arg Ile Asp Arg Lys Ile Glu Phe Pro Asn Pro Asn
305 310 315 320
Glu Glu Ser Arg Phe Asp Ile Leu Lys Ile His Ser Arg Lys Met Asn
325 330 335
Leu Met Arg Gly Ile Asp Leu Lys Lys Ile Ala Glu Lys Met Asn Gly
340 345 350
Ala Ser Gly Ala Glu Leu Lys Ala Val Cys Thr Glu Ala Gly Met Phe
355 360 365
Ala Leu Arg Glu Arg Arg Val His Val Thr Gln Glu Asp Phe Glu Met
370 375 380
Ala Val Ala Lys Val Met Lys Lys Asp Thr Glu Lys Asn Met Ser Leu
385 390 395 400
Arg Lys Leu Trp Lys
405

(2) INFORMATION FOR SEQ ID NO:1261:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 350 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..350

(D) OTHER INFORMATION: / Ceres Seq. ID 1569438

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1261:

Met	Leu	Arg	Glu	Glu	Leu	Gln	Leu	Leu	Gln	Pro	Gly	Ser	Tyr	Val
1			5						10				15	
Gly	Glu	Val	Val	Lys	Val	Met	Gly	Lys	Asn	Lys	Val	Leu	Val	Lys
			20				25					30		
His	Pro	Glu	Gly	Lys	Tyr	Val	Val	Asp	Ile	Asp	Lys	Ser	Ile	Asp
			35				40					45		
Thr	Lys	Leu	Thr	Pro	Ser	Thr	Arg	Val	Ala	Leu	Arg	Asn	Asp	Ser
			50				55				60			
Val	Leu	His	Leu	Val	Leu	Pro	Ser	Lys	Val	Asp	Pro	Leu	Val	Asn
65					70				75					80
Met	Lys	Val	Glu	Lys	Val	Pro	Asp	Ser	Thr	Tyr	Asp	Met	Ile	Gly
			85						90				95	
Leu	Asp	Gln	Gln	Ile	Lys	Glu	Ile	Lys	Glu	Val	Ile	Glu	Leu	Pro
			100					105				110		
Lys	His	Pro	Glu	Leu	Phe	Glu	Ser	Leu	Gly	Ile	Ala	Gln	Pro	Lys
			115				120					125		
Val	Leu	Leu	Tyr	Gly	Pro	Pro	Gly	Thr	Gly	Lys	Thr	Leu	Leu	Ala
			130				135				140			
Ala	Val	Ala	His	His	Thr	Asp	Cys	Thr	Phe	Ile	Arg	Val	Ser	Gly
145					150				155					160
Glu	Leu	Val	Gln	Lys	Tyr	Ile	Gly	Glu	Gly	Ser	Arg	Met	Val	Arg
			165					170					175	
Leu	Phe	Val	Met	Ala	Arg	Glu	His	Ala	Pro	Ser	Ile	Ile	Phe	Met
			180					185					190	
Glu	Ile	Asp	Ser	Ile	Gly	Ser	Ala	Arg	Met	Glu	Ser	Gly	Ser	Gly
			195				200					205		
Gly	Asp	Ser	Glu	Val	Gln	Arg	Thr	Met	Leu	Glu	Leu	Leu	Asn	Gln
			210				215				220			
Asp	Gly	Phe	Glu	Ala	Ser	Asn	Lys	Ile	Lys	Val	Leu	Met	Ala	Thr
225					230					235				240
Arg	Ile	Asp	Ile	Leu	Asp	Gln	Ala	Leu	Leu	Arg	Pro	Gly	Arg	Ile
			245						250				255	
Arg	Lys	Ile	Glu	Phe	Pro	Asn	Pro	Asn	Glu	Glu	Ser	Arg	Phe	Asp
			260					265					270	
Leu	Lys	Ile	His	Ser	Arg	Lys	Met	Asn	Leu	Met	Arg	Gly	Ile	Asp
			275				280					285		
Lys	Lys	Ile	Ala	Glu	Lys	Met	Asn	Gly	Ala	Ser	Gly	Ala	Glu	Leu
			290				295				300			
Ala	Val	Cys	Thr	Glu	Ala	Gly	Met	Phe	Ala	Leu	Arg	Glu	Arg	Val
305					310				315					320
His	Val	Thr	Gln	Glu	Asp	Phe	Glu	Met	Ala	Val	Ala	Lys	Val	Met
			325					330					335	
Lys	Asp	Thr	Glu	Lys	Asn	Met	Ser	Leu	Arg	Lys	Leu	Trp	Lys	
			340					345					350	

(2) INFORMATION FOR SEQ ID NO:1262:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1188 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1188

(D) OTHER INFORMATION: / Ceres Seq. ID 1569439

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1262:

aatctagaac	aagaaaccaa	aacatacacc	actctgttt	ttaaaggtaa	aaaagatcaa	60
gaagaaacca	aagaaatca	gacagcaaca	agaaaagatc	agtttttaag	agaaggaaag	120
taggaaacgg	gtcagattgt	tggatagaga	gaggaagcga	aaaaagagtc	gcagtgttct	180

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ttttccactg cgtgggtttg gtataatcag ctgtggctac aacgaggagg cataatctac 240
cgacgtcgga ttccgggtgc ttaccgcact gggcgggcac gacgacgaca cttccocgtg 300
ccaccgagga tctctctctt ggtttcaatg ctggttccctc cgctcatccac ggtgggtttag 360
gctcagcttc agtcgcgcgc ggCgttccat catggcctccc gggatctctct gtccgtttacg 420
gcctacacctc ttccggcgggc gcgacggaga tgggcatggt tgggtctaaga gatgttttcc 480
ttgttgctcc gggtttatcac caccagaacgc ccggagtgat atctggatgcc gatcatatga 540
acagtaatgc agctgcggcg gcggcgctcg ctgtcggagt gattcctcta ctcacggcgg 600
gtccaccgca gcaaaaactg gaagactccg acattaaact cctcggaaac aaccggagat 660
ggcagaataa caacaacaac caccgaaacgc agtatcttca cttcaagagt actaacgaga 720
caacggtcgg aacgagctcg aacaactcgg ggtctggctc aggcgcatac ggaaccggcca 780
cgtgtcaaga ctgtggaaat caggcggaaga aagaatgtaa gcagaggcgg ttaggactt 840
gctgcgaagg cgtggctctt gatgtttcta ctcaagtgaa gagcacgtgg gtctctgctg 900
ctcggcgagg agagaggcag gtcacGccta ccggcgctaa tccaacggct ggctctgtct 960
tttcgacctc ctccgggagc aagaagccga ggatcgtagg gtctcaacaa caacaacaac 1020
aacaacaaca aacaacaagc acttctcata cttcaacttc taacacacca cctcaaaagt 1080
tcgagaccag ctccagccga caaggtagtt ttacattttc attagtatac atagctacat 1140
gattttatgt atgtatatat atgcataata cactattagc ccttcttg

```

(2) INFORMATION FOR SEQ ID NO:1263:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 230 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..230

(D) OTHER INFORMATION: / Ceres Seq. ID 1569440

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1263:

```

Met Gly Met Val Gly Leu Arg Asp Val Phe Leu Val Ala Pro Ala Tyr
1 5 10 15
His His Gln Asn Ala Gly Val Ile Ser Gly Ser Asp His Met Asn Ser
20 25 30
Asn Ala Ala Ala Ala Ala Leu Ala Val Gly Val Ile Pro Leu Leu
35 40 45
Thr Ala Gly Pro Pro Gln Gln Asn Val Glu Asp Ser Asp Ile Asn Phe
50 55 60
Leu Gly Asn Asn Arg Arg Trp Gln Asn Asn Asn Asn His Glu Thr
65 70 75 80
Gln Tyr Leu His Phe Pys Ser Thr Asn Gln Thr Thr Val Gly Thr Ser
85 90 95
Ser Asn Asn Ser Gly Ser Gly Ser Gly Ala Ser Gly Thr Ala Thr Cys
100 105 110
Gln Asp Cys Gly Asn Gln Ala Lys Lys Glu Cys Lys Gln Arg Arg Cys
115 120 125
Arg Thr Cys Cys Lys Ser Arg Gly Phe Asp Cys Ser Thr His Val Lys
130 135 140
Ser Thr Trp Val Ser Ala Ala Arg Arg Arg Glu Arg Gln Val Met Pro
145 150 155 160
Thr Gly Ala Asn Pro Thr Ala Gly Ser Ser Leu Ser Thr Ser Ser Gly
165 170 175
Thr Lys Lys Pro Arg Ile Val Gly Ser Gln Gln Gln Gln Gln Gln
180 185 190
Gln Gln Gln Gln Ala Thr Ser His Thr Ser Thr Ser Asn Thr Pro Pro
195 200 205
Gln Ser Phe Glu Thr Ser Ser Ser Arg Gln Gly Ser Phe Thr Phe Ser
210 215 220
Leu Val Tyr Ile Ala Thr
225 230

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(2) INFORMATION FOR SEQ ID NO:1264:

(i) SEQUENCE CHARACTERISTICS:

SEQUENCE LISTING

- (A) LENGTH: 228 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..228
(D) OTHER INFORMATION: / Ceres Seq. ID 1569441
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1264:

Met Val Gly Leu Arg Asp Val Phe Leu Val Ala Pro Ala Tyr His His
1 5 10 15
Gln Asn Ala Gly Val Ile Ser Gly Ser Asp His Met Asn Ser Asn Ala
20 25 30
Ala Ala Ala Ala Ala Leu Ala Val Gly Val Ile Pro Leu Leu Thr Ala
35 40 45
Gly Pro Pro Gln Gln Asn Val Glu Asp Ser Asp Ile Asn Phe Leu Gly
50 55 60
Asn Asn Arg Arg Trp Gln Asn Asn Asn Asn His Glu Thr Gln Tyr
65 70 75 80
Leu His Phe Lys Ser Thr Asn Gln Thr Thr Val Gly Thr Ser Ser Asn
85 90 95
Asn Ser Gly Ser Gly Ser Gly Ala Ser Gly Thr Ala Thr Cys Gln Asp
100 105 110
Cys Gly Asn Gln Ala Lys Lys Glu Cys Lys Gln Arg Arg Cys Arg Thr
115 120 125
Cys Cys Lys Ser Arg Gly Phe Asp Cys Ser Thr His Val Lys Ser Thr
130 135 140
Trp Val Ser Ala Ala Arg Arg Arg Glu Arg Gln Val Met Pro Thr Gly
145 150 155 160
Ala Asn Pro Thr Ala Gly Ser Ser Leu Ser Thr Ser Ser Gly Thr Lys
165 170 175
Lys Pro Arg Ile Val Gly Ser Gln Gln Gln Gln Gln Gln Gln
180 185 190
Gln Gln Ala Thr Ser His Thr Ser Thr Ser Asn Thr Pro Pro Gln Ser
195 200 205
Phe Glu Thr Ser Ser Ser Arg Gln Gly Ser Phe Thr Phe Ser Leu Val
210 215 220
Tyr Ile Ala Thr
225

(2) INFORMATION FOR SEQ ID NO:1265:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 201 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..201
(D) OTHER INFORMATION: / Ceres Seq. ID 1569442

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1265:

Met Asn Ser Asn Ala Ala Ala Ala Ala Ala Leu Ala Val Gly Val Ile
1 5 10 15
Pro Leu Leu Thr Ala Gly Pro Pro Gln Gln Asn Val Glu Asp Ser Asp
20 25 30
Ile Asn Phe Leu Gly Asn Asn Arg Arg Trp Gln Asn Asn Asn Asn Asn
35 40 45
His Glu Thr Gln Tyr Leu His Phe Lys Ser Thr Asn Gln Thr Thr Val
50 55 60
Gly Thr Ser Ser Asn Asn Ser Gly Ser Gly Ser Gly Ala Ser Gly Thr

65	70	75	80
Ala Thr Cys Gln Asp Cys Gly Asn Gln Ala Lys Lys Glu Cys Lys Gln			
	85	90	95
Arg Arg Cys Arg Thr Cys Cys Lys Ser Arg Gly Phe Asp Cys Ser Thr			
	100	105	110
His Val Lys Ser Thr Trp Val Ser Ala Ala Arg Arg Arg Glu Arg Gln			
	115	120	125
Val Met Pro Thr Thr Gly Ala Asn Pro Thr Ala Gly Ser Ser Leu Ser Thr			
	130	135	140
Ser Ser Gly Thr Lys Lys Pro Arg Ile Val Gly Ser Gln Gln Gln Gln			
	145	150	155
Gln Gln Gln Gln Gln Gln Gln Ala Thr Ser His Thr Ser Thr Ser Asn			
	165	170	175
Thr Pro Pro Gln Ser Phe Glu Thr Ser Ser Ser Arg Gln Gly Ser Phe			
	180	185	190
Thr Phe Ser Leu Val Tyr Ile Ala Thr			
	195	200	

(2) INFORMATION FOR SEQ ID NO:1266:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1210 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1210
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569451

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1266:

tcaatggtga	tacttttgat	gagaaatcca	ggattctcga	tcctaataagg	atgattcagag	60
cttacactca	atctgcagct	actttgaato	ttcttagagc	ctttgccact	ggaggttacg	120
ctgcattcca	aagagttact	caatggaacc	tgatttttgt	tgaacaaagt	gagcaagctg	180
acaggtacca	ggagtttagc	aacagggttg	atgagccctt	ggggttcagt	ctctcatgtg	240
gacttggcac	ggatcatcca	cttatgacta	caactgattt	ctacacatcc	catgagtgtt	300
tgctctgcc	ttatgaacag	tcccttacc	ggttggattc	aactcttgtt	ctctactatg	360
attgtcttgc	acacatggct	tggtgcggag	agcgtaccag	acaattggat	ggcgcctaag	420
tcgagtttct	cagggggatt	gctaactctc	tgggcattaa	gggtgagcac	aaaatggatc	480
ccaatgagct	ggttaaagct	gtagaaatcc	tgaatcctaa	taacaagcct	ggaagaatca	540
ctgtaattgt	gagaatgggt	gctgagaaca	tgagagttaa	ggttccccac	ctgatcagag	600
cagtcgccag	atcaggccag	attgtgacat	gggtctgcga	tccaatgcac	ggaacaccca	660
tcaaagcaCc	ttgcggtctt	aaaacacgtg	cccttgactc	aatactggct	gaagtccagag	720
cattctctga	tgtgcacag	caagaaggaa	gtcacgcggg	cggatctcat	ctcagagatg	780
caggtcaagaa	cgtgacagaa	gtgattggag	gggtccgcac	tgtgacctac	gatgacctca	840
gttctcgtca	ccacacacac	tgtgacctaa	gggtgaacgc	gtcacagtct	cttgaaactg	900
cttctcattg	tgcagaacgc	ctcaggaaga	gaagaacgcg	tagccagcgt	gtgtctttgag	960
tcgggtttct	cccttttata	cactttttga	ttccaaacaa	ctctttttct	tttgtctcgt	1020
gaactgtgag	tggtgtcttt	atgacttaag	ttaaaagccc	aaaagcctct	ctaggaggag	1080
taaaacctgt	tctgtctgtg	acagaccatg	tcagtctcat	gtctctttag	ttactcttaa	1140
tgtcaaaccc	tgtgacttac	actagtgtat	atttattttt	acgtatctac	acaaacatga	1200
aacttggtct						

(2) INFORMATION FOR SEQ ID NO:1267:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 318 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..318
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569452

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1267:

Asn	Gly	Asp	Thr	Phe	Asp	Glu	Lys	Ser	Arg	Ile	Pro	Asp	Pro	Asn	Arg
1				5					10					15	
Met	Ile	Arg	Ala	Tyr	Thr	Gln	Ser	Ala	Ala	Thr	Leu	Asn	Leu	Leu	Arg
			20					25					30		
Ala	Phe	Ala	Thr	Gly	Gly	Tyr	Ala	Ala	Ile	Gln	Arg	Val	Thr	Gln	Trp
		35					40					45			
Asn	Leu	Asp	Phe	Val	Glu	Gln	Ser	Glu	Gln	Ala	Asp	Arg	Tyr	Gln	Glu
	50				55					60					
Leu	Ala	Asn	Arg	Val	Asp	Glu	Ala	Leu	Gly	Phe	Met	Ser	Ala	Cys	Gly
	65				70				75					80	
Leu	Gly	Thr	Asp	His	Pro	Leu	Met	Thr	Thr	Asp	Phe	Tyr	Thr	Ser	
			85					90					95		
His	Glu	Cys	Leu	Leu	Pro	Tyr	Glu	Gln	Ser	Leu	Thr	Arg	Leu	Asp	
		100					105						110		
Ser	Thr	Ser	Gly	Leu	Tyr	Tyr	Asp	Cys	Ser	Ala	His	Met	Val	Trp	Cys
		115					120					125			
Gly	Glu	Arg	Thr	Arg	Gln	Leu	Asp	Gly	Ala	His	Val	Glu	Phe	Leu	Arg
	130				135						140				
Gly	Ile	Ala	Asn	Pro	Leu	Gly	Ile	Lys	Val	Ser	Asn	Lys	Met	Asp	Pro
	145				150					155				160	
Asn	Glu	Leu	Val	Lys	Leu	Val	Glu	Ile	Leu	Asn	Pro	Asn	Asn	Lys	Pro
			165						170					175	
Gly	Arg	Ile	Thr	Val	Ile	Val	Arg	Met	Gly	Ala	Glu	Asn	Met	Arg	Val
		180					185						190		
Lys	Leu	Pro	His	Leu	Ile	Arg	Ala	Val	Arg	Arg	Ser	Gly	Gln	Ile	Val
		195					200					205			
Thr	Trp	Val	Cys	Asp	Pro	Met	His	Gly	Asn	Thr	Ile	Lys	Ala	Pro	Cys
	210					215					220				
Gly	Leu	Lys	Thr	Arg	Ala	Phe	Asp	Ser	Ile	Leu	Ala	Glu	Val	Arg	Ala
	225				230					235				240	
Phe	Leu	Asp	Val	His	Glu	Gln	Glu	Gly	Ser	His	Ala	Gly	Gly	Ile	His
		245						250						255	
Leu	Glu	Met	Thr	Gly	Gln	Asn	Val	Thr	Glu	Cys	Ile	Gly	Gly	Ser	Arg
		260					265						270		
Thr	Val	Thr	Tyr	Asp	Asp	Leu	Ser	Ser	Arg	Tyr	His	Thr	His	Cys	Asp
		275					280					285			
Pro	Arg	Leu	Asn	Ala	Ser	Gln	Ser	Leu	Glu	Leu	Ala	Phe	Ile	Val	Ala
	290					295					300				
Glu	Arg	Leu	Arg	Lys	Arg	Arg	Thr	Gly	Ser	Gln	Arg	Val	Ser		
	305			310						315					

(2) INFORMATION FOR SEQ ID NO:1268:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 302 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..302

(D) OTHER INFORMATION: / Ceres Seq. ID 1569453

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1268:

Met	Ile	Arg	Ala	Tyr	Thr	Gln	Ser	Ala	Ala	Thr	Leu	Asn	Leu	Leu	Arg
1				5					10					15	
Ala	Phe	Ala	Thr	Gly	Gly	Tyr	Ala	Ala	Ile	Gln	Arg	Val	Thr	Gln	Trp
		20					25						30		
Asn	Leu	Asp	Phe	Val	Glu	Gln	Ser	Glu	Gln	Ala	Asp	Arg	Tyr	Gln	Glu
		35				40					45				
Leu	Ala	Asn	Arg	Val	Asp	Glu	Ala	Leu	Gly	Phe	Met	Ser	Ala	Cys	Gly
	50				55						60				

Leu Gly Thr Asp His Pro Leu Met Thr Thr Thr Asp Phe Tyr Thr Ser
65 70 75 80
His Glu Cys Leu Leu Pro Tyr Glu Gln Ser Leu Thr Arg Leu Asp
85 90 95
Ser Thr Ser Gly Leu Tyr Tyr Asp Cys Ser Ala His Met Val Trp Cys
100 105 110
Gly Glu Arg Thr Arg Gln Leu Asp Gly Ala His Val Glu Phe Leu Arg
115 120 125
Gly Ile Ala Asn Pro Leu Gly Ile Lys Val Ser Asn Lys Met Asp Pro
130 135 140
Asn Glu Leu Val Lys Leu Val Glu Ile Leu Asn Pro Asn Asn Lys Pro
145 150 155 160
Gly Arg Ile Thr Val Ile Val Arg Met Gly Ala Glu Asn Met Arg Val
165 170 175
Lys Leu Pro His Leu Ile Arg Ala Val Arg Arg Ser Gly Gln Ile Val
180 185 190
Thr Trp Val Cys Asp Pro Met His Gly Asn Thr Ile Lys Ala Pro Cys
195 200 205
Gly Leu Lys Thr Arg Ala Phe Asp Ser Ile Leu Ala Glu Val Arg Ala
210 215 220
Phe Leu Asp Val His Glu Gln Glu Gly Ser His Ala Gly Gly Ile His
225 230 235 240
Leu Glu Met Thr Gly Gln Asn Val Thr Glu Cys Ile Gly Gly Ser Arg
245 250 255
Thr Val Thr Tyr Asp Asp Leu Ser Ser Arg Tyr His Thr Cys Asp
260 265 270
Pro Arg Leu Asn Ala Ser Gln Ser Leu Glu Leu Ala Phe Ile Val Ala
275 280 285
Glu Arg Leu Arg Lys Arg Arg Thr Gly Ser Gln Arg Val Ser
290 295 300

(2) INFORMATION FOR SEQ ID NO:1269:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 243 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..243
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569454

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1269:

Met Ser Ala Cys Gly Leu Gly Thr Asp His Pro Leu Met Thr Thr Thr
1 5 10 15
Asp Phe Tyr Thr Ser His Glu Cys Leu Leu Pro Tyr Glu Gln Ser
20 25 30
Leu Thr Arg Leu Asp Ser Thr Ser Gly Leu Tyr Tyr Asp Cys Ser Ala
35 40 45
His Met Val Trp Cys Gly Glu Arg Thr Arg Gln Leu Asp Gly Ala His
50 55 60
Val Glu Phe Leu Arg Gly Ile Ala Asn Pro Leu Gly Ile Lys Val Ser
65 70 75 80
Asn Lys Met Asp Pro Asn Glu Leu Val Lys Leu Val Glu Ile Leu Asn
85 90 95
Pro Asn Asn Lys Pro Gly Arg Ile Thr Val Ile Val Arg Met Gly Ala
100 105 110
Glu Asn Met Arg Val Lys Leu Pro His Leu Ile Arg Ala Val Arg Arg
115 120 125
Ser Gly Gln Ile Val Thr Trp Trp Cys Asp Pro Met His Gly Asn Thr
130 135 140
Ile Lys Ala Pro Cys Gly Leu Lys Thr Arg Ala Phe Asp Ser Ile Leu

145	150	155	160
Ala Glu Val Arg	Ala Phe Leu Asp Val	His Glu Gln Glu Gly Ser His	
	165	170	175
Ala Gly Gly Ile	His Leu Glu Met Thr Gly Gln Asn Val Thr Glu Cys		
	180	185	190
Ile Gly Gly Ser Arg Thr Val Thr Tyr Asp Asp Leu Ser Ser Arg Tyr			
	195	200	205
His Thr His Cys Asp Pro Arg Leu Asn Ala Ser Gln Ser Leu Glu Leu			
	210	215	220
Ala Phe Ile Val Ala Glu Arg Leu Arg Lys Arg Thr Gly Ser Gln			
	225	230	235
Arg Val Ser			240

(2) INFORMATION FOR SEQ ID NO:1270:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1748 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1748
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569470

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1270:

aggtccagca	cacgataccta	aatcctgtga	gcacgtcttc	catcgctggt	ttccattat	60
tgacgaatct	ctttgacctt	ttttcttct	tcttaaacaa	acccaattcg	atttcaacga	120
acgcctcttc	tctctcaact	tctttcgatt	tggtctttgc	cggagctcgt	agtgtaacgg	180
tgatccgcgg	cgagagagatg	gctcctaagt	atccataaaa	agccgttggt	ggcggcgcaa	240
gtggttttct	cgcctctctt	gcttcgtcga	tctccaattt	gggatctgct	atgaccaaat	300
cagtttaagt	tttggttccc	tatgagggac	ttgaagttaa	caatctcgaa	ggaagtacag	360
atgatctgga	ggaggaagca	agcagaggaa	gatggaagca	agaggatcga	gatgctatt	420
ggaagatgat	gcagaagtac	ataggatctg	atgttacatc	aattggtgac	cttcctgtga	480
ttatttttga	accaatgaca	atgcttcaga	aaatggcgga	gttgatggaA	tactcgcatc	540
tgctagacat	ggcagacaaa	accgaggacc	cttattttgc	catggtgtat	gcatactcgt	600
gggctatata	cgtgtattat	gctttccaac	gtacctggaa	accattcaat	ccaatccttg	660
gtgagactta	tgagatggct	aattacaatg	gtgttaactt	catatctgaa	caggtcagcc	720
atccaccacc	aatgagtgtc	ggctcatgct	aaaatagaca	ttttacgtat	gattgtactt	780
caaaactgaa	aacaaaattt	ttgggcaatt	ccattgactg	ttaccagta	ggaaggacac	840
gggtgacact	taaaagagat	ggagtgtgtc	ttgacttggt	acctctctg	accaaagtcc	900
acaacctata	ctttggagca	attcgggtcg	attcgctcgt	ggaattatgc	atgacaaaac	960
agaccaccgg	tgacaaagtc	gtgctttact	tccaacctat	tggtctgttc	ggatctgctc	1020
gatataaggt	ggatggatat	gtctataaac	cctctgagga	gcctaagata	ctcatgactc	1080
gcaaatggaa	cgagtccatg	agttatcagc	cggtgtgatg	tgaaggtgaa	ccctcccagc	1140
gcaccgaact	gaaagaggta	tggaaaactc	ctgatgtgoc	aaagatgac	aaatatcaat	1200
acactcactt	tgctcacaa	attaatagct	tcgacactgc	cccgaataag	ctgttgccct	1260
ctgattcacg	gttacgaact	gatagatacg	cacttgagat	gggcgcacgt	tccaataatcag	1320
gctatgagaa	gagcagcatg	gaagagagac	agagagctga	aaagagagac	cgcgaagaga	1380
aaggccaacg	cttctactcca	aaatggttcg	atgtaacgga	agaagtcaat	gctacacact	1440
ggggtgatct	ggaagtttac	caattcaatg	gaaagtactc	ggaactcgtc	gcagctgcgg	1500
ataactctga	agataaacac	gacctaaagt	cgatccaatt	caacccatgc	caattccaag	1560
atctgtctac	ttaaatgtat	cgtcccaaaa	gacagaaaag	atcaaatctt	tttgaaaaca	1620
aattgtattc	tattctctcg	tagttacaaa	aaactttgtt	ctacatctgc	tagctttccc	1680
attgctttct	ctagtattag	tgtacaactt	ctactgtttt	gtcttaaaat	cattcaaatc	1740
ttctcttg						

(2) INFORMATION FOR SEQ ID NO:1271:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 523 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..523
 (D) OTHER INFORMATION: / Ceres Seq. ID 1569471
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1271:

Val	Gln	His	Thr	Ile	Leu	Asn	Pro	Val	Ser	Ile	Val	Ser	Ile	Ala	Gly
1				5					10					15	
Leu	Pro	Leu	Leu	Thr	Asn	Leu	Phe	Ala	Phe	Phe	Ser	Ser	Phe	Leu	Asn
				20				25					30		
Lys	Pro	Asn	Ser	Ile	Ser	Thr	Asn	Ala	Ser	Ser	Leu	Ser	Leu	Ser	Phe
		35					40				45				
Asp	Leu	Phe	Phe	Ala	Gly	Ala	Arg	Ser	Val	Ser	Val	Ile	Arg	Gly	Gly
	50					55					60				
Glu	Met	Ala	Pro	Asn	Asp	Pro	Lys	Lys	Ala	Val	Gly	Gly	Gly	Gly	Ser
	65			70					75				80		
Gly	Phe	Phe	Ala	Ser	Leu	Ala	Ser	Ser	Ile	Ser	Asn	Leu	Gly	Ser	Ala
			85						90				95		
Met	Thr	Lys	Ser	Val	Asn	Gly	Leu	Val	Pro	Tyr	Glu	Gly	Leu	Glu	Val
			100				105						110		
Ile	Asn	Pro	Glu	Gly	Ser	Thr	Asp	Asp	Ala	Glu	Glu	Glu	Ala	Ser	Arg
		115					120					125			
Gly	Arg	Trp	Lys	Gln	Glu	Asp	Arg	Asp	Gly	Tyr	Trp	Lys	Met	Met	Gln
	130				135						140				
Lys	Tyr	Ile	Gly	Ser	Asp	Val	Thr	Ser	Met	Val	Thr	Leu	Pro	Val	Ile
	145			150					155					160	
Ile	Phe	Glu	Pro	Met	Thr	Met	Leu	Gln	Lys	Met	Ala	Glu	Leu	Met	Glu
			165						170				175		
Tyr	Ser	His	Leu	Leu	Asp	Met	Ala	Asp	Lys	Thr	Glu	Asp	Pro	Tyr	Leu
		180					185						190		
Arg	Met	Val	Tyr	Ala	Ser	Ser	Trp	Ala	Ile	Ser	Val	Tyr	Tyr	Ala	Phe
		195					200					205			
Gln	Arg	Thr	Trp	Lys	Pro	Phe	Asn	Pro	Ile	Leu	Gly	Glu	Thr	Tyr	Glu
	210					215					220				
Met	Ala	Asn	Tyr	Asn	Gly	Val	Asn	Phe	Ile	Ser	Glu	Gln	Val	Ser	His
	225				230				235					240	
His	Pro	Pro	Met	Ser	Ala	Gly	His	Ala	Glu	Asn	Glu	His	Phe	Thr	Tyr
			245						250				255		
Asp	Cys	Thr	Ser	Lys	Leu	Lys	Thr	Lys	Phe	Leu	Gly	Asn	Ser	Ile	Asp
		260					265						270		
Val	Tyr	Pro	Val	Gly	Arg	Thr	Arg	Val	Thr	Leu	Lys	Arg	Asp	Gly	Val
		275					280					285			
Val	Leu	Asp	Leu	Val	Pro	Pro	Leu	Thr	Lys	Val	His	Asn	Leu	Ile	Phe
	290					295					300				
Gly	Arg	Thr	Trp	Val	Asp	Ser	Pro	Gly	Glu	Met	Ile	Met	Thr	Asn	Gln
	305				310				315					320	
Thr	Thr	Gly	Asp	Lys	Val	Val	Leu	Tyr	Phe	Gln	Pro	Cys	Gly	Trp	Phe
			325						330				335		
Gly	Ser	Gly	Arg	Tyr	Glu	Val	Asp	Gly	Tyr	Val	Tyr	Asn	Ala	Ser	Glu
		340					345					350			
Glu	Pro	Lys	Ile	Leu	Met	Thr	Gly	Lys	Trp	Asn	Glu	Ser	Met	Ser	Tyr
		355					360				365				
Gln	Pro	Cys	Asp	Gly	Glu	Gly	Glu	Pro	Leu	Pro	Gly	Thr	Glu	Leu	Lys
	370					375					380				
Glu	Val	Trp	Lys	Leu	Ala	Asp	Val	Pro	Lys	Asp	Asp	Lys	Tyr	Gln	Tyr
	385				390				395					400	
Thr	His	Phe	Ala	His	Lys	Ile	Asn	Ser	Phe	Asp	Thr	Ala	Pro	Lys	Lys
			405						410				415		
Leu	Leu	Pro	Ser	Asp	Ser	Arg	Leu	Arg	Pro	Asp	Arg	Tyr	Ala	Leu	Glu
		420					425					430			
Met	Gly	Asp	Met	Ser	Lys	Ser	Gly	Tyr	Glu	Lys	Ser	Ser	Met	Glu	Glu

(2) INFORMATION FOR SEQ ID NO:1272:

(A) LENGTH: 458 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: 1 in

MOLECULE TYPE: peptide

(18) FEATURE:

(D) NAM

(A) NAME/REF: peptide
(B) LOCATION: 1 458

(D) OTHER INFORMATION

(D) OTHER INFORMATION: / Ceres Seq. ID: 1585472
SEQUENCE DESCRIPTION: SEQ ID NO:1272:

(X1) SEQUENCE DESCRIPTION: SEQ ID NO:1272:
Ala Pro Arg Arg Pro Lys Lys Ala Val Gly Gl

Met	Ala	Pro	Asn	Asp	Pro	Lys	Lys	Ala	Val	Gly	Gly	Gly	Gly	Ser	Gly
1			5					10						15	
Phe	Phe	Ala	Leu	Ala	Ser	Ser	Ile	Ser	Asn	Leu	Gly	Ser	Ala	Met	
			20				25					30			
Thr	Lys	Ser	Val	Asn	Gly	Leu	Val	Pro	Tyr	Glu	Gly	Leu	Glu	Val	Ile
		35					40				45				
Asn	Pro	Glu	Gly	Ser	Thr	Asp	Asp	Ala	Glu	Glu	Glu	Ala	Ser	Arg	Gly
		50				55					60				
Arg	Trp	Lys	Gln	Glu	Asp	Arg	Asp	Gly	Tyr	Trp	Lys	Met	Met	Gln	Lys
65					70					75					80
Tyr	Ile	Gly	Ser	Asp	Val	Thr	Ser	Met	Val	Thr	Leu	Pro	Val	Ile	Ile
			85						90					95	
Phe	Glu	Pro	Met	Thr	Met	Leu	Gln	Lys	Met	Ala	Glu	Leu	Met	Glu	Tyr
			100					105					110		
Ser	His	Leu	Leu	Asp	Met	Ala	Asp	Lys	Thr	Glu	Asp	Pro	Tyr	Leu	Arg
		115					120					125			
Met	Val	Tyr	Ala	Ser	Ser	Trp	Ala	Ile	Ser	Val	Tyr	Tyr	Ala	Phe	Gln
		130				135					140				
Arg	Thr	Trp	Lys	Pro	Phe	Asn	Pro	Ile	Leu	Gly	Gly	Thr	Tyr	Glu	Met
145					150					155					160
Ala	Asn	Tyr	Asn	Gly	Val	Asn	Phe	Ile	Ser	Glu	Gln	Val	Ser	His	His
			165					170						175	
Pro	Pro	Met	Ser	Ala	Gly	His	Ala	Glu	Asn	Glu	His	Phe	Thr	Tyr	Asp
			180					185					190		
Cys	Thr	Ser	Lys	Leu	Lys	Thr	Lys	Phe	Leu	Gly	Asn	Ser	Ile	Asp	Val
		195					200					205			
Tyr	Pro	Val	Gly	Arg	Thr	Arg	Val	Thr	Leu	Lys	Arg	Asp	Gly	Val	Val
		210				215					220				
Leu	Asp	Leu	Val	Pro	Pro	Leu	Thr	Lys	Val	His	Asn	Leu	Ile	Phe	Gly
225					230					235					240
Arg	Thr	Trp	Val	Asp	Ser	Pro	Gly	Glu	Met	Ile	Met	Thr	Asn	Gln	Thr
			245					250						255	
Thr	Gly	Asp	Lys	Val	Val	Leu	Tyr	Phe	Gln	Pro	Cys	Gly	Tyr	Phe	Gly
			260					265				270			
Ser	Gly	Arg	Tyr	Glu	Val	Asp	Gly	Tyr	Val	Tyr	Asn	Ala	Ser	Glu	Glu
		275					280					285			
Pro	Lys	Ile	Leu	Met	Thr	Gly	Lys	Trp	Asn	Glu	Ser	Met	Ser	Tyr	Gln
		290				295					300				

Pro Cys Asp Gly Glu Gly Glu Pro Leu Pro Gly Thr Glu Leu Lys Glu
305 310 315 320
Val Trp Lys Leu Ala Asp Val Pro Lys Asp Asp Lys Tyr Gln Tyr Thr
325 330 335
His Phe Ala His Lys Ile Asn Ser Phe Asp Thr Ala Pro Lys Lys Leu
340 345 350
Leu Pro Ser Asp Ser Arg Leu Arg Pro Asp Arg Tyr Ala Leu Glu Met
355 360 365
Gly Asp Met Ser Lys Ser Gly Tyr Glu Lys Ser Ser Met Glu Glu Arg
370 375 380
Gln Arg Ala Glu Lys Arg Thr Arg Glu Glu Lys Gly Gln Ala Phe Thr
385 390 395 400
Pro Lys Trp Phe Asp Val Thr Glu Glu Val Thr Ala Thr Pro Trp Gly
405 410 415
Asp Leu Glu Val Tyr Gln Phe Asn Gly Lys Tyr Ser Glu His Arg Ala
420 425 430
Ala Ala Asp Asn Ser Glu Asp Asn Thr Asp Pro Lys Ser Ile Gln Phe
435 440 445
Asn Pro Trp Gln Phe Gln Asp Leu Ser Thr
450 455

(2) INFORMATION FOR SEQ ID NO:1273:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 427 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..427

(D) OTHER INFORMATION: / Ceres Seq. ID 1569473

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1273:

Met Thr Lys Ser Val Asn Gly Leu Val Pro Tyr Glu Gly Leu Glu Val
1 5 10 15
Ile Asn Pro Glu Gly Ser Thr Asp Asp Ala Glu Glu Glu Ala Ser Arg
20 25 30
Gly Arg Trp Lys Gln Glu Asp Arg Asp Gly Tyr Trp Lys Met Met Gln
35 40 45
Lys Tyr Ile Gly Ser Asp Val Thr Ser Met Val Thr Leu Pro Val Ile
50 55 60
Ile Phe Glu Pro Met Thr Met Leu Gln Lys Met Ala Glu Leu Met Glu
65 70 75 80
Tyr Ser His Leu Leu Asp Met Ala Asp Lys Thr Glu Asp Pro Tyr Leu
85 90 95
Arg Met Val Tyr Ala Ser Ser Trp Ala Ile Ser Val Tyr Tyr Ala Phe
100 105 110
Gln Arg Thr Trp Lys Pro Phe Asn Pro Ile Leu Gly Glu Thr Tyr Glu
115 120 125
Met Ala Asn Tyr Asn Gly Val Asn Phe Ile Ser Glu Gln Val Ser His
130 135 140
His Pro Pro Met Ser Ala Gly His Ala Glu Asn Glu His Phe Thr Tyr
145 150 155 160
Asp Cys Thr Ser Lys Leu Lys Thr Lys Phe Leu Gly Asn Ser Ile Asp
165 170 175
Val Tyr Pro Val Gly Arg Thr Arg Val Thr Leu Lys Arg Asp Gly Val
180 185 190
Val Leu Asp Leu Val Pro Pro Leu Thr Lys Val His Asn Leu Ile Phe
195 200 205
Gly Arg Thr Trp Val Asp Ser Pro Gly Glu Met Ile Met Thr Asn Gln
210 215 220
Thr Thr Gly Asp Lys Val Val Leu Tyr Phe Gln Pro Cys Gly Trp Phe

225				230				235				240			
Gly	Ser	Gly	Arg	Tyr	Glu	Val	Asp	Gly	Tyr	Val	Tyr	Asn	Ala	Ser	Glu
				245				250						255	
Glu	Pro	Lys	Ile	Leu	Met	Thr	Gly	Lys	Trp	Asn	Glu	Ser	Met	Ser	Tyr
			260					265						270	
Gln	Pro	Cys	Asp	Gly	Glu	Gly	Glu	Pro	Leu	Pro	Gly	Thr	Glu	Leu	Lys
			275					280					285		
Glu	Val	Trp	Lys	Leu	Ala	Asp	Val	Pro	Lys	Asp	Asp	Lys	Tyr	Gln	Tyr
			290				295				300				
Thr	His	Phe	Ala	His	Lys	Ile	Asn	Ser	Phe	Asp	Thr	Ala	Pro	Lys	Lys
				310					315					320	
Leu	Leu	Pro	Ser	Asp	Ser	Arg	Leu	Arg	Pro	Asp	Arg	Tyr	Ala	Leu	Glu
				325					330					335	
Met	Gly	Asp	Met	Ser	Lys	Ser	Gly	Tyr	Glu	Lys	Ser	Ser	Met	Glu	Glu
			340					345					350		
Arg	Gln	Arg	Ala	Glu	Lys	Arg	Thr	Arg	Glu	Glu	Lys	Gly	Gln	Ala	Phe
			355				360					365			
Thr	Pro	Lys	Trp	Phe	Asp	Val	Thr	Glu	Glu	Val	Thr	Ala	Thr	Pro	Trp
			370				375				380				
Gly	Asp	Leu	Glu	Val	Tyr	Gln	Phe	Asn	Gly	Lys	Tyr	Ser	Glu	His	Arg
			385				390			395				400	
Ala	Ala	Ala	Asp	Asn	Ser	Glu	Asp	Asn	Thr	Asp	Pro	Lys	Ser	Ile	Gln
				405					410					415	
Phe	Asn	Pro	Trp	Gln	Phe	Gln	Asp	Leu	Ser	Thr					
				420											

(2) INFORMATION FOR SEQ ID NO:1274:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 606 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..606

(D) OTHER INFORMATION: / Ceres Seq. ID 1569509

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1274:

atcacaaactc	tcatttttctt	ctctctcgat	tTcttgatat	atcagtaacc	aaaaaAcaca	60
gagaattaaa	acatggctta	cttctccaca	gcgacatctc	ttctctctct	ctgctctctct	120
gtttctcttc	cttatgttca	tggagcctcc	gactgcgaca	cccttgatgt	taccctgttc	180
ccatgtttac	cttttatatc	gatcgggggt	acggccgata	caccaacagc	ttcatgtctc	240
tcacgtctca	aaaatattct	cgatacgaag	ccgatatgtc	tatgcgaagg	gttgaagaag	300
gcacctttag	gaatcaagga	gaggacacta	cggacgagga	ggaggccacg	gtggtggttg	360
acactatgga	ggtggaggag	accatggagg	aggaggctac	gggctgaacg	aaactgttca	420
gacgaagccg	ggtgtttaaa	agttataact	atcaataaaa	ttcaccatgc	ataattgcat	480
ctctatatac	acttatgtct	tatatgtatc	catcaaaata	aaccatgggt	agtttgtaat	540
gcagttcctt	cagaaatgtg	tggaaataatg	tttcacaata	ataatagaat	atctctgttg	600
attctg						

(2) INFORMATION FOR SEQ ID NO:1275:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 134 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..134

(D) OTHER INFORMATION: / Ceres Seq. ID 1569510

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1275:

His Asn Ser His Phe Leu Leu Ser Arg Phe Leu Asp Ile Ser Val Thr

1	5	10	15
Lys Lys His Arg Glu Leu Lys His Gly Leu Leu Leu His Ser Asp Ile	20	25	30
Ser Ser Pro Pro Arg Pro Leu Cys Phe Leu Ser Leu Cys Ser Trp Ser	35	40	45
Leu Arg Leu Arg His Pro Cys Asp Tyr Pro Val Pro Met Phe Thr Phe	50	55	60
Tyr Ile Asp Arg Gly Tyr Gly Arg Tyr Thr His Ser Phe Met Leu Leu	65	70	75
Gln Ser Gln Lys Tyr Ser Arg Tyr Glu Thr Asp Met Ser Met Arg Arg	85	90	95
Val Glu Glu Gly Thr Phe Arg Asn Gln Gly Glu Asp Thr Thr Asp Glu	100	105	110
Glu Glu Ala Thr Val Val Val Asp Thr Met Glu Val Glu Asp Thr Met	115	120	125
Glu Glu Glu Val Thr Gly			
130			

(2) INFORMATION FOR SEQ ID NO:1276:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 128 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..128

(D) OTHER INFORMATION: / Ceres Seq. ID 1569511

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1276:

Met Ala Tyr Phe Ser Thr Ala Thr Ser Leu Leu Leu Val Leu Ser	1	5	10	15
Val Ser Ser Pro Tyr Val His Gly Ala Ser Asp Cys Asp Thr Leu Val	20	25	30	
Ile Thr Leu Phe Pro Cys Leu Pro Phe Ile Ser Ile Gly Thr Ala	35	40	45	
Asp Thr Pro Thr Ala Ser Cys Cys Ser Ser Leu Lys Asn Ile Leu Asp	50	55	60	
Thr Lys Pro Ile Cys Leu Cys Glu Gly Leu Lys Lys Ala Pro Leu Gly	65	70	75	80
Ile Lys Glu Arg Thr Leu Arg Thr Arg Arg Arg Pro Arg Trp Trp Trp	85	90	95	
Thr Leu Trp Arg Trp Arg Thr Pro Trp Arg Arg Arg Ser Arg Ala Glu	100	105	110	
Arg Thr Cys Ser Asp Glu Ala Gly Cys Leu Lys Val Ile Thr Ile Lys	115	120	125	

(2) INFORMATION FOR SEQ ID NO:1277:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 74 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..74

(D) OTHER INFORMATION: / Ceres Seq. ID 1569512

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1277:

Met Phe Thr Phe Tyr Ile Asp Arg Gly Tyr Gly Arg Tyr Thr His Ser	1	5	10	15
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Phe Met Leu Leu Gln Ser Gln Lys Tyr Ser Arg Tyr Glu Thr Asp Met
20 25 30
Ser Met Arg Arg Val Glu Glu Gly Thr Phe Arg Asn Gln Gly Glu Asp
35 40 45
Thr Thr Asp Glu Glu Glu Ala Thr Val Val Val Asp Thr Met Glu Val
50 55 60
Glu Asp Thr Met Glu Glu Val Thr Gly
65 70

(2) INFORMATION FOR SEQ ID NO:1278:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 985 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..985

(D) OTHER INFORMATION: / Ceres Seq. ID 1569522

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1278:

acttttttca	gctccgacaa	aaatggctgc	aatcaccatt	tcttctctct	tcacagcctc	60
agcctctctcg	cgtgttgttc	gtccacatgt	tcttcgaaat	accctgtgta	tcacctctta	120
ttcacgcttc	acaccatcct	tctccttccc	atctctctcc	ttcacactcc	gtgacacagc	180
tccgtctcgt	cgtcgttctc	tctttatcgc	ctccgccgtc	aaatctctaa	cggagacgga	240
gctgcttcca	atcacagagg	ctgattcaat	cccgtccgct	tccggtgtat	acgctgtata	300
cgataaagagc	gacgagcttc	agttcgtcgg	aatatctcgg	aacatcgcgtg	cgagtgtctc	360
tgctcatctc	aaatctgtgc	cggagctttg	tggctccgtt	aaggttgaaa	tagtagaaga	420
accagataaa	cgagttttta	cacaagcatg	gaaattatgg	atagaagaac	atataaaagt	480
aaactgaaaa	gttccgccgg	ggaataagtc	agggaaacaac	acatttgtca	aaacaaactcc	540
gaggaagAaa	atccgatatac	cgtctcactc	caggtcgcca	tgTttgagct	cacggttctt	600
ttgggaGgAac	tgattgaCcg	TtagtgAaa	gagagcAaag	tggtagcttt	cataaaagga	660
tcaaggagtg	ctcctcaatg	tggattctca	cagagagttg	ttgggattct	tgaaggccaa	720
ggagttgatt	atgaaactgt	tgatgttctt	gacgatgagt	ataatcatgg	gctaaggagg	780
acgcttaaga	actacagcaa	ttggccaaag	tttccacaga	tatttgtgaa	aggagaactt	840
gtaggaggat	gtgatatttt	gacctcaatg	tatgaaatgt	gtgaacttgc	caatatcttg	900
aactagtttc	atccgatttt	cttctctatt	tctagtgtga	actccaaaca	ttcattatag	960
agaaaacatg	cttggattct	cttcc				

(2) INFORMATION FOR SEQ ID NO:1279:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 203 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..203

(D) OTHER INFORMATION: / Ceres Seq. ID 1569523

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1279:

Leu Phe Ser Ala Pro Thr Lys Met Ala Ala Ile Thr Ile Ser Ser Ser	
1 5 10 15	
Leu His Ala Ser Ala Ser Pro Arg Val Val Arg Pro His Val Ser Arg	
20 25 30	
Asn Thr Pro Val Ile Thr Leu Tyr Ser Arg Phe Thr Pro Ser Phe Ser	
35 40 45	
Phe Pro Ser Leu Ser Phe Thr Leu Arg Asp Thr Ala Pro Ser Arg Arg	
50 55 60	
Arg Ser Phe Phe Ile Ala Ser Ala Val Lys Ser Leu Thr Glu Thr Glu	
65 70 75 80	
Leu Leu Pro Ile Thr Glu Ala Asp Ser Ile Pro Ser Ala Ser Gly Val	
85 90 95	

Tyr Ala Val Tyr Asp Lys Ser Asp Glu Leu Gln Phe Val Gly Ile Ser
100 105 110
Arg Asn Ile Ala Ala Ser Val Ser Ala His Leu Lys Ser Val Pro Glu
115 120 125
Leu Cys Gly Ser Val Lys Val Gly Ile Val Glu Glu Pro Asp Lys Ala
130 135 140
Val Leu Thr Gln Ala Trp Lys Leu Trp Ile Glu Glu His Ile Lys Val
145 150 155 160
Thr Gly Lys Val Pro Gly Asn Lys Ser Gly Asn Asn Thr Phe Val
165 170 175
Lys Gln Thr Pro Arg Lys Lys Ile Arg Tyr Pro Ser His Ser Arg Ser
180 185 190
Pro Cys Leu Ser Ser Arg Phe Xaa Trp Arg Asn
195 200

(2) INFORMATION FOR SEQ ID NO:1280:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 196 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..196
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569524

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1280:

Met Ala Ala Ile Thr Ile Ser Ser Ser Leu His Ala Ser Ala Ser Pro
1 5 10 15
Arg Val Val Arg Pro His Val Ser Arg Asn Thr Pro Val Ile Thr Leu
20 25 30
Tyr Ser Arg Phe Thr Pro Ser Phe Ser Phe Pro Ser Leu Ser Phe Thr
35 40 45
Leu Arg Asp Thr Ala Pro Ser Arg Arg Arg Ser Phe Phe Ile Ala Ser
50 55 60
Ala Val Lys Ser Leu Thr Glu Thr Glu Leu Leu Pro Ile Thr Glu Ala
65 70 75 80
Asp Ser Ile Pro Ser Ala Ser Gly Val Tyr Ala Val Tyr Asp Lys Ser
85 90 95
Asp Glu Leu Gln Phe Val Gly Ile Ser Arg Asn Ile Ala Ala Ser Val
100 105 110
Ser Ala His Leu Lys Ser Val Pro Glu Leu Cys Gly Ser Val Lys Val
115 120 125
Gly Ile Val Glu Glu Pro Asp Lys Ala Val Leu Thr Gln Ala Trp Lys
130 135 140
Leu Trp Ile Glu Glu His Ile Lys Val Thr Gly Lys Val Pro Pro Gly
145 150 155 160
Asn Lys Ser Gly Asn Asn Thr Phe Val Lys Gln Thr Pro Arg Lys Lys
165 170 175
Ile Arg Tyr Pro Ser His Ser Arg Ser Pro Cys Leu Ser Ser Arg Phe
180 185 190
Xaa Trp Arg Asn
195

(2) INFORMATION FOR SEQ ID NO:1281:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 108 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide

(B) LOCATION: 1..108
(D) OTHER INFORMATION: / Ceres Seq. ID 1569525
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1281:
Met Phe Glu Leu Thr Val Xaa Leu Glu Glu Leu Ile Asp Arg Leu Val
1 5 10 15
Lys Glu Ser Lys Val Val Ala Phe Ile Lys Gly Ser Arg Ser Ala Pro
20 25 30
Gln Cys Gly Phe Ser Gln Arg Val Val Gly Ile Leu Glu Ser Gln Gly
35 40 45
Val Asp Tyr Glu Thr Val Asp Val Leu Asp Asp Glu Tyr Asn His Gly
50 55 60
Leu Arg Glu Thr Leu Lys Asn Tyr Ser Asn Trp Pro Thr Phe Pro Gln
65 70 75 80
Ile Phe Val Lys Gly Glu Leu Val Gly Gly Cys Asp Ile Leu Thr Ser
85 90 95
Met Tyr Glu Asn Gly Glu Leu Ala Asn Ile Leu Asn
100 105

(2) INFORMATION FOR SEQ ID NO:1282:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 654 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..654
(D) OTHER INFORMATION: / Ceres Seq. ID 1569526

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1282:

atatttgaag ttctgtgatt ttgaaggatt tgattggttt ccatgatcta gagttttgag 60
aatggcgatg gtatcaggaa gacgatctac tctaaacccc gacgcacctc tttttattcc 120
ggcagctgta cgacaagtgg aagattcttc accggagtgg tggcaattgg tgacaacttc 180
gacttggtac cctgattact ggatcatgca gcacgagcaa ggccgggatg gtttctatga 240
caacggagag aatgagaatg gtggaggtoa tatcgatgta gctgatcttc ttccagaatc 300
attttatatt gatgatatgg aagatttttt tgacactgat gctgctgagt ttgatcaagg 360
attcgatgga agaattgatt accaagcacc ttccgaattt ggctttggaa agaattggtga 420
gatggttaag aaatcaaagt gaaacaggag cccgagatcg attgtggaac cagctaaaga 480
tgcggaataa ccagcgaaat ggggaaacca gagggttgct gctgctccga gaaacatcca 540
ccagcctcgc tgaagagata gtgtgttaac tagtcagaga agtcagagca gttcggctcg 600
tgtatcttta gccaccactg tacctttgta atYYYtttta gtatttgctt ccac

(2) INFORMATION FOR SEQ ID NO:1283:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 163 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..163
(D) OTHER INFORMATION: / Ceres Seq. ID 1569527

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1283:

Met Ala Met Val Ser Gly Arg Arg Ser Thr Leu Asn Pro Asp Ala Pro
1 5 10 15
Leu Phe Ile Pro Ala Ala Val Arg Gln Val Glu Asp Phe Ser Pro Glu
20 25 30
Trp Trp Gln Leu Val Thr Thr Ser Thr Trp Tyr Pro Asp Tyr Trp Ile
35 40 45
Ser Gln Gln Gln Gln Gly Ala Asp Gly Phe Tyr Asp Asn Gly Glu Asn
50 55 60
Glu Asn Gly Gly Gly His Ile Asp Val Ala Asp Leu Leu Pro Glu Ser

65		70		75		80
Phe Tyr Phe Asp Asp Met Glu Asp Phe Phe Asp Thr Asp Ala Ala Glu						
	85			90		95
Phe Asp Gln Gly Phe Asp Gly Arg Met Tyr Tyr Gln Ala Pro Ser Glu						
	100			105		110
Phe Gly Phe Gly Lys Asn Gly Glu Met Val Lys Lys Ser Ser Gly Asn						
	115			120		125
Arg Ser Pro Arg Ser Ile Val Glu Pro Ala Lys Tyr Ala Glu Lys Pro						
	130			135		140
Ala Lys Trp Gly Asn Gln Arg Val Ala Ala Ala Pro Arg Asn Ile His						
	145			150		155
						160
Gln Pro Arg						

(2) INFORMATION FOR SEQ ID NO:1284:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 161 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..161
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569528

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1284:

Met Val Ser Gly Arg Arg Ser Thr Leu Asn Pro Asp Ala Pro Leu Phe						
1	5			10		15
Ile Pro Ala Ala Val Arg Gln Val Glu Asp Phe Ser Pro Glu Trp Trp						
	20			25		30
Gln Leu Val Thr Thr Ser Thr Trp Tyr Pro Asp Tyr Trp Ile Ser Gln						
	35			40		45
Gln Gln Gln Gly Ala Asp Gly Phe Tyr Asp Asn Gly Glu Asn Glu Asn						
	50			55		60
Gly Gly Gly His Ile Asp Val Ala Asp Leu Leu Pro Glu Ser Phe Tyr						
	65			70		75
Phe Asp Asp Met Glu Asp Phe Phe Asp Thr Asp Ala Ala Glu Phe Asp						
	85			90		95
Gln Gly Phe Asp Gly Arg Met Tyr Tyr Gln Ala Pro Ser Glu Phe Gly						
	100			105		110
Phe Gly Lys Asn Gly Glu Met Val Lys Lys Ser Ser Gly Asn Arg Ser						
	115			120		125
Pro Arg Ser Ile Val Glu Pro Ala Lys Tyr Ala Glu Lys Pro Ala Lys						
	130			135		140
Trp Gly Asn Gln Arg Val Ala Ala Ala Pro Arg Asn Ile His Gln Pro						
	145			150		155
Arg						160

(2) INFORMATION FOR SEQ ID NO:1285:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 85 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..85
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569529

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1285:

Met Ile Trp Lys Ile Ser Leu Thr Leu Met Leu Leu Ser Leu Ile Lys					
1	5			10	15

Asp Ser Met Glu Glu Cys Ile Thr Lys His Leu Pro Asn Leu Ala Leu
20 25 30
Glu Arg Met Val Arg Trp Leu Arg Asn Gln Val Glu Thr Gly Ala Arg
35 40 45
Asp Arg Leu Trp Asn Gln Leu Ser Met Arg Lys Ser Gln Arg Asn Gly
50 55 60
Glu Thr Arg Gly Leu Leu Leu Arg Glu Thr Ser Thr Ser Leu Ala
65 70 75 80
Glu Glu Ile Cys Cys
85

(2) INFORMATION FOR SEQ ID NO:1286:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1195 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1195

(D) OTHER INFORMATION: / Ceres Seq. ID 1569530

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1286:

ttttcggcgtt	caacggaacc	gcgcgaatat	ggagaatagc	ggcgataaat	gaagctgggtg	60
gggtgaaaga	tcggaccacc	gtggaagata	tggatctcgc	cgctccgagca	agtcttcgcg	120
gctggaaatt	tctctacctc	ggtgaccttc	aggtgaaaag	tgagcttcca	agtactttta	180
gagccttcgc	ttttcagcaa	catagatggt	cttgtggacc	tgcaaatctc	tttaggaaaa	240
tggttatgga	gatcgtaa	aacaagaaag	tgagattctg	gaagaaagt	tacgtgat	300
acagctctct	ctttgtgagg	aaaatcattg	cacatttggt	cacattttgt	ttctactcgc	360
ttgtttcttc	tctcacaa	ctcgtcccg	agggttaagt	tccgatttgg	gggttcggtt	420
atatcccatc	catcatact	atcctcaatt	ccgtcggta	tcCaaggtca	attcatctgc	480
tgttctattg	gattctatc	gagaatgtga	tgtcgtcgca	ccggacaaa	gccactctca	540
ttggtctggt	tgaggcagga	agggtcaacg	agttggtagt	gactgctaag	cttggaagcg	600
gtcagagcgc	taaaggaaac	actaaaggga	tcaaaaggtt	cccaagaatc	ttcaaattgc	660
ctgatcgatt	gaatacattg	gagcttggat	ttcggcgctt	cttgttcgtg	tgccggatgct	720
atgactttgt	gcacgggaag	aacaattact	tcatctacct	gtttcttcag	acaatgtctt	780
tccttcacag	tgggctgggc	tggatcggga	cttatgtccc	gagtttagtag	ttgtgttgtt	840
tcagagagaa	aagagaatgt	tattaatttt	cttgagaaat	aaagacaatt	ttcattgaaa	900
tgacaaagga	aaattgatag	gggagataga	gacgtaccgg	tacaacaag	taggaagaaa	960
ggagaagact	tttatcaaa	accaggaaa	aggagaagct	ccaagggttc	ttttgattta	1020
tttttatttt	ttctgtgttt	tatttatata	gctatgggat	tgttgattca	gtttgtgtga	1080
gatttttaatt	ttcgtttctt	gttttttatt	ttggtttttg	ggattttttt	cggttttgaaa	1140
gtgttagtct	ttttgttttt	tttttaatt	aaattccaag	taaaaattaa	attcc	

(2) INFORMATION FOR SEQ ID NO:1287:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 274 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..274

(D) OTHER INFORMATION: / Ceres Seq. ID 1569531

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1287:

Phe Gly Phe Asn Gly Thr Ala Gly Ile Trp Arg Ile Ala Ala Ile Asn	
1 5 10 15	
Glu Ala Gly Gly Trp Lys Asp Arg Thr Thr Val Glu Asp Met Asp Leu	
20 25 30	
Ala Val Arg Ala Ser Leu Arg Gly Trp Lys Phe Leu Tyr Leu Gly Asp	
35 40 45	
Leu Gln Val Lys Ser Glu Leu Pro Ser Thr Phe Arg Ala Phe Arg Phe	

WUOLAH

(i) SEQUENCE CHARACTERISTICS:

(ii) MOLECULE TYPE: peptide

(A) NAME/KEY: peptide

(D) OTHER INFORMATION

Asp Leu Ala Val Arg Ala Ser Leu Arg Gly Tr

1	2	3	4	5	6	7	8	9	10	11	12	13	14	15
Leu	Gly	Asp	Leu	Gln	Val	Lys	Ser	Glu	Leu	Pro	Ser	Thr	Phe	Arg
			20					25					30	
Phe	Arg	Phe	Gln	Gln	His	Arg	Trp	Ser	Cys	Gly	Pro	Ala	Asn	Leu
		35					40					45		Thr
Arg	Lys	Met	Val	Met	Glu	Ile	Val	Arg	Asn	Lys	Lys	Val	Arg	Phe
	50					55					60			Thr
Lys	Lys	Val	Tyr	Val	Ile	Tyr	Ser	Phe	Phe	Phe	Val	Arg	Lys	Ile
	65				70					75				80
Ala	His	Trp	Val	Thr	Phe	Cys	Phe	Tyr	Cys	Val	Val	Leu	Pro	Leu
				85					90				95	Thr
Ile	Leu	Val	Pro	Glu	Val	Lys	Val	Pro	Ile	Trp	Gly	Ser	Val	Tyr
			100					105					110	Ile
Pro	Ser	Ile	Ile	Thr	Ile	Leu	Asn	Ser	Val	Gly	Thr	Pro	Arg	Ser
		115					120					125		Ile
His	Leu	Leu	Phe	Tyr	Trp	Ile	Leu	Phe	Glu	Asn	Val	Met	Ser	Leu
	130					135					140			His
Arg	Thr	Lys	Ala	Thr	Leu	Ile	Gly	Leu	Phe	Glu	Ala	Gly	Arg	Ala
	145				150					155				160

Glu Leu Val Val Thr Ala Lys Leu Gly Ser Gly Gln Ser Ala Lys Gly
165 170 175
Asn Thr Lys Gly Ile Lys Arg Phe Pro Arg Ile Phe Lys Leu Pro Asp
180 185 190
Arg Leu Asn Thr Leu Glu Leu Gly Phe Ala Ala Phe Leu Phe Val Cys
195 200 205
Gly Cys Tyr Asp Phe Val His Gly Lys Asn Asn Tyr Phe Ile Tyr Leu
210 215 220
Phe Leu Gln Thr Met Ser Phe Phe Ile Ser Gly Leu Gly Trp Ile Gly
225 230 235 240
Thr Tyr Val Pro Ser
245

(2) INFORMATION FOR SEQ ID NO:1289:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 195 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..195

(D) OTHER INFORMATION: / Ceres Seq. ID 1569533

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1289:

Met Val Met Glu Ile Val Arg Asn Lys Lys Val Arg Phe Trp Lys Lys
1 5 10 15
Val Tyr Val Ile Tyr Ser Phe Phe Phe Val Arg Lys Ile Ile Ala His
20 25 30
Trp Val Thr Phe Cys Phe Tyr Cys Val Val Leu Pro Leu Thr Ile Leu
35 40 45
Val Pro Glu Val Lys Val Pro Ile Trp Gly Ser Val Tyr Ile Pro Ser
50 55 60
Ile Ile Thr Ile Leu Asn Ser Val Gly Thr Pro Arg Ser Ile His Leu
65 70 75 80
Leu Phe Tyr Trp Ile Leu Phe Glu Asn Val Met Ser Leu His Arg Thr
85 90 95
Lys Ala Thr Leu Ile Gly Leu Phe Glu Ala Gly Arg Ala Asn Glu Leu
100 105 110
Val Val Thr Ala Lys Leu Gly Ser Gly Gln Ser Ala Lys Gly Asn Thr
115 120 125
Lys Gly Ile Lys Arg Phe Pro Arg Ile Phe Lys Leu Pro Asp Arg Leu
130 135 140
Asn Thr Leu Glu Leu Gly Phe Ala Ala Phe Leu Phe Val Cys Gly Cys
145 150 155 160
Tyr Asp Phe Val His Gly Lys Asn Asn Tyr Phe Ile Tyr Leu Phe Leu
165 170 175
Gln Thr Met Ser Phe Phe Ile Ser Gly Leu Gly Trp Ile Gly Thr Tyr
180 185 190
Val Pro Ser
195

(2) INFORMATION FOR SEQ ID NO:1290:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1212 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1212

(D) OTHER INFORMATION: / Ceres Seq. ID 1569538

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1290:

gcagacattt	tagacaaagt	tactctcttt	ctttctcatg	ttcttttcgg	acagaaacaaa	60
actcccta	ccaatgtc	attcctttgg	tctctctctg	aataatcatc	tctcttccaaa	120
ccctattcca	ttttaactat	cgatctctgg	ctaagtcctc	aatggcgggg	gcggttgctt	180
ctcttcccaa	atttagtg	gtcaattcct	ccagatttcc	cagaagaaga	atcggttttt	240
ctgtctccaa	aaagccctc	gaagtttgtt	gttcttccgg	caatactcgt	tacactaagc	300
agagaggggc	atttacatca	ttagaaagat	gtgcgatttc	attagcttta	tccggttggtt	360
taatgggttc	agtagctctg	attgtcttgc	ctcccaatgc	tcaogcagtg	gcgaatccag	420
tgtattccaga	tgtttcaagt	ttagatctccg	gtctctccgt	taaagatccg	gaagctttac	480
taagatatgc	attgctctatt	gacaaacaa	ccatcaggga	agtgacaga	ccctctgagg	540
atgactcaga	tagctctcaag	attgtctggc	taaaggctct	agattctgtt	gaacgggaatg	600
tgaggcaggc	aagttagaaca	ttgcagcaag	ggaaaaagta	aattgtggca	ggttttgcgt	660
aatcgaga	ggaatcatgt	aatgaaatga	ttagaaaagt	ggaagctggg	atgcaagata	720
tgtcttaagt	agtgaagat	cgaaaaagag	acgcagttgc	tccaaaaacag	aaagaaattc	780
tcaaatatgt	tggcggaata	gaagaggata	tgggttgatg	ctttccatat	gaagtgcogg	840
aaagatgatc	Cgaacatgcc	tctctccaag	ggaagagcta	gtgtggacat	gaaggtcaag	900
atcaaggaca	atcccaacat	cgaggactgt	gtgttccgca	tgttttatac	tgtttataac	960
gccccgttta	ccgccggaaa	ctttgtggac	tgtgtagaga	ggcatttcta	cgatgctctt	1020
ccggcgcttc	atatggaaa	ccatcaacca	tatctctctc	tattccatgt	ttctgttttt	1080
tgtttttac	tgtgtattca	atacaatttg	tcttttccct	tctgtcattt	ttgtcagatg	1140
ttatttagtt	ttgttcaagt	taactcttgt	tggttatctt	actttaagag	ctcatatgga	1200
tctgtctctt	cc					

(2) INFORMATION FOR SEQ ID NO:1291:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 239 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..239

(D) OTHER INFORMATION: / Ceres Seq. ID 1569539

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1291:

Met	Ala	Ala	Ala	Phe	Ala	Ser	Leu	Pro	Thr	Phe	Ser	Val	Val	Asn	Ser	
1				5					10					15		
Ser	Arg	Phe	Pro	Arg	Arg	Arg	Ile	Gly	Phe	Ser	Cys	Ser	Lys	Lys	Pro	
			20					25					30			
Leu	Glu	Val	Arg	Cys	Ser	Ser	Gly	Asn	Thr	Arg	Tyr	Thr	Lys	Gln	Arg	
			35				40					45				
Gly	Ala	Phe	Thr	Ser	Leu	Lys	Glu	Cys	Ala	Ile	Ser	Leu	Ala	Leu	Ser	
			50				55				60					
Val	Gly	Leu	Met	Val	Ser	Val	Pro	Ser	Ile	Ala	Leu	Pro	Pro	Asn	Ala	
			65				70			75				80		
His	Ala	Val	Ala	Asn	Pro	Val	Ile	Pro	Asp	Val	Ser	Val	Leu	Ile	Ser	
			85					90						95		
Gly	Pro	Pro	Ile	Lys	Asp	Pro	Glu	Ala	Leu	Leu	Arg	Tyr	Ala	Leu	Pro	
			100				105						110			
Ile	Asp	Asn	Lys	Ala	Ile	Arg	Glu	Val	Gln	Lys	Pro	Leu	Glu	Asp	Ile	
			115				120					125				
Thr	Asp	Ser	Leu	Lys	Ile	Ala	Gly	Val	Lys	Ala	Leu	Asp	Ser	Val	Glu	
			130				135					140				
Arg	Asn	Val	Arg	Gln	Ala	Ser	Arg	Thr	Leu	Gln	Gln	Gly	Lys	Ser	Ile	
			145				150				155				160	
Ile	Val	Ala	Gly	Phe	Ala	Glu	Ser	Lys	Lys	Asp	His	Gly	Asn	Glu	Met	
			165					170						175		
Ile	Glu	Lys	Leu	Glu	Ala	Gly	Met	Gln	Asp	Met	Leu	Lys	Ile	Val	Glu	
			180				185					190				
Asp	Arg	Lys	Arg	Asp	Ala	Val	Ala	Pro	Lys	Gln	Lys	Glu	Ile	Leu	Lys	
			195				200					205				
Tyr	Val	Gly	Gly	Ile	Glu	Glu	Asp	Met	Val	Asp	Gly	Phe	Pro	Tyr	Glu	

210 215 220
Val Pro Glu Glu Tyr Arg Glu His Ala Ser Pro Gln Gly Lys Ser
225 230 235
(2) INFORMATION FOR SEQ ID NO:1292:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 172 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..172
(D) OTHER INFORMATION: / Ceres Seq. ID 1569540
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1292:
Met Val Ser Val Pro Ser Ile Ala Leu Pro Pro Asn Ala His Ala Val
1 5 10 15
Ala Asn Pro Val Ile Pro Asp Val Ser Val Leu Ile Ser Gly Pro Pro
20 25 30
Ile Lys Asp Pro Glu Ala Leu Leu Arg Tyr Ala Leu Pro Ile Asp Asn
35 40 45
Lys Ala Ile Arg Glu Val Gln Lys Pro Leu Glu Asp Ile Thr Asp Ser
50 55 60
Leu Lys Ile Ala Gly Val Lys Ala Leu Asp Ser Val Glu Arg Asn Val
65 70 75 80
Arg Gln Ala Ser Arg Thr Leu Gln Gln Gly Lys Ser Ile Ile Val Ala
85 90 95
Gly Phe Ala Glu Ser Lys Lys Asp His Gly Asn Glu Met Ile Glu Lys
100 105 110
Leu Glu Ala Gly Met Gln Asp Met Leu Lys Ile Val Glu Asp Arg Lys
115 120 125
Arg Asp Ala Val Ala Pro Lys Gln Lys Glu Ile Leu Lys Tyr Val Gly
130 135 140
Gly Ile Glu Glu Asp Met Val Asp Gly Phe Pro Tyr Glu Val Pro Glu
145 150 155 160
Glu Tyr Arg Glu His Ala Ser Pro Gln Gly Lys Ser
165 170

(2) INFORMATION FOR SEQ ID NO:1293:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 132 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..132
(D) OTHER INFORMATION: / Ceres Seq. ID 1569541
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1293:
Met Ala Phe His Met Lys Cys Arg Lys Ser Ile Ala Asn Met Pro Leu
1 5 10 15
Leu Lys Gly Arg Ala Ser Val Asp Met Lys Val Lys Ile Lys Asp Asn
20 25 30
Pro Asn Ile Glu Asp Cys Val Phe Arg Ile Val Leu Asp Gly Tyr Asn
35 40 45
Ala Pro Val Thr Ala Gly Asn Phe Val Asp Leu Val Glu Arg His Phe
50 55 60
Tyr Asp Ala Leu Pro Ala Leu His Met Glu Ser His Gln Pro Tyr Pro
65 70 75 80
Pro Leu Phe His Val Ser Val Phe Trp Phe Leu Leu Gly Ile Glu Tyr
85 90 95

Asn Leu Ser Phe Pro Phe Cys His Phe Cys Gln Met Leu Phe Ser Phe
100 105 110
Val Gln Val Asn Ser Cys Trp Leu Ser Tyr Phe Lys Ser Ser Tyr Gly
115 120 125
Ser Arg Ser Ser
130

(2) INFORMATION FOR SEQ ID NO:1294:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 684 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..684
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569546

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1294:

acatctcaact	gctcaactact	ctcactgtaa	tcctttagat	ctTcttttca	aattTcaatg	60
gcgtccCggt	gatgttgagt	atcggtgctt	cggtggaggt	ctagcatggg	ccactgatga	120
cagagctctt	gagactgcct	tcgctcaata	cgccgacgtt	attgattcca	agatcattaa	180
cgatcgtgag	actggaagat	caaggggatt	cggtatcgct	accttcaagg	atgagaaaagc	240
catgaagat	gcgattgagg	gaatgaacgg	acaagatctc	gatggccgta	gcatactgt	300
taacgaggt	cagtcagcgt	gaagcgggtg	cgccgggaggc	caccgtggag	gtggtggcgg	360
tgatatacgc	agcggcggtg	gtggaagacg	tgagggagga	ggaggatacg	gtggtgggta	420
aggagaggt	tacggaggaa	gcggtgggtg	tgaggagatg	taattccctt	aattaggttt	480
gggattacca	atgaatgttc	ttctctctgc	ttgttatgct	ttctacttgt	tttgtgtgtt	540
ctctattttg	ttctggtttc	gctttagatt	tgatgtaaca	gtctgtgatt	aggatattttg	600
gtatctggaa	acgtaatggt	aagtcacttg	tcattctcta	aataacaaat	ttcttcggag	660
atattatctc	tggtgattga	ttct				

(2) INFORMATION FOR SEQ ID NO:1295:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 153 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..153
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569547

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1295:

His	Leu	Thr	Ala	His	Tyr	Ser	His	Cys	Asn	Pro	Leu	Asp	Leu	Leu	Phe
1				5				10					15		
Lys	Phe	Gln	Trp	Arg	Pro	Gly	Asp	Val	Glu	Tyr	Arg	Cys	Phe	Val	Gly
				20				25					30		
Gly	Leu	Ala	Trp	Ala	Thr	Asp	Asp	Arg	Ala	Leu	Glu	Thr	Ala	Phe	Ala
				35				40					45		
Gln	Tyr	Gly	Asp	Val	Ile	Asp	Ser	Lys	Ile	Ile	Asn	Asp	Arg	Glu	Thr
				50				55					60		
Gly	Arg	Ser	Arg	Gly	Phe	Gly	Phe	Val	Thr	Phe	Lys	Asp	Glu	Lys	Ala
				65				70					75		80
Met	Lys	Asp	Ala	Ile	Glu	Gly	Met	Asn	Gly	Gln	Asp	Leu	Asp	Gly	Arg
				85				90					95		
Ser	Ile	Thr	Val	Asn	Glu	Ala	Gln	Ser	Arg	Gly	Ser	Gly	Gly	Gly	Gly
				100				105					110		
Gly	His	Arg	Gly	Gly	Gly	Gly	Gly	Tyr	Arg	Ser	Gly	Gly	Gly	Gly	Gly
				115				120					125		
Arg	Arg	Glu	Gly	Gly	Gly	Gly	Tyr	Gly	Gly	Gly	Glu	Gly	Gly	Gly	Tyr
				130				135					140		
Gly	Gly	Ser	Gly	Gly	Gly	Gly	Gly	Trp							

145 150
(2) INFORMATION FOR SEQ ID NO:1296:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 773 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..773
(D) OTHER INFORMATION: / Ceres Seq. ID 1569552
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1296:
tcacataaaa ttgttccaaa ttctattcgt atcctttccg ctgctgcgcgt cttcgtctct 60
gagataataa ggaacttgtgt atttttccat cgttaaaaagg catttcaaa agacaatatg 120
tcaggtagat aggcctgcccc ttgtgttgtt cctccccccg ttgctgagcc agcgcccatc 180
ccagaggaca tggacttaaat gactgcattg gaggtagact ttaggaaaag cgtgtcctat 240
ggtaggtgtt ttctgtgtct ccatgagtggt gctaagctta ttgagaagcg tgtggctcaa 300
ctcgttgtct tggctgaaga ctgcaaccag cctgattatg tcaagcttgt gaaggctctc 360
tgtctgcatc acgaagtcaag gttgctaaca gttccaagtg ccaagaccct tggcgaatgg 420
gctggctctc gcaagattga ttctgagggt aatgccagga aggttggttg atgctcatgt 480
cttgtgttca aggacttcgg cgaggagaca actgccctca gtatcgtaaa taagcatatt 540
gcttctcaat aaaatgccat gaagcatatc taaactcgga ttcatatgt ttccaccctc 600
caatgctgtt Attctctctgg tttgtatata ttaactaata tttacgggac agctcttgag 660
atatttttgg aacatgatca agttttgttg ttatctagac ttactcttc caaggccaaa 720
tttgcttagg atttatttgg ctcatctact tttatcataa ttttttttt cct
(2) INFORMATION FOR SEQ ID NO:1297:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 144 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..144
(D) OTHER INFORMATION: / Ceres Seq. ID 1569553
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1297:
Met Ser Gly Asp Glu Ala Ala Pro Val Val Val Pro Pro Val Ala
1 5 10 15
Glu Pro Ala Ala Ile Pro Glu Asp Met Asp Leu Met Thr Ala Leu Glu
20 25 30
Leu Thr Leu Arg Lys Ala Arg Ala Tyr Gly Gly Val Val Arg Gly Leu
35 40 45
His Glu Cys Ala Lys Leu Ile Glu Lys Arg Val Ala Gln Leu Val Val
50 55 60
Leu Ala Glu Asp Cys Asn Gln Pro Asp Tyr Val Lys Leu Val Lys Ala
65 70 75 80
Leu Cys Ala Asp His Glu Val Arg Leu Leu Thr Val Pro Ser Ala Lys
85 90 95
Thr Leu Gly Glu Trp Ala Gly Leu Cys Lys Ile Asp Ser Glu Gly Asn
100 105 110
Ala Arg Lys Val Val Gly Cys Ser Cys Leu Val Val Lys Asp Phe Gly
115 120 125
Glu Glu Thr Thr Ala Leu Ser Ile Val Asn Lys His Ile Ala Ser Gln
130 135 140
(2) INFORMATION FOR SEQ ID NO:1298:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 120 amino acids

(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..120
 (D) OTHER INFORMATION: / Ceres Seq. ID 1569554
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1298:
Met Asp Leu Met Thr Ala Leu Glu Leu Thr Leu Arg Lys Ala Arg Ala
1 5 10 15
Tyr Gly Gly Val Val Arg Gly Leu His Glu Cys Ala Lys Leu Ile Glu
 20 25 30
Lys Arg Val Ala Gln Leu Val Val Leu Ala Glu Asp Cys Asn Gln Pro
 35 40 45
Asp Tyr Val Lys Leu Val Lys Ala Leu Cys Ala Asp His Glu Val Arg
 50 55 60
Leu Leu Thr Val Pro Ser Ala Lys Thr Leu Gly Glu Trp Ala Gly Leu
65 70 75 80
Cys Lys Ile Asp Ser Glu Gly Asn Ala Arg Lys Val Val Gly Cys Ser
 85 90 95
Cys Leu Val Val Lys Asp Phe Gly Glu Glu Thr Thr Ala Leu Ser Ile
 100 105 110
Val Asn Lys His Ile Ala Ser Gln
 115 120
(2) INFORMATION FOR SEQ ID NO:1299:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 117 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..117
 (D) OTHER INFORMATION: / Ceres Seq. ID 1569555
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1299:
Met Thr Ala Leu Glu Leu Thr Leu Arg Lys Ala Arg Ala Tyr Gly Gly
1 5 10 15
Val Val Arg Gly Leu His Glu Cys Ala Lys Leu Ile Glu Lys Arg Val
 20 25 30
Ala Gln Leu Val Val Leu Ala Glu Asp Cys Asn Gln Pro Asp Tyr Val
 35 40 45
Lys Leu Val Lys Ala Leu Cys Ala Asp His Glu Val Arg Leu Leu Thr
 50 55 60
Val Pro Ser Ala Lys Thr Leu Gly Glu Trp Ala Gly Leu Cys Lys Ile
65 70 75 80
Asp Ser Glu Gly Asn Ala Arg Lys Val Val Gly Cys Ser Cys Leu Val
 85 90 95
Val Lys Asp Phe Gly Glu Glu Thr Thr Ala Leu Ser Ile Val Asn Lys
 100 105 110
His Ile Ala Ser Gln
 115
(2) INFORMATION FOR SEQ ID NO:1300:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1141 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: DNA (genomic)
 (ix) FEATURE:

(A) NAME/KEY: -
(B) LOCATION: 1..1141
(D) OTHER INFORMATION: / Ceres Seq. ID 1569579

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1300:

atttagccct	tgttttctct	acacacatct	cacatccccc	tatctctctc	tctcttcaaa	60
cgtttttagt	ccccaaaaaa	atatcaaaag	aactaaaaag	aaaaccctag	agccogaaga	120
ctctctact	cggtgtcgat	cggatcacct	aactaattac	tcgttgataa	tcattatatac	180
gagaaatag	attaattttg	aggccaacga	gctgagatta	gggtaccggg	gtgggaatca	240
cgaggagaa	atggctggaa	aaaataatgg	taaaagagga	ttttctgaga	ctgttgatct	300
caaacctga	ctttcatcga	cggctatgga	ttcagtttcc	aaagtctgatt	tagagaaat	360
gaaggagaa	gtcgtaaacc	caccagccaa	ggcacaagtt	gtgggatggc	caccggtacg	420
atcttctcgc	aagaaacgtca	tgctcggcca	aaaaccgacc	accggaatg	ccaccgaagg	480
aaacgataag	acttctggca	cgagtggagc	cacctcatcc	gcctccgcgt	gtgccaccgt	540
ggcttatgtg	aagggttagca	tggacgggtg	accgtaccta	cggaaaattg	acttgaaact	600
ctacaaaact	taccaagatc	tctccaacgc	cttaagcaaa	atgttttagct	cttttaccat	660
aggcaactat	ggaccacaag	gaatgaaga	tttcatgaat	gagagttaaa	tgatcgatct	720
cttaaacgga	tcagattatg	ttccaacata	tgaagataaa	gatggcgact	ggatgcttgt	780
aggagacgta	ccgtgggaga	tgtttgttga	ttcatgcaaa	cgtatacgaa	taatgaagg	840
atcagaagca	atcggaactg	ctccaaggcg	attagaaaaa	tgcaagaaca	gaagttagt	900
ctcgcagcac	attcttgtgt	cttacctaaa	aaagggaaga	agcctgtttc	gatcgtgttg	960
atatctcgaa	ccgagaaagc	taaacccggc	cgaaaatttt	gttcccgagca	aggagctttg	1020
ttataatatt	aattaataat	aatattaata	ttgtCggtg	attacatttt	aaaaaattaa	1080
atcgtttttg	ttatatgtat	tatatacata	tattaatatg	tatatattaat	taggttgcat	1140

(2) INFORMATION FOR SEQ ID NO:1301:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 298 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1..298
(D) OTHER INFORMATION: / Ceres Seq. ID 1569580

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1301:

Ph	Ser	Pro	Leu	Phe	Leu	Tyr	Thr	His	Leu	Thr	Ser	Pro	Tyr	Leu	Ser
1				5				10						15	
Leu	Ser	Ser	Asn	Val	Leu	Val	Pro	Gln	Lys	Asn	Ile	Lys	Arg	Thr	Lys
			20				25						30		
Arg	Lys	Thr	Leu	Glu	Ala	Glu	Glu	Ser	Pro	Thr	Arg	Cys	Arg	Ser	Asp
		35					40					45			
His	Leu	Thr	Asn	Tyr	Ser	Leu	Ile	Ile	Ile	Ile	Ser	Arg	Asn	Met	Ile
		50					55					60			
Asn	Phe	Glu	Ala	Thr	Glu	Leu	Arg	Leu	Gly	Leu	Pro	Gly	Gly	Asn	His
65				70					75					80	
Gly	Gly	Glu	Met	Ala	Gly	Lys	Asn	Asn	Gly	Lys	Arg	Gly	Phe	Ser	Glu
			85						90				95		
Thr	Val	Asp	Leu	Lys	Leu	Asn	Leu	Ser	Ser	Thr	Ala	Met	Asp	Ser	Val
			100					105					110		
Ser	Lys	Val	Asp	Leu	Glu	Asn	Met	Lys	Glu	Lys	Val	Val	Lys	Pro	Pro
		115					120						125		
Ala	Lys	Ala	Gln	Val	Val	Gly	Trp	Pro	Pro	Val	Arg	Ser	Phe	Arg	Lys
		130					135					140			
Asn	Val	Met	Ser	Gly	Gln	Lys	Pro	Thr	Thr	Gly	Asp	Ala	Thr	Glu	Gly
145				150					155				160		
Asn	Asp	Lys	Thr	Ser	Gly	Ser	Ser	Gly	Ala	Thr	Ser	Ser	Ala	Ser	Ala
			165						170				175		
Cys	Ala	Thr	Val	Ala	Tyr	Val	Lys	Val	Ser	Met	Asp	Gly	Ala	Pro	Tyr
		180						185					190		
Leu	Arg	Lys	Ile	Asp	Leu	Lys	Leu	Tyr	Lys	Thr	Tyr	Gln	Asp	Leu	Ser

195	200	205
Asn Ala Leu Ser Lys Met Phe Ser Ser Phe Thr Ile Gly Asn Tyr Gly		
210	215	220
Pro Gln Gly Met Lys Asp Phe Met Asn Glu Ser Lys Leu Ile Asp Leu		
225	230	235
Leu Asn Gly Ser Asp Tyr Val Pro Thr Tyr Glu Asp Lys Asp Gly Asp		
245	250	255
Trp Met Leu Val Gly Asp Val Pro Trp Glu Met Phe Val Asp Ser Cys		
260	265	270
Lys Arg Ile Arg Ile Met Lys Gly Ser Glu Ala Ile Gly Leu Ala Pro		
275	280	285
Arg Ala Leu Glu Lys Cys Lys Asn Arg Ser		
290	295	

(2) INFORMATION FOR SEQ ID NO:1302:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 236 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..236
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569581

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1302:

Met Ile Asn Phe Glu Ala Thr Glu Leu Arg Leu Gly Leu Pro Gly Gly	
1	5
Asn His Gly Gly Glu Met Ala Gly Lys Asn Asn Gly Lys Arg Gly Phe	
20	25
Ser Glu Thr Val Asp Leu Lys Leu Asn Leu Ser Ser Thr Ala Met Asp	
35	40
Ser Val Ser Lys Val Asp Leu Glu Asn Met Lys Glu Lys Val Val Lys	
50	55
Pro Pro Ala Lys Ala Gln Val Val Gly Trp Pro Val Arg Ser Phe	
65	70
Arg Lys Asn Val Met Ser Gly Gln Lys Pro Thr Thr Gly Asp Ala Thr	
85	90
Glu Gly Asn Asp Lys Thr Ser Gly Ser Ser Gly Ala Thr Ser Ser Ala	
100	105
Ser Ala Cys Ala Thr Val Ala Tyr Val Lys Val Ser Met Asp Gly Ala	
115	120
Pro Tyr Leu Arg Lys Ile Asp Leu Lys Leu Tyr Lys Thr Tyr Gln Asp	
130	135
Leu Ser Asn Ala Leu Ser Lys Met Phe Ser Ser Phe Thr Ile Gly Asn	
145	150
Tyr Gly Pro Gln Gly Met Lys Asp Phe Met Asn Glu Ser Lys Leu Ile	
165	170
Asp Leu Leu Asn Gly Ser Asp Tyr Val Pro Thr Tyr Glu Asp Lys Asp	
180	185
Gly Asp Trp Met Leu Val Gly Asp Val Pro Trp Glu Met Phe Val Asp	
195	200
Ser Cys Lys Arg Ile Arg Ile Met Lys Gly Ser Glu Ala Ile Gly Leu	
210	215
Ala Pro Arg Ala Leu Glu Lys Cys Lys Asn Arg Ser	
225	230
	235

(2) INFORMATION FOR SEQ ID NO:1303:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 215 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ix) FEATURE:

(B) LOCATION: 1..215

(D) OTHER INFORMATION

SEQUENCE DESCRIPTION: SEQ ID NO:1303:

Ala Gly Lys Asn Asn Gly Lys Arg Gly Phe Ser

[illegible]

(2) INFORMATION FOR SEQ ID NO:1304:

(i) SEQUENCE CHARACTERISTICS:

{A} LENGTH: 929 base pairs

(B) TYPE: nucleic acid

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(C) STRANDEDNESS: single
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(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..929

(D) OTHER INFORMATION: / Ceres Seq. ID 1569583

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1304:

aaaaacatta	gttacagctcg	gaattctcgaa	aaacccctaatt	tcagctaaag	gttgatcggt	60
gattctaaaa	ctcgagtgat	gaaggggaaat	tggctcgatcg	tacgaaaggt	tcttcctatc	120
caggtctcca	ctctccgctt	ctcgacacca	tgtctgcgat	taacataatc	catccgacgc	180
ctgtgtcttc	ccccaaactc	gatatctgct	ctaatcgcta	gaactcatt	gtttactgcc	240
tcacaattg	gtgcttcact	cgatttttgc	ttctccaca	ctctgcgttc	tcatcgagga	300
agcctctctg	cggagagctg	aggtgaaaaa	ggtgttttct	tagtgaattc	agaggaagag	360
ttcatcaatg	caatgagcaa	agctcaagat	ggatctttac	catcgctctt	ctattttact	420
gcgcctgggt	gtggaccatg	cagggttttc	ttctctgtaa	tctgtgaagt	tagtaaaaca	480
tatcccgatg	taactacgta	taaaagctgac	attgatgagg	gccggatttc	gaacatactc	540
acaagtgatg	atatacaggc	tgtgcccaaa	ctgcattttc	cgaagagagg	ctcgaagcaa	600
ggcgaggttg	tgggtgcaga	tgtcagcaga	ctgaagaata	cttggaaca	gcctctcaag	660
tgaagacctg	atccgtctca	gtaaaagaac	tgttgtaaat	ttccaagata	gtttaagact	720
gaaattttga	aatacaatcta	aaaaataatg	atgctgctgaa	ccagtttctg	ctttgttccc	780
ccctcgttgt	tcaggaattgt	aaattgccctt	tgttttttgt	agttttcccc	attctcttgg	840
cgcgttaatt	ctcaagattt	ctttgtgttc	ctgggtgaca	acttcaataa	atatcgacaa	900

gtcataactt tttatcaaaa ttttGsmcc

(2) INFORMATION FOR SEQ ID NO:1305:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 194 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..194
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569584

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1305:

Met	Lys	Gly	Asn	Trp	Ser	Ile	Val	Arg	Lys	Val	Leu	His	Arg	Gln	Phe	
1			5						10					15		
Ser	Thr	Leu	Arg	Ser	Ser	Thr	Pro	Ser	Ser	Arg	Leu	Ser	Thr	Ser	Ile	
			20						25					30		
Arg	Pro	Leu	Val	Leu	Ala	Pro	Asn	Ser	Ile	Ser	Ser	Leu	Ile	Ala	Arg	
			35						40					45		
Asn	Ser	Leu	Phe	Thr	Ala	Ser	Asn	Ile	Gly	Pro	Ser	Ile	Asp	Phe	Asn	
			50						55					60		
Phe	Ser	Asn	Thr	Ser	Leu	Pro	His	Arg	Arg	Ser	Leu	Cys	Ser	Glu	Ala	
			65						70					75		
Gly	Gly	Glu	Asn	Gly	Val	Val	Leu	Val	Lys	Ser	Glu	Glu	Glu	Phe	Ile	
			85						90					95		
Asn	Ala	Met	Ser	Lys	Ala	Gln	Asp	Gly	Ser	Leu	Pro	Ser	Val	Phe	Tyr	
			100						105					110		
Phe	Thr	Ala	Ala	Trp	Cys	Gly	Pro	Cys	Arg	Phe	Ile	Ser	Pro	Val	Ile	
			115						120					125		
Val	Glu	Leu	Ser	Lys	Gln	Tyr	Pro	Asp	Val	Thr	Thr	Tyr	Lys	Val	Asp	
			130						135					140		
Ile	Asp	Glu	Gly	Gly	Ile	Ser	Asn	Thr	Ile	Ser	Lys	Leu	Asn	Ile	Thr	
			145						150					155		
Ala	Val	Pro	Thr	Leu	His	Phe	Phe	Lys	Gly	Ser	Lys	Gln	Gly	Glu		
			165						170					175		
Val	Val	Gly	Ala	Asp	Val	Thr	Lys	Leu	Lys	Asn	Leu	Met	Glu	Gln	Leu	
			180						185					190		
Tyr	Lys															

(2) INFORMATION FOR SEQ ID NO:1306:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1340 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1340
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569585

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1306:

gccgcagagt	gttgatgctg	ttacgttttag	tactttgatg	aatgggtatc	ttcaggtttc	60
taagaaagcg	ttggcctttg	atttgttttag	gattatgaga	aaaagtgag	tggtcggttaa	120
tgtcagtacg	ttgcttagct	ttctttcggc	tattagtgat	ctaggagatt	tgctcggagc	180
agaatctgct	catgtgttat	gcatacaagt	tggccttgat	ttagacttgc	atttaatac	240
agctttgata	gggatgtacg	gcaaaactgg	gggtatcagt	tcagcacgca	ggatccttga	300
ttggcccat	cgaaaggatg	tgtttacatg	gaactgtatg	atagaccaat	atgccaaaac	360
gggtctcctt	gaagagtgtg	tatggctact	gaggcagatg	aagtatga	aaatgaac	420
gaattactct	acgtttgttg	ctgtgtgttc	ttcctgtgcg	tacagtgaag	cagcatctgt	480
aggacgtact	gttTgctgat	ctattggaag	aggaagaagt	agctttggat	gcaatactgt	540
gaactgcact	cgttgatatg	tatgcataag	taggattgct	tgaaaaagct	gttgagattt	600

tcaatagaat	gaagcataag	gatgtaaaagt	cctggaccgc	gatgatctcg	ggttatggag	660
ctcatggagt	agcaagagaa	gcagtaacac	tattcaataa	gatggaggaa	gagaactgca	720
aagtggagacc	caatgagatt	acctctttgg	ttgtgctgaa	tgcttttagc	catggagggt	780
tggtaatgga	aggaatcaga	tgcttttaaga	ggatggttga	ggcttacacg	ttcacgcccc	840
aagttgaaca	ttatgtgtgt	gtggttgatc	ttttaggtcg	agcggggcag	ttagaggaaq	900
cgtatgagtt	aataaggaac	ttaccgatca	caagtgaattc	aacgggttgg	cgtgctctgc	960
tagctgcttg	tagagtatac	gggaatgcag	atttggggga	aagtgtgatg	atgagattgg	1020
ctgaaatggg	tgagacacat	cggcagatg	caattcttct	agctggggaca	cacgtgtgtg	1080
cagggaaccc	acaaaaatca	ttagataatg	agttgaataa	agggagaaaa	gaagctggat	1140
acagcgccat	tgaatataga	tagagttagc	aatctctggc	gttcattcac	ctctgacctt	1200
ttgtttgaaa	actatatcag	caaaatgttg	ttcaataaag	taaacccctg	tatttactct	1260
ttctttatgc	tttaaaacag	taacttatgt	ataaagaaag	gagacaattg	atcttaattga	1320

aacagttttg atggattgtg

(2) INFORMATION FOR SEQ ID NO:1307:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 201 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..201
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569586

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1307:

Met	Tyr	Ala	Lys	Val	Gly	Leu	Leu	Glu	Lys	Ala	Val	Glu	Ile	Phe	Asn
1			5					10						15	
Arg	Met	Lys	Asp	Lys	Asp	Val	Lys	Ser	Trp	Thr	Ala	Met	Ile	Ser	Gly
		20					25					30			
Tyr	Gly	Ala	His	Gly	Leu	Ala	Arg	Glu	Ala	Val	Thr	Leu	Phe	Asn	Lys
		35					40				45				
Met	Glu	Glu	Glu	Asn	Cys	Lys	Val	Arg	Pro	Asn	Glu	Ile	Thr	Phe	Leu
		50				55				60					
Val	Val	Leu	Asn	Ala	Cys	Ser	His	Gly	Gly	Leu	Val	Met	Glu	Gly	Ile
		65				70				75				80	
Arg	Cys	Phe	Lys	Arg	Met	Val	Glu	Ala	Tyr	Ser	Phe	Thr	Pro	Lys	Val
			85						90					95	
Glu	His	Tyr	Gly	Cys	Val	Val	Asp	Leu	Leu	Gly	Arg	Ala	Gly	Gln	Leu
			100				105						110		
Glu	Glu	Ala	Tyr	Glu	Leu	Ile	Arg	Asn	Leu	Pro	Ile	Thr	Ser	Asp	Ser
		115					120					125			
Thr	Ala	Trp	Arg	Ala	Leu	Leu	Ala	Ala	Cys	Arg	Val	Tyr	Gly	Asn	Ala
		130				135					140				
Asp	Leu	Gly	Glu	Ser	Val	Met	Met	Arg	Leu	Ala	Glu	Met	Gly	Glu	Thr
		145				150				155				160	
His	Pro	Ala	Asp	Ala	Ile	Leu	Leu	Ala	Gly	Thr	His	Ala	Val	Ala	Gly
			165						170				175		
Asn	Pro	Gln	Lys	Ser	Leu	Asp	Asn	Glu	Leu	Asn	Lys	Gly	Arg	Lys	Glu
			180					185					190		
Ala	Gly	Tyr	Ser	Ala	Ile	Glu	Ile	Glu							
		195				200									

(2) INFORMATION FOR SEQ ID NO:1308:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 184 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..184

(D) OTHER INFORMATION: / Ceres Seq. ID 1569587

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1308:

Met	Lys	Asp	Lys	Asp	Val	Lys	Ser	Trp	Thr	Ala	Met	Ile	Ser	Gly	Tyr
1			5					10						15	
Gly	Ala	His	Gly	Leu	Ala	Arg	Glu	Ala	Val	Thr	Leu	Phe	Asn	Lys	Met
			20				25						30		
Glu	Glu	Glu	Asn	Cys	Lys	Val	Arg	Pro	Asn	Glu	Ile	Thr	Phe	Leu	Val
		35				40					45				
Val	Leu	Asn	Ala	Cys	Ser	His	Gly	Gly	Leu	Val	Met	Glu	Gly	Ile	Arg
	50				55					60					
Cys	Phe	Lys	Arg	Met	Val	Glu	Ala	Tyr	Ser	Phe	Thr	Pro	Lys	Val	Glu
65				70					75					80	
His	Tyr	Gly	Cys	Val	Val	Asp	Leu	Leu	Gly	Arg	Ala	Gly	Gln	Leu	Glu
			85						90				95		
Glu	Ala	Tyr	Glu	Leu	Ile	Arg	Asn	Leu	Pro	Ile	Thr	Ser	Asp	Ser	Thr
			100				105						110		
Ala	Trp	Arg	Ala	Leu	Leu	Ala	Ala	Cys	Arg	Val	Tyr	Gly	Asn	Ala	Asp
		115				120						125			
Leu	Gly	Glu	Ser	Val	Met	Met	Arg	Leu	Ala	Glu	Met	Gly	Glu	Thr	His
	130				135					140					
Pro	Ala	Asp	Ala	Ile	Leu	Leu	Ala	Gly	Thr	His	Ala	Val	Ala	Gly	Asn
145				150					155					160	
Pro	Gln	Lys	Ser	Leu	Asp	Asn	Glu	Leu	Asn	Lys	Gly	Arg	Lys	Glu	Ala
			165				170							175	
Gly	Tyr	Ser	Ala	Ile	Glu	Ile	Glu								
			180												

(2) INFORMATION FOR SEQ ID NO:1309:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 173 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..173

(D) OTHER INFORMATION: / Ceres Seq. ID 1569588

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1309:

Met	Ile	Ser	Gly	Tyr	Gly	Ala	His	Gly	Leu	Ala	Arg	Glu	Ala	Val	Thr
1			5					10						15	
Leu	Phe	Asn	Lys	Met	Glu	Glu	Glu	Asn	Cys	Lys	Val	Arg	Pro	Asn	Glu
			20				25						30		
Ile	Thr	Phe	Leu	Val	Val	Leu	Asn	Ala	Cys	Ser	His	Gly	Gly	Leu	Val
		35				40					45				
Met	Glu	Gly	Ile	Arg	Cys	Phe	Lys	Arg	Met	Val	Glu	Ala	Tyr	Ser	Phe
	50				55					60					
Thr	Pro	Lys	Val	Glu	His	Tyr	Gly	Cys	Val	Val	Asp	Leu	Leu	Gly	Arg
65				70				75						80	
Ala	Gly	Gln	Leu	Glu	Glu	Ala	Tyr	Glu	Leu	Ile	Arg	Asn	Leu	Pro	Ile
		85						90				95			
Thr	Ser	Asp	Ser	Thr	Ala	Trp	Arg	Ala	Leu	Leu	Ala	Ala	Cys	Arg	Val
		100				105						110			
Tyr	Gly	Asn	Ala	Asp	Leu	Gly	Glu	Ser	Val	Met	Met	Arg	Leu	Ala	Glu
	115				120							125			
Met	Gly	Glu	Thr	His	Pro	Ala	Asp	Ala	Ile	Leu	Leu	Ala	Gly	Thr	His
	130				135					140					
Ala	Val	Ala	Gly	Asn	Pro	Gln	Lys	Ser	Leu	Asp	Asn	Glu	Leu	Asn	Lys
145				150					155					160	
Gly	Arg	Lys	Glu	Ala	Gly	Tyr	Ser	Ala	Ile	Glu	Ile	Glu			
			165				170								

(2) INFORMATION FOR SEQ ID NO:1310:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1666 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..1666
(D) OTHER INFORMATION: / Ceres Seq. ID 1569589
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1310:
aaatataatt tcaacgacgt gctctctttt cttcttcgga tctctcttc gccgagtgaa 60
gccgcgactg tgaatcatgt agaggagtaa aacgcgcgcg catctccgaa tcgaatgact 120
ctccccttaa gaatgcaaaa ccgggtgggg gaatctcttt tggtagctag aagaatgtgg 180
ccccgatgca gcagagtcga ttaacatcag catcatgtga taaacagagg gctgagttag 240
ctaggaaagca tgtgagactt cttataaacc aatttgttaag ttgggtgcag ttacagctga 300
agaatcatcc tgaatgaact tgggaagatg ggatgaatga ctacattacg catgcttcaa 360
acattcttga aaagttttaag gatgtggtca gctggcttaa agaaaaataag ggaaaggggg 420
agaattttat ccctgaatct cgtggagcag aaaagaaatt agtggctgaa gtcaaagata 480
ccaatgttaa atcattttca aacaatatct cttttgcttc aaacaatcaa cctgggactt 540
tctcaaaaac tcaatcttcc gatttttcca gtgctcagtc tggtttcttt tcaagccaat 600
ctggagcatt ctcacgagct cttctcgttt taatatccaa tagccagact ggatctttta 660
gcagtggtcca gtttggtagc acaaaaagca gccaaaccaag cctatttttc ggcagtcagg 720
ccggagcaat gttctaaagc caacctggaa ctttctccag cagtctctct ggtataaacat 780
ctaattagcca gacgggatct ttttagtagt gccaatattg tcagacaaaa agcagcccaat 840
caagcctact tctcggcagt caagcaggag taatctctag tagccaacct tcttttcaat 900
tttctaaacg tcaatccccct ttacatctct cagtacctcc agtgtccata ccggcaaaag 960
aggatcactc agatgatgcg gatgtgtgag acgaacaatc tcaaccgagc agccactctg 1020
tcaaaaagac ggaagaaaaa ggtattactg tggttcatga agtcaaatgc aaactttatg 1080
tcaagtcaag tgaccacgca gataaaaggt ggaagactgg aaactctaca 1140
taaatgtcaa agaaggagtc gacaagggGa caaaagaatc aaaaaccaca attcttgtcc 1200
gaaaagatgt tggaaaaact cttctgaatg cactactgta cgtctgaatg aagacaagcc 1260
cacagaagaa cgctcttgtt gcaatatctt actcctcgga tgattccaac gagaatgtaa 1320
caccgagaac ctttctgata aggacaaaag acgcagaagc tagagataat tttagcaacg 1380
ccatccaaga atacgcccct tcttcataga ttgcccraag ccaggttgag attcttactg 1440
taacttttaa aagccttatc gactcgtcct ctctctatat ttttttctct atttgaata 1500
ttaggaaggg tcttaagact aacgtaaaag ttgataaagg gcacaaaaat gttgtatgat 1560
tgtgagagag agagaggggc aaaggagttc gtactgtatt agagaattgt gtccaatct 1620
tctttgtaac ttaaaaaaca gaacaataa aatcacttct ttttat

(2) INFORMATION FOR SEQ ID NO:1311:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 443 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..443
(D) OTHER INFORMATION: / Ceres Seq. ID 1569590
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1311:
Met Arg Gly Val Lys Arg Ala Ala Ile Ser Glu Ser Asn Asp Ser Pro
1 5 10 15
Phe Lys Asn Ala Lys Pro Val Gly Gly Ile Phe Phe Gly Thr Gln Lys
20 25 30
Asn Val Ala Pro Met Gln Gln Ser Pro Leu Thr Ser Ala Ser Leu Asp
35 40 45
Lys Gln Arg Ala Glu Leu Ala Arg Lys His Val Arg Ala Leu Asn Asn
50 55 60
Gln Phe Val Ser Trp Val Gln Leu Gln Leu Lys Asn His Pro Asp Glu
65 70 75 80

Leu Trp Glu Asp Gly Met Asn Asp Tyr Ile Thr His Ala Ser Asn Ile
85 90 95
Leu Glu Lys Phe Lys Asp Val Val Ser Trp Leu Lys Glu Asn Lys Gly
100 105 110
Lys Gly Glu Asn Leu Ser Pro Glu Ser Arg Gly Ala Glu Lys Lys Leu
115 120 125
Val Ala Glu Val Lys Asn Thr Asn Val Lys Ser Phe Ser Asn Asn Ile
130 135 140
Pro Phe Ala Ser Asn Asn Gln Pro Gly Ile Phe Ser Asn Asn Gln Ser
145 150 155 160
Ser Asp Phe Ser Ser Ser Gln Ser Gly Phe Phe Ser Ser Gln Ser Gly
165 170 175
Ala Phe Ser Ser Ser Pro Ser Gly Leu Ile Ser Asn Ser Gln Thr Gly
180 185 190
Ser Phe Ser Ser Gly Gln Phe Gly Thr Thr Lys Ser Ser Gln Pro Ser
195 200 205
Leu Phe Ser Gly Ser Gln Ala Gly Ala Ile Ser Asn Ser Gln Pro Gly
210 215 220
Thr Phe Ser Ser Ser Pro Ser Gly Ile Thr Ser Asn Ser Gln Thr Gly
225 230 235 240
Ser Phe Ser Ser Gly Gln Phe Gly Gln Thr Lys Ser Ser Gln Pro Ser
245 250 255
Leu Leu Ser Gly Ser Gln Ala Gly Val Ile Ser Ser Ser Gln Pro Ser
260 265 270
Phe Gln Phe Ser Asn Ser Gln Ser Pro Phe Thr Ser Ala Val Pro Pro
275 280 285
Val Ser Ile Pro Ala Lys Gln Asp His Ser Asp Asp Ala Asp Gly Gly
290 295 300
Asp Glu Gln Ser Gln Pro Ser Ser Pro Ser Val Lys Lys Thr Glu Glu
305 310 315 320
Lys Gly Ile Thr Val Val His Glu Val Lys Cys Lys Leu Tyr Val Lys
325 330 335
Ser Ser Asp Pro Ala Asp Lys Gly Trp Lys Asp Lys Gly Thr Gly Asn
340 345 350
Leu Tyr Ile Lys Cys Lys Glu Gly Val Asp Lys Gly Thr Lys Glu Ser
355 360 365
Lys Pro Thr Ile Leu Val Arg Asn Asp Val Gly Lys Leu Leu Asn
370 375 380
Ala Leu Leu Tyr Ala Gly Met Lys Thr Ser Pro Gln Lys Asn Ala Leu
385 390 395 400
Val Ala Ile Phe His Ser Ser Asp Asp Ser Asn Glu Asn Val Thr Pro
405 410 415
Arg Thr Phe Leu Ile Arg Thr Lys Asn Ala Glu Ala Arg Asp Asn Leu
420 425 430
Ala Thr Ala Ile Gln Glu Tyr Ala Pro Ser Ser
435 440

(2) INFORMATION FOR SEQ ID NO:1312:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 407 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..407

(D) OTHER INFORMATION: / Ceres Seq. ID 1569591

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1312:

Met Gln Gln Ser Pro Leu Thr Ser Ala Ser Leu Asp Lys Gln Arg Ala
1 5 10 15
Glu Leu Ala Arg Lys His Val Arg Ala Leu Asn Asn Gln Phe Val Ser

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1313:

```

Met Asn Asp Tyr Ile Thr His Ala Ser Asn Ile Leu Glu Lys Phe Lys
1      5      10      15
Asp Val Val Ser Trp Leu Lys Glu Asn Lys Gly Lys Gly Glu Asn Leu
20      25      30
Ser Pro Glu Ser Arg Gly Ala Glu Lys Lys Leu Val Ala Glu Val Lys
35      40      45
Asn Thr Asn Val Lys Ser Phe Ser Asn Asn Ile Pro Phe Ala Ser Asn
50      55      60
Asn Gln Pro Gly Ile Phe Ser Asn Asn Gln Ser Ser Asp Phe Ser Ser
65      70      75      80
Ser Gln Ser Gly Phe Phe Ser Ser Gln Ser Gly Ala Phe Ser Ser Ser
85      90      95
Pro Ser Gly Leu Ile Ser Asn Ser Gln Thr Gly Ser Phe Ser Ser Gly
100      105      110
Gln Phe Gly Thr Thr Lys Ser Ser Gln Pro Ser Leu Phe Ser Gly Ser
115      120      125
Gln Ala Gly Ala Ile Ser Asn Ser Gln Pro Gly Thr Phe Ser Ser Ser
130      135      140
Pro Ser Gly Ile Thr Ser Asn Ser Gln Thr Gly Ser Phe Ser Ser Gly
145      150      155      160
Gln Phe Gly Gln Thr Lys Ser Ser Gln Pro Ser Leu Leu Ser Gly Ser
165      170      175
Gln Ala Gly Val Ile Ser Ser Ser Gln Pro Ser Phe Gln Phe Ser Asn
180      185      190
Ser Gln Ser Pro Phe Thr Ser Ala Val Pro Pro Val Ser Ile Pro Ala
195      200      205
Lys Gln Asp His Ser Asp Asp Ala Asp Gly Gly Asp Glu Gln Ser Gln
210      215      220
Pro Ser Ser Pro Ser Val Lys Lys Thr Glu Glu Lys Gly Ile Thr Val
225      230      235      240
Val His Glu Val Lys Cys Lys Leu Tyr Val Lys Ser Ser Asp Pro Ala
245      250      255
Asp Lys Gly Trp Lys Asp Lys Gly Thr Gly Asn Leu Tyr Ile Lys Cys
260      265      270
Lys Glu Gly Val Asp Lys Gly Thr Lys Glu Ser Lys Pro Thr Ile Leu
275      280      285
Val Arg Asn Asp Val Gly Lys Leu Leu Asn Ala Leu Leu Tyr Ala
290      295      300
Gly Met Lys Thr Ser Pro Gln Lys Asn Ala Leu Val Ala Ile Phe His
305      310      315      320
Ser Ser Asp Asp Ser Asn Glu Asn Val Thr Pro Arg Thr Phe Leu Ile
325      330      335
Arg Thr Lys Asn Ala Glu Ala Arg Asp Asn Leu Ala Thr Ala Ile Gln
340      345      350
Glu Tyr Ala Pro Ser Ser
355

```

(2) INFORMATION FOR SEQ ID NO:1314:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1306 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1306
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569603

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1314:

```

aaccacaag aagaatccaa agacatgaaa cttctcttta ttgttctcat ctcttttctt      60
tcctctctcc aagcatcaaa aggattcgat ttgcacgaaa aagaattaga aaccgaagag      120
aacctatgga agctctatga gaggtggaga gggccaccact ctgtatccCa gagcttctca      180

```

tgaggcaata	aagcgggttca	acgttttttag	acacaatgtc	cttcgatgtcc	acaggactaa	240
caagaagaac	aagcctttaca	aactcaagat	caatagattc	gccgcacaacg	caccacgagt	300
ttagaagctc	ctacgctggc	ttaaatgtta	agcatcaccg	aatgcttctg	ggaccgaagc	360
cgggatctgg	tggtttcatg	tatgagaatg	tgaccagagt	tcgagattct	gttgattggc	420
gagagaaagg	agctgtcaat	gaagtcaaga	atcaacagg	ttgtggaaat	tgctggcgct	480
tttcgacggt	tgacgacgtg	gaagggataa	acaagatcgg	aacaacaaaa	ctagtttcat	540
tgtctgaaca	agagcttgtg	gattgtgaca	ctgaagagaa	tcaaggttgt	gcaggaggct	600
tcattggaac	tgcgtttgaa	tttataaaga	acaatggtgg	aatcaaaaac	gaagagacct	660
atcccttaaga	ttccagtgac	gttcaattct	gtagagctaa	gagtatgtgt	ggagaaactg	720
taaccatoga	tggaacagaa	cacgtccctg	agaatgatga	ggaagaacct	ctcaaaagctg	780
ttgctcacca	gcctgtctct	gtagctattg	atgctgggag	ctcagatttc	cagctttact	840
ctgaggggtg	gtttatcgga	gaatgcggga	ctcagttgaa	ccacgggggtg	gtgattgttg	900
ggtatggaga	gaccaaaaat	ggaacaaaat	attggatagt	aaggaactca	tggggacctg	960
aatggggaga	aggaggtcat	gttcggatag	aaagaggaaat	atcgagaaat	gaaggacggt	1020
gcggtatagc	catggaggct	tcttatccca	ccaagctctc	ttcgactcct	tctactcatg	1080
agtcagtagt	tcgtgatgat	gttaaagacg	agctctagag	actttaagtc	attgaaaact	1140
gaatttcgaa	ccattcttct	agtgcgctta	cactgagttt	attattttaa	tggtattgag	1200
ttcattgggt	tcaattttaca	catctatcgt	gtattcatct	taagtttgaga	cgatttttat	1260
ctccttgtaa	tattggccag	catttgcctt	gcggaaaaat	ggcggtt		

(2) INFORMATION FOR SEQ ID NO:1315:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 300 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..300

(D) OTHER INFORMATION: / Ceres Seq. ID 1569604

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1315:

Met	Ser	Phe	Met	Ser	Thr	Gly	Leu	Thr	Arg	Arg	Thr	Ser	Leu	Thr	Asn
1			5					10					15		
Ser	Arg	Ser	Ile	Asp	Ser	Pro	Thr	Thr	His	His	Glu	Phe	Arg	Ser	Ser
			20					25					30		
Tyr	Ala	Gly	Ser	Asn	Val	Lys	His	His	Arg	Met	Leu	Arg	Gly	Pro	Lys
			35				40					45			
Arg	Gly	Ser	Gly	Gly	Phe	Met	Tyr	Glu	Asn	Val	Thr	Arg	Val	Pro	Ser
			50				55					60			
Ser	Val	Asp	Trp	Arg	Gly	Lys	Gly	Ala	Val	Thr	Glu	Val	Lys	Asn	Gln
			65				70				75			80	
Gln	Asp	Cys	Gly	Ser	Cys	Trp	Ala	Phe	Ser	Thr	Val	Ala	Ala	Val	Glu
			85						90				95		
Gly	Ile	Asn	Lys	Ile	Gly	Thr	Asn	Lys	Leu	Val	Ser	Leu	Ser	Glu	Gln
			100				105					110			
Glu	Leu	Val	Asp	Cys	Asp	Thr	Glu	Glu	Asn	Gln	Gly	Cys	Ala	Gly	Gly
			115				120					125			
Leu	Met	Glu	Pro	Ala	Phe	Glu	Phe	Ile	Lys	Asn	Asn	Gly	Gly	Ile	Lys
			130				135					140			
Thr	Glu	Glu	Thr	Tyr	Pro	Tyr	Asp	Ser	Ser	Asp	Val	Gln	Phe	Cys	Arg
			145				150				155			160	
Ala	Lys	Ser	Ile	Gly	Gly	Glu	Thr	Val	Thr	Ile	Asp	Gly	His	Glu	His
			165						170				175		
Val	Pro	Glu	Asn	Asp	Glu	Glu	Glu	Leu	Lys	Ala	Val	Ala	His	Gln	
			180					185				190			
Pro	Val	Ser	Val	Ala	Ile	Asp	Ala	Gly	Ser	Ser	Asp	Phe	Gln	Leu	Tyr
			195				200					205			
Ser	Glu	Gly	Val	Phe	Ile	Gly	Glu	Cys	Gly	Thr	Gln	Leu	Asn	His	Gly
			210				215					220			
Val	Val	Ile	Val	Gly	Tyr	Gly	Glu	Thr	Lys	Asn	Gly	Thr	Lys	Tyr	Trp
			225				230				235				

Ile	Val	Arg	Asn	Ser	Trp	Gly	Pro	Glu	Trp	Gly	Glu	Gly	Gly	Tyr	Val
			245						250					255	
Arg	Ile	Glu	Arg	Gly	Ile	Ser	Glu	Asn	Glu	Gly	Arg	Cys	Gly	Ile	Ala
			260					265					270		
Met	Glu	Ala	Ser	Tyr	Pro	Thr	Lys	Leu	Ser	Ser	Thr	Pro	Ser	Thr	His
			275				280					285			
Glu	Ser	Val	Val	Arg	Asp	Asp	Val	Lys	Asp	Glu	Leu				
			290			295					300				

(2) INFORMATION FOR SEQ ID NO:1316:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 297 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..297

(D) OTHER INFORMATION: / Ceres Seq. ID 1569605

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1316:

Met	Ser	Thr	Gly	Leu	Thr	Arg	Arg	Thr	Ser	Leu	Thr	Asn	Ser	Arg	Ser
1				5				10						15	
Ile	Asp	Ser	Pro	Thr	Thr	His	His	Glu	Phe	Arg	Ser	Ser	Tyr	Ala	Gly
			20					25					30		
Ser	Asn	Val	Lys	His	His	Arg	Met	Leu	Arg	Gly	Pro	Lys	Arg	Gly	Ser
			35				40					45			
Gly	Gly	Phe	Met	Tyr	Glu	Asn	Val	Thr	Arg	Val	Pro	Ser	Ser	Val	Asp
			50			55				60					
Trp	Arg	Glu	Lys	Gly	Ala	Val	Thr	Glu	Val	Lys	Asn	Gln	Gln	Asp	Cys
			65			70				75				80	
Gly	Ser	Cys	Trp	Ala	Phe	Ser	Thr	Val	Ala	Ala	Val	Glu	Gly	Ile	Asn
			85						90				95		
Lys	Ile	Gly	Thr	Asn	Lys	Leu	Val	Ser	Leu	Ser	Glu	Gln	Glu	Leu	Val
			100				105						110		
Asp	Cys	Asp	Thr	Glu	Glu	Asn	Gln	Gly	Cys	Ala	Gly	Gly	Leu	Met	Glu
			115				120					125			
Pro	Ala	Phe	Glu	Phe	Ile	Lys	Asn	Asn	Gly	Gly	Ile	Lys	Thr	Glu	Glu
			130				135					140			
Thr	Tyr	Pro	Tyr	Asp	Ser	Ser	Asp	Val	Gln	Phe	Cys	Arg	Ala	Lys	Ser
			145			150				155				160	
Ile	Gly	Gly	Glu	Thr	Val	Thr	Ile	Asp	Gly	His	Glu	His	Val	Pro	Glu
			165					170					175		
Asn	Asp	Glu	Glu	Glu	Leu	Leu	Lys	Ala	Val	Ala	His	Gln	Pro	Val	Ser
			180				185						190		
Val	Ala	Ile	Asp	Ala	Gly	Ser	Ser	Asp	Phe	Gln	Leu	Tyr	Ser	Glu	Gly
			195				200					205			
Val	Phe	Ile	Gly	Glu	Cys	Gly	Thr	Gln	Leu	Asn	His	Gly	Val	Val	Ile
			210			215					220				
Val	Gly	Tyr	Gly	Glu	Thr	Lys	Asn	Gly	Thr	Lys	Tyr	Trp	Ile	Val	Arg
			225			230				235				240	
Asn	Ser	Trp	Gly	Pro	Glu	Trp	Gly	Glu	Gly	Gly	Tyr	Val	Arg	Ile	Glu
			245				250						255		
Arg	Gly	Ile	Ser	Glu	Asn	Glu	Gly	Arg	Cys	Gly	Ile	Ala	Met	Glu	Ala
			260				265						270		
Ser	Tyr	Pro	Thr	Lys	Leu	Ser	Ser	Thr	Pro	Ser	Thr	His	Glu	Ser	Val
			275				280					285			
Val	Arg	Asp	Asp	Val	Lys	Asp	Glu	Leu							
			290			295									

(2) INFORMATION FOR SEQ ID NO:1317:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 258 amino acids

(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..258
(D) OTHER INFORMATION: / Ceres Seq. ID 1569606
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1317:

Met	Leu	Arg	Gly	Pro	Lys	Arg	Gly	Ser	Gly	Phe	Met	Tyr	Glu	Asn	
1			5					10					15		
Val	Thr	Arg	Val	Pro	Ser	Ser	Val	Asp	Trp	Arg	Glu	Lys	Gly	Ala	Val
			20					25					30		
Thr	Glu	Val	Lys	Asn	Gln	Gln	Asp	Cys	Gly	Ser	Cys	Trp	Ala	Phe	Ser
			35				40					45			
Thr	Val	Ala	Ala	Val	Glu	Gly	Ile	Asn	Lys	Ile	Gly	Thr	Asn	Lys	Leu
			50			55					60				
Val	Ser	Leu	Ser	Glu	Gln	Glu	Leu	Val	Asp	Cys	Asp	Thr	Glu	Glu	Asn
65					70				75					80	
Gln	Gly	Cys	Ala	Gly	Gly	Leu	Met	Glu	Pro	Ala	Phe	Glu	Phe	Ile	Lys
			85					90					95		
Asn	Asn	Gly	Gly	Ile	Lys	Thr	Glu	Glu	Thr	Tyr	Pro	Tyr	Asp	Ser	Ser
			100					105					110		
Asp	Val	Gln	Phe	Cys	Arg	Ala	Lys	Ser	Ile	Gly	Gly	Glu	Thr	Val	Thr
			115				120					125			
Ile	Asp	Gly	His	Glu	His	Val	Pro	Glu	Asn	Asp	Glu	Glu	Glu	Leu	Leu
			130			135					140				
Lys	Ala	Val	Ala	His	Gln	Pro	Val	Ser	Val	Ala	Ile	Asp	Ala	Gly	Ser
145					150					155				160	
Ser	Asp	Phe	Gln	Leu	Tyr	Ser	Glu	Gly	Val	Phe	Ile	Gly	Glu	Cys	Gly
			165					170					175		
Thr	Gln	Leu	Asn	His	Gly	Val	Val	Ile	Val	Gly	Tyr	Gly	Glu	Thr	Lys
			180				185						190		
Asn	Gly	Thr	Lys	Tyr	Trp	Ile	Val	Arg	Asn	Ser	Trp	Gly	Pro	Glu	Trp
			195				200					205			
Gly	Glu	Gly	Gly	Tyr	Val	Arg	Ile	Glu	Arg	Gly	Ile	Ser	Glu	Asn	Glu
			210			215					220				
Gly	Arg	Cys	Gly	Ile	Ala	Met	Glu	Ala	Ser	Tyr	Pro	Thr	Lys	Leu	Ser
225					230					235				240	
Ser	Thr	Pro	Ser	Thr	His	Glu	Ser	Val	Val	Arg	Asp	Asp	Val	Lys	Asp
			245					250					255		

Glu Leu

(2) INFORMATION FOR SEQ ID NO:1318:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2081 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..2081
(D) OTHER INFORMATION: / Ceres Seq. ID 1569611
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1318:

aaaagcttct	tcataaatg	agaagcaagg	atgtgagatc	gaagctttg	atattgatta	60
caacatcttt	gtaaggaaga	ttaattgttaa	tccttttga	atcttttagc	ggaaaccgcg	120
gcgggaagct	gaccagccgg	taaagacaga	ggaagagtca	ttgaagctag	aggatgaaac	180
cggtaacaaa	gtcaagcatg	tactaaaagg	agtgaattgc	agagcccaac	catgggaagt	240
tccttgctatt	gttggtcccaa	gtgggtgcagg	gaagtgcgtc	ttgcttgaaa	ttctatgctg	300
tagactcatc	cctcaaaccc	ggtcgggtta	tgtcaacaag	agccccgggtg	atagagccaa	360

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tttcaagaaa atctctgtgtt atgtcactca gaaggatact ctgtttccct tgcttacggg 420
ggaggaaacc ctctctgttca gtgctaagct gcgtttaaag ctccctcgag atgaactcgag 480
atcacggggt aagtcttttg tccatgagct tggggttgaa gctgttgcca cggctcgtgt 540
tgggcgtgat agtgcagag gtatatcggt ttgagagaga cgtcgtgtct ccatgaggat 600
tgaagtattt cagcaccta aagtcttgat ccttgatgag ccaacctctg gtcttgatag 660
tacttcggct ctgctgatca tagacatgct caaacacatg gctgaaacac gaggcaggac 720
cataattctt actatccacc aaccgggatt tcggtatgct aaacagtcca atctctgttt 780
cttgttgccc aatggctcga ccttgaagca ggggtcggtg gatcagcttg ggtttactt 840
aaggtcaaat gggttgaccc ctctcttcca tgaataacatc gttgaatttg ccatgtaact 900
aatcgaaatc atcacaatac agcaacggct acaggaaagc agaagagcag ctoatgtctt 960
aacacacaaa acaacattac aagagaagag atcagaagat agtcaagggt agagcaaaag 1020
tgggcaatac acactacaac agctgtttca acaacaaggt gtgcgtgat taggaacagt 1080
gaacatagca acagagtcca caagagattt tgcaaatcca agattagaag aaactatgat 1140
actcacacat aggtttctcca agaacatttt cagaaccaag gagctttttg cgtgcaggac 1200
ggttcagatg tttaggttcag gaattgtctt agtctgtatt ttcataatct caaagacgat 1260
ttaaaagggt cgcgagaaaag agtcggcctc ttgtcattca tattgacctt tctgctaact 1320
tcgacaatag aggcactccc tataattctg caagaaagag agattctgat gaaggagacc 1380
tctagtggaa gctacagagt gtctctatct gcgcctcgta atggactagt ttacttgcca 1440
tttctgtcca tcttagctat tctattctca accccagtgt actggctggt gggactgaac 1500
cccagtttca tggcgtttct acacttttct ctctcattt ggttaactct ctacacagca 1560
aactcgggtg ttgtgtgctt tagtgcactg gttcctaatt tcatagttgg aaactcagt 1620
atttcgggtg tgatgggttg ctctttttct ttctcgggt acttcatac gaacctgatg 1680
atccctggtt actcgatttt catgcactac atctcctgt tcaagtaccg gttcgaagga 1740
tttctgatta acgagttctt aaaatcaaac aagtgttttg agtatggatt cggaaaatgt 1800
ttgtgtgacc agaggagtat actcaagaaa gaaaggtacg gaaggaaaag tagatgaga 1860
aatgttgtga tcatgctatg ttttgtctg ctctacaggt tcatttctca tgtgattctg 1920
aggtgtagat gtccccaacg aagtttcaaa accactctgc ctaataaat gtggtagcaa 1980
taagtctctt ttctgaaaaa attgggttac aggtttgttc atgtgtttaa ttatttactT 2040
cgtacagcaa ccgaagatgt gaaagaaaat gttgtttctg c

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(2) INFORMATION FOR SEQ ID NO:1319:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 411 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..411
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569612

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1319:

```

Lys Ala Ser Ser Ser Met Glu Lys Gln Gly Cys Glu Ile Glu Ala Leu
1      5      10      15
Asp Ile Asp Tyr Asn Ile Phe Val Arg Lys Ile Asn Val Asn Pro Phe
20     25     30
Gly Ile Phe Arg Arg Lys Pro Arg Pro Glu Ala Asp Gln Pro Val Lys
35     40     45
Thr Glu Glu Glu Ser Leu Lys Leu Glu Asp Glu Thr Gly Asn Lys Val
50     55     60
Lys His Val Leu Lys Gly Val Thr Cys Arg Ala Lys Pro Trp Glu Ile
65     70     75     80
Leu Ala Ile Val Gly Pro Ser Gly Ala Gly Lys Ser Ser Leu Leu Glu
85     90     95
Ile Leu Ala Ala Arg Leu Ile Pro Gln Thr Gly Ser Val Tyr Val Asn
100    105    110
Lys Ser Pro Val Asp Arg Ala Asn Phe Lys Lys Ile Ser Gly Tyr Val
115    120    125
Thr Gln Lys Asp Thr Leu Phe Pro Leu Leu Thr Val Glu Glu Thr Leu
130    135    140
Leu Phe Ser Ala Lys Leu Arg Leu Lys Leu Pro Ala Asp Glu Leu Arg
145    150    155    160

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Ser Arg Val Lys Ser Leu Val His Glu Leu Gly Leu Glu Ala Val Ala
165 170 175
Thr Ala Arg Val Gly Asp Asp Ser Val Arg Gly Ile Ser Gly Gly Glu
180 185 190
Arg Arg Arg Val Ser Ile Gly Val Glu Val Ile His Asp Pro Lys Val
195 200 205
Leu Ile Leu Asp Glu Pro Thr Ser Gly Leu Asp Ser Thr Ser Ala Leu
210 215 220
Leu Ile Ile Asp Met Leu Lys His Met Ala Glu Thr Arg Gly Arg Thr
225 230 235
Ile Ile Leu Thr Ile His Gln Pro Gly Phe Arg Ile Val Lys Gln Phe
245 250 255
Asn Ser Val Leu Leu Leu Ala Asn Gly Ser Thr Leu Lys Gln Gly Ser
260 265 270
Val Asp Gln Leu Gly Val Tyr Leu Arg Ser Asn Gly Leu His Pro Pro
275 280 285
Leu His Glu Asn Ile Val Glu Phe Ala Ile Glu Ser Ile Glu Ser Ile
290 295 300
Thr Lys Gln Gln Arg Leu Gln Glu Ser Arg Arg Ala Ala His Val Leu
305 310 315
Thr Pro Gln Thr Thr Leu Gln Glu Lys Arg Ser Glu Asp Ser Gln Gly
325 330 335
Glu Ser Lys Ser Gly Lys Phe Thr Leu Gln Gln Leu Phe Gln Gln Thr
340 345 350
Arg Val Ala Asp Val Gly Thr Met Asn Ile Ala Thr Glu Phe Thr Arg
355 360 365
Asp Phe Ala Asn Ser Arg Leu Glu Glu Thr Met Ile Leu Thr His Arg
370 375 380
Phe Ser Lys Asn Ile Phe Arg Thr Lys Glu Leu Phe Ala Cys Arg Thr
385 390 395
Val Gln Met Leu Gly Ser Gly Ile Val Leu Val
405 410

(2) INFORMATION FOR SEQ ID NO:1320:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 406 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..406

(D) OTHER INFORMATION: / Ceres Seq. ID 1569613

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1320:

Met Glu Lys Gln Gly Cys Glu Ile Glu Ala Leu Asp Ile Asp Tyr Asn
1 5 10 15
Ile Phe Val Arg Lys Ile Asn Val Asn Pro Phe Gly Ile Phe Arg Arg
20 25 30
Lys Pro Arg Pro Glu Ala Asp Gln Pro Val Lys Thr Glu Glu Ser
35 40 45
Leu Lys Leu Glu Asp Glu Thr Gly Asn Lys Val Lys His Val Leu Lys
50 55 60
Gly Val Thr Cys Arg Ala Lys Pro Trp Glu Ile Leu Ala Ile Val Gly
65 70 75 80
Pro Ser Gly Ala Gly Lys Ser Ser Leu Leu Glu Ile Leu Ala Ala Arg
85 90 95
Leu Ile Pro Gln Thr Gly Ser Val Tyr Val Asn Lys Ser Pro Val Asp
100 105 110
Arg Ala Asn Phe Lys Lys Ile Ser Gly Tyr Val Thr Gln Lys Asp Thr
115 120 125
Leu Phe Pro Leu Leu Thr Val Glu Glu Thr Leu Leu Phe Ser Ala Lys

130	135	140
Leu Arg Leu Lys Leu	Pro Ala Asp Glu Leu Arg Ser Arg Val Lys Ser	
145	150	155
Leu Val His Glu Leu Gly Leu Glu Ala Val Ala Thr Ala Arg Val Gly		160
	165	170
Asp Asp Ser Val Arg Gly Ile Ser Gly Gly Glu Arg Arg Arg Val Ser		175
	180	185
Ile Gly Val Glu Glu Val Ile His Asp Pro Lys Val Leu Ile Leu Asp Glu		190
	195	200
Pro Thr Ser Gly Leu Asp Ser Thr Ser Ala Leu Leu Ile Ile Asp Met		205
	210	215
Leu Lys His Met Ala Glu Thr Arg Gly Arg Thr Ile Ile Leu Thr Ile		220
225	230	235
His Gln Pro Gly Phe Arg Ile Val Lys Gln Phe Asn Ser Val Leu Leu		240
	245	250
Leu Ala Asn Gly Ser Thr Leu Lys Gln Gly Ser Val Asp Gln Leu Gly		255
	260	265
Val Tyr Leu Arg Ser Asn Gly Leu His Pro Pro Leu His Glu Asn Ile		270
	275	280
Val Glu Phe Ala Ile Glu Ser Ile Glu Ser Ile Thr Lys Gln Gln Arg		285
	290	295
Leu Gln Glu Ser Arg Arg Ala Ala His Val Leu Thr Pro Gln Thr Thr		300
305	310	315
Leu Gln Glu Lys Arg Ser Glu Asp Ser Gln Gly Glu Ser Lys Ser Gly		320
	325	330
Lys Phe Thr Leu Gln Gln Leu Phe Gln Gln Thr Arg Val Ala Asp Val		335
	340	345
Gly Thr Met Asn Ile Ala Thr Glu Phe Thr Arg Asp Phe Ala Asn Ser		350
	355	360
Arg Leu Glu Glu Thr Met Ile Leu Thr His Arg Phe Ser Lys Asn Ile		365
	370	375
Phe Arg Thr Lys Glu Leu Phe Ala Cys Arg Thr Val Gln Met Leu Gly		380
385	390	395
Ser Gly Ile Val Leu Val		400
	405	

(2) INFORMATION FOR SEQ ID NO:1321:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 470 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..470
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569614

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1321:

acgatctggt gctggataag ctttttgctt cattctcact tcttctctca tccaaaaaag	60
ctctctccatt tcaattggcga cagcatcatc tctctcatca ctctcttcac tctcaactcca	120
caccogaacc tcttctctca tctctcttct ctcacacaaa tccatcgctc ttttctctct	180
cttctctcaac cgcgcgtctt catctctcac tctcgtcaaa gcctcatcga ccgataccga	240
aaccatcttc ttctgaagacg aaacaccaga aataaccgca aatgtcgtct tcgacccacc	300
aattgtctcc gaagatttcg tctctctctc gtatttcgac gaagggaagcg acgagacaga	360
ggaagagatc gCtaaccgtt ttgaagagct ctatggacct gcgtatagtg gtgagagtat	420
gctttgagtc catcacataa atatctttcc caagcatact ctccaccgac	

(2) INFORMATION FOR SEQ ID NO:1322:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 127 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..127
 (D) OTHER INFORMATION: / Ceres Seq. ID 1569615
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1322:

Thr	Ile	Trp	Cys	Trp	Ile	Ser	Leu	Leu	Leu	His	Ser	His	Phe	Leu	Pro
1			5					10						15	
His	Pro	Lys	Lys	Leu	Leu	His	Phe	Asn	Gly	Asp	Ser	Ile	Ile	Ser	Leu
			20					25					30		
Ile	Thr	Leu	Phe	Thr	Leu	Thr	Pro	His	Pro	Asn	Leu	Phe	Ser	His	Leu
		35					40					45			
Leu	Phe	Leu	His	Lys	Ile	His	Arg	Leu	Phe	Leu	Leu	Pro	Gln	Pro	
		50				55				60					
Pro	Leu	Leu	Ile	Ser	His	Ser	Arg	Gln	Ser	Leu	Ile	Asp	Arg	Tyr	Arg
		65			70				75				80		
Asn	His	Leu	Leu	Arg	Arg	Arg	Asn	Thr	Arg	Asn	Asn	Arg	Lys	Cys	Arg
			85					90					95		
Leu	Arg	Pro	Thr	Asn	Cys	Ser	Arg	Arg	Ile	Arg	Leu	Ser	Ser	Val	Phe
			100					105					110		
Arg	Arg	Arg	Lys	Arg	Arg	Asp	Arg	Gly	Arg	Asp	Arg	Tyr	Arg	Phe	
		115					120						125		

(2) INFORMATION FOR SEQ ID NO:1323:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 90 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..90
 (D) OTHER INFORMATION: / Ceres Seq. ID 1569616
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1323:

Asp	Leu	Val	Leu	Asp	Lys	Pro	Phe	Ala	Ser	Phe	Ser	Leu	Pro	Ser	Ser
1			5						10					15	
Ser	Lys	Lys	Ala	Pro	Pro	Phe	Gln	Trp	Arg	Gln	His	His	Leu	Ser	His
			20					25					30		
His	Ser	Leu	His	Ser	His	Ser	Thr	Pro	Glu	Pro	Leu	Leu	Ser	Ser	Pro
		35					40					45			
Leu	Pro	Pro	Gln	Asn	Pro	Ser	Ser	Leu	Ser	Pro	Pro	Ser	Ser	Thr	Ala
		50				55				60					
Ala	Ser	His	Leu	Ser	Leu	Ser	Ser	Lys	Pro	His	Arg	Pro	Ile	Pro	Lys
		65			70				75					80	
Pro	Ser	Ser	Ser	Lys	Thr	Lys	His	Gln	Lys						
			85					90							

(2) INFORMATION FOR SEQ ID NO:1324:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 117 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..117
 (D) OTHER INFORMATION: / Ceres Seq. ID 1569617
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1324:

Met	Ala	Thr	Ala	Ser	Ser	Leu	Ser	Ser	Leu	Ser	Ser	Leu	Ser	Leu	His
1				5					10					15	
Thr	Arg	Thr	Ser	Ser	Leu	Ile	Ser	Ser	Ser	Thr	Lys	Ser	Ile	Val	

	20		25		30	
Ser	Phe	Ser	Ser	Phe	Leu	Asn
	35		40		45	
Lys	Ala	Ser	Ser	Thr	Asp	Thr
	50		55		60	
Pro	Glu	Ile	Thr	Ala	Asn	Val
	65		70		75	
Gly	Phe	Val	Ser	Pro	Tyr	Phe
	85		90		95	
Glu	Glu	Ile	Ala	Thr	Ala	Phe
	100		105		110	
Gly	Glu	Ser	Met	Leu		
	115					

(2) INFORMATION FOR SEQ ID NO:1325:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1356 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1356
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569618

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1325:

aaaccccaaac	atttttcgat	tttcccgac	tttctccgac	gatgcgatgg	cgatagCgat	60
gggtattccg	gtgacttatg	ctccgacgat	tgacacgatc	atttgaggca	gtctcccttg	120
tccagatttt	ctttttcaac	ctctttctct	tgcttaccga	ccaaattcat	catctttgaa	180
actgcttcac	ccctttcgct	ttgggtatcc	tgaagactcc	gctttatacc	cattttgatc	240
tggagaagga	tatagatgaa	gtgctacagt	cgcatactgt	ttattcaaat	gtttcgaagg	300
gagttctctg	aaaatcgaaa	gacttgatga	agtcggttgg	atcagatgat	catcacgaaa	360
tatgcattga	tatttttgag	aaagagagag	ttcaagtggc	tggaaaaaaa	agagaatcac	420
agttctcaag	ccagtttcgg	gatatagcaa	cgattgttat	cgagaaaact	atcaacctgt	480
aaacacaacg	acctttatac	atcagcatgg	tagagcgctc	aatgcattga	attcattttg	540
ctgttgatcc	tcatagtaat	tccaagaagc	aggcacttga	tgtcatccgt	gagctgcata	600
agcacttccc	tataaagcgt	tttccaatga	gactgcgtct	tactgttctc	gttcaaaatt	660
tcccctcgct	tctggagaag	ctaaaagaat	gggatggtag	tgtgtgtctc	aaagacgaat	720
ctggaaacac	gatgtccact	gtctgcgaga	tggaaacggg	ccatttccga	gagtggtgat	780
cccatgtgag	gagtatccag	ggaagactag	aaataactgc	tgtatcagtt	catcgagaag	840
gtgacacaag	catgatgatc	tacgatgagc	atgatgatat	ggcattcgaa	acccacaagg	900
cgttgttacc	tgctgagact	gagactaaag	atttgaccga	tccctgcgtt	gaactatgca	960
agaaaactga	gaagcaagag	ataagtacta	cgatatacat	aaagcaagaa	gggtggaagg	1020
aaaagaaggg	gaccaagtgc	agcacttgca	acacgttctg	tgagagagct	aagcataaca	1080
gagagcactg	taagagtatg	tggcacaacg	acacacttaa	cggttaagct	cggaacttcc	1140
ctctctattg	tgtctgcaga	tgcattgtct	agattgacat	ggacgactct	agagcagatt	1200
tgaagactac	ctctttctga	aactacaatt	ttctctcttt	gtgcttttaa	ttttgtcaat	1260
gtgttaaatc	tctgtatcat	atgtgagtat	gaatacaca	aacttgtgga	atgaaatttt	1320
gcgaagaact	taagagtaaa	aacttgtgtt	taagag			

(2) INFORMATION FOR SEQ ID NO:1326:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 297 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..297
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569619

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1326:

Met Lys Ser Phe Gly Ser Asp Asp His Thr Lys Ile Cys Ile Asp Ile

1	5	10	15
Leu Glu Lys Gly Glu Leu Gln Val Ala Gly Lys Glu Arg Glu Ser Gln	20	25	30
Phe Ser Ser Gln Phe Arg Asp Ile Ala Thr Ile Val Met Gln Lys Thr	35	40	45
Ile Asn Pro Glu Thr Gln Arg Pro Tyr Thr Ile Ser Met Val Glu Arg	50	55	60
Leu Met His Glu Ile His Phe Ala Val Asp Pro His Ser Asn Ser Lys	65	70	75
Lys Gln Ala Leu Asp Val Ile Arg Glu Leu Gln Lys His Phe Pro Ile	85	90	95
Lys Arg Ser Pro Met Arg Leu Arg Leu Thr Val Pro Val Gln Asn Phe	100	105	110
Pro Ser Leu Leu Glu Lys Leu Lys Glu Trp Asp Gly Ser Val Val Ser	115	120	125
Lys Asp Glu Ser Gly Thr Gln Met Ser Thr Val Cys Glu Met Glu Pro	130	135	140
Gly Leu Phe Arg Glu Cys Asp Ser His Val Arg Ser Ile Gln Gly Arg	145	150	155
Leu Glu Ile Leu Ala Val Ser Val His Ala Glu Gly Asp Thr Ser Met	165	170	175
Asp His Tyr Asp Glu His Asp Asp Met Ala Leu Gln Thr His Lys Pro	180	185	190
Leu Leu Pro Ala Glu Thr Glu Thr Lys Asp Leu Thr Asp Pro Val Val	195	200	205
Glu Leu Ser Lys Lys Leu Gln Lys Gln Glu Ile Ser Thr Thr Asp Asn	210	215	220
Ile Lys Gln Glu Gly Gly Glu Glu Lys Lys Gly Thr Lys Cys Ser Thr	225	230	235
Cys Asn Thr Phe Val Gly Glu Ala Lys Gln Tyr Arg Glu His Cys Lys	245	250	255
Ser Asp Trp His Lys His Asn Leu Lys Asp Lys Thr Arg Lys Leu Pro	260	265	270
Pro Ile Ser Ala Asp Glu Cys Met Ser Glu Ile Asp Met Asp Asp Ser	275	280	285
Arg Ala Asp Leu Lys Asp Tyr Ser Phe	290	295	

(2) INFORMATION FOR SEQ ID NO:1327:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 253 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..253
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569620

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1327:

Met Gln Lys Thr Ile Asn Pro Glu Thr Gln Arg Pro Tyr Thr Ile Ser	5	10	15
Met Val Glu Arg Leu Met His Glu Ile His Phe Ala Val Asp Pro His	20	25	30
Ser Asn Ser Lys Lys Gln Ala Leu Asp Val Ile Arg Glu Leu Gln Lys	35	40	45
His Phe Pro Ile Lys Arg Ser Pro Met Arg Leu Arg Leu Thr Val Pro	50	55	60
Val Gln Asn Phe Pro Ser Leu Leu Glu Lys Leu Lys Glu Trp Asp Gly	65	70	75
Ser Val Val Ser Lys Asp Glu Ser Gly Thr Gln Met Ser Thr Val Cys	85	90	95

Glu	Met	Glu	Pro	Gly	Leu	Phe	Arg	Glu	Cys	Asp	Ser	His	Val	Arg	Ser
			100					105					110		
Ile	Gln	Gly	Arg	Leu	Glu	Ile	Leu	Ala	Val	Ser	Val	His	Ala	Glu	Gly
		115					120					125			
Asp	Thr	Ser	Met	Asp	His	Tyr	Asp	Glu	His	Asp	Asp	Met	Ala	Leu	Gln
		130				135					140				
Thr	His	Lys	Pro	Leu	Leu	Pro	Ala	Glu	Thr	Thr	Lys	Asp	Leu	Thr	
		145			150					155				160	
Asp	Pro	Val	Val	Glu	Leu	Ser	Lys	Lys	Leu	Gln	Lys	Gln	Glu	Ile	Ser
				165					170					175	
Thr	Thr	Asp	Asn	Ile	Lys	Gln	Glu	Gly	Gly	Glu	Glu	Lys	Lys	Gly	Thr
			180					185					190		
Lys	Cys	Ser	Thr	Cys	Asn	Thr	Phe	Val	Gly	Glu	Ala	Lys	Gln	Tyr	Arg
			195				200					205			
Glu	His	Cys	Lys	Ser	Asp	Trp	His	Lys	His	Asn	Leu	Lys	Arg	Lys	Thr
			210			215					220				
Arg	Lys	Leu	Pro	Pro	Ile	Ser	Ala	Asp	Glu	Cys	Met	Ser	Glu	Ile	Asp
				230						235					240
Met	Asp	Asp	Ser	Arg	Ala	Asp	Leu	Lys	Asp	Tyr	Ser	Phe			
				245					250						

(2) INFORMATION FOR SEQ ID NO:1328:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 237 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..237

(D) OTHER INFORMATION: / Ceres Seq. ID 1569621

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1328:

Met	Val	Glu	Arg	Leu	Met	His	Glu	Ile	His	Phe	Ala	Val	Asp	Pro	His
1			5					10					15		
Ser	Asn	Ser	Lys	Lys	Gln	Ala	Leu	Asp	Val	Ile	Arg	Glu	Leu	Gln	Lys
			20					25					30		
His	Phe	Pro	Ile	Lys	Arg	Ser	Pro	Met	Arg	Leu	Arg	Leu	Thr	Val	Pro
		35					40					45			
Val	Gln	Asn	Phe	Pro	Ser	Leu	Leu	Glu	Lys	Leu	Lys	Glu	Trp	Asp	Gly
		50			55						60				
Ser	Val	Val	Ser	Lys	Asp	Glu	Ser	Gly	Thr	Gln	Met	Ser	Thr	Val	Cys
				70					75					80	
Glu	Met	Glu	Pro	Gly	Leu	Phe	Arg	Glu	Cys	Asp	Ser	His	Val	Arg	Ser
				85					90				95		
Ile	Gln	Gly	Arg	Leu	Glu	Ile	Leu	Ala	Val	Ser	Val	His	Ala	Glu	Gly
		100					105						110		
Asp	Thr	Ser	Met	Asp	His	Tyr	Asp	Glu	His	Asp	Asp	Met	Ala	Leu	Gln
		115				120						125			
Thr	His	Lys	Pro	Leu	Leu	Pro	Ala	Glu	Thr	Glu	Thr	Lys	Asp	Leu	Thr
		130				135					140				
Asp	Pro	Val	Val	Glu	Leu	Ser	Lys	Lys	Leu	Gln	Lys	Gln	Glu	Ile	Ser
				145		150				155				160	
Thr	Thr	Asp	Asn	Ile	Lys	Gln	Glu	Gly	Gly	Glu	Glu	Lys	Lys	Gly	Thr
				165					170					175	
Lys	Cys	Ser	Thr	Cys	Asn	Thr	Phe	Val	Gly	Glu	Ala	Lys	Gln	Tyr	Arg
			180				185						190		
Glu	His	Cys	Lys	Ser	Asp	Trp	His	Lys	His	Asn	Leu	Lys	Arg	Lys	Thr
			195			200						205			
Arg	Lys	Leu	Pro	Pro	Ile	Ser	Ala	Asp	Glu	Cys	Met	Ser	Glu	Ile	Asp
		210				215					220				
Met	Asp	Asp	Ser	Arg	Ala	Asp	Leu	Lys	Asp	Tyr	Ser	Phe			

225

230

235

(2) INFORMATION FOR SEQ ID NO:1329:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1511 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1511

(D) OTHER INFORMATION: / Ceres Seq. ID 1569652

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1329:

```
aaattcaaaa ttttaacacac aaacacaaac acacacacca aaaaaaaaca cagacctttaa      60
aaaaataaaa atggttgata tggattggaa gaggaagatg gtatcatcag atttaccaaa      120
ctcacctaaag cttttcttcaa agcttcacgt aactattcca tcaccgttca aaatcgtccc      180
tgtttcatct cggatctcat gttcagcacc tgctctttgc tctgcttacg agctttacct      240
tcgtctccct gagctaagaa agctcttggtc atctcgtgat ttctctcaat ggacatcaga      300
gcgcattctc aaaccagctc ttcaagcttt ggagatcagt ttctgcgcgt ttttcgcgtt      360
ttgttctgat actagaccgt acatcaacca ccgtgaatgg aaccggaggg tagattctct      420
catcacgaag cagatccagc ttgtagcagc gatctgcgaa gatgaagaag aagaaggtat      480
atacagcggag cctccgctgc gcggtggagc gagttcgttg agtttgttac cgcagctagc      540
tacgtggagg agatcaaggc ctttggggaa gaagatctta tatacgatcg ataacagatg      600
gagtcggtgt aagtacacgc tcggactcgg tgaacaaaac atcgcgggaa aaccaaatct      660
cgggtacgat gcgatttgcg gaccaaaacg gatctatagc ctcaaggata atccatacgc      720
agatacatatc gataatcacg agaatcaaac tctctatatac attcaccaga tctctgaatc      780
gtggatctac gcactctgaa atctcttgaa tcgaatcgct tcaagtatcg aagaagagaa      840
attcgaaaaa cgttcaaacg atgtttactt gctggagaag attcggaaaa ttttagcgga      900
gattgaagat ctctcatagt tgatggatcc ggaagatttt ttgaattga agaaacagatt      960
acagatcaaa tcgacgggta aaaacgatgc gttttgtttc agatctaaaq gattagtga      1020
gatgatgaag atgtcgaagg atctgagaca gaaagtaccg gcggtcttgg cggttgaggt      1080
agatccaacg ggaggaccga gattAcaaga ggcggcgatg aagctttacg cgcgaagagc      1140
agagtcgcat aaagattcat tgcttcaggc gatgcaagcg gtggaagcgg cgcgcaagag      1200
tttctcttct gggtataggc agttagtggc ggctatgatg ggaagtgcgg agatgaacgc      1260
gacggcgagt caagagtcgt gtgactcact gactcagata ttatggagc gcacgtattt      1320
cccgagcctt gacgcggcaa agacgtttct gggagagttt tggagtcatt tgggagatt      1380
aaattttaat tctgcgtggt ataattattt aatataaatt taaatttggt gtttggttta      1440
atttactttg taagatagtg aaatttttgg aacatttgac gatccatatt tgaatacaaa      1500
ttcattttta c
```

(2) INFORMATION FOR SEQ ID NO:1330:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 458 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..458

(D) OTHER INFORMATION: / Ceres Seq. ID 1569653

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1330:

```
Asn Ser Lys Phe Asn Thr Gln Thr Gln Thr His Thr Pro Lys Lys Asn
1      5      10      15
Thr Asp Leu Lys Lys Ile Lys Met Val Asp Met Asp Trp Lys Arg Lys
20     25     30
Met Val Ser Ser Asp Leu Pro Asn Ser Pro Lys Leu Ser Ser Lys Leu
35     40     45
His Val Thr Ile Pro Ser Pro Phe Lys Ile Val Pro Val Ser Ser Pro
50     55     60
Ile Ser Cys Ser Ala Pro Ala Leu Cys Ser Ala Tyr Glu Leu Tyr Leu
65     70     75     80
```

Arg Leu Pro Glu Leu Arg Lys Leu Trp Ser Ser Arg Asp Phe Pro Gln
85 90 95
Trp Thr Ser Glu Pro Ile Leu Lys Pro Ala Leu Gln Ala Leu Glu Ile
100 105 110
Ser Phe Arg Leu Val Phe Ala Val Cys Ser Asp Thr Arg Pro Tyr Ile
115 120 125
Asn His Arg Glu Trp Asn Arg Arg Leu Asp Ser Leu Ile Thr Lys Gln
130 135 140
Ile Gln Leu Val Ala Ala Ile Cys Glu Asp Glu Glu Glu Gly Ile
145 150 155 160
Ser Ala Glu Ala Pro Val Gly Gly Gly Arg Ser Ser Leu Ser Leu Leu
165 170 175
Pro Gln Leu Ala Thr Trp Arg Arg Ser Glu Ala Leu Gly Lys Lys Ile
180 185 190
Leu Tyr Thr Ile Asp Asn Glu Met Ser Arg Cys Lys Tyr Thr Leu Gly
195 200 205
Leu Gly Glu Gln Asn Ile Ala Gly Lys Pro Asn Leu Arg Tyr Asp Ala
210 215 220
Ile Cys Arg Pro Asn Glu Ile Tyr Ser Leu Lys Asp Asn Pro Tyr Ala
225 230 235 240
Asp His Ile Asp Asn His Glu Asn Gln Thr Leu Tyr Ile Ile His Gln
245 250 255
Ile Leu Glu Ser Trp Ile Tyr Ala Ser Gly Asn Leu Leu Asn Arg Ile
260 265 270
Val Ser Ser Ile Glu Glu Glu Lys Phe Glu Lys Ala Ser Asn Asp Val
275 280 285
Tyr Leu Leu Glu Lys Ile Trp Lys Ile Leu Ala Glu Ile Glu Asp Leu
290 295 300
His Met Leu Met Asp Pro Glu Asp Phe Leu Lys Leu Lys Lys Gln Leu
305 310 315 320
Gln Ile Lys Ser Thr Gly Lys Asn Asp Ala Phe Cys Phe Arg Ser Lys
325 330 335
Gly Leu Val Glu Met Met Lys Met Ser Lys Asp Leu Arg Gln Lys Val
340 345 350
Pro Ala Val Leu Ala Val Glu Val Asp Pro Thr Gly Gly Pro Arg Leu
355 360 365
Gln Glu Ala Ala Met Lys Leu Tyr Ala Arg Lys Thr Glu Cys Asp Lys
370 375 380
Ile His Leu Leu Gln Gly Met Gln Ala Val Glu Ala Ala Ala Lys Ser
385 390 395 400
Phe Phe Phe Gly Tyr Arg Gln Leu Val Ala Met Met Gly Ser Ala
405 410 415
Glu Met Asn Ala Thr Ala Ser Gln Glu Ser Cys Asp Ser Leu Ser Gln
420 425 430
Ile Phe Met Glu Pro Thr Tyr Phe Pro Ser Leu Asp Ala Ala Lys Thr
435 440 445
Phe Leu Gly Glu Phe Trp Ser His Leu Gly
450 455

(2) INFORMATION FOR SEQ ID NO:1331:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 435 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..435

(D) OTHER INFORMATION: / Ceres Seq. ID 1569654

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1331:

Met Val Asp Met Asp Trp Lys Arg Lys Met Val Ser Ser Asp Leu Pro

1	5	10	15
Asn Ser Pro Lys Leu Ser Ser Lys Leu His Val Thr Ile Pro Ser Pro	20	25	30
Phe Lys Ile Val Pro Val Ser Ser Pro Ile Ser Cys Ser Ala Pro Ala	35	40	45
Leu Cys Ser Ser Ala Tyr Glu Leu Tyr Leu Arg Leu Pro Glu Leu Arg Lys	50	55	60
Leu Trp Ser Ser Arg Asp Phe Pro Gln Trp Thr Ser Glu Pro Ile Leu	65	70	75
Lys Pro Ala Leu Gln Ala Leu Glu Ile Ser Phe Arg Leu Val Phe Ala	85	90	95
Val Cys Ser Asp Thr Arg Pro Tyr Ile Asn His Arg Glu Trp Asn Arg	100	105	110
Arg Leu Asp Ser Leu Ile Thr Lys Gln Ile Gln Leu Val Ala Ala Ile	115	120	125
Cys Glu Asp Glu Glu Glu Glu Gly Ile Ser Ala Glu Ala Pro Val Gly	130	135	140
Gly Gly Arg Ser Ser Leu Ser Leu Leu Pro Gln Leu Ala Thr Trp Arg	145	150	155
Arg Ser Glu Ala Leu Gly Lys Lys Ile Leu Tyr Thr Ile Asp Asn Glu	165	170	175
Met Ser Arg Cys Lys Tyr Thr Leu Gly Leu Gly Glu Gln Asn Ile Ala	180	185	190
Gly Lys Pro Asn Leu Arg Tyr Asp Ala Ile Cys Arg Pro Asn Glu Ile	195	200	205
Tyr Ser Leu Lys Asp Asn Pro Tyr Ala Asp His Ile Asp Asn His Glu	210	215	220
Asn Gln Thr Leu Tyr Ile Ile His Gln Ile Leu Glu Ser Trp Ile Tyr	225	230	235
Ala Ser Gly Asn Leu Leu Asn Arg Ile Val Ser Ser Ile Glu Glu Glu	245	250	255
Lys Phe Glu Lys Ala Ser Asn Asp Val Tyr Leu Leu Glu Lys Ile Trp	260	265	270
Lys Ile Leu Ala Glu Ile Glu Asp Leu His Met Leu Met Asp Pro Glu	275	280	285
Asp Phe Leu Lys Leu Lys Lys Gln Leu Gln Ile Lys Ser Thr Gly Lys	290	295	300
Asn Asp Ala Phe Cys Phe Arg Ser Lys Gly Leu Val Glu Met Met Lys	305	310	315
Met Ser Lys Asp Leu Arg Gln Lys Val Pro Ala Val Leu Ala Val Glu	325	330	335
Val Asp Pro Thr Gly Gly Pro Arg Leu Gln Glu Ala Ala Met Lys Leu	340	345	350
Tyr Ala Arg Lys Thr Glu Cys Asp Lys Ile His Leu Leu Gln Gly Met	355	360	365
Gln Ala Val Glu Ala Ala Ala Lys Ser Phe Phe Phe Gly Tyr Arg Gln	370	375	380
Leu Val Ala Ala Met Met Gly Ser Ala Glu Met Asn Ala Thr Ala Ser	385	390	395
Gln Glu Ser Cys Asp Ser Leu Ser Gln Ile Phe Met Glu Pro Thr Tyr	405	410	415
Phe Pro Ser Leu Asp Ala Ala Lys Thr Phe Leu Gly Glu Phe Trp Ser	420	425	430
His Leu Gly	435		

(2) INFORMATION FOR SEQ ID NO:1332:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 432 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(2) INFORMATION FOR SEQ ID NO:1333:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1276 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1276

(D) OTHER INFORMATION: / Ceres Seq. ID 1569656

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1333:

acttaaaagcc	ctcaaaaatct	cagagaacgc	tcgctgatca	aatccgctcg	ctttcaaccg	60
tcgcctcctc	cgctcatgaca	attgagtgcg	ttaataccga	aggtctctga	ttcaaccaaa	120
tgaagaagctc	ctctcatcaa	accctagaaa	cgaggatgag	gccgattttg	atgaagggac	180
atgaacgctc	attgacgttc	ctgaggtaca	acagaaatgg	tgatctgctt	ttctcctgag	240
ccaagagacca	cactcccaca	gtctgggttg	ccgataacgg	cgagcgtctt	ggcacttacc	300
gtggccacag	tgggtcgtgt	tgggtcgtgt	atatctccag	agactcgtct	agattgatca	360
ctggtagtcg	tgatcagact	gcaaaagctg	gggagtgtga	atctggcaaa	gaattgttca	420
ctttcaagtt	tgggtccctc	gcaaGgtctg	tggatttctc	tgttggtgat	catcttgtag	480
tgattaccac	tgatcacttc	gtgggaactt	cctctgctat	tcatgtcaaa	cgatttgtag	540
aagatcccca	agaccagggt	ggtgattctg	tgcttgctct	tcaaaagtct	gatgaaaaga	600
agaagatcaa	tagagctgtt	tggggctccc	tgaaccaaac	cattgttagt	gggtgtgaag	660
atgctgctat	cagaactctg	gatgcagaga	ctagaaaatt	gcttaagcaa	tcagatgagg	720
aagtgggtca	caaggaggcc	attacatccc	tctgcaaaag	agctgatgac	tctcacttCc	780
ttacaaagttc	acatgacaaa	actgcaaaag	tttgggacat	gagaaacgtg	actcttatta	840
agacttacac	cactgtgggtg	cctgtaaaatG	ctgtcgccat	gtctccactt	ctcaaccatg	900
ttgtgctagg	aggtgtgtcaa	gatgcacatg	ctgtgactac	cactgatcat	cgtgctggga	960
agtttgaaac	taagtgtttac	gacacagattc	tgcaagagga	aattgtgggc	gtgaagagtc	1020
attttggacc	tattaatgct	ttggcatttca	gtccctgatg	gaagagtttc	tctagtggag	1080
gtgaagagcg	ctacgtgaga	gtgcactcatt	ttgactccaa	ttacttcaac	atcaagattt	1140
agattctttg	aacatgtctt	tccatttttt	catcattcca	cataatattt	ttctcttttt	1200
taacattttc	agaattgatg	tactaccaaa	ttaccaatat	actaacttga	tgataaagct	1260
tggtgttgtt	cttttc					

(2) INFORMATION FOR SEQ ID NO:1334:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 379 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..379

(D) OTHER INFORMATION: / Ceres Seq. ID 1569657

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1334:

Leu	Lys	Pro	Ser	Lys	Ser	Gln	Arg	Thr	Leu	Ala	Asp	Gln	Ile	Arg	Arg	
1				5				10					15			
Pro	Ser	Thr	Val	Ala	Ser	Ser	Val	Met	Thr	Ile	Glu	Cys	Val	Asn	Pro	
			20					25					30			
Glu	Gly	Leu	Arg	Phe	Asn	Gln	Met	Lys	Ser	Ser	Ser	His	Gln	Thr	Leu	
		35				40						45				
Glu	Thr	Arg	Met	Arg	Pro	Ile	Leu	Met	Lys	Gly	His	Glu	Arg	Pro	Leu	
		50				55						60				
Thr	Phe	Leu	Arg	Tyr	Asn	Arg	Asn	Gly	Asp	Leu	Phe	Ser	Cys	Ala		
		65			70				75				80			
Lys	Asp	His	Thr	Pro	Thr	Val	Trp	Phe	Ala	Asp	Asn	Gly	Glu	Arg	Leu	
			85					90					95			
Gly	Thr	Tyr	Arg	Gly	His	Ser	Gly	Ala	Val	Trp	Cys	Cys	Asp	Ile	Ser	
			100					105					110			

Arg Asp Ser Ser Arg Leu Ile Thr Gly Ser Ala Asp Gln Thr Ala Lys
115 120 125
Leu Trp Asp Val Lys Ser Gly Lys Glu Leu Phe Thr Phe Lys Phe Gly
130 135 140
Ala Pro Ala Arg Ser Val Asp Phe Ser Val Gly Asp His Leu Ala Val
145 150 155 160
Ile Thr Thr Asp His Phe Val Gly Thr Ser Ala Ile His Val Lys
165 170 175
Arg Ile Ala Glu Asp Pro Glu Asp Gln Val Gly Asp Ser Val Leu Val
180 185 190
Leu Gln Ser Pro Asp Gly Lys Lys Lys Ile Asn Arg Ala Val Trp Gly
195 200 205
Pro Leu Asn Gln Thr Ile Val Ser Gly Gly Glu Asp Ala Ala Ile Arg
210 215 220
Ile Trp Asp Ala Glu Thr Arg Lys Leu Leu Lys Gln Ser Asp Glu Glu
225 230 235 240
Val Gly His Lys Glu Ala Ile Thr Ser Leu Cys Lys Ala Ala Asp Asp
245 250 255
Ser His Phe Leu Thr Gly Ser His Asp Lys Thr Ala Lys Leu Trp Asp
260 265 270
Met Arg Thr Leu Thr Leu Ile Lys Thr Tyr Thr Thr Val Val Pro Val
275 280 285
Asn Ala Val Ala Met Ser Pro Leu Leu Asn His Val Val Leu Gly Gly
290 295 300
Gly Gln Asp Ala Ser Ala Val Thr Thr Thr Asp His Arg Ala Gly Lys
305 310 315 320
Phe Glu Ala Lys Phe Tyr Asp Thr Ile Leu Gln Glu Glu Ile Gly Gly
325 330 335
Val Lys Gly His Phe Gly Pro Ile Asn Ala Leu Ala Phe Ser Pro Asp
340 345 350
Gly Lys Ser Phe Ser Ser Gly Gly Glu Asp Gly Tyr Val Arg Leu His
355 360 365
His Phe Asp Ser Asn Tyr Phe Asn Ile Lys Ile
370 375

(2) INFORMATION FOR SEQ ID NO:1335:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 355 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..355
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569658

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1335:

Met Thr Ile Glu Cys Val Asn Pro Glu Gly Leu Arg Phe Asn Gln Met
1 5 10 15
Lys Ser Ser Ser His Gln Thr Leu Glu Thr Arg Met Arg Pro Ile Leu
20 25 30
Met Lys Gly His Glu Arg Pro Leu Thr Phe Leu Arg Tyr Asn Arg Asn
35 40 45
Gly Asp Leu Leu Phe Ser Cys Ala Lys Asp His Thr Pro Thr Val Trp
50 55 60
Phe Ala Asp Asn Gly Glu Arg Leu Gly Thr Tyr Arg Gly His Ser Gly
65 70 75 80
Ala Val Trp Cys Cys Asp Ile Ser Arg Asp Ser Ser Arg Leu Ile Thr
85 90 95
Gly Ser Ala Asp Gln Thr Ala Lys Leu Trp Asp Val Lys Ser Gly Lys
100 105 110
Glu Leu Phe Thr Phe Lys Phe Gly Ala Pro Ala Arg Ser Val Asp Phe

Figure 6

(1) SEQUENCE CHARACTERISTICS:

(ii) MOLECULE TYPE: peptide

(A) NAME/KEY: peptide

(B) LOCATION: 1..340

(D) OTHER INFORMATION: / Ceres Seq. ID 1569659

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1336:

Met	Lys	Ser	Ser	Ser	His	Gln	Thr	Leu	Glu	Thr	Arg	Met	Arg	Pro	Ile
1				5					10					15	
Leu	Met	Lys	Gly	His	Glu	Arg	Pro	Leu	Thr	Phe	Leu	Arg	Tyr	Asn	Arg
			20					25					30		
Asn	Gly	Asp	Leu	Leu	Phe	Ser	Cys	Ala	Lys	Asp	His	Thr	Pro	Thr	Val
		35					40					45			
Trp	Phe	Ala	Asp	Asn	Gly	Glu	Arg	Leu	Gly	Thr	Tyr	Arg	Gly	His	Ser
	50				55						60				
Gly	Ala	Val	Trp	Cys	Cys	Asp	Ile	Ser	Arg	Asp	Ser	Ser	Arg	Leu	Ile
65				70						75				80	
Thr	Gly	Ser	Ala	Asp	Gln	Thr	Ala	Lys	Leu	Trp	Asp	Val	Lys	Ser	Gly
			85					90					95		
Lys	Glu	Leu	Phe	Thr	Phe	Lys	Phe	Gly	Ala	Pro	Ala	Arg	Ser	Val	Asp
		100						105				110			
Phe	Ser	Val	Gly	Asp	His	Leu	Ala	Val	Ile	Thr	Thr	Asp	His	Phe	Val
		115				120						125			
Gly	Thr	Ser	Ser	Ala	Ile	His	Val	Lys	Arg	Ile	Ala	Glu	Asp	Pro	Glu
	130					135				140					

Asp Gln Val Gly Asp Ser Val Leu Val Leu Gln Ser Pro Asp Gly Lys
145 150 155 160
Lys Lys Ile Asn Arg Ala Val Trp Gly Pro Leu Asn Gln Thr Ile Val
165 170 175
Ser Gly Gly Glu Asp Ala Ala Ile Arg Ile Trp Asp Ala Glu Thr Arg
180 185 190
Lys Leu Leu Lys Gln Ser Asp Glu Glu Val Gly His Lys Glu Ala Ile
195 200 205
Thr Ser Leu Cys Lys Ala Ala Asp Asp Ser His Phe Leu Thr Gly Ser
210 215 220
His Asp Lys Thr Ala Lys Leu Trp Asp Met Arg Thr Leu Thr Leu Ile
225 230 235 240
Lys Thr Tyr Thr Thr Val Val Pro Val Asn Ala Val Ala Met Ser Pro
245 250 255
Leu Leu Asn His Val Val Leu Gly Gly Gly Gln Asp Ala Ser Ala Val
260 265 270
Thr Thr Thr Asp His Arg Ala Gly Lys Phe Glu Ala Lys Phe Tyr Asp
275 280 285
Thr Ile Leu Gln Glu Glu Ile Gly Gly Val Lys Gly His Phe Gly Pro
290 295 300
Ile Asn Ala Leu Ala Phe Ser Pro Asp Gly Lys Ser Phe Ser Ser Gly
305 310 315 320
Gly Glu Asp Gly Tyr Val Arg Leu His His Phe Asp Ser Asn Tyr Phe
325 330 335
Asn Ile Lys Ile
340

(2) INFORMATION FOR SEQ ID NO:1337:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1213 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1213
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569667

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1337:

atctctctct	ctctaaacct	ctctctcaat	ggccgtcgat	gctcaccatc	tctttctttc	60
tcctctctca	ctctctctcca	acagagaatt	aacgatgaat	aataaacacta	tggaaaccaac	120
tagtgccggt	tctgtcaata	acaatcaaac	cggttacggc	ctctgtttcac	ctttctccgt	180
tccaacaact	acatcaacaa	caacaacagc	aacgcctcct	cttcttccata	tgtagcgcg	240
ctctgatact	attcccacca	cgcgcgggta	ctacgcgcga	ggtgctacta	atctcgactg	300
tgaatttttc	ctttaccaca	cgagaaaacg	ctcaagagat	tcttcaagat	caaatattca	360
tcactctctt	cttcagaaac	cgagatcatc	atcatgtgtt	aacgctgcta	ctacaacaac	420
tacaacaact	ccgttctcgt	ttcttggcca	agacattgat	atctctcttc	acatgaatca	480
acaacaacac	gaatatagat	gatctgtctc	cttccactta	tatcagatgg	agagatgtga	540
atatgagata	gaagagaaga	ggaaaaagaca	agcgagaaag	ataatggagg	cgatagagca	600
aggactgggt	aaaagggttc	gtgtcaaaaga	agaagaaaga	gagaggatcg	gcaagggtta	660
ccacgcgctt	gaggagcgag	tgaagtcaat	tcttatagag	aaccaaatct	ggagagacct	720
tgctcagacg	aacgaagcca	cggctaacca	cctccgaacc	aacctcgagc	atgttctggc	780
gcagggttaag	gacgtatcac	gcgcgcgcagg	attagagaaa	aacatgaacg	aagaggagca	840
tgcggagtcg	tgctgcggaa	cgacgtgtgg	tgtgtgtgtg	gaagaaacgg	taaggcgacg	900
ggtaggatta	gaaaggagg	gcagagataa	ggcggagagg	aggaggagga	ggaatgtgtg	960
aaactgtggg	gaggaggaa	cgtgtgtgtt	gctgttaccg	tgacagacat	tgtgtgtgtg	1020
tggagtagtc	gggtccagtg	tgcacacgtg	tccatctgt	acatcttcta	aaaacgctag	1080
cgttcatgtc	aacatgtcat	cttgaccocg	tcccggttat	ggaatactcc	tcttctctct	1140
tttttWttt	tttttttgtt	ctttagaaaa	tttgaagga	tatttttagt	gaatattatt	1200
attattttta	gct					

(2) INFORMATION FOR SEQ ID NO:1338:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 358 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..358
(D) OTHER INFORMATION: / Ceres Seq. ID 1569668
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1338:

```

Met Ala Val Asp Ala His His Leu Phe Leu Ser Pro Pro Gln Leu Phe
1      5      10      15
Ser Asn Arg Glu Leu Thr Met Asn Asn Asn Thr Met Glu Pro Thr Ser
20      25      30
Gly Gly Phe Cys Asn Asn Asn Gln Thr Gly Tyr Gly Val Val Ser Pro
35      40      45
Phe Ser Val Pro Asn His Thr Ser Thr Thr Thr Thr Ala Thr Pro Pro
50      55      60
Leu Leu His Met Tyr Gly Gly Ser Asp Thr Ile Pro Thr Thr Ala Gly
65      70      75      80
Tyr Tyr Ala Asp Gly Ala Thr Asn Leu Asp Cys Glu Phe Phe Pro Leu
85      90      95
Pro Thr Arg Lys Arg Ser Arg Asp Ser Ser Arg Ser Asn Tyr His His
100      105      110
Leu Leu Leu Gln Asn Pro Arg Ser Ser Cys Val Asn Ala Ala Thr
115      120      125
Thr Thr Thr Thr Thr Thr Phe Ser Phe Leu Gly Gln Asp Ile Asp
130      135      140
Ile Ser Ser His Met Asn Gln Gln Gln His Glu Ile Asp Arg Phe Val
145      150      155      160
Ser Leu His Leu Tyr Gln Met Glu Arg Val Lys Tyr Glu Ile Glu Glu
165      170      175
Lys Arg Lys Arg Gln Ala Arg Thr Ile Met Glu Ala Ile Glu Gln Gly
180      185      190
Leu Val Lys Arg Leu Arg Val Lys Glu Glu Glu Arg Glu Arg Ile Gly
195      200      205
Lys Val Asn His Ala Leu Glu Glu Arg Val Lys Ser Leu Ser Ile Glu
210      215      220
Asn Gln Ile Trp Arg Asp Leu Ala Gln Thr Asn Glu Ala Thr Ala Asn
225      230      235
His Leu Arg Thr Asn Leu Glu His Val Leu Ala Gln Val Lys Asp Val
245      250      255
Ser Arg Gly Ala Gly Leu Glu Lys Asn Met Asn Glu Glu Asp Asp Ala
260      265      270
Glu Ser Cys Cys Gly Ser Ser Cys Gly Gly Gly Glu Thr Val
275      280      285
Arg Arg Arg Val Gly Leu Glu Arg Glu Ala Gln Asp Lys Ala Glu Arg
290      295      300
Arg Arg Arg Arg Met Cys Arg Asn Cys Gly Glu Glu Glu Ser Cys Val
305      310      315
Leu Leu Leu Pro Cys Arg His Leu Cys Leu Cys Gly Val Cys Gly Ser
325      330      335
Ser Val His Thr Cys Pro Ile Cys Thr Ser Pro Lys Asn Ala Ser Val
340      345      350
His Val Asn Met Ser Ser
355

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(2) INFORMATION FOR SEQ ID NO:1339:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 336 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:

(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..336
(D) OTHER INFORMATION: / Ceres Seq. ID 1569669
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1339:
Met Asn Asn Asn Thr Met Glu Pro Thr Ser Gly Gly Phe Cys Asn Asn
1 5 10 15
Asn Gln Thr Gly Tyr Gly Val Val Ser Pro Phe Ser Val Pro Asn His
20 25 30
Thr Ser Thr Thr Thr Ala Thr Pro Leu Leu His Met Tyr Gly
35 40 45
Gly Ser Asp Thr Ile Pro Thr Thr Ala Gly Tyr Tyr Ala Asp Gly Ala
50 55 60
Thr Asn Leu Asp Cys Glu Phe Phe Pro Leu Pro Thr Arg Lys Arg Ser
65 70 75 80
Arg Asp Ser Ser Arg Ser Asn Tyr His His Leu Leu Leu Gln Asn Pro
85 90 95
Arg Ser Ser Ser Cys Val Asn Ala Ala Thr Thr Thr Thr Thr Thr
100 105 110
Pro Phe Ser Phe Leu Gly Gln Asp Ile Asp Ile Ser Ser His Met Asn
115 120 125
Gln Gln Gln His Glu Ile Asp Arg Phe Val Ser Leu His Leu Tyr Gln
130 135 140
Met Glu Arg Val Lys Tyr Glu Ile Glu Glu Lys Arg Lys Arg Gln Ala
145 150 155
Arg Thr Ile Met Glu Ala Ile Glu Gln Gly Leu Val Lys Arg Leu Arg
160 165 170 175
Val Lys Glu Glu Glu Arg Glu Arg Ile Gly Lys Val Asn His Ala Leu
180 185 190
Glu Glu Arg Val Lys Ser Leu Ser Ile Glu Asn Gln Ile Trp Arg Asp
195 200 205
Leu Ala Gln Thr Asn Glu Ala Thr Ala Asn His Leu Arg Thr Asn Leu
210 215 220
Glu His Val Leu Ala Gln Val Lys Asp Val Ser Arg Gly Ala Gly Leu
225 230 235 240
Glu Lys Asn Met Asn Glu Glu Asp Asp Ala Glu Ser Cys Cys Gly Ser
245 250 255
Ser Cys Gly Gly Gly Gly Glu Glu Thr Val Arg Arg Arg Val Gly Leu
260 265 270
Glu Arg Glu Ala Gln Asp Lys Ala Glu Arg Arg Arg Arg Met Cys
275 280 285
Arg Asn Cys Gly Glu Glu Glu Ser Cys Val Leu Leu Leu Pro Cys Arg
290 295 300
His Leu Cys Leu Cys Gly Val Cys Gly Ser Ser Val His Thr Cys Pro
305 310 315 320
Ile Cys Thr Ser Pro Lys Asn Ala Ser Val His Val Asn Met Ser Ser
325 330 335

(2) INFORMATION FOR SEQ ID NO:1340:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 331 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..331

(D) OTHER INFORMATION: / Ceres Seq. ID 1569670
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1340:

Met	Glu	Pro	Thr	Ser	Gly	Gly	Phe	Cys	Asn	Asn	Asn	Gln	Thr	Gly	Tyr
1				5				10						15	
Gly	Val	Val	Ser	Pro	Phe	Ser	Val	Pro	Asn	His	Thr	Ser	Thr	Thr	
				20				25					30		
Thr	Ala	Thr	Pro	Pro	Leu	Leu	His	Met	Tyr	Gly	Gly	Ser	Asp	Thr	Ile
				35			40					45			
Pro	Thr	Thr	Ala	Gly	Tyr	Tyr	Ala	Asp	Gly	Ala	Thr	Asn	Leu	Asp	Cys
				50		55					60				
Glu	Phe	Phe	Pro	Leu	Pro	Thr	Arg	Lys	Arg	Ser	Arg	Asp	Ser	Ser	Arg
65				70					75					80	
Ser	Asn	Tyr	His	His	Leu	Leu	Leu	Gln	Asn	Pro	Arg	Ser	Ser	Ser	Cys
				85					90					95	
Val	Asn	Ala	Ala	Thr	Thr	Thr	Thr	Thr	Thr	Thr	Pro	Phe	Ser	Phe	Leu
				100				105					110		
Gly	Gln	Asp	Ile	Asp	Ile	Ser	Ser	His	Met	Asn	Gln	Gln	Gln	His	Glu
				115			120					125			
Ile	Asp	Arg	Phe	Val	Ser	Leu	His	Leu	Tyr	Gln	Met	Glu	Arg	Val	Lys
				130		135					140				
Tyr	Glu	Ile	Glu	Glu	Lys	Arg	Lys	Arg	Gln	Ala	Arg	Thr	Ile	Met	Glu
145					150				155					160	
Ala	Ile	Glu	Gln	Gly	Leu	Val	Lys	Arg	Leu	Arg	Val	Lys	Glu	Glu	Glu
				165				170						175	
Arg	Glu	Arg	Ile	Gly	Lys	Val	Asn	His	Ala	Leu	Glu	Glu	Arg	Val	Lys
				180				185					190		
Ser	Leu	Ser	Ile	Glu	Asn	Gln	Ile	Trp	Arg	Asp	Leu	Ala	Gln	Thr	Asn
				195			200					205			
Glu	Ala	Thr	Ala	Asn	His	Leu	Arg	Thr	Asn	Leu	Glu	His	Val	Leu	Ala
				210		215					220				
Gln	Val	Lys	Asp	Val	Ser	Arg	Gly	Ala	Gly	Leu	Glu	Lys	Asn	Met	Asn
225					230					235				240	
Glu	Glu	Asp	Asp	Ala	Glu	Ser	Cys	Cys	Gly	Ser	Ser	Cys	Gly	Gly	Gly
				245					250					255	
Gly	Glu	Glu	Thr	Val	Arg	Arg	Arg	Val	Gly	Leu	Glu	Arg	Glu	Ala	Gln
				260				265					270		
Asp	Lys	Ala	Glu	Arg	Arg	Arg	Arg	Met	Cys	Arg	Asn	Cys	Gly	Glu	
				275			280				285				
Glu	Glu	Ser	Cys	Val	Leu	Leu	Leu	Pro	Cys	Arg	His	Leu	Cys	Leu	Cys
				290		295					300				
Gly	Val	Cys	Gly	Ser	Ser	Val	His	Thr	Cys	Pro	Ile	Cys	Thr	Ser	Pro
305					310					315					320
Lys	Asn	Ala	Ser	Val	His	Val	Asn	Met	Ser	Ser					
				325					330						

(2) INFORMATION FOR SEQ ID NO:1341:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1169 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1169
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569671

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1341:

acacccaaac	acgcgacgcg	agcgaaAgaa	gacgatgacg	aacaaggaga	aagctcgaga	60
gagaaggagg	aaaaaaatgc	aggagatctc	tctccttcga	actattcctt	actctgacca	120
ccataggttgG	tggtcttggt	aaaatgtagc	agtagtgact	ggttcaaacc	gcgggattgg	180
attcgagatt	gcaagacagc	ttcggttcca	cggattgacg	gttggtctta	cagctagaaa	240
cgtgaatgct	ggtcttgaag	cagttaaatc	tttgaggcac	caagaagaag	gtctcaaggt	300

ttattttcat	caacttgatg	tcacagactc	ttcctcgatt	agagagtttg	gttgctggct	360
taagcaaaaca	tttgagggtt	tagatattct	cgtgaataat	Ygcaggtggt	aactacaatc	420
tcggctcaga	taatacgggt	gaatttgctg	aaacagttat	atctactaac	taccaaggaa	480
ccaaaaacat	gacaaaaagt	atgataccCt	tgatgagacc	atctcctcat	ggcgctcgtg	540
tagtcaatgt	tagttctcgg	ctaggttagag	taaatggaag	acgtaataga	ctggcaaatg	600
tagagttgag	agatcagcta	agcagtcacg	atttgctgac	cgaggaaactt	atagacagaa	660
ctgtctctaa	attcatcaac	caagtaaaag	acggaacttg	ggaatcaggc	gggtggcctc	720
agacattcac	tgactactcc	atgtctaagc	ttgcagtgaa	tgcttacacg	agactaatgg	780
caaaagaact	tgagagacga	ggagaggaag	agaagattta	tgttaacagc	ttttgccctg	840
gttggggtgaa	gactcgcatg	aNctgGctac	gccggaaata	tgcacactga	agatgcagct	900
gatactggag	tttggttag	ccgtgctctt	tccgaagagt	cagtaaccgg	aaaattcttc	960
gcagagagac	gtgagatcaa	cttctgaggg	ttgttgaatg	tttgtaaacg	ttggaataga	1020
ttgtgtcgtc	ttcgtttagt	gccatagttt	tagtcaaaag	tttcaaaaat	caattgtaat	1080
tggttaagtga	atggttgtag	tcagtgtacg	cgtcagattt	gccacaaaaa	taggagttta	1140
taatttaaat	atgaattaatt	tttaattgc				

(2) INFORMATION FOR SEQ ID NO:1342:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 136 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..136
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569672

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1342:

His	Pro	Asn	Thr	Arg	Arg	Glu	Arg	Lys	Lys	Thr	Met	Thr	Asn	Lys	Glu
1				5					10					15	
Lys	Ala	Arg	Glu	Arg	Arg	Glu	Lys	Lys	Met	Gln	Glu	Ile	Ser	Leu	Leu
			20					25					30		
Arg	Thr	Ile	Pro	Tyr	Ser	Asp	His	His	Arg	Trp	Trp	Ser	Cys	Glu	Asn
			35				40					45			
Val	Ala	Val	Val	Thr	Gly	Ser	Asn	Arg	Gly	Ile	Gly	Phe	Glu	Ile	Ala
			50			55					60				
Arg	Gln	Leu	Ala	Val	His	Gly	Leu	Thr	Val	Val	Leu	Thr	Ala	Arg	Asn
			65			70			75					80	
Val	Asn	Ala	Gly	Leu	Glu	Ala	Val	Lys	Ser	Leu	Arg	His	Gln	Glu	Glu
			85					90					95		
Gly	Leu	Lys	Val	Tyr	Phe	His	Gln	Leu	Asp	Val	Thr	Asp	Ser	Ser	Ser
			100					105					110		
Ile	Arg	Glu	Phe	Gly	Cys	Trp	Leu	Lys	Gln	Thr	Phe	Gly	Gly	Leu	Asp
			115				120						125		
Ile	Leu	Val	Asn	Asn	Xaa	Arg	Cys								
			130			135									

(2) INFORMATION FOR SEQ ID NO:1343:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 133 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..133
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569673

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1343:

Met	Thr	Lys	Ala	Met	Ile	Pro	Leu	Met	Arg	Pro	Ser	Pro	His	Gly	Ala
1				5				10					15		
Arg	Val	Val	Asn	Val	Ser	Ser	Arg	Leu	Gly	Arg	Val	Asn	Gly	Arg	Arg
			20					25					30		

Asn Arg Leu Ala Asn Val Glu Leu Arg Asp Gln Leu Ser Ser Pro Asp
35 40 45
Leu Leu Thr Glu Glu Leu Ile Asp Arg Thr Val Ser Lys Phe Ile Asn
50 55 60
Gln Val Lys Asp Gly Thr Trp Glu Ser Gly Gly Trp Pro Gln Thr Phe
65 70 75 80
Thr Asp.Tyr Ser Met Ser Lys Leu Ala Val Asn Ala Tyr Thr Arg Leu
85 90 95
Met Ala Lys Glu Leu Glu Arg Arg Gly Glu Glu Lys Ile Tyr Val
100 105 110
Asn Ser Phe Cys Pro Gly Trp Val Lys Thr Ala Met Xaa Trp Leu Arg
115 120 125
Arg Lys Tyr Ala Thr
130

(2) INFORMATION FOR SEQ ID NO:1344:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..129

(D) OTHER INFORMATION: / Ceres Seq. ID 1569674

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1344:

Met Ile Pro Leu Met Arg Pro Ser Pro His Gly Ala Arg Val Val Asn
1 5 10 15
Val Ser Ser Arg Leu Gly Arg Val Asn Gly Arg Arg Asn Arg Leu Ala
20 25 30
Asn Val Glu Leu Arg Asp Gln Leu Ser Ser Pro Asp Leu Leu Thr Glu
35 40 45
Glu Leu Ile Asp Arg Thr Val Ser Lys Phe Ile Asn Gln Val Lys Asp
50 55 60
Gly Thr Trp Glu Ser Gly Gly Trp Pro Gln Thr Phe Thr Asp Tyr Ser
65 70 75 80
Met Ser Lys Leu Ala Val Asn Ala Tyr Thr Arg Leu Met Ala Lys Glu
85 90 95
Leu Glu Arg Arg Gly Glu Glu Glu Lys Ile Tyr Val Asn Ser Phe Cys
100 105 110
Pro Gly Trp Val Lys Thr Ala Met Xaa Trp Leu Arg Arg Lys Tyr Ala
115 120 125
Thr

(2) INFORMATION FOR SEQ ID NO:1345:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1214 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1214

(D) OTHER INFORMATION: / Ceres Seq. ID 1569685

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1345:

aatcaaaaag	gcaaaaagca	aagagagaga	gagagagaag	aagaagtggag	actttgtgttc	60
ttacgggtgtt	tatagcttct	ttgttttgtc	ttttagggttc	ttgccttttt	cogatcaatc	120
agaccaatcc	ctccctcaact	tttagcatct	tattctcttt	cgctctcttt	atatctctgg	180
gaattttctt	caatcgatcc	ctcttttgtg	taatctcaaca	attAgagaga	gagatrtgtg	240
Gtaatcagtt	ggcgatatct	tgcgtcttct	catcttsttc	gtactatgaa	tctttgaagg	300

ttttggaagc	tgtatgttcaa	cacgctaatt	ctttggcaga	agcaattcca	atggggaaga	360
acaatgtgcg	gcttcagatg	aaactgggtc	atagtaactt	tgcttCatta	ttactcttct	420
tgcttgggtg	gattgatctt	tcttctcat	gtcttattcc	tcgtactacta	aaactcttct	480
atgttttgtt	ctacaaggtc	cagtcgtatg	gacaacctaa	gcttaccacg	cacggaagga	540
aagcaacgat	tagtgagttc	tatggtgtga	tactaccatc	actgcagcta	ttacacagca	600
acttagatga	gttggaiaac	acagacatcg	ggtttgacct	taaaagactc	agtaagaaga	660
taacaaaaga	ggctcgtagt	agtagattca	gcaatgccgg	tttagagcgt	gaagaagaat	720
gcgggtatct	tttagaaaact	tgacccaaaa	tggtgttgcc	taattgttgc	cattctatgt	780
gcatcaaatG	ctatcgcaat	tggaacttga	agtctcagtc	atgcccggtt	tgctgaggca	840
gcatgaagag	agtgaaactca	gaggacttgt	gggtgcttgc	gggtgataac	gatgtgggtg	900
atacaaggac	ggcttcaagg	gaagatttgt	tcagatttcta	ttctctacat	aatagccttc	960
ccaagattta	cccaagaagct	ctctttgtgg	tttactatga	gtactcaaat	ctgctataga	1020
atctggacaa	acaaaacttt	gtacagattt	tttagatggta	aatgtattgt	atagaatgta	1080
aaactgtgtt	aaggcttttg	gatgatatga	tgcaaatgcc	aaagctctca	gtttttacat	1140
acttaataat	tgtcaaatg	cgagaaaaaa	aaaaagcttg	aatgcagcaa	agaataaaga	1200
ttctatttca	tctc					

(2) INFORMATION FOR SEQ ID NO:1346:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 338 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..338
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569686

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1346:

Ser	Lys	Arg	Gln	Lys	Ala	Lys	Arg	Glu	Arg	Glu	Arg	Arg	Ser	Glu
1			5					10				15		
Thr	Cys	Val	Leu	Thr	Val	Phe	Ile	Ala	Ser	Leu	Phe	Cys	Leu	Gly
			20					25				30		
Ser	Cys	Leu	Phe	Pro	Ile	Asn	Gln	Thr	Asn	Pro	Ser	Phe	Thr	Ser
			35				40					45		
Ile	Leu	Phe	Ser	Phe	Val	Leu	Leu	Ile	Phe	Leu	Gly	Ile	Phe	Asn
			50				55				60			
Arg	Phe	Leu	Phe	Val	Val	Ile	Ser	Gln	Leu	Glu	Arg	Glu	Xaa	Ser
			65				70				75			80
Asn	Gln	Leu	Ala	Ile	Ser	Ser	Ser	Ser	Ser	Xaa	Ser	Tyr	Tyr	Glu
			85					90				95		
Ser	Leu	Lys	Val	Leu	Glu	Ala	Asp	Val	Gln	His	Ala	Asn	Ser	Leu
			100					105				110		
Glu	Ala	Ile	Pro	Met	Gly	Lys	Asn	Asn	Val	Arg	Leu	Gln	Met	Lys
			115				120					125		
Val	His	Ser	Asn	Phe	Ala	Ser	Leu	Leu	Phe	Leu	Leu	Arg	Trp	Ile
			130				135					140		
Asp	Leu	Ser	Ser	Ser	Cys	Leu	Ile	Pro	Arg	Tyr	Leu	Asn	Leu	His
			145				150				155			160
Val	Leu	Val	Tyr	Lys	Val	Gln	Ser	Asp	Gly	Gln	Pro	Lys	Leu	Thr
			165					170				175		
His	Gly	Arg	Lys	Ala	Thr	Ile	Ser	Glu	Phe	Tyr	Gly	Val	Ile	Pro
			180					185				190		
Ser	Leu	Gln	Leu	Leu	His	Ser	Asn	Leu	Asp	Glu	Leu	Glu	Thr	Asp
			195				200					205		
Ile	Gly	Phe	Asp	Leu	Lys	Arg	Leu	Ser	Lys	Lys	Ile	Thr	Lys	Glu
			210				215					220		
Arg	Ser	Ser	Arg	Phe	Ser	Asn	Ala	Gly	Leu	Glu	Arg	Glu	Glu	Cys
			225				230				235			240
Gly	Ile	Cys	Leu	Glu	Thr	Cys	Thr	Lys	Met	Val	Leu	Pro	Asn	Cys
			245					250				255		
His	Ser	Met	Cys	Ile	Lys	Cys	Tyr	Arg	Asn	Trp	Asn	Leu	Lys	Gln

2025 RELEASE UNDER E.O. 14176

(2) INFORMATION FOR SEQ ID NO:1347:

(A) LENGTH: 222 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

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(D) TOPOLOGY: lin
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MOLECULE TYPE: peptid

(ii) MOLECULE TYPE: peptide

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(ix) FEATURE:
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(A) NAME/KEY: peptide

(B) LOCATION: 1..222

(D) OTHER INFORMATION: / Ceres Seq. ID 1569687

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1347:

Met	Gly	Lys	Asn	Asn	Val	Arg	Leu	Gln	Met	Lys	Leu	Val	His	Ser	Asn
1			5					10						15	
Phe	Ala	Ser	Leu	Leu	Leu	Phe	Leu	Leu	Arg	Trp	Ile	Asp	Leu	Ser	Ser
			20					25					30		
Ser	Cys	Leu	Ile	Pro	Arg	Tyr	Leu	Asn	Leu	Phe	His	Val	Leu	Val	Tyr
		35					40					45			
Lys	Val	Gln	Ser	Asp	Gly	Gln	Pro	Lys	Leu	Thr	Thr	His	Gly	Arg	Lys
		50				55					60				
Ala	Thr	Ile	Ser	Glu	Phe	Tyr	Gly	Val	Ile	Leu	Pro	Ser	Leu	Gln	Leu
65					70					75					80
Leu	His	Ser	Asn	Leu	Asp	Glu	Leu	Glu	Thr	Thr	Asp	Ile	Gly	Phe	Asp
				85					90					95	
Leu	Lys	Arg	Leu	Ser	Lys	Lys	Ile	Thr	Lys	Glu	Ala	Arg	Ser	Ser	Arg
			100					105					110		
Phe	Ser	Asn	Ala	Gly	Leu	Glu	Arg	Glu	Glu	Glu	Cys	Gly	Ile	Cys	Leu
		115					120					125			
Glu	Thr	Cys	Thr	Lys	Met	Val	Leu	Pro	Asn	Cys	Cys	His	Ser	Met	Cys
					135						140				
Ile	Lys	Cys	Tyr	Arg	Asn	Trp	Asn	Leu	Lys	Ser	Gln	Ser	Cys	Pro	Phe
145					150					155					160
Cys	Arg	Gly	Ser	Met	Lys	Arg	Val	Asn	Ser	Glu	Asp	Leu	Trp	Val	Leu
				165					170					175	
Ala	Gly	Asp	Asn	Asp	Val	Val	Asp	Thr	Arg	Thr	Ala	Ser	Arg	Glu	Asp
			180					185					190		
Leu	Phe	Arg	Phe	Tyr	Leu	Tyr	Ile	Asn	Ser	Leu	Pro	Lys	Asp	Tyr	Pro
		195					200					205			
Glu	Ala	Leu	Phe	Val	Val	Tyr	Tyr	Glu	Tyr	Ser	Asn	Leu	Leu		
		210				215					220				

(2) INFORMATION FOR SEQ ID NO:1348:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 213 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

```
(ix) FEATURE:
```

(A) NAME/KEY: peptide

(B) LOCATION: 1..213

(D) OTHER INFORMATION: / Ceres Seq. ID 1569688

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1348:

Met	Lys	Leu	Val	His	Ser	Asn	Phe	Ala	Ser	Leu	Leu	Leu	Phe	Leu	Leu
1				5					10					15	
Arg	Trp	Ile	Asp	Leu	Ser	Ser	Ser	Cys	Leu	Ile	Pro	Arg	Tyr	Leu	Asn
				20				25					30		
Leu	Phe	His	Val	Leu	Val	Tyr	Lys	Val	Gln	Ser	Asp	Gly	Gln	Pro	Lys
				35				40					45		
Leu	Thr	Thr	His	Gly	Arg	Lys	Ala	Thr	Ile	Ser	Glu	Phe	Tyr	Gly	Val
				50				55					60		
Ile	Leu	Pro	Ser	Leu	Gln	Leu	Leu	His	Ser	Asn	Leu	Asp	Glu	Leu	Glu
				65				70					75		80
Thr	Thr	Asp	Ile	Gly	Phe	Asp	Leu	Lys	Arg	Leu	Ser	Lys	Lys	Ile	Thr
				85				90					95		
Lys	Glu	Ala	Arg	Ser	Ser	Arg	Phe	Ser	Asn	Ala	Gly	Leu	Glu	Arg	Glu
				100				105					110		
Glu	Glu	Cys	Gly	Ile	Cys	Leu	Glu	Thr	Cys	Thr	Lys	Met	Val	Leu	Pro
				115				120					125		
Asn	Cys	Cys	His	Ser	Met	Cys	Ile	Lys	Cys	Tyr	Arg	Asn	Trp	Asn	Leu
				130				135					140		
Lys	Ser	Gln	Ser	Cys	Pro	Phe	Cys	Arg	Gly	Ser	Met	Lys	Arg	Val	Asn
				145				150					155		160
Ser	Glu	Asp	Leu	Trp	Val	Leu	Ala	Gly	Asp	Asn	Asp	Val	Val	Asp	Thr
				165				170					175		
Arg	Thr	Ala	Ser	Arg	Glu	Asp	Leu	Phe	Arg	Phe	Tyr	Leu	Tyr	Ile	Asn
				180				185					190		
Ser	Leu	Pro	Lys	Asp	Tyr	Pro	Glu	Ala	Leu	Phe	Val	Val	Tyr	Tyr	Glu
				195				200					205		
Tyr	Ser	Asn	Leu	Leu											
				210											

(2) INFORMATION FOR SEQ ID NO:1349:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 792 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..792

(D) OTHER INFORMATION: / Ceres Seq. ID 1569697

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1349:

gattcagagt	ttgtcagcga	gagagacgaa	gaaagaaaga	gaggagaggt	ggaagatgat	60
taaggcagtg	atgatgatga	acacacaagg	caaaccacgt	ctagctaaaat	tctacgatta	120
catgccctgtg	gagaagcagc	aggagcttat	tcgcggcgtg	ttttcagtat	tgtgcagtag	180
acctgagaac	gtaagcaaat	ttctggagat	cgaatcattg	tttggaccgg	actcgcggct	240
tggtatataag	cattatgcta	cactctattt	tgttcttgta	tttgatgggt	cagaaaatga	300
gcttgctatg	cttgatctca	tttaagttct	tgttgaaaca	ctggacaaat	gcttcagcaa	360
tgtctgcgaa	ctcgacattg	Gtggtcaact	acagcaagat	gcacgcgggt	ttagGatgag	420
attgattctg	gaggacaaAg	tactggaaac	tagttctgct	gaagtcatga	aggctgttga	480
agaaatatca	aaattagaag	ctgcctcaaa	ttcgatttca	cttgctccca	agtcctgttc	540
cgggtggcgt	ggccggttagc	ttcgaaaaaa	cttgcctgaa	taagtcagag	aacatgtaac	600
aaaagcttat	ccaagtcttg	atccaaacat	gtttgtttaa	tgagcgtgga	atgttgcgtg	660
gatgggctca	gtagtctaac	gtgggcctgt	gaattgtaat	tgggtaacgg	acggaactgc	720
ttgctatttt	tgagaatgta	acaaaaacga	cgagaagtta	agatctataa	atgataaaat	780
atgtccaaat	cc					

(2) INFORMATION FOR SEQ ID NO:1350:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:

(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..107
 (D) OTHER INFORMATION: / Ceres Seq. ID 1569698
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1350:
Ile Gln Ser Leu Ser Ala Arg Glu Thr Lys Lys Glu Arg Glu Glu Arg
1 5 10 15
Trp Lys Met Ile Lys Ala Val Met Met Met Asn Thr Gln Gly Lys Pro
 20 25 30
Arg Leu Ala Lys Phe Tyr Asp Tyr Met Pro Val Glu Lys Gln Gln Glu
 35 40 45
Leu Ile Arg Gly Val Phe Ser Val Leu Cys Ser Arg Pro Glu Asn Val
 50 55 60
Ser Asn Phe Leu Glu Ile Glu Ser Leu Phe Gly Pro Asp Ser Arg Leu
65 70 75 80
Val Tyr Lys His Tyr Ala Thr Leu Tyr Phe Val Leu Val Phe Asp Gly
 85 90 95
Ser Glu Asn Glu Leu Ala Met Leu Asp Leu Ile
 100 105
(2) INFORMATION FOR SEQ ID NO:1351:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 89 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..89
 (D) OTHER INFORMATION: / Ceres Seq. ID 1569699
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1351:
Met Ile Lys Ala Val Met Met Met Asn Thr Gln Gly Lys Pro Arg Leu
1 5 10 15
Ala Lys Phe Tyr Asp Tyr Met Pro Val Glu Lys Gln Gln Glu Leu Ile
 20 25 30
Arg Gly Val Phe Ser Val Leu Cys Ser Arg Pro Glu Asn Val Ser Asn
 35 40 45
Phe Leu Glu Ile Glu Ser Leu Phe Gly Pro Asp Ser Arg Leu Val Tyr
 50 55 60
Lys His Tyr Ala Thr Leu Tyr Phe Val Leu Val Phe Asp Gly Ser Glu
65 70 75 80
Asn Glu Leu Ala Met Leu Asp Leu Ile
 85
(2) INFORMATION FOR SEQ ID NO:1352:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 84 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..84
 (D) OTHER INFORMATION: / Ceres Seq. ID 1569700
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1352:
Met Met Met Asn Thr Gln Gly Lys Pro Arg Leu Ala Lys Phe Tyr Asp
1 5 10 15
Tyr Met Pro Val Glu Lys Gln Gln Glu Leu Ile Arg Gly Val Phe Ser
 20 25 30

Val Leu Cys Ser Arg Pro Glu Asn Val Ser Asn Phe Leu Glu Ile Glu
35 40 45
Ser Leu Phe Gly Pro Asp Ser Arg Leu Val Tyr Lys His Tyr Ala Thr
50 55 60
Leu Tyr Phe Val Leu Val Phe Asp Gly Ser Glu Asn Glu Leu Ala Met
65 70 75 80
Leu Asp Leu Ile

(2) INFORMATION FOR SEQ ID NO:1353:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1377 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1377

(D) OTHER INFORMATION: / Ceres Seq. ID 1569717

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1353:

aaaccaAgt	cCAagtTCct	gtTaaatggc	gaaaaaagaa	gggtcaaaaga	tgaacatcgc	60
cattatacat	ccagatctgtt	gaatagcgcg	aGcagagaga	ttgattgttg	atgcggccgt	120
tgagcttgcc	tgcacgcttg	ataaagtcca	tatcttcacc	tctcaccacg	acaaatccag	180
atgcttccag	gaactctttt	cgggtatctt	tcaagttacg	gtgatgtgat	ctttctctgc	240
acggcatatt	ttctaccagc	tacacgcagt	KgtGgcata	ttgcgggtgc	tggtttgtgc	300
tctctgtgtt	cttttggggt	gggtcttcatt	cgatgttgta	ctagcagacc	aagtttcagt	360
cgtagtccca	ttgtggaac	tcaaaaggct	acttaaggtt	gttttctact	gccatttccc	420
ggatctctgt	ctagctaaag	atacaacaac	acttagacgg	atgtatcggg	aaccattgga	480
tttcattgaa	gaacaaacaa	cagggatggc	tgatgatgat	cttgtaacaa	gtaaactcac	540
ggcatcaaca	tttgccaata	catttaaaag	gctaaatgca	caaggggagt	gccccagctg	600
actttacccc	cgagtcgaata	ttgatcagtt	cattgaaccc	cacacttata	agttgaattt	660
ctctccata	aaacgctttt	agaggaaaaa	gaacatcgat	ctagctgttt	cagcttttgc	720
tatctctatg	aaacataagc	aaaatctgag	tgatgttacc	cttaccgctg	caggtggata	780
tgacgacgca	ttgaaggaga	atgttgagta	cttgaggagg	ctcagaagtt	tagccagaaa	840
agaaggagtt	tctgatcgag	ttaaactttat	cacatcttgt	tcaaccgcgt	aaagaatatg	900
actttctgca	agctgcttgt	gcgttctctc	cacccccaag	gatgaacatt	ttggtattgt	960
tccattagaa	gcaatggctg	catacaaaac	ogtगतagcc	tgcaacagtg	gtggcccccgt	1020
ggagacggta	aagaatggag	taacaggcta	tctttgtgaa	ccaactccag	aagatttcag	1080
ttcggcgatg	gctagattca	tgcgaaatcc	tgagttggcg	aatagaatgg	gagctgaagc	1140
caggaaacct	gtcgttgaat	cattctctgt	gaagacgttt	ggacagagat	tgaatcagta	1200
tctcgttgat	gtcgtatcaa	gtcctaaga	agattgagat	tctctgttgt	agtaatacata	1260
gatcgttgtg	gaacacagct	actttaggct	tagttctgaa	actacagagg	ctttattctc	1320
ggatacctca	tcttgacogt	gaagatttgt	taaatctagg	tgaacagttt	tttggttt	

(2) INFORMATION FOR SEQ ID NO:1354:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 403 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..403

(D) OTHER INFORMATION: / Ceres Seq. ID 1569718

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1354:

Met	Ala	Lys	Lys	Glu	Gly	Ser	Lys	Met	Asn	Ile	Ala	Ile	Ile	His	Pro
1				5					10					15	
Asp	Leu	Gly	Ile	Gly	Gly	Ala	Glu	Arg	Leu	Ile	Val	Asp	Ala	Ala	Val
			20				25				30				
Glu	Leu	Ala	Ser	His	Gly	His	Lys	Val	His	Ile	Phe	Thr	Ser	His	His
			35				40				45				

```

Asp Lys Ser Arg Cys Phe Glu Glu Thr Leu Ser Gly Ile Phe Gln Val
50      55      60
Thr Val Tyr Gly Ser Phe Leu Pro Arg His Ile Phe Tyr Arg Leu His
65      70      75      80
Ala Xaa Val Ala Tyr Leu Arg Cys Leu Phe Val Ala Leu Cys Val Leu
85      90      95
Leu Gly Trp Ser Ser Phe Asp Val Val Leu Ala Asp Gln Val Ser Val
100     105     110
Val Val Pro Leu Leu Lys Leu Lys Arg Ser Ser Lys Val Val Phe Tyr
115     120     125
Cys His Phe Pro Asp Leu Leu Leu Ala Lys His Thr Thr Thr Leu Arg
130     135     140
Arg Met Tyr Arg Lys Pro Ile Asp Phe Ile Glu Glu Gln Thr Thr Gly
145     150     155     160
Met Ala Asp Met Ile Leu Val Asn Ser Asn Phe Thr Ala Ser Thr Phe
165     170     175
Ala Asn Thr Phe Lys Arg Leu Asn Ala Gln Gly Ser Arg Pro Ala Val
180     185     190
Leu Tyr Pro Ala Val Asn Ile Asp Gln Phe Ile Glu Pro His Thr Tyr
195     200     205
Lys Leu Asn Phe Leu Ser Ile Asn Arg Phe Glu Arg Lys Lys Asn Ile
210     215     220
Asp Leu Ala Val Ser Ala Phe Ala Ile Leu Cys Lys His Lys Gln Asn
225     230     235     240
Leu Ser Asp Val Thr Leu Thr Val Ala Gly Tyr Asp Glu Arg Leu
245     250     255
Lys Glu Asn Val Glu Tyr Leu Glu Glu Leu Arg Ser Leu Ala Glu Lys
260     265     270
Glu Gly Val Ser Asp Arg Val Asn Phe Ile Thr Ser Cys Ser Thr Ala
275     280     285
Glu Arg Asn Glu Leu Leu Ser Ser Cys Leu Cys Val Leu Tyr Thr Pro
290     295     300
Thr Asp Glu His Phe Gly Ile Val Pro Leu Glu Ala Met Ala Ala Tyr
305     310     315     320
Lys Pro Val Ile Ala Cys Asn Ser Gly Gly Pro Val Glu Thr Val Lys
325     330     335
Asn Gly Val Thr Gly Tyr Leu Cys Glu Pro Thr Pro Glu Asp Phe Ser
340     345     350
Ser Ala Met Ala Arg Phe Ile Glu Asn Pro Glu Leu Ala Asn Arg Met
355     360     365
Gly Ala Glu Ala Arg Asn His Val Val Glu Ser Phe Ser Val Lys Thr
370     375     380
Phe Gly Gln Lys Leu Asn Gln Tyr Leu Val Asp Val Val Ser Ser Pro
385     390     395     400
Lys Glu Asp

```

(2) INFORMATION FOR SEQ ID NO:1355:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 395 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..395

(D) OTHER INFORMATION: / Ceres Seq. ID 1569719

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1355:

```

Met Asn Ile Ala Ile Ile His Pro Asp Leu Gly Ile Gly Gly Ala Glu
1      5      10      15
Arg Leu Ile Val Asp Ala Ala Val Glu Leu Ala Ser His Gly His Lys

```

	20		25		30
Val His Ile Phe Thr Ser His His Asp Lys Ser Arg Cys Phe Glu Glu	35	40		45	
Thr Leu Ser Gly Ile Phe Gln Val Thr Val Tyr Gly Ser Phe Leu Pro	50	55		60	
Arg His Ile Phe Tyr Arg Leu His Ala Xaa Val Ala Tyr Leu Arg Cys	65	70		75	
Leu Phe Val Ala Leu Cys Val Leu Leu Gly Trp Ser Ser Phe Asp Val	85	90		95	
Val Leu Ala Asp Gln Val Ser Val Val Val Pro Leu Leu Lys Leu Lys	100	105		110	
Arg Ser Ser Lys Val Val Phe Tyr Cys His Phe Pro Asp Leu Leu Leu	115	120		125	
Ala Lys His Thr Thr Thr Leu Arg Arg Met Tyr Arg Lys Pro Ile Asp	130	135		140	
Phe Ile Glu Glu Gln Thr Thr Gly Met Ala Asp Met Ile Leu Val Asn	145	150		155	
Ser Asn Phe Thr Ala Ser Thr Phe Ala Asn Thr Phe Lys Arg Leu Asn	165	170		175	
Ala Gln Gly Ser Arg Pro Ala Val Leu Tyr Pro Ala Val Asn Ile Asp	180	185		190	
Gln Phe Ile Glu Pro His Thr Tyr Lys Leu Asn Phe Leu Ser Ile Asn	195	200		205	
Arg Phe Glu Arg Lys Lys Asn Ile Asp Leu Ala Val Ser Ala Phe Ala	210	215		220	
Ile Leu Cys Lys His Lys Gln Asn Leu Ser Asp Val Thr Leu Thr Val	225	230		235	
Ala Gly Gly Tyr Asp Glu Arg Leu Lys Glu Asn Val Glu Tyr Leu Glu	245	250		255	
Glu Leu Arg Ser Leu Ala Glu Lys Glu Gly Val Ser Asp Arg Val Asn	260	265		270	
Phe Ile Thr Ser Cys Ser Thr Ala Glu Arg Asn Glu Leu Leu Ser Ser	275	280		285	
Cys Leu Cys Val Leu Tyr Thr Pro Thr Asp Glu His Phe Gly Ile Val	290	295		300	
Pro Leu Glu Ala Met Ala Ala Tyr Lys Pro Val Ile Ala Cys Asn Ser	305	310		315	
Gly Gly Pro Val Glu Thr Val Lys Asn Gly Val Thr Gly Tyr Leu Cys	325	330		335	
Glu Pro Thr Pro Glu Asp Phe Ser Ser Ala Met Ala Arg Phe Ile Glu	340	345		350	
Asn Pro Glu Leu Ala Asn Arg Met Gly Ala Glu Ala Arg Asn His Val	355	360		365	
Val Glu Ser Phe Ser Val Lys Thr Phe Gly Gln Lys Leu Asn Gln Tyr	370	375		380	
Leu Val Asp Val Val Ser Ser Pro Lys Glu Asp	385	390		395	

(2) INFORMATION FOR SEQ ID NO:1356:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 258 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..258
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569720

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1356:

Met Tyr Arg Lys Pro Ile Asp Phe Ile Glu Glu Gln Thr Thr Gly Met		
1	5	10

Ala Asp Met Ile Leu Val Asn Ser Asn Phe Thr Ala Ser Thr Phe Ala
20 25 30
Asn Thr Phe Lys Arg Leu Asn Ala Gln Gly Ser Arg Pro Ala Val Leu
35 40 45
Tyr Pro Ala Val Asn Ile Asp Gln Phe Ile Glu Pro His Thr Tyr Lys
50 55 60
Leu Asn Phe Leu Ser Ile Asn Arg Phe Glu Arg Lys Lys Asn Ile Asp
65 70 75 80
Leu Ala Val Ser Ala Phe Ala Ile Leu Cys Lys His Lys Gln Asn Leu
85 90 95
Ser Asp Val Thr Leu Thr Val Ala Gly Gly Tyr Asp Glu Arg Leu Lys
100 105 110
Glu Asn Val Glu Tyr Leu Glu Glu Leu Arg Ser Leu Ala Glu Lys Glu
115 120 125
Gly Val Ser Asp Arg Val Asn Phe Ile Thr Ser Cys Ser Thr Ala Glu
130 135 140
Arg Asn Glu Leu Leu Ser Ser Cys Leu Cys Val Leu Tyr Thr Pro Thr
145 150 155 160
Asp Glu His Phe Gly Ile Val Pro Leu Glu Ala Met Ala Tyr Lys
165 170 175
Pro Val Ile Ala Cys Asn Ser Gly Gly Pro Val Glu Thr Val Lys Asn
180 185 190
Gly Val Thr Gly Tyr Leu Cys Glu Pro Thr Pro Glu Asp Phe Ser Ser
195 200 205
Ala Met Ala Arg Phe Ile Glu Asn Pro Glu Leu Ala Asn Arg Met Gly
210 215 220
Ala Glu Ala Arg Asn His Val Val Glu Ser Phe Ser Val Lys Thr Phe
225 230 235 240
Gly Gln Lys Leu Asn Gln Tyr Leu Val Asp Val Val Ser Ser Pro Lys
245 250 255
Glu Asp

(2) INFORMATION FOR SEQ ID NO:1357:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 662 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..662
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569721

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1357:

actcgatcat	agaataaaaa	acaaaaaccc	ttgaagtcac	taagttgatt	caaaatggtt	60
gcgagaagt	aggaagtga	gatagtggaa	gatacggcg	cgaaatgatt	gatgttgta	120
tcaagagttg	gagaaggcgg	cggaggagga	gagaaacgag	ttttccgatg	caagacttgt	180
cttaaaagat	tttctcgatt	tcaagctttg	ggaggtcac	gtgcaagcca	caacaaactc	240
attaacagta	gcgatccatc	actctctgga	tctctgtcta	acaagaaaaa	taaaacggcg	300
acgtctcatc	cttgtccgat	atgtggcggt	gagtttccga	tggggcaagc	tcttggtggt	360
cacatgagga	gacataggag	tgagaaagcc	tcaccaggca	cgttggtgta	acagttcttt	420
tttaccggag	acgacgacgg	tgacgacttt	gaagaaatcg	agtagtgga	agagagtggc	480
ttgtttgac	ttagatccga	tgagaggttt	agtcaattgg	aagtgtgagt	tggaagaagc	540
gatttcttga	tctgttttat	tcttccatat	tcgttatagg	gttttaacat	attttcatac	600
agtttcatt	tgtaaatctt	gtagatccat	ttatcttaac	gatcgatgty	aatattattt	660

(2) INFORMATION FOR SEQ ID NO:1358:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 136 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:

- (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1..136
(D) OTHER INFORMATION: / Ceres Seq. ID 1569722

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1358:

```
Met Val Ala Arg Ser Glu Glu Val Glu Ile Val Glu Asp Thr Ala Ala
1      5      10      15
Lys Cys Leu Met Leu Leu Ser Arg Val Gly Glu Gly Gly Gly Gly
20      25      30
Glu Lys Arg Val Phe Arg Cys Lys Thr Cys Leu Lys Glu Phe Ser Ser
35      40      45
Phe Gln Ala Leu Gly Gly His Arg Ala Ser His Asn Lys Leu Ile Asn
50      55      60
Ser Ser Asp Pro Ser Leu Leu Gly Ser Leu Ser Asn Lys Lys Thr Lys
65      70      75      80
Thr Ala Thr Ser His Pro Cys Pro Ile Cys Gly Val Glu Phe Pro Met
85      90      95
Gly Gln Ala Leu Gly Gly His Met Arg Arg His Arg Ser Glu Lys Ala
100      105      110
Ser Pro Gly Thr Leu Gly Tyr Thr Phe Phe Phe Thr Gly Asp Asp Asp
115      120      125
Gly Asp Asp Phe Glu Glu Ile Glu
130      135
```

- (2) INFORMATION FOR SEQ ID NO:1359:

- (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 117 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide

- (ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1..117
(D) OTHER INFORMATION: / Ceres Seq. ID 1569723

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1359:

```
Met Leu Leu Ser Arg Val Gly Glu Gly Gly Gly Gly Glu Lys Arg
1      5      10      15
Val Phe Arg Cys Lys Thr Cys Leu Lys Glu Phe Ser Ser Phe Gln Ala
20      25      30
Leu Gly Gly His Arg Ala Ser His Asn Lys Leu Ile Asn Ser Ser Asp
35      40      45
Pro Ser Leu Leu Gly Ser Leu Ser Asn Lys Lys Thr Lys Thr Ala Thr
50      55      60
Ser His Pro Cys Pro Ile Cys Gly Val Glu Phe Pro Met Gly Gln Ala
65      70      75      80
Leu Gly Gly His Met Arg Arg His Arg Ser Glu Lys Ala Ser Pro Gly
85      90      95
Thr Leu Gly Tyr Thr Phe Phe Phe Thr Gly Asp Asp Asp Gly Asp Asp
100      105      110
Phe Glu Glu Ile Glu
115
```

- (2) INFORMATION FOR SEQ ID NO:1360:

- (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1488 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)

- (ix) FEATURE:

(A) NAME/KEY: -
(B) LOCATION: 1.1488
(D) OTHER INFORMATION: / Ceres Seq. ID 1569724

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1360:

cttagcagat	gcttttttgc	aaaaaaaata	tacaaaaaaa	aaaaaatctg	catctgcctt	60
cgtctctctc	cttgccctcta	aaatttaatta	cccatttttt	ccgataaaat	tttgttgagg	120
aaagaatttt	gttgtaaaaga	gagtttaatt	aaattatgcc	ttcaatagaa	gatgagctgt	180
ttccgtcaac	gcggggtaaa	ttcaaaattg	accggtcaaa	ccgtcagctc	caccgttgtt	240
tgcgtctcat	gagcaccatg	tttctttggg	ctctcttctc	catcgctctc	accgctttct	300
acttgagttt	ccaaagcttt	gtcgattccg	gtagccgtta	tctaaccgct	ttttggggcg	360
gcattccaat	ggagaaacag	gttcgtacct	ccgctcagat	ccatcgctcc	ggcggatctc	420
ccgtccttgt	taccggcgct	accggattcg	tcggtagcoa	cggtcgaact	ccgttgagga	480
aaacgcgcga	tggtgtcggt	ggacttgata	atttcaacaa	ttactacgat	ccgtctttga	540
aaagtgcctg	tagatctctg	ttgtcgtcga	gagggatctt	cgctgttgaa	ggagatctaa	600
acgacgcgaa	gctgttagca	aaagcttttc	atgtggttgc	tttactcac	gtgatgcac	660
tcgtctgcta	agctgtgtgt	agatacgtct	tggagaatcc	tcaatcgat	gtctcatagca	720
acatgcgcgg	acttgtgaat	cttctcgaga	tttgcaaaag	ggcgaatcct	cagccgcgca	780
ttgtttgggc	ttcatcgagc	tccgtttatg	gactcaacga	gaaagttcca	ttctctgaat	840
ctgacccgac	ggatcaacgc	gcgagttctc	acgccgcac	gaaaaaagcc	ggcgaagaaa	900
tcaccacac	ttataaccat	atttagcggt	ttgccattac	cggtttaaga	ttcttcacg	960
tttacggacc	atggggtaga	ccgatatagg	cttaactctc	cttcaccaga	aacatcctac	1020
aaagtaaac	gcatacaatc	taccggggca	aaaacccggg	cgatttagcc	cgggatttca	1080
catatcagca	cgatatagtg	aaaggatgtt	taggatctct	ggaattcctg	ggtaaaagta	1140
ccgggtcggg	gtaaaaaacg	tggagcagca	cCgtaccgga	tatttaacct	gggaaacaca	1200
ttctcggtta	cagtaccgat	tctgtgtgat	atatgtggag	agcattttaa	ggtgaaagcg	1260
aaagggaaat	tcgtggagat	gccaggaac	ggcgacgtac	cgttcacaca	tgccaatatt	1320
agctcagccc	gaatatgaat	ccggtataaa	ccgacaacgc	atttggaac	ccgggttgag	1380
aaagtctgta	gatgttatct	tctttattac	ggatacaata	ctaaagccaa	gctgtgtacat	1440
taaccgtgac	tattattatt	atttttaagt	aaattatttt	ttctctcc		

(2) INFORMATION FOR SEQ ID NO:1361:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 332 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1.332
(D) OTHER INFORMATION: / Ceres Seq. ID 1569725

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1361:

Met	Pro	Ser	Ile	Glu	Asp	Glu	Leu	Phe	Pro	Ser	Thr	Pro	Gly	Lys	Phe
1			5				10						15		
Lys	Ile	Asp	Arg	Ser	Asn	Arg	Gln	Leu	His	Arg	Cys	Phe	Ala	Ser	Thr
			20				25						30		
Ser	Thr	Met	Phe	Leu	Trp	Ala	Leu	Phe	Leu	Ile	Ala	Leu	Thr	Ala	Ser
			35				40						45		
Tyr	Leu	Ser	Phe	Gln	Ser	Phe	Val	Asp	Ser	Gly	Ser	Arg	Tyr	Leu	Thr
			50				55						60		
Ala	Ser	Trp	Gly	Gly	Ile	Gln	Trp	Glu	Lys	Gln	Val	Arg	Thr	Ser	Ala
			65				70						75		
Gln	Ile	His	Arg	Ser	Gly	Gly	Ile	Ser	Val	Leu	Val	Thr	Gly	Ala	Thr
			85				90						95		
Gly	Val	Val	Gly	Ser	His	Val	Ser	Leu	Ala	Leu	Arg	Lys	Arg	Gly	Asp
			100				105						110		
Gly	Val	Val	Gly	Leu	Asp	Asn	Phe	Asn	Asn	Tyr	Tyr	Asp	Pro	Ser	Leu
			115				120						125		
Lys	Arg	Ala	Arg	Arg	Ser	Leu	Leu	Ser	Ser	Arg	Gly	Ile	Phe	Val	Val
			130				135						140		
Glu	Gly	Asp	Leu	Asn	Asp	Ala	Lys	Leu	Leu	Ala	Lys	Leu	Phe	Asp	Val
			145				150						155		

Val Ala Phe Thr His Val Met His Leu Ala Ala Gln Ala Gly Val Arg
165 170 175
Tyr Ala Leu Glu Asn Pro Gln Ser Tyr Val His Ser Asn Ile Ala Gly
180 185 190
Leu Val Asn Leu Leu Glu Ile Cys Lys Ala Ala Asn Pro Gln Pro Ala
195 200 205
Ile Val Trp Ala Ser Ser Ser Val Tyr Gly Leu Asn Glu Lys Val
210 215 220
Pro Phe Ser Glu Ser Asp Arg Thr Asp Gln Pro Ala Ser Leu Tyr Ala
225 230 235 240
Ala Thr Lys Lys Ala Gly Glu Glu Ile Thr His Thr Tyr Asn His Ile
245 250 255
Tyr Gly Leu Ala Ile Thr Gly Leu Arg Phe Phe Thr Val Tyr Gly Pro
260 265 270
Trp Gly Arg Pro Asp Met Ala Tyr Phe Ser Phe Thr Arg Asn Ile Leu
275 280 285
Gln Gly Lys Pro Ile Thr Ile Tyr Arg Gly Lys Asn Arg Val Asp Leu
290 295 300
Ala Arg Asp Phe Thr Tyr Ile Asp Asp Ile Val Lys Gly Cys Leu Gly
305 310 315 320
Ser Leu Asp Ser Ser Gly Lys Ser Thr Gly Ser Gly
325 330

(2) INFORMATION FOR SEQ ID NO:1362:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 298 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..298

(D) OTHER INFORMATION: / Ceres Seq. ID 1569726

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1362:

Met Phe Leu Trp Ala Leu Phe Leu Ile Ala Leu Thr Ala Ser Tyr Leu
1 5 10 15
Ser Phe Gln Ser Phe Val Asp Ser Gly Ser Arg Tyr Leu Thr Ala Ser
20 25 30
Trp Gly Gly Ile Gln Trp Glu Lys Gln Val Arg Thr Ser Ala Gln Ile
35 40 45
His Arg Ser Gly Gly Ile Ser Val Leu Val Thr Gly Ala Thr Gly Phe
50 55 60
Val Gly Ser His Val Ser Leu Ala Leu Arg Lys Arg Gly Asp Gly Val
65 70 75 80
Val Gly Leu Asp Asn Phe Asn Asn Tyr Tyr Asp Pro Ser Leu Lys Arg
85 90 95
Ala Arg Arg Ser Leu Leu Ser Ser Arg Gly Ile Phe Val Val Glu Gly
100 105 110
Asp Leu Asn Asp Ala Lys Leu Leu Ala Lys Leu Phe Asp Val Val Ala
115 120 125
Phe Thr His Val Met His Leu Ala Ala Gln Ala Gly Val Arg Tyr Ala
130 135 140
Leu Glu Asn Pro Gln Ser Tyr Val His Ser Asn Ile Ala Gly Leu Val
145 150 155 160
Asn Leu Leu Glu Ile Cys Lys Ala Ala Asn Pro Gln Pro Ala Ile Val
165 170 175
Trp Ala Ser Ser Ser Ser Val Tyr Gly Leu Asn Glu Lys Val Pro Phe
180 185 190
Ser Glu Ser Asp Arg Thr Asp Gln Pro Ala Ser Leu Tyr Ala Ala Thr
195 200 205
Lys Lys Ala Gly Glu Glu Ile Thr His Thr Tyr Asn His Ile Tyr Gly

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210	215	220
Leu Ala Ile Thr Gly	Leu Arg Phe Phe Thr Val Tyr Gly	Pro Trp Gly
225	230	235
Arg Pro Asp Met Ala Tyr Phe Ser Phe Thr Arg Asn Ile Leu Gln Gly		240
	245	250
Lys Pro Ile Thr Ile Tyr Arg Gly Lys Asn Arg Val Asp Leu Ala Arg		255
	260	265
Asp Phe Thr Tyr Ile Asp Asp Ile Val Lys Gly Cys Leu Gly Ser Leu		270
	275	280
Asp Ser Ser Gly Lys Ser Thr Gly Ser Gly		285
290	295	

(2) INFORMATION FOR SEQ ID NO:1363:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 166 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..166

(D) OTHER INFORMATION: / Ceres Seq. ID 1569727

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1363:

Met His Leu Ala Ala Gln Ala Gly Val Arg Tyr Ala Leu Glu Asn Pro	
1 5 10 15	
Gln Ser Tyr Val His Ser Asn Ile Ala Gly Leu Val Asn Leu Leu Glu	
20 25 30	
Ile Cys Lys Ala Ala Asn Pro Gln Pro Ala Ile Val Trp Ala Ser Ser	
35 40 45	
Ser Ser Val Tyr Gly Leu Asn Glu Lys Val Pro Phe Ser Glu Ser Asp	
50 55 60	
Arg Thr Asp Gln Pro Ala Ser Leu Tyr Ala Ala Thr Lys Lys Ala Gly	
65 70 75 80	
Glu Glu Ile Thr His Thr Tyr Asn His Ile Tyr Gly Leu Ala Ile Thr	
85 90 95	
Gly Leu Arg Phe Phe Thr Val Tyr Gly Pro Trp Gly Arg Pro Asp Met	
100 105 110	
Ala Tyr Phe Ser Phe Thr Arg Asn Ile Leu Gln Gly Lys Pro Ile Thr	
115 120 125	
Ile Tyr Arg Gly Lys Asn Arg Val Asp Leu Ala Arg Asp Phe Thr Tyr	
130 135 140	
Ile Asp Asp Ile Val Lys Gly Cys Leu Gly Ser Leu Asp Ser Ser Gly	
145 150 155 160	
Lys Ser Thr Gly Ser Gly	
165	

(2) INFORMATION FOR SEQ ID NO:1364:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1142 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1142

(D) OTHER INFORMATION: / Ceres Seq. ID 1569732

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1364:

aagtcatctt ctctctcTtt tttttagtgt gtgcaaagtc atcttctctt ttaatattta	60
cctaaaaattc caaacaaaag agaacgttat gaaaccaaag agcaaaagttg cagaatctac	120
agctgcacaa tgtttttctcg tcatgagctt gttatgcagc tgcattattg gtgaccaa	180
ggagactaat aatgaaggct tgtcttacag ttactacgag aaaacttgtc ccaaagtcca	240

agagatagtg	agatcttcac	tttcatcaat	gtttatactt	gatactactt	ctctcgcagc	300
cttgctaagg	cttatgtttc	atgactgcca	agttcaggga	tgtagacgat	ctatctactt	360
cgagccaat	agagaccaac	agttcaccca	gcttgattca	gccaaagaat	tcggatacag	420
aaagagggac	ctggttggct	ctatcaaaac	ctcactagag	cttgagtgct	ccsagcaagt	480
ctcatgtctt	gaagtcata	tcctcgccgc	cagagacgcc	gtggctctca	cgggagcccc	540
actcatctcc	gtgccattag	gacgaaaaga	ctccctctcc	actccaagca	aacacgtggc	600
agactctgag	cttctctcct	ccactgctga	cgttgacact	accttaagcc	tattcgctaa	660
caaaggcatg	accatcgaag	agtcctgtgc	catactgggt	gcacatacga	taggagtcac	720
acattgcaac	aacgtattat	cgcgttttca	taacgcaaac	gcgacaagcg	agaacatgga	780
tcacgttttt	caaacgtttc	tgcggtttgc	ttgtccagag	ttttctccaa	cttctcaagc	840
tgccgaagcg	acattttgtc	ccaacgatca	aacttcggtg	atcttcgata	cagcttatta	900
cgatgatgcc	atcgccggac	gtggcaatct	taggattgac	tcggagattg	gagctgatcc	960
acgtacacgt	ccattttgtg	aagcgtttgc	agctgatcaa	gaccgtttct	tcaacgcott	1020
ctctctccgc	tttgtaaaat	tgctgtctta	caaagtgtaa	accgggaatg	aaggagtaat	1080
tagaagcggt	tgtgacaaag	ttgattgatg	tatatattata	attatcaaat	gttaaaaaata	1140
tt						

(2) INFORMATION FOR SEQ ID NO:1365:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 368 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..368
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569733

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1365:

Ser	His	Leu	Leu	Ser	Leu	Phe	Phe	Ser	Val	Cys	Lys	Val	Ile	Phe	Ser
1			5						10				15		
Phe	Asn	Ile	Tyr	Leu	Lys	Phe	Gln	Thr	Lys	Glu	Asn	Val	Met	Lys	Pro
			20					25					30		
Lys	Ser	Lys	Val	Ala	Glu	Ser	Thr	Ala	Ala	Ser	Cys	Phe	Leu	Val	Met
			35					40					45		
Ser	Leu	Leu	Cys	Ser	Cys	Ile	Ile	Gly	Asp	Gln	Met	Glu	Thr	Asn	Asn
			50				55				60				
Glu	Gly	Leu	Ser	Tyr	Ser	Tyr	Tyr	Glu	Lys	Thr	Cys	Pro	Lys	Val	Glu
			70					75					80		
Glu	Ile	Val	Arg	Ser	Ser	Leu	Ser	Ser	Met	Phe	Ile	Leu	Asp	Pro	Thr
			85					90					95		
Ser	Pro	Ala	Ala	Leu	Leu	Arg	Leu	Met	Phe	His	Asp	Cys	Gln	Val	Gln
			100					105					110		
Gly	Cys	Asp	Ala	Ser	Ile	Leu	Leu	Glu	Pro	Ile	Arg	Asp	Gln	Gln	Phe
			115					120					125		
Thr	Glu	Leu	Asp	Ser	Ala	Lys	Asn	Phe	Gly	Ile	Arg	Lys	Arg	Asp	Leu
			130				135						140		
Val	Gly	Ser	Ile	Lys	Thr	Ser	Leu	Glu	Leu	Glu	Cys	Pro	Lys	Gln	Val
			145				150				155			160	
Ser	Cys	Ser	Asp	Val	Ile	Ile	Leu	Ala	Ala	Arg	Asp	Ala	Val	Ala	Leu
			165					170					175		
Thr	Gly	Gly	Pro	Leu	Ile	Ser	Val	Pro	Leu	Gly	Arg	Lys	Asp	Ser	Leu
			180					185					190		
Ser	Thr	Pro	Ser	Lys	His	Val	Ala	Asp	Ser	Glu	Leu	Pro	Pro	Ser	Thr
			195				200					205			
Ala	Asp	Val	Asp	Thr	Thr	Leu	Ser	Leu	Phe	Ala	Asn	Lys	Gly	Met	Thr
			210				215					220			
Ile	Glu	Glu	Ser	Val	Ala	Ile	Met	Gly	Ala	His	Thr	Ile	Gly	Val	Thr
			225				230			235				240	
His	Cys	Asn	Asn	Val	Leu	Ser	Arg	Phe	Asp	Asn	Ala	Asn	Ala	Thr	Ser
			245					250					255		
Glu	Asn	Met	Asp	Pro	Arg	Phe	Gln	Thr	Phe	Leu	Arg	Val	Ala	Cys	Pro

										260											265											270
Glu	Phe	Ser	Pro	Thr	Ser	Gln	Ala	Ala	Glu	Ala	Thr	Phe	Val	Pro	Asn																	
										275											280											285
Asp	Gln	Thr	Ser	Val	Ile	Phe	Asp	Thr	Ala	Tyr	Tyr	Asp	Asp	Ala	Ile																	
										290											295											300
Ala	Gly	Arg	Gly	Asn	Leu	Arg	Ile	Asp	Ser	Glu	Ile	Gly	Ala	Asp	Pro																	
										305											310											315
Arg	Thr	Arg	Pro	Phe	Val	Glu	Ala	Phe	Ala	Ala	Asp	Gln	Asp	Arg	Phe																	
										325											330											335
Phe	Asn	Ala	Phe	Ser	Ser	Ala	Phe	Val	Lys	Leu	Ser	Ser	Tyr	Lys	Val																	
										340											345											350
Leu	Thr	Gly	Asn	Glu	Gly	Val	Ile	Arg	Ser	Val	Cys	Asp	Lys	Val	Asp																	
										355											360											365

(2) INFORMATION FOR SEQ ID NO:1366:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 339 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..339

(D) OTHER INFORMATION: / Ceres Seq. ID 1569734

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1366:

Met	Lys	Pro	Lys	Ser	Lys	Val	Ala	Glu	Ser	Thr	Ala	Ala	Ser	Cys	Phe
1			5					10						15	
Leu	Val	Met	Ser	Leu	Leu	Cys	Ser	Cys	Ile	Ile	Gly	Asp	Gln	Met	Glu
			20					25					30		
Thr	Asn	Asn	Glu	Gly	Leu	Ser	Tyr	Ser	Tyr	Tyr	Glu	Lys	Thr	Cys	Pro
			35				40					45			
Lys	Val	Glu	Glu	Ile	Val	Arg	Ser	Ser	Leu	Ser	Ser	Met	Phe	Ile	Leu
			50				55					60			
Asp	Pro	Thr	Ser	Pro	Ala	Ala	Leu	Leu	Arg	Leu	Met	Phe	His	Asp	Cys
			65				70					75			80
Gln	Val	Gln	Gly	Cys	Asp	Ala	Ser	Ile	Leu	Leu	Glu	Pro	Ile	Arg	Asp
			85					90						95	
Gln	Gln	Phe	Thr	Glu	Leu	Asp	Ser	Ala	Lys	Asn	Phe	Gly	Ile	Arg	Lys
			100					105					110		
Arg	Asp	Leu	Val	Gly	Ser	Ile	Lys	Thr	Ser	Leu	Glu	Leu	Glu	Cys	Pro
			115				120						125		
Lys	Gln	Val	Ser	Cys	Ser	Asp	Val	Ile	Ile	Leu	Ala	Ala	Arg	Asp	Ala
			130				135					140			
Val	Ala	Leu	Thr	Gly	Gly	Pro	Leu	Ile	Ser	Val	Pro	Leu	Gly	Arg	Lys
			145				150					155			160
Asp	Ser	Leu	Ser	Thr	Pro	Ser	Lys	His	Val	Ala	Asp	Ser	Glu	Leu	Pro
			165					170					175		
Pro	Ser	Thr	Ala	Asp	Val	Asp	Thr	Thr	Leu	Ser	Leu	Phe	Ala	Asn	Lys
			180				185						190		
Gly	Met	Thr	Ile	Glu	Glu	Ser	Val	Ala	Ile	Met	Gly	Ala	His	Thr	Ile
			195				200					205			
Gly	Val	Thr	His	Cys	Asn	Asn	Val	Leu	Ser	Arg	Phe	Asp	Asn	Ala	Asn
			210				215					220			
Ala	Thr	Ser	Glu	Asn	Met	Asp	Pro	Arg	Phe	Gln	Thr	Phe	Leu	Arg	Val
			225				230					235			240
Ala	Cys	Pro	Glu	Phe	Ser	Pro	Thr	Ser	Gln	Ala	Ala	Glu	Ala	Thr	Phe
			245					250					255		
Val	Pro	Asn	Asp	Gln	Thr	Ser	Val	Ile	Phe	Asp	Thr	Ala	Tyr	Tyr	Asp
			260					265					270		

Asp Ala Ile Ala Gly Arg Gly Asn Leu Arg Ile Asp Ser Glu Ile Gly
275 280 285
Ala Asp Pro Arg Thr Arg Pro Phe Val Glu Ala Phe Ala Ala Asp Gln
290 295 300
Asp Arg Phe Phe Asn Ala Phe Ser Ser Ala Phe Val Lys Leu Ser Ser
305 310 315 320
Tyr Lys Val Leu Thr Gly Asn Glu Gly Val Ile Arg Ser Val Cys Asp
325 330 335
Lys Val Asp

(2) INFORMATION FOR SEQ ID NO:1367:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 321 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..321

(D) OTHER INFORMATION: / Ceres Seq. ID 1569735

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1367:

Met Ser Leu Leu Cys Ser Cys Ile Ile Gly Asp Gln Met Glu Thr Asn
1 5 10 15
Asn Glu Gly Leu Ser Tyr Ser Tyr Tyr Glu Lys Thr Cys Pro Lys Val
20 25 30
Glu Glu Ile Val Arg Ser Ser Leu Ser Ser Met Phe Ile Leu Asp Pro
35 40 45
Thr Ser Pro Ala Ala Leu Leu Arg Leu Met Phe His Asp Cys Gln Val
50 55 60
Gln Gly Cys Asp Ala Ser Ile Leu Leu Glu Pro Ile Arg Asp Gln Gln
65 70 75 80
Phe Thr Glu Leu Asp Ser Ala Lys Asn Phe Gly Ile Arg Lys Arg Asp
85 90 95
Leu Val Gly Ser Ile Lys Thr Ser Leu Glu Leu Glu Cys Pro Lys Gln
100 105 110
Val Ser Cys Ser Asp Val Ile Ile Leu Ala Ala Arg Asp Ala Val Ala
115 120 125
Leu Thr Gly Gly Pro Leu Ile Ser Val Pro Leu Gly Arg Lys Asp Ser
130 135 140
Leu Ser Thr Pro Ser Lys His Val Ala Asp Ser Glu Leu Pro Pro Ser
145 150 155 160
Thr Ala Asp Val Asp Thr Thr Leu Ser Leu Phe Ala Asn Lys Gly Met
165 170 175
Thr Ile Glu Glu Ser Val Ala Ile Met Gly Ala His Thr Ile Gly Val
180 185 190
Thr His Cys Asn Asn Val Leu Ser Arg Phe Asp Asn Ala Asn Ala Thr
195 200 205
Ser Glu Asn Met Asp Pro Arg Phe Gln Thr Phe Leu Arg Val Ala Cys
210 215 220
Pro Glu Phe Ser Pro Thr Ser Gln Ala Ala Glu Ala Thr Phe Val Pro
225 230 235 240
Asn Asp Gln Thr Ser Val Ile Phe Asp Thr Ala Tyr Tyr Asp Asp Ala
245 250 255
Ile Ala Gly Arg Gly Asn Leu Arg Ile Asp Ser Glu Ile Gly Ala Asp
260 265 270
Pro Arg Thr Arg Pro Phe Val Glu Ala Phe Ala Ala Asp Gln Asp Arg
275 280 285
Phe Phe Asn Ala Phe Ser Ser Ala Phe Val Lys Leu Ser Ser Tyr Lys
290 295 300
Val Leu Thr Gly Asn Glu Gly Val Ile Arg Ser Val Cys Asp Lys Val

305 310 315 320
Asp

(2) INFORMATION FOR SEQ ID NO:1368:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1672 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1672

(D) OTHER INFORMATION: / Ceres Seq. ID 1569744

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1368:

```
tacgaagcag aagacagaac ccaaaaacog acaaaagctcc cctattctct cgaaaattca 60
ttactcttaa agatggatgt tgtagggtggc tgatgactct tcttccctag catgaccttt 120
attgatacca agatgtgtat gagaagaacac aacatcaatt taacaacagt catagattct 180
aacgaagcca ttggtatgga acatgaatta gattctgcta gacatcaata ttcttcagtg 240
ctcactgcaa ttccattctt ctccgctaca ttgtttatct ctctctcttt gaaaatacat 300
atacgtgacg gggttcacga aagtcctttaa taacatttcc atacacaaaa cacaaatagt 360
ttagagattt gtctctaggg agattttagct atctctctgt tcaaaagatt ggctctaaag 420
tgcaagcttt tgctttaagt gggaagaaaa ggattgtgaa tcacggcatg tgtttttcca 480
aaggaatctt tgatctcggt tcacgcctgt ctgagaattt tatggatgat cctttgatcc 540
cgggattgct tgaatgtgtc ctgaagcagt gtctagcgct tgttcccggt gctaggttcc 600
catccatggg aagtgtatgc aagaaatgga gggtttgtgt ccagagcaaa gagtttatta 660
ctgtgagaag actcgtctgt atgcttgagg agtggcttta tgtcttaacg atgaatgctg 720
gtgggaaaaga taaccgatgg gaggtgatgg actggttggg acagaagcta tcatctcttc 780
caccgatgcc ttggtctgca aaaaacaggtt ttaaggttgt tgtggttgat gggaaacttc 840
ttgtcattgt ttgtgttgtt atgatcaacg gttcgttgtt tgatctgct gatgtttatc 900
agtatgatac atgcctcaat agctggagta gactagcaga cctggaagta gctcggatgt 960
atttctgttg ttctgaggtg aacgggcatg tttatgttgt ggagggtgat ggggttagtg 1020
gtgagagctt gtcaagtgca gaggtgTatG aTctgatctt gagacgtgta catggaactt 1080
catagagctc ttaaggcgct cgagggtggg ttgtttcGct agcgcttca acgggaagct 1140
atatgtgatg ggtgggaagt ccaacttcac tattgaaac tcaaaaattc ttgatgtgta 1200
caacactcaa tgtggctctt ggcattgtag caaaaaaggt ttaacgatgg tcaacagctca 1260
tggtgaagta gggaaaaagc tgttctgtat cgaactggaag aaccaccgga agatgtcggt 1320
gttcaatgcg gaagacgaac cctgggaagt ggtggctctt ccgctatcag gaagctcgag 1380
ggcggggttt cagtttggtta agctgagttg gaagcttttg ctattctcgt ctacggaaga 1440
aaccggtcaa tgtactttac tgtatgacct ggatgtctca ccaggcacac agtggaaaaa 1500
gtctgagatc aaactctctg ttcttctcgt atgcagtgtc acaatcacag cctgattgat 1560
accatttgtt tgtttacatt tctttttatg atccaaatcc aaagagagca ttgtcgtctc 1620
ttttaagttg atgataacac tgattttaa aagtggagag tgtttttggt gg
```

(2) INFORMATION FOR SEQ ID NO:1369:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 221 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..221

(D) OTHER INFORMATION: / Ceres Seq. ID 1569745

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1369:

```
Met Gln Ala Phe Ala Leu Ser Gly Lys Lys Arg Ile Val Asn His Gly
1 5 10 15
Met Cys Phe Ser Lys Gly Asn Leu Asp Leu Gly Ser Arg Leu Ser Glu
20 25 30
Asn Phe Met Asp Asp Pro Leu Ile Pro Gly Leu Pro Asp Asp Val Ala
35 40 45
```

```

Lys Gln Cys Leu Ala Leu Val Pro Arg Ala Arg Phe Pro Ser Met Gly
50 55 60
Ser Val Cys Lys Lys Trp Arg Phe Val Val Gln Ser Lys Glu Phe Ile
65 70 75 80
Thr Val Arg Arg Leu Ala Gly Met Leu Glu Glu Trp Leu Tyr Val Leu
85 90 95
Thr Met Asn Ala Gly Gly Lys Asp Asn Arg Trp Glu Val Met Asp Cys
100 105 110
Leu Gly Gln Lys Leu Ser Ser Leu Pro Pro Met Pro Gly Pro Ala Lys
115 120 125
Thr Gly Phe Lys Val Val Val Val Asp Gly Lys Leu Leu Val Ile Ala
130 135 140
Gly Cys Cys Met Ile Asn Gly Ser Leu Val Ala Ser Ala Asp Val Tyr
145 150 155 160
Gln Tyr Asp Thr Cys Leu Asn Ser Trp Ser Arg Leu Ala Asp Leu Glu
165 170 175
Val Ala Arg Tyr Asp Phe Ala Cys Ala Glu Val Asn Gly His Val Tyr
180 185 190
Val Val Gly Gly His Gly Val Asp Gly Glu Ser Leu Ser Ser Ala Glu
195 200 205
Val Tyr Asp Leu Ile Leu Arg Arg Val His Gly Leu Ser
210 215 220

```

(2) INFORMATION FOR SEQ ID NO:1370:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 205 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..205

(D) OTHER INFORMATION: / Ceres Seq. ID 1569746

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1370:

```

Met Cys Phe Ser Lys Gly Asn Leu Asp Leu Gly Ser Arg Leu Ser Glu
1 5 10 15
Asn Phe Met Asp Asp Pro Leu Ile Pro Gly Leu Pro Asp Asp Val Ala
20 25 30
Lys Gln Cys Leu Ala Leu Val Pro Arg Ala Arg Phe Pro Ser Met Gly
35 40 45
Ser Val Cys Lys Lys Trp Arg Phe Val Val Gln Ser Lys Glu Phe Ile
50 55 60
Thr Val Arg Arg Leu Ala Gly Met Leu Glu Glu Trp Leu Tyr Val Leu
65 70 75 80
Thr Met Asn Ala Gly Gly Lys Asp Asn Arg Trp Glu Val Met Asp Cys
85 90 95
Leu Gly Gln Lys Leu Ser Ser Leu Pro Pro Met Pro Gly Pro Ala Lys
100 105 110
Thr Gly Phe Lys Val Val Val Val Asp Gly Lys Leu Leu Val Ile Ala
115 120 125
Gly Cys Cys Met Ile Asn Gly Ser Leu Val Ala Ser Ala Asp Val Tyr
130 135 140
Gln Tyr Asp Thr Cys Leu Asn Ser Trp Ser Arg Leu Ala Asp Leu Glu
145 150 155 160
Val Ala Arg Tyr Asp Phe Ala Cys Ala Glu Val Asn Gly His Val Tyr
165 170 175
Val Val Gly Gly His Gly Val Asp Gly Glu Ser Leu Ser Ser Ala Glu
180 185 190
Val Tyr Asp Leu Ile Leu Arg Arg Val His Gly Leu Ser
195 200 205

```

(2) INFORMATION FOR SEQ ID NO:1371:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 187 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..187
(D) OTHER INFORMATION: / Ceres Seq. ID 1569747
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1371:
Met Asp Asp Pro Leu Ile Pro Gly Leu Pro Asp Asp Val Ala Lys Gln
1 5 10 15
Cys Leu Ala Leu Val Pro Arg Ala Arg Phe Pro Ser Met Gly Ser Val
20 25 30
Cys Lys Lys Trp Arg Phe Val Val Gln Ser Lys Glu Phe Ile Thr Val
35 40 45
Arg Arg Leu Ala Gly Met Leu Glu Glu Trp Leu Tyr Val Leu Thr Met
50 55 60
Asn Ala Gly Gly Lys Asp Asn Arg Trp Glu Val Met Asp Cys Leu Gly
65 70 75 80
Gln Lys Leu Ser Ser Leu Pro Pro Met Pro Gly Pro Ala Lys Thr Gly
85 90 95
Phe Lys Val Val Val Val Asp Gly Lys Leu Leu Val Ile Ala Gly Cys
100 105 110
Cys Met Ile Asn Gly Ser Leu Val Ala Ser Ala Asp Val Tyr Gln Tyr
115 120 125
Asp Thr Cys Leu Asn Ser Trp Ser Arg Leu Ala Asp Leu Glu Val Ala
130 135 140
Arg Tyr Asp Phe Ala Cys Ala Glu Val Asn Gly His Val Tyr Val Val
145 150 155 160
Gly Gly His Gly Val Asp Gly Glu Ser Leu Ser Ser Ala Glu Val Tyr
165 170 175
Asp Leu Ile Leu Arg Arg Val His Gly Leu Ser
180 185

(2) INFORMATION FOR SEQ ID NO:1372:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1412 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1412

(D) OTHER INFORMATION: / Ceres Seq. ID 1569748

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1372:

actcaatcgt	cattctctcg	gtatctctctc	ctcgaaagaa	gaatgcctgg	aattagaggt	60
ccttcggaat	actgcagga	accactctctg	cacctctctc	tcaaggtcaa	cgcaaggaa	120
ccttccaaag	ccgagcctcc	ccgctcggcc	ttagtctctac	cttatgtcac	tcccgtcgac	180
ctttctotaca	agcgaatca	tggtcccatc	cccattgttg	atcaccttca	aagctactcc	240
gtcacccotta	ctggattgat	ccagaaccgc	agaaaagctct	ttatcaaga	catcaggctcc	300
ctcccaaagt	acaatgtttac	tgctactctt	cttggtccgg	taacagaagg	actgccaatga	360
gcaaaagttag	gaatgttaga	ggtgttggat	gggatgtttc	tgctattggc	aacgctgtct	420
gggggtggggc	gaaactggcc	gatgttcttg	agcttctggg	gataccaaag	ctgactgott	480
ctaccaattt	aggagccaga	catgtttgagt	tcgttagtgt	tgatcgtctg	aaggaggaaa	540
atggggggccc	ttataaggcg	ctaatcactc	taagtcaagc	cacaaatctc	gaagcgggatg	600
ttctacccct	tatgatagta	atggagagac	cctgaacagg	gatcacggat	ttccgttaag	660
gggtgttgtc	cctggttgtga	ttggtgctcg	tatcagwcaa	atggcttgat	tcacatcaatg	720
tcatcgctga	agaaagccag	ggattctctc	tgcaaaaaga	ttacaaaatg	tttccacacct	780
ctgtcaattg	ggataaatc	aactgggtcc	ctaggagacc	gcaaatggat	ttccctgttcc	840

agagtgc	atgctctgtg	gaggtatgtc	aaatggtgaa	gcctggaaa	gtaagtatca	900
aaggtatgc	gggttcagga	ggtggacg	ggatagaaa	agtgacata	tccttggtg	960
gagga	ctgggtgaa	gcttctagaa	cgaggaacc	aggaagcag	tacatctcag	1020
aaacacgctc	cagtgacaaa	tggtcatggg	tggtgttga	agccaccatt	gatgtttcac	1080
agactacaga	ggtcatgcc	aaagcggttg	attcggcggc	gaatgttcaa	ccggaaaatg	1140
tggtgtcgtg	gtggaacctc	agaggagttc	tcaaCacttc	gtggcacctg	gtccttctcc	1200
ggcttgccca	ctctaaactg	tagaccaagt	taccactatg	ctgtcgtgtc	ctctttatct	1260
tttctttaag	aactaaaaa	tccttgaata	tgcttgcct	tggtgatctg	tgagagcaaa	1320
atactgttta	tagttaaata	aaatgggaaa	accatctgt	tgctatgtgg	tggattataa	1380
attatttatt	tatatgatag	aactgttatt	cg			

(2) INFORMATION FOR SEQ ID NO:1373:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 157 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..157

(D) OTHER INFORMATION: / Ceres Seq. ID 1569749

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1373:

Met	Gln	Lys	Asp	Tyr	Lys	Met	Phe	Pro	Pro	Ser	Val	Asn	Trp	Asp	Asn
1				5						10				15	
Ile	Asn	Trp	Ser	Ser	Arg	Arg	Pro	Gln	Met	Asp	Phe	Pro	Val	Gln	Ser
			20						25					30	
Ala	Ile	Cys	Ser	Val	Glu	Asp	Val	Gln	Met	Val	Lys	Pro	Gly	Lys	Val
			35				40					45			
Ser	Ile	Lys	Gly	Tyr	Ala	Val	Ser	Gly	Gly	Gly	Arg	Gly	Ile	Glu	Arg
			50				55				60				
Val	Asp	Ile	Ser	Leu	Asp	Gly	Gly	Lys	Asn	Trp	Val	Glu	Ala	Ser	Arg
			65			70				75				80	
Thr	Gln	Glu	Pro	Gly	Lys	Gln	Tyr	Ile	Ser	Glu	His	Ser	Ser	Ser	Asp
				85					90					95	
Lys	Trp	Ala	Trp	Val	Leu	Phe	Glu	Ala	Thr	Ile	Asp	Val	Ser	Gln	Thr
			100					105						110	
Thr	Glu	Val	Ile	Ala	Lys	Ala	Val	Asp	Ser	Ala	Ala	Asn	Val	Gln	Pro
			115				120					125			
Glu	Asn	Val	Glu	Ser	Val	Trp	Asn	Leu	Arg	Gly	Val	Leu	Asn	Thr	Ser
			130				135					140			
Trp	His	Arg	Val	Leu	Leu	Arg	Leu	Gly	His	Ser	Asn	Leu			
			145			150			155						

(2) INFORMATION FOR SEQ ID NO:1374:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 151 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..151

(D) OTHER INFORMATION: / Ceres Seq. ID 1569750

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1374:

Met	Phe	Pro	Pro	Ser	Val	Asn	Trp	Asp	Asn	Ile	Asn	Trp	Ser	Ser	Arg
1				5					10				15		
Arg	Pro	Gln	Met	Asp	Phe	Pro	Val	Gln	Ser	Ala	Ile	Cys	Ser	Val	Glu
			20					25					30		
Asp	Val	Gln	Met	Val	Lys	Pro	Gly	Lys	Val	Ser	Ile	Lys	Gly	Tyr	Ala
			35				40					45			
Val	Ser	Gly	Gly	Gly	Arg	Gly	Ile	Glu	Arg	Val	Asp	Ile	Ser	Leu	Asp

50	55	60
Gly Gly Lys Asn Trp Val Glu Ala Ser Arg Thr Gln Glu Pro Gly Lys		
65	70	75
Gln Tyr Ile Ser Glu His Ser Ser Ser Asp Lys Trp Ala Trp Val Leu		80
	85	90
Phe Glu Ala Thr Ile Asp Val Ser Gln Thr Thr Glu Val Ile Ala Lys		95
	100	105
Ala Val Asp Ser Ala Ala Asn Val Gln Pro Glu Asn Val Glu Ser Val		110
	115	120
Trp Asn Leu Arg Gly Val Leu Asn Thr Ser Trp His Arg Val Leu Leu		125
	130	135
Arg Leu Gly His Ser Asn Leu		140
	145	150

(2) INFORMATION FOR SEQ ID NO:1375:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 132 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..132
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569751

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1375:

Met Asp Phe Pro Val Gln Ser Ala Ile Cys Ser Val Glu Asp Val Gln	
1	5
Met Val Lys Pro Gly Lys Val Ser Ile Lys Gly Tyr Ala Val Ser Gly	
	20
Gly Gly Arg Gly Ile Glu Arg Val Asp Ile Ser Leu Asp Gly Gly Lys	
	35
Asn Trp Val Glu Ala Ser Arg Thr Gln Glu Pro Gly Lys Gln Tyr Ile	
	50
Ser Glu His Ser Ser Ser Asp Lys Trp Ala Trp Val Leu Phe Glu Ala	
	65
Thr Ile Asp Val Ser Gln Thr Thr Glu Val Ile Ala Lys Ala Val Asp	
	85
Ser Ala Ala Asn Val Gln Pro Glu Asn Val Glu Ser Val Trp Asn Leu	
	100
Arg Gly Val Leu Asn Thr Ser Trp His Arg Val Leu Leu Arg Leu Gly	
	115
His Ser Asn Leu	
	130

(2) INFORMATION FOR SEQ ID NO:1376:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1221 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1221

(D) OTHER INFORMATION: / Ceres Seq. ID 1569760

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1376:

aattctataat cattttgtga ctcttgagc actctctct ctttgtctct gtgactcaca	60
ttcatccaat ccaggaggca tgtcgacatc tgaggataaa ccggaataca tcagtagagt	120
agttcatcag gaggtgtgacg tggaaaAtcg tcgatagaag tcagaaggat aagmcgagg	180
aaaaagaaga aggraaaaggt ggattctctg ataaggtgaa agatttcatt catgcacattg	240
gtgagaaact cgagggaacc attggctttg ggaagccaac tgctgatgtc tctgcgattc	300
atatccctaa gatcaattct gagaggcgac atattgttgt ggatgtgctt gtcaagaacc	360

cgaatccagt	tccatccct	ctcatcgatg	tcaactacct	ggtcgagagc	gatgggagga	420
aactgggttc	tgggtttgatc	cgggatgctg	gaacactcaa	ggctcatgga	gaagaaactg	480
tgaagatacc	attgaagcttg	atNcTatgat	gacatcaaga	gcacttacaa	cgatatacaac	540
cccgggatga	tcatacctta	cagaatcaa	gttgatctga	ttgtggatgt	gccagattatg	600
ggaagactga	cattgccgct	ggagaaatgt	ggagagatcc	caattccaaa	gaaacctgat	660
gttgatatac	agaagattaa	gttccagaag	ttctcttttg	aggaaacctg	ggcgattctc	720
catgtgaggg	ttcagaacat	gaatgatctc	gactttgggg	tcaatgactt	ggactgtgaa	780
gtttggctct	gtgatgttaag	cattgggaaa	gcagagatcg	cggactcgat	caagcttgac	840
aaaaacggaa	gcggattgat	taatgtgccg	atgacattcc	gaccaaaagg	ctttggttct	900
gcgctttggg	atatgatttc	tggttaaagg	acagggtaca	caatcaaagg	taattattgat	960
gttgatacac	catttgagac	tatgaagctt	cttattatca	aggaaggtgg	agagaccctg	1020
ctgaagaagg	aagatgatga	tgacgacgat	gagtaataag	gaaacaaagt	gctgcagaga	1080
cagaatggtc	atagtacta	aatctccgat	cttgaaatgt	ctatttaaaa	ttaaaaaaa	1140
aaagaaaagac	ttgtttttgt	tgcttttga	taactgatgg	atcagacttt	tgaatagagc	1200
cgctcttttta	ttggactctt	t				

(2) INFORMATION FOR SEQ ID NO:1377:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 169 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..169

(D) OTHER INFORMATION: / Ceres Seq. ID 1569761

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1377:

Met	Ile	Ile	Pro	Tyr	Arg	Ile	Lys	Val	Asp	Leu	Ile	Val	Asp	Val	Pro
1			5					10						15	
Val	Leu	Gly	Arg	Leu	Thr	Leu	Pro	Leu	Glu	Lys	Cys	Gly	Glu	Ile	Pro
			20					25					30		
Ile	Pro	Lys	Lys	Pro	Asp	Val	Asp	Ile	Glu	Lys	Ile	Lys	Phe	Gln	Lys
			35				40					45			
Phe	Ser	Leu	Glu	Glu	Thr	Val	Ala	Ile	Leu	His	Val	Arg	Leu	Gln	Asn
			50				55				60				
Met	Asn	Asp	Phe	Asp	Leu	Gly	Leu	Asn	Asp	Leu	Asp	Cys	Glu	Val	Trp
			65			70			75					80	
Leu	Cys	Asp	Val	Ser	Ile	Gly	Lys	Ala	Glu	Ile	Ala	Asp	Ser	Ile	Lys
			85						90					95	
Leu	Asp	Lys	Asn	Gly	Ser	Gly	Leu	Ile	Asn	Val	Pro	Met	Thr	Phe	Arg
			100					105					110		
Pro	Lys	Asp	Phe	Gly	Ser	Ala	Leu	Trp	Asp	Met	Ile	Arg	Gly	Lys	Gly
			115				120					125			
Thr	Gly	Tyr	Thr	Ile	Lys	Gly	Asn	Ile	Asp	Val	Asp	Thr	Pro	Phe	Gly
			130				135					140			
Ala	Met	Lys	Leu	Pro	Ile	Ile	Lys	Glu	Gly	Gly	Glu	Thr	Arg	Leu	Lys
			145				150			155				160	
Lys	Glu	Asp	Asp	Asp	Asp	Asp	Asp	Glu							
															165

(2) INFORMATION FOR SEQ ID NO:1378:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 105 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..105

(D) OTHER INFORMATION: / Ceres Seq. ID 1569762

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1378:

Met Asn Asp Phe Asp Leu Gly Leu Asn Asp Leu Asp Cys Glu Val Trp
1 5 10 15
Leu Cys Asp Val Ser Ile Gly Lys Ala Glu Ile Ala Asp Ser Ile Lys
20 25 30
Leu Asp Lys Asn Gly Ser Gly Leu Ile Asn Val Pro Met Thr Phe Arg
35 40 45
Pro Lys Asp Phe Gly Ser Ala Leu Trp Asp Met Ile Arg Gly Lys Gly
50 55 60
Thr Gly Tyr Thr Ile Lys Gly Asn Ile Asp Val Asp Thr Pro Phe Gly
65 70 75 80
Ala Met Lys Leu Pro Ile Ile Lys Glu Gly Glu Thr Arg Leu Lys
85 90 95
Lys Glu Asp Asp Asp Asp Asp Glu
100 105

(2) INFORMATION FOR SEQ ID NO:1379:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1355 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1355
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569775

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1379:

aactctcttc	tcttctctag	tcttctcttc	tattatgcaa	aaggtctctt	tggccatgga	60
tacttctgct	ctagtaaatcc	atcagttctct	gtctcgcatc	aaactttctc	ctcccaaatc	120
tcttctcttc	tcttctcttc	ctgtcttctc	ccctgaatcc	ttaccgatca	gacggatcca	180
gtctgttttc	cgaggagcta	tatgtgcgcc	cgtacaaaga	aactacgaag	aaacgacctc	240
ctccgtggaa	gaggcagagg	aagatgatga	gtcatcatca	tcgtacggag	aagtgaacaa	300
gatacttggg	agccgaacgg	cgBgggaagg	agccatggag	tacctatcgc	agtggaagaa	360
cgccattctc	ccgtcgtggg	ttccatcgag	ctacatcgca	gcagacgtaG	tgtcggagta	420
cgagacaccc	tgtgtggacgg	cagctagaaa	agccgacgag	caggccctgt	cacagctcct	480
ggaggaccga	gacgtcgatg	ccgtggacga	aagcggccgg	acggctctgc	ttttcgtggc	540
aggtctgggg	tccggacaagt	gcgtaaaggct	tctggccggag	gctggagcgc	atctcgacca	600
ccgagacatg	aggggaggct	tgacggcgct	gcacatggcg	gctgttlaag	tgaggccgga	660
ggtgtgtggg	gcgctgtggg	agctggggag	tgatattgaa	gtggaagacg	agagaggggt	720
aacggcggtt	gaactagcga	gggagattct	gaagacgacg	ccgaagggga	atccgatcca	780
gttcggggag	agaatttggg	tagagaaagt	gatcaatgtc	ctggaaggac	aagtggtcca	840
gtaccccgag	gtggatgaga	ctgtagagaa	acgagggaaa	ggcaagacgc	ttgaatatct	900
ggtaagtgag	aaggacgggt	gagattgcga	gtgggtgaaa	ggtgtacacg	tgccgggaag	960
tgtggctaa	gactacgagg	atgggcttga	gtacgctgta	gcggagagtg	ttgatcgggaa	1020
gagggtggga	gacgatggga	agaccatcga	gtatcttctc	aatggactgc	atatgtctga	1080
tgccacttgg	gaagctcagg	acaatgtcga	ctctactctt	gttctactct	accaacaaca	1140
acaaccaata	aatgaatgat	tgattttgat	gattacattc	ttctcaattt	gctttctttt	1200
catatgtgtt	ggttcatctg	accggttcgg	ttggtaacga	coggtacatt	ttcattttct	1260
tttaagatgt	gattcttgat	gtttttggcc	ttttggggag	actatttgat	ttatatatcca	1320
tgctttgaat	ttgtcttccc	tttttgggga	gattc			

(2) INFORMATION FOR SEQ ID NO:1380:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 385 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..385
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569776

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1380:

DECEMBER 1971

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      (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 374 amino acids
          (B) TYPE: amino acid
          (C) STRANDEDNESS:
          (D) TOPOLOGY: linear
      (ii) MOLECULE TYPE: peptide
      (ix) FEATURE:

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(A) NAME/KEY: peptide
(B) LOCATION: 1..374
(D) OTHER INFORMATION: / Ceres Seq. ID 1569777

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1381:

Met	Gln	Lys	Val	Phe	Leu	Ala	Met	Asp	Thr	Cys	Ala	Leu	Val	Ile	His
1			5						10					15	
Gln	Ser	Leu	Ser	Arg	Ile	Lys	Leu	Ser	Pro	Pro	Lys	Ser	Ser	Ser	
			20					25					30		
Ser	Ser	Ser	Ser	Ala	Phe	Ser	Pro	Glu	Ser	Leu	Pro	Ile	Arg	Arg	Ile
			35				40					45			
Glu	Leu	Cys	Phe	Arg	Gly	Ala	Ile	Cys	Ala	Ala	Val	Gln	Arg	Asn	Tyr
			50			55					60				
Glu	Glu	Thr	Thr	Ser	Ser	Val	Glu	Glu	Ala	Glu	Glu	Asp	Asp	Glu	Ser
						70				75				80	
Ser	Ser	Ser	Tyr	Gly	Glu	Val	Asn	Lys	Ile	Ile	Gly	Ser	Arg	Thr	Ala
				85					90					95	
Xaa	Glu	Gly	Ala	Met	Glu	Tyr	Leu	Ile	Glu	Trp	Lys	Asp	Gly	His	Ser
			100					105						110	
Pro	Ser	Thr	Val	Pro	Ser	Ser	Tyr	Ile	Ala	Ala	Asp	Val	Val	Ser	Glu
			115				120					125			
Tyr	Glu	Thr	Pro	Trp	Trp	Thr	Ala	Ala	Arg	Lys	Ala	Asp	Glu	Gln	Ala
			130				135				140				
Leu	Ser	Gln	Leu	Leu	Glu	Asp	Arg	Asp	Val	Asp	Ala	Val	Asp	Glu	Ser
			145			150				155				160	
Gly	Arg	Thr	Ala	Leu	Leu	Phe	Val	Ala	Gly	Leu	Gly	Ser	Asp	Lys	Cys
				165					170					175	
Val	Arg	Leu	Leu	Ala	Glu	Ala	Gly	Ala	Asp	Leu	Asp	His	Arg	Asp	Met
			180					185						190	
Arg	Gly	Gly	Leu	Thr	Ala	Leu	His	Met	Ala	Ala	Gly	Tyr	Val	Arg	Pro
			195				200					205			
Glu	Val	Val	Glu	Ala	Leu	Val	Glu	Leu	Gly	Ala	Asp	Ile	Glu	Val	Glu
			210			215					220				
Asp	Glu	Arg	Gly	Leu	Thr	Ala	Leu	Glu	Leu	Ala	Arg	Glu	Ile	Leu	Lys
				230						235				240	
Thr	Thr	Pro	Lys	Gly	Asn	Pro	Met	Gln	Phe	Gly	Arg	Arg	Ile	Gly	Leu
				245					250					255	
Glu	Lys	Val	Ile	Asn	Val	Leu	Glu	Gly	Gln	Val	Phe	Glu	Tyr	Ala	Glu
			260					265					270		
Val	Asp	Glu	Ile	Val	Glu	Lys	Arg	Gly	Lys	Gly	Lys	Asp	Val	Glu	Tyr
			275				280					285			
Leu	Val	Arg	Trp	Lys	Asp	Gly	Gly	Asp	Cys	Glu	Trp	Val	Lys	Gly	Val
			290			295					300				
His	Val	Ala	Glu	Asp	Val	Ala	Lys	Asp	Tyr	Glu	Asp	Gly	Leu	Glu	Tyr
					310					315				320	
Ala	Val	Ala	Glu	Ser	Val	Ile	Gly	Lys	Arg	Val	Gly	Asp	Asp	Gly	Lys
				325					330					335	
Thr	Ile	Glu	Tyr	Leu	Val	Lys	Trp	Thr	Asp	Met	Ser	Asp	Ala	Thr	Trp
				340				345					350		
Glu	Pro	Gln	Asp	Asn	Val	Asp	Ser	Thr	Leu	Val	Leu	Leu	Tyr	Gln	Gln
			355				360						365		
Gln	Gln	Pro	Ile	Asn	Glu										
			370												

(2) INFORMATION FOR SEQ ID NO:1382:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 367 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..367

(D) OTHER INFORMATION: / Ceres Seq. ID 1569778

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1382:

Met Asp Thr Cys Ala Leu Val Ile His Gln Ser Leu Ser Arg Ile Lys
1 5 10 15
Leu Ser Pro Pro Lys Ser Ser Ser Ser Ser Ser Ser Ala Phe Ser
20 25 30
Pro Glu Ser Leu Pro Ile Arg Arg Ile Glu Leu Cys Phe Arg Gly Ala
35 40 45
Ile Cys Ala Ala Val Gln Arg Asn Tyr Glu Glu Thr Thr Ser Ser Val
50 55 60
Glu Glu Ala Glu Glu Asp Asp Glu Ser Ser Ser Ser Tyr Gly Glu Val
65 70 75 80
Asn Lys Ile Ile Gly Ser Arg Thr Ala Xaa Glu Gly Ala Met Glu Tyr
85 90 95
Leu Ile Glu Trp Lys Asp Gly His Ser Pro Ser Trp Val Pro Ser Ser
100 105 110
Tyr Ile Ala Ala Asp Val Val Ser Glu Tyr Glu Thr Pro Trp Trp Thr
115 120 125
Ala Ala Arg Lys Ala Asp Glu Gln Ala Leu Ser Gln Leu Leu Glu Asp
130 135 140
Arg Asp Val Asp Ala Val Asp Glu Ser Gly Arg Thr Ala Leu Leu Phe
145 150 155 160
Val Ala Gly Leu Gly Ser Asp Lys Cys Val Arg Leu Leu Ala Glu Ala
165 170 175
Gly Ala Asp Leu Asp His Arg Asp Met Arg Gly Gly Leu Thr Ala Leu
180 185 190
His Met Ala Ala Gly Tyr Val Arg Pro Glu Val Val Glu Ala Leu Val
195 200 205
Glu Leu Gly Ala Asp Ile Glu Val Glu Asp Glu Arg Gly Leu Thr Ala
210 215 220
Leu Glu Leu Ala Arg Glu Ile Leu Lys Thr Thr Pro Lys Gly Asn Pro
225 230 235 240
Met Gln Phe Gly Arg Arg Ile Gly Leu Glu Lys Val Ile Asn Val Leu
245 250 255
Glu Gly Gln Val Phe Glu Tyr Ala Glu Val Asp Glu Ile Val Glu Lys
260 265 270
Arg Gly Lys Gly Lys Asp Val Glu Tyr Leu Val Arg Trp Lys Asp Gly
275 280 285
Gly Asp Cys Glu Trp Val Lys Gly Val His Val Ala Glu Asp Val Ala
290 295 300
Lys Asp Tyr Glu Asp Gly Leu Glu Tyr Ala Val Ala Glu Ser Val Ile
305 310 315 320
Gly Lys Arg Val Gly Asp Asp Gly Lys Thr Ile Glu Tyr Leu Val Lys
325 330 335
Trp Thr Asp Met Ser Asp Ala Thr Trp Glu Pro Gln Asp Asn Val Asp
340 345 350
Ser Thr Leu Val Leu Leu Tyr Gln Gln Gln Pro Ile Asn Glu
355 360 365

(2) INFORMATION FOR SEQ ID NO:1383:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1287 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1287
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569787

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1383:

acactttctt tagccattta taaacgcttc attttctatat aaacatctct tatcttgttg	60
aaaatctctc gcagcttttg aaaaacatga cttttctaaa aatgaaaagc cttttctttc	120
tcttcaccat cctctctctc ctctcgaccc tcttcaccat ctccaacgca cggaagttta	180

atgtcggagg	cagtgccgcg	tgggttacaa	acccacctga	aaactacgaa	tcttggtctg	240
gcataaaccc	tttctctgtt	caogacactc	tctatttttag	ctatgctaa	ggagctgaat	300
cgggtcctaga	gggtgaacaag	gctgattacg	acgcttgtaa	tacaaagaat	ccgatcaaaa	360
gagtgagcaga	tggagattct	gagatctctc	ttgatcgtaa	tggtccggtt	tacttcatca	420
gtggcaatga	agataactgt	aagaagggtc	aaaagcttaa	tgctgtgttc	atatctgtca	480
ggattccatc	aacggctcag	tctctctcag	ccgctgcacc	gggaagctct	acgcggggat	540
caatgaactcc	gcggggagga	gcccaactcg	ctaaatcttc	ctccctctgt	tctccgcaga	600
cttctctctc	gggatcgact	actccgctcg	gaggagctca	ctcgctcaaa	tcttcatcag	660
ctgtctctcc	ggcgacttct	cctccaggat	caatggcgcc	taaactccgc	tcctctgttt	720
ctccgagcac	tTcAcGcacc	ggcaccacct	aaatccacgt	ccctgttttc	cccatctctc	780
gctccgatga	cttccaccgc	ggcaccgaat	gcacctaaat	catcttcaac	tattctctcg	840
tcttctgtc	cgatgacttc	accacotgga	tcaatggcac	ctaaatcttc	gtccctctgt	900
tcaaaactcac	ccacccgttc	tccatcgttg	gctccgggag	gctctacttc	ttcttcaccg	960
tcagattctc	cgtaaggctg	ggcgatgggt	cctTcaggag	atggtccatc	agccgctggg	1020
gatatctcta	cgccgggttg	agctccaggg	cagaaaaaat	cgctggcgaa	tgyatgacc	1080
gttatgtcka	ttactacggg	tytaagtttg	gttttgacca	tctttctgtc	agcttaagaa	1140
cacttggtgag	acttggttca	tgtcggatcc	gatttgttct	gtttcgggtt	gagtttccaa	1200
ctttgtttta	aattgwtttt	ggatccccat	ttgattctgt	attattcagt	atagttggat	1260
tgttttgtta	taataatag	acagtttc				

(2) INFORMATION FOR SEQ ID NO:1384:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 221 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..221

(D) OTHER INFORMATION: / Ceres Seq. ID 1569788

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1384:

Met	Thr	Phe	Leu	Lys	Met	Lys	Ser	Leu	Ser	Phe	Phe	Thr	Ile	Leu
1			5					10					15	
Leu	Ser	Leu	Ser	Thr	Leu	Phe	Thr	Ile	Ser	Asn	Ala	Arg	Lys	Phe
			20					25					30	Asn
Val	Gly	Gly	Ser	Gly	Ala	Trp	Val	Thr	Asn	Pro	Pro	Glu	Asn	Tyr
			35					40				45		Glu
Ser	Trp	Ser	Gly	Lys	Asn	Arg	Phe	Leu	Val	His	Asp	Thr	Leu	Tyr
			50					55				60		Phe
Ser	Tyr	Ala	Lys	Gly	Ala	Asp	Ser	Val	Leu	Glu	Val	Asn	Lys	Ala
			65					70				75		Asp
Tyr	Asp	Ala	Cys	Asn	Thr	Lys	Asn	Pro	Ile	Lys	Arg	Val	Asp	Asp
			85					90				95		Gly
Asp	Ser	Glu	Ile	Ser	Leu	Asp	Arg	Tyr	Gly	Pro	Phe	Tyr	Phe	Ile
			100					105				110		Ser
Gly	Asn	Glu	Asp	Asn	Cys	Lys	Lys	Gly	Gln	Lys	Leu	Asn	Val	Val
			115					120				125		Val
Ile	Ser	Ala	Arg	Ile	Pro	Ser	Thr	Ala	Gln	Ser	Pro	His	Ala	Ala
			130					135				140		Ala
Pro	Gly	Ser	Ser	Thr	Pro	Gly	Ser	Met	Thr	Pro	Pro	Gly	Gly	Ala
			145					150				155		His
Ser	Pro	Lys	Ser	Ser	Ser	Pro	Val	Ser	Pro	Thr	Thr	Ser	Pro	Gly
			165					170				175		Gly
Ser	Thr	Thr	Pro	Gly	Gly	Ala	His	Ser	Pro	Lys	Ser	Ser	Ser	Ala
			180					185				190		Ala
Val	Ser	Pro	Ala	Thr	Ser	Pro	Pro	Gly	Ser	Met	Ala	Pro	Lys	Ser
			195					200				205		Gly
Ser	Pro	Val	Ser	Pro	Thr	Thr	Ser	Arg	Thr	Gly	Thr	Thr		
			210					215				220		

(2) INFORMATION FOR SEQ ID NO:1385:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 216 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..216
(D) OTHER INFORMATION: / Ceres Seq. ID 1569789
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1385:

```
Met Lys Ser Leu Ser Phe Phe Phe Thr Ile Leu Leu Ser Leu Ser Thr
1      5      10      15
Leu Phe Thr Ile Ser Asn Ala Arg Lys Phe Asn Val Gly Gly Ser Gly
20     25     30
Ala Trp Val Thr Asn Pro Pro Glu Asn Tyr Glu Ser Trp Ser Gly Lys
35     40     45
Asn Arg Phe Leu Val His Asp Thr Leu Tyr Phe Ser Tyr Ala Lys Gly
50     55     60
Ala Asp Ser Val Leu Glu Val Asn Lys Ala Asp Tyr Asp Ala Cys Asn
65     70     75     80
Thr Lys Asn Pro Ile Lys Arg Val Asp Asp Gly Asp Ser Glu Ile Ser
85     90     95
Leu Asp Arg Tyr Gly Pro Phe Tyr Phe Ile Ser Gly Asn Glu Asp Asn
100    105    110
Cys Lys Lys Gly Gln Lys Leu Asn Val Val Val Ile Ser Ala Arg Ile
115    120    125
Pro Ser Thr Ala Gln Ser Pro His Ala Ala Pro Gly Ser Ser Thr
130    135    140
Pro Gly Ser Met Thr Pro Pro Gly Gly Ala His Ser Pro Lys Ser Ser
145    150    155    160
Ser Pro Val Ser Pro Thr Thr Ser Pro Pro Gly Ser Thr Thr Pro Pro
165    170    175
Gly Gly Ala His Ser Pro Lys Ser Ser Ser Ala Val Ser Pro Ala Thr
180    185    190
Ser Pro Pro Gly Ser Met Ala Pro Lys Ser Gly Ser Pro Val Ser Pro
195    200    205
Thr Thr Ser Arg Thr Gly Thr Thr
210    215
```

(2) INFORMATION FOR SEQ ID NO:1386:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 116 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..116
(D) OTHER INFORMATION: / Ceres Seq. ID 1569790
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1386:

```
Met Thr Ser Pro Pro Ala Pro Met Ala Pro Lys Ser Ser Ser Thr Ile
1      5      10      15
Pro Pro Ser Ser Ala Pro Met Thr Ser Pro Pro Gly Ser Met Ala Pro
20     25     30
Lys Ser Ser Ser Pro Val Ser Asn Ser Pro Thr Val Ser Pro Ser Leu
35     40     45
Ala Pro Gly Gly Ser Thr Ser Ser Ser Pro Ser Asp Ser Pro Ser Gly
50     55     60
Ser Ala Met Gly Pro Ser Gly Asp Gly Pro Ser Ala Ala Gly Asp Ile
65     70     75     80
Ser Thr Pro Ala Gly Ala Pro Gly Gln Lys Lys Ser Ser Ala Asn Xaa
```

85 90 95
Met Thr Val Met Xaa Ile Thr Thr Val Xaa Ser Leu Val Leu Thr Ile
100 105 110
Phe Leu Ser Ala
115

(2) INFORMATION FOR SEQ ID NO:1387:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1481 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1481
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569799

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1387:

gattactt	gt	tcttttgatt	tctccttcca	tagaaccgaa	ttgttttcag	ctcgagatt	60
ctcctgcgca	gagaacgatt	ttaatctatt	tctcctcgaga	gtagaaaatg	gctgagtggt		120
aagatattca	accctctgtc	tgtgacaagt	gaactggaat	gggttaagct	ggtttttgcgt		180
gggatgatgc	accgagggtc	gtgttttccaa	gtattgttgg	ccgtcctcgc	cacactggag		240
tgatgtgttg	aattggacac	aaggatgcat	atgttggcga	tgaagctcaa	tccaagcgtg		300
gtattctttac	cccttaaatc	ccattatgac	acggtattgt	caacaattgg	gatgatattg		360
aaaaaatctg	gcatactact	ttctacaatg	agctccgtgt	tgctcccag	gagcatccta		420
tctctgctac	tgaagcgctc	cttaacccaa	aggctaaccg	tgaagaagatg	actcagatca		480
tgtttgaac	cttttaacgct	ccggctatgt	atgtcgccat	tcaagctgtc	ctgtgcttt		540
atgctagtgg	ctgtactact	ggattgtgct	ttgactctgg	agatggtgtg	agtcacacgg		600
tccctatctc	tgaagggttac	gctctcccg	atgcaatcct	acgtcttgat	cttgacagtc		660
gtgacctcac	agatgctctg	atgaagatcc	tcaatgagcg	tggttactct	ttcaccacaa		720
cagctgagcg	tgaattgtc	agagacatca	aggagaagct	ttgctacatt	gctcttgact		780
atgacgagga	ctgtgagacg	gctaaaacca	gctctctgtg	agagaagaac	tatgagttac		840
ctgatggcca	agtgatcacc	attggatctg	agcgtttccg	ttgccccgag	gttctttacc		900
agccatctat	gatcggatg	gagaatgctg	gtatccatga	aaccacctac	aactccataa		960
tgaatgtga	tggtgacatc	agaaaggact	tgtatggtaa	catttgtgctc	agtgggtgaa		1020
caactatggt	ccctggaaat	gctgacagaa	tgagcaaaag	gattcactgt	ttggcaccga		1080
gcagcatgaa	gatcaaaagt	gttgacacct	ctgagaggaa	atactctgtc	tgatttggag		1140
gatccatctt	ggcctccctc	agtaaccttc	agcagatgtg	gatcgcaag	gcagaatatg		1200
atgagtcagg	ccctgcgatt	gttcaccgga	aatgcttttg	agcttgaagt	taagtctgct		1260
tccggagaag	ccctgggggt	tttccagttt	gtccttaactg	ggttttttac	ttcgtttctct		1320
gctcttcttt	gtttttcttc	ttcaatattt	tcagattctg	gcctaaagaca	ttttgaagaa		1380
tttacaattat	ctgttttgatg	tgtaaaactg	ttgtcttctg	ctcttttattt	attttggatg		1440
acacaactgt	gttttgatga	ataagaactc	ctgatttttc	c			

(2) INFORMATION FOR SEQ ID NO:1388:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 377 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..377
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569800

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1388:

Met	Ala	Asp	Gly	Glu	Asp	Ile	Gln	Pro	Leu	Val	Cys	Asp	Asn	Gly	Thr
1				5					10					15	
Gly	Met	Val	Lys	Ala	Gly	Phe	Ala	Gly	Asp	Asp	Ala	Pro	Arg	Ala	Val
				20					25					30	
Phe	Pro	Ser	Ile	Val	Gly	Arg	Pro	Gly	His	Thr	Gly	Val	Met	Val	Gly
				35					40					45	
Met	Gly	Gln	Lys	Asp	Ala	Tyr	Val	Gly	Asp	Glu	Ala	Gln	Ser	Lys	Arg

[illegible]

Asp Asp Met Glu Lys Ile Trp His His Thr Phe Tyr Asn Glu Leu Arg
65 70 75 80
Val Ala Pro Glu Glu His Pro Ile Leu Leu Thr Glu Ala Pro Leu Asn
85 90 95
Pro Lys Ala Asn Arg Glu Lys Met Thr Gln Ile Met Phe Glu Thr Phe
100 105 110
Asn Ala Pro Ala Met Tyr Val Ala Ile Gln Ala Val Leu Ser Leu Tyr
115 120 125
Ala Ser Gly Arg Thr Thr Gly Ile Val Leu Asp Ser Gly Asp Gly Val
130 135 140
Ser His Thr Val Pro Ile Tyr Glu Gly Tyr Ala Leu Pro His Ala Ile
145 150 155 160
Leu Arg Leu Asp Leu Ala Gly Arg Asp Leu Thr Asp Ala Leu Met Lys
165 170 175
Ile Leu Thr Glu Arg Gly Tyr Ser Phe Thr Thr Thr Ala Glu Arg Glu
180 185 190
Ile Val Arg Asp Ile Lys Glu Lys Leu Cys Tyr Ile Ala Leu Asp Tyr
195 200 205
Glu Gln Glu Leu Glu Thr Ala Lys Thr Ser Ser Ser Val Glu Lys Asn
210 215 220
Tyr Glu Leu Pro Asp Gly Gln Val Ile Thr Ile Gly Ser Glu Arg Phe
225 230 235 240
Arg Cys Pro Glu Val Leu Tyr Gln Pro Ser Met Ile Gly Met Glu Asn
245 250 255
Ala Gly Ile His Glu Thr Thr Tyr Asn Ser Ile Met Lys Cys Asp Val
260 265 270
Asp Ile Arg Lys Asp Leu Tyr Gly Asn Ile Val Leu Ser Gly Gly Thr
275 280 285
Thr Met Phe Pro Gly Ile Ala Asp Arg Met Ser Lys Glu Ile Thr Ala
290 295 300
Leu Ala Pro Ser Ser Met Lys Ile Lys Val Val Ala Pro Pro Glu Arg
305 310 315 320
Lys Tyr Ser Val Trp Ile Gly Gly Ser Ile Leu Ala Ser Leu Ser Thr
325 330 335
Phe Gln Gln Met Trp Ile Ala Lys Ala Glu Tyr Asp Glu Ser Gly Pro
340 345 350
Ser Ile Val His Arg Lys Cys Phe
355 360

(2) INFORMATION FOR SEQ ID NO:1390:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 332 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..332
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569802

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1390:

Met Val Gly Met Gly Gln Lys Asp Ala Tyr Val Gly Asp Glu Ala Gln
1 5 10 15
Ser Lys Arg Gly Ile Leu Thr Leu Lys Tyr Pro Ile Glu His Gly Ile
20 25 30
Val Asn Asn Trp Asp Asp Met Glu Lys Ile Trp His His Thr Phe Tyr
35 40 45
Asn Glu Leu Arg Val Ala Pro Glu Glu His Pro Ile Leu Leu Thr Glu
50 55 60
Ala Pro Leu Asn Pro Lys Ala Asn Arg Glu Lys Met Thr Gln Ile Met
65 70 75 80
Phe Glu Thr Phe Asn Ala Pro Ala Met Tyr Val Ala Ile Gln Ala Val

85 90 95
Leu Ser Leu Tyr Ala Ser Gly Arg Thr Thr Gly Ile Val Leu Asp Ser
100 105 110
Gly Asp Gly Val Ser His Thr Val Pro Ile Tyr Glu Gly Tyr Ala Leu
115 120 125
Pro His Ala Ile Leu Arg Leu Asp Leu Ala Gly Arg Asp Leu Thr Asp
130 135 140
Ala Leu Met Lys Ile Leu Thr Glu Arg Gly Tyr Ser Phe Thr Thr Thr
145 150 155 160
Ala Glu Arg Glu Ile Val Arg Asp Ile Lys Glu Lys Leu Cys Tyr Ile
165 170 175
Ala Leu Asp Tyr Glu Gln Glu Leu Glu Thr Ala Lys Thr Ser Ser Ser
180 185 190
Val Glu Lys Asn Tyr Glu Leu Pro Asp Gly Gln Val Ile Thr Ile Gly
195 200 205
Ser Glu Arg Phe Arg Cys Pro Glu Val Leu Tyr Gln Pro Ser Met Ile
210 215 220
Gly Met Glu Asn Ala Gly Ile His Glu Thr Tyr Asn Ser Ile Met
225 230 235 240
Lys Cys Asp Val Asp Ile Arg Lys Asp Leu Tyr Gly Asn Ile Val Leu
245 250 255
Ser Gly Gly Thr Thr Met Phe Pro Gly Ile Ala Asp Arg Met Ser Lys
260 265 270
Glu Ile Thr Ala Leu Ala Pro Ser Ser Met Lys Ile Lys Val Val Ala
275 280 285
Pro Pro Glu Arg Lys Tyr Ser Val Trp Ile Gly Gly Ser Ile Leu Ala
290 295 300
Ser Leu Ser Thr Phe Gln Gln Met Trp Ile Ala Lys Ala Glu Tyr Asp
305 310 315 320
Glu Ser Gly Pro Ser Ile Val His Arg Lys Cys Phe
325 330

(2) INFORMATION FOR SEQ ID NO:1391:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1439 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1439

(D) OTHER INFORMATION: / Ceres Seq. ID 1569807

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1391:

caagaaaaaa	aagaaacgat	gaggcttaat	ggggattcgg	gtccgggtca	ggatgaaccc	60
ggttcgagcg	gggtttcacg	cggaaatcaga	cgattcccg	tagcagctca	gcggagatt	120
atgagagctg	ctgagaaaga	cgatcaatac	gcttctttca	tccacgaagc	ttgccgcgat	180
gccttcgcgac	accttttcgg	tacaagaatc	gctcttgctt	accagaagga	gatgaagcta	240
cttggaacaga	tgcttttacta	tggtctttacg	acagggttcag	ggcaacaaac	tttaggagag	300
gaatattgtg	acattatata	gggtgcagg	ccttatggac	tctctctact	accagctaga	360
cgtgctttgt	tcatattgta	ccagaccgca	gttccatata	tcgcagagag	aattagcaat	420
cgagctgtcta	cgcaagcagt	cacctttgat	gagctctgat	agtttttttg	tgatagctat	480
atccactcac	caagaatgat	agatcttcca	tcttcatctc	aagttgaaac	ttcaactctc	540
gtagtatcta	gggttaaacga	tagacttaag	agatbttggc	accgagctWt	tcagcgatgg	600
cctgggtgttc	ttctgtttgc	cgcggaagtc	ttacaactgg	ttttgcgtgc	caatctgatg	660
cttttctact	ctgaaggttt	ttattatcat	atatcgaaac	gtgcatcccg	ggttcgcttat	720
gttttctatg	gaaagcaact	gaatcagaga	cctagatacc	aaattcttgg	ggttttccct	780
ctaattccaat	tgtgctatct	tgctgctgag	ggcttcgctc	ggagtaattt	gtcatctatc	840
acctgttcca	ttcagcaggc	tcttatagga	tcttatcaaa	cttcaggagg	gagaggttta	900
cctgtttttca	atgaagagg	gaatttgata	acttcggaag	ctgaaaagg	aaactgtgct	960
acctccgatt	caacttcaac	ggaggcagta	gggaaatgca	ctctctgctt	aagcaccgct	1020
cagcaccctaa	cggccaactc	ttgtgggtcat	gtgtttttgt	ggagctgcgat	tatggaatgg	1080

tgcaacgaga atcaagaatg cctcttttgt cgaacgcccc ataccattc aagtttggtt	1140
tgtttgtatc attctgattt ttaggcacaa tgggatcaac aaggacaggc actgcagaaa	1200
ggcaaaagcag ctaagacagt gacacctaa gacagtgcac ctgctacagg aatggaatct	1260
gcttcggcgt cagacttttt gagtaagatc aacaagttat gagagaagac agaataaata	1320
tattttcgac atcattctcg atcccatgcc tacctttttc tctatgat ttatgtcaga	1380
aaccacagag gtttggtgtt ttacatttca ttaaaaagag ttggagatgt taggtggtt	

(2) INFORMATION FOR SEQ ID NO:1392:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 387 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..387

(D) OTHER INFORMATION: / Ceres Seq. ID 1569808

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1392:

His Glu Lys Lys Glu Thr Met Arg Leu Asn Gly Asp Ser Gly Pro Gly	
1 5 10 15	
Gln Asp Glu Pro Gly Ser Ser Gly Phe His Gly Gly Ile Arg Arg Phe	
20 25 30	
Pro Leu Ala Ala Gln Pro Glu Ile Met Arg Ala Ala Glu Lys Asp Asp	
35 40 45	
Gln Tyr Ala Ser Phe Ile His Glu Ala Cys Arg Asp Ala Phe Arg His	
50 55 60	
Leu Phe Gly Thr Arg Ile Ala Leu Ala Tyr Gln Lys Glu Met Lys Leu	
65 70 75 80	
Leu Gly Gln Met Leu Tyr Tyr Val Leu Thr Thr Gly Ser Gly Gln Gln	
85 90 95	
Thr Leu Gly Glu Glu Tyr Cys Asp Ile Ile Gln Val Ala Gly Pro Tyr	
100 105 110	
Gly Leu Ser Pro Thr Pro Ala Arg Arg Ala Leu Phe Ile Leu Tyr Gln	
115 120 125	
Thr Ala Val Pro Tyr Ile Ala Glu Arg Ile Ser Thr Arg Ala Ala Thr	
130 135 140	
Gln Ala Val Thr Phe Asp Glu Ser Asp Glu Phe Phe Gly Asp Ser His	
145 150 155 160	
Ile His Ser Pro Arg Met Ile Asp Leu Pro Ser Ser Ser Gln Val Glu	
165 170 175	
Thr Ser Thr Ser Val Val Ser Arg Leu Asn Asp Arg Leu Lys Arg Xaa	
180 185 190	
Trp His Arg Ala Xaa Gln Arg Trp Pro Val Val Leu Pro Val Ala Arg	
195 200 205	
Glu Val Leu Gln Leu Val Leu Arg Ala Asn Leu Met Leu Phe Tyr Ser	
210 215 220	
Glu Gly Phe Tyr Tyr His Ile Ser Lys Arg Ala Ser Gly Val Arg Tyr	
225 230 235 240	
Val Phe Ile Gly Lys Gln Leu Asn Gln Arg Pro Arg Tyr Gln Ile Leu	
245 250 255	
Gly Val Phe Leu Leu Ile Gln Leu Cys Ile Leu Ala Ala Glu Gly Leu	
260 265 270	
Arg Arg Ser Asn Leu Ser Ser Ile Thr Ser Ser Ile Gln Gln Ala Ser	
275 280 285	
Ile Gly Ser Tyr Gln Thr Ser Gly Gly Arg Gly Leu Pro Val Leu Asn	
290 295 300	
Glu Glu Gly Asn Leu Ile Thr Ser Glu Ala Glu Lys Gly Asn Trp Ser	
305 310 315 320	
Thr Ser Asp Ser Thr Ser Thr Glu Ala Val Gly Lys Cys Thr Leu Cys	
325 330 335	
Leu Ser Thr Arg Gln His Pro Thr Ala Thr Pro Cys Gly His Val Phe	

340 345 350
Cys Trp Ser Cys Ile Met Glu Trp Cys Asn Glu Asn Gln Glu Cys Pro
355 360 365
Leu Cys Arg Thr Pro Asn Thr His Ser Ser Leu Val Cys Leu Tyr His
370 375 380
Ser Asp Phe
385

(2) INFORMATION FOR SEQ ID NO:1393:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 381 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..381
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569809

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1393:

Met Arg Leu Asn Gly Asp Ser Gly Pro Gly Gln Asp Glu Pro Gly Ser
1 5 10 15
Ser Gly Phe His Gly Gly Ile Arg Arg Phe Pro Leu Ala Ala Gln Pro
20 25 30
Glu Ile Met Arg Ala Ala Glu Lys Asp Asp Gln Tyr Ala Ser Phe Ile
35 40 45
His Glu Ala Cys Arg Asp Ala Phe Arg His Leu Phe Gly Thr Arg Ile
50 55 60
Ala Leu Ala Tyr Gln Lys Glu Met Lys Leu Leu Gly Gln Met Leu Tyr
65 70 75 80
Tyr Val Leu Thr Thr Gly Ser Gly Gln Gln Thr Leu Gly Glu Glu Tyr
85 90 95
Cys Asp Ile Ile Gln Val Ala Gly Pro Tyr Gly Leu Ser Pro Thr Pro
100 105 110
Ala Arg Arg Ala Leu Phe Ile Leu Tyr Gln Thr Ala Val Pro Tyr Ile
115 120 125
Ala Glu Arg Ile Ser Thr Arg Ala Ala Thr Gln Ala Val Thr Phe Asp
130 135 140
Glu Ser Asp Glu Phe Phe Gly Asp Ser His Ile His Ser Pro Arg Met
145 150 155 160
Ile Asp Leu Pro Ser Ser Ser Gln Val Glu Thr Ser Thr Ser Val Val
165 170 175
Ser Arg Leu Asn Asp Arg Leu Lys Arg Xaa Trp His Arg Ala Xaa Gln
180 185 190
Arg Trp Pro Val Val Leu Pro Val Ala Arg Glu Val Leu Gln Leu Val
195 200 205
Leu Arg Ala Asn Leu Met Leu Phe Tyr Ser Glu Gly Phe Tyr Tyr His
210 215 220
Ile Ser Lys Arg Ala Ser Gly Val Arg Tyr Val Phe Ile Gly Lys Gln
225 230 235 240
Leu Asn Gln Arg Pro Arg Tyr Gln Ile Leu Gly Val Phe Leu Leu Ile
245 250 255
Gln Leu Cys Ile Leu Ala Ala Glu Gly Leu Arg Arg Ser Asn Leu Ser
260 265 270
Ser Ile Thr Ser Ser Ile Gln Gln Ala Ser Ile Gly Ser Tyr Gln Thr
275 280 285
Ser Gly Gly Arg Gly Leu Pro Val Leu Asn Glu Glu Gly Asn Leu Ile
290 295 300
Thr Ser Glu Ala Glu Lys Gly Asn Trp Ser Thr Ser Asp Ser Thr Ser
305 310 315 320
Thr Glu Ala Val Gly Lys Cys Thr Leu Cys Leu Ser Thr Arg Gln His
325 330 335

Pro Thr Ala Thr Pro Cys Gly His Val Phe Cys Trp Ser Cys Ile Met
340 345 350
Glu Trp Cys Asn Glu Asn Gln Glu Cys Pro Leu Cys Arg Thr Pro Asn
355 360 365
Thr His Ser Ser Leu Val Cys Leu Tyr His Ser Asp Phe
370 375 380

(2) INFORMATION FOR SEQ ID NO:1394:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 347 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..347

(D) OTHER INFORMATION: / Ceres Seq. ID 1569810

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1394:

Met Arg Ala Ala Glu Lys Asp Asp Gln Tyr Ala Ser Phe Ile His Glu
1 5 10 15
Ala Cys Arg Asp Ala Phe Arg His Leu Phe Gly Thr Arg Ile Ala Leu
20 25 30
Ala Tyr Gln Lys Glu Met Lys Leu Leu Gly Gln Met Leu Tyr Tyr Val
35 40 45
Leu Thr Thr Gly Ser Gly Gln Gln Thr Leu Gly Glu Glu Tyr Cys Asp
50 55 60
Ile Ile Gln Val Ala Gly Pro Tyr Gly Leu Ser Pro Thr Pro Ala Arg
65 70 75 80
Arg Ala Leu Phe Ile Leu Tyr Gln Thr Ala Val Pro Tyr Ile Ala Glu
85 90 95
Arg Ile Ser Thr Arg Ala Ala Thr Gln Ala Val Thr Phe Asp Glu Ser
100 105 110
Asp Glu Phe Phe Gly Asp Ser His Ile His Ser Pro Arg Met Ile Asp
115 120 125
Leu Pro Ser Ser Ser Gln Val Glu Thr Ser Thr Ser Val Val Ser Arg
130 135 140
Leu Asn Asp Arg Leu Lys Arg Xaa Trp His Arg Ala Xaa Gln Arg Trp
145 150 155 160
Pro Val Val Leu Pro Val Ala Arg Glu Val Leu Gln Leu Val Leu Arg
165 170 175
Ala Asn Leu Met Leu Phe Tyr Ser Glu Gly Phe Tyr Tyr His Ile Ser
180 185 190
Lys Arg Ala Ser Gly Val Arg Tyr Val Phe Ile Gly Lys Gln Leu Asn
195 200 205
Gln Arg Pro Arg Tyr Gln Ile Leu Gly Val Phe Leu Leu Ile Gln Leu
210 215 220
Cys Ile Leu Ala Ala Glu Gly Leu Arg Arg Ser Asn Leu Ser Ser Ile
225 230 235 240
Thr Ser Ser Ile Gln Gln Ala Ser Ile Gly Ser Tyr Gln Thr Ser Gly
245 250 255
Gly Arg Gly Leu Pro Val Leu Asn Glu Glu Gly Asn Leu Ile Thr Ser
260 265 270
Glu Ala Glu Lys Gly Asn Trp Ser Thr Ser Asp Ser Thr Ser Thr Glu
275 280 285
Ala Val Gly Lys Cys Thr Leu Cys Leu Ser Thr Arg Gln His Pro Thr
290 295 300
Ala Thr Pro Cys Gly His Val Phe Cys Trp Ser Cys Ile Met Glu Trp
305 310 315 320
Cys Asn Glu Asn Gln Glu Cys Pro Leu Cys Arg Thr Pro Asn Thr His
325 330 335
Ser Ser Leu Val Cys Leu Tyr His Ser Asp Phe

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340 345
(2) INFORMATION FOR SEQ ID NO:1395:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1824 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..1824
(D) OTHER INFORMATION: / Ceres Seq. ID 1569815
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1395:
aagggtgacct tggctcttgg ttgaccatca aaaaactacaa cgctctttct ccgtaGgaaa 60
ggggaagcaa ataaattatc gaagcccact ggtttcggag ctgatcggtc tctattttct 120
ctttcataca tatctcaagc agataaagtt gatcggatgc tagaatggga ggaggattta 180
gagtttttga tttggtgagg ccattcttgg cttttctgcc tgaggttcag agtgcgtgata 240
ggaaggttcc attcagagag aaggttatct acactgtcat ctctctcttc atctttctgt 300
ctcgagtcga gctctctctt tatggaatcc attccaccac cggtgcggat ccattctatt 360
ggatgcgtgt cattcttggc tccaaccgtg gaactgtcat ggagctcggg attactctca 420
ttgttacatc tggacttggg atgcaactct tggctgggtc caagattatt gaggttgaca 480
acaatgttgc tgaggatcgt gccctcttga atggtgtcga gaagcttcta ggtattctga 540
ttgccattgt tgagcgtggt gcatatgttc tttctggaat gtatgggtccc gttggacagc 600
ttggtgttgg aaatgccatt ctgatcatcc ttacagctttt cttgtctgga atcatttgtta 660
ctgcgttga tgaactcctt cagaagggat atggctctcg atcaggaatc tcccttttca 720
ttgccaccaa cattttgtaa agcattatct ggaaggcatt tagcccaact accatcaaca 780
ccgggcgtgg agctgagttt gaaggtgctg ttaattgcact gtcccatatg ctgataacca 840
agtccaacaa ggttgcgggt ctccgccaag ctttctaacc gcaaaacctt ccaaatgtta 900
ccaacttggc tgccacagtc ttgatcttcc tgatttgtat ctacttccaa ggtttccgtg 960
tggtttggcc tgtgagatca aagaatgccc gtggacaaca ggttctttac ccaatcaagc 1020
tgtttacaac ctctaaacat cccatcatcc tccaatccgc cctgtctcca aatctttact 1080
tcatttctca gcttctctac cgggaagttca cgggaaattt ctttggtaac ctttgggac 1140
aatggaagaa atctgagtac agtggacaat ctattccagt tagtggtctg gcttacctca 1200
tcacagctcc agcaagtttc tctgacatgg cagctcaacc ctgccatgca ctggttctaca 1260
tcgtcttcat gctcactgct tgtgctcttt tctcaaaagc atggattgaa gtctctggat 1320
cttctgctag ggatgtagct aagcagctaa aggaacaaca aatggtgatg ccaggacaca 1380
gagaatcaaa cttacagaag gaactgaaca gatacatccc aacagcagca gcttttgag 1440
gagtttgtat cgggtgcactt accgttttgg ctgatttcat gggagccatc gggctcggaa 1500
ccggaattct gttggcggtc acgatcatat accagtatct cgagaccttt gagaaggaaa 1560
aagccagtga actcggcttc ttccgggttct aagttagctt aaagaagggt taaactttgc 1620
ctgaggcaaa aaagcagagc aagaagaggct ttgctctctg tgcccacctc aaacacagac 1680
aattttgtgt ggcacttggg ttgactactt ttttttgtt gttgttgaaa cgaatttttc 1740
tcattagtca tttatgtttt ttgttactt tttaacaagt aaaaaactta tgtgatagac 1800
gctttttcaa tgtatgtttc twgc
(2) INFORMATION FOR SEQ ID NO:1396:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 475 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..475
(D) OTHER INFORMATION: / Ceres Seq. ID 1569816
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1396:
Met Gly Gly Gly Phe Arg Val Leu His Leu Val Arg Pro Phe Leu Ala
1 5 10 15
Phe Leu Pro Glu Val Gln Ser Ala Asp Arg Lys Val Pro Phe Arg Glu
20 25 30
Lys Val Ile Tyr Thr Val Ile Ser Leu Phe Ile Phe Leu Val Cys Ser

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..409

(D) OTHER INFORMATION: / Ceres Seq. ID 1569817

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1397:

Met	Arg	Val	Ile	Leu	Ala	Ser	Asn	Arg	Gly	Thr	Val	Met	Glu	Leu	Gly
1			5					10					15		
Ile	Thr	Pro	Ile	Val	Thr	Ser	Gly	Leu	Val	Met	Gln	Leu	Leu	Ala	Gly
			20				25					30			
Ser	Lys	Ile	Ile	Glu	Val	Asp	Asn	Asn	Val	Arg	Glu	Asp	Arg	Ala	Leu
		35				40					45				
Leu	Asn	Gly	Ala	Gln	Lys	Leu	Leu	Gly	Ile	Leu	Ile	Ala	Ile	Gly	Glu
	50				55				60						
Ala	Val	Ala	Tyr	Val	Leu	Ser	Gly	Met	Tyr	Gly	Pro	Val	Gly	Gln	Leu
65			70						75					80	
Gly	Val	Gly	Asn	Ala	Ile	Leu	Ile	Ile	Leu	Gln	Leu	Phe	Phe	Ala	Gly
			85						90					95	
Ile	Ile	Val	Ile	Cys	Leu	Asp	Glu	Leu	Leu	Gln	Lys	Gly	Tyr	Gly	Leu
		100					105						110		
Gly	Ser	Gly	Ile	Ser	Leu	Phe	Ile	Ala	Thr	Asn	Ile	Cys	Gly	Ser	Ile
		115					120					125			
Ile	Trp	Lys	Ala	Phe	Ser	Pro	Thr	Thr	Ile	Asn	Thr	Gly	Arg	Gly	Ala
130					135						140				
Glu	Phe	Glu	Gly	Ala	Val	Ile	Ala	Leu	Phe	His	Met	Leu	Ile	Thr	Lys
145				150					155						160
Ser	Asn	Lys	Val	Ala	Ala	Leu	Arg	Gln	Ala	Phe	Tyr	Arg	Gln	Asn	Leu
			165					170					175		
Pro	Asn	Val	Thr	Asn	Leu	Leu	Ala	Thr	Val	Leu	Ile	Phe	Leu	Ile	Val
		180					185						190		
Ile	Tyr	Phe	Gln	Gly	Phe	Arg	Val	Val	Leu	Pro	Val	Arg	Ser	Lys	Asn
		195					200					205			
Ala	Arg	Gly	Gln	Gln	Gly	Ser	Tyr	Pro	Ile	Lys	Leu	Phe	Tyr	Thr	Ser
210					215						220				
Asn	Met	Pro	Ile	Ile	Leu	Gln	Ser	Ala	Leu	Val	Ser	Asn	Leu	Tyr	Phe
225					230					235					240
Ile	Ser	Gln	Leu	Leu	Tyr	Arg	Lys	Phe	Ser	Gly	Asn	Phe	Phe	Val	Asn
			245					250					255		
Leu	Leu	Gly	Gln	Trp	Lys	Glu	Ser	Glu	Tyr	Ser	Gly	Gln	Ser	Ile	Pro
		260					265					270			
Val	Ser	Gly	Leu	Ala	Tyr	Leu	Ile	Thr	Ala	Pro	Ala	Ser	Phe	Ser	Asp
		275					280					285			
Met	Ala	Ala	His	Pro	Phe	His	Ala	Leu	Phe	Tyr	Ile	Val	Phe	Met	Leu
290					295					300					
Thr	Ala	Cys	Ala	Leu	Phe	Ser	Lys	Thr	Trp	Ile	Glu	Val	Ser	Gly	Ser
305				310						315					320
Ser	Ala	Arg	Asp	Val	Ala	Lys	Gln	Leu	Lys	Glu	Gln	Gln	Met	Val	Met
			325					330					335		
Pro	Gly	His	Arg	Glu	Ser	Asn	Leu	Gln	Lys	Glu	Leu	Asn	Arg	Tyr	Ile
		340					345						350		
Pro	Thr	Ala	Ala	Ala	Phe	Gly	Gly	Val	Cys	Ile	Gly	Ala	Leu	Thr	Val
		355					360					365			
Leu	Ala	Asp	Phe	Met	Gly	Ala	Ile	Gly	Ser	Gly	Thr	Gly	Ile	Leu	Leu
		370				375					380				
Ala	Val	Thr	Ile	Ile	Tyr	Gln	Tyr	Phe	Glu	Thr	Phe	Glu	Lys	Glu	Lys
385					390					395					400
Ala	Ser	Glu	Leu	Gly	Phe	Phe	Gly	Phe							
					405										

(2) INFORMATION FOR SEQ ID NO:1398:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 397 amino acids

(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..397
(D) OTHER INFORMATION: / Ceres Seq. ID 1569818

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1398:
Met Glu Leu Gly Ile Thr Pro Ile Val Thr Ser Gly Leu Val Met Gln
1 5 10 15
Leu Leu Ala Gly Ser Lys Ile Ile Glu Val Asp Asn Asn Val Arg Glu
20 25 30
Asp Arg Ala Leu Leu Asn Gly Ala Gln Lys Leu Gly Ile Leu Ile
35 40 45
Ala Ile Gly Glu Ala Val Ala Tyr Val Leu Ser Gly Met Tyr Gly Pro
50 55 60
Val Gly Gln Leu Gly Val Gly Asn Ala Ile Leu Ile Ile Leu Gln Leu
65 70 75 80
Phe Phe Ala Gly Ile Ile Val Ile Cys Leu Asp Glu Leu Leu Gln Lys
85 90 95
Gly Tyr Gly Leu Gly Ser Gly Ile Ser Leu Phe Ile Ala Thr Asn Ile
100 105 110
Cys Glu Ser Ile Ile Trp Lys Ala Phe Ser Pro Thr Thr Ile Asn Thr
115 120 125
Gly Arg Gly Ala Glu Phe Glu Gly Ala Val Ile Ala Leu Phe His Met
130 135 140
Leu Ile Thr Lys Ser Asn Lys Val Ala Ala Leu Arg Gln Ala Phe Tyr
145 150 155 160
Arg Gln Asn Leu Pro Asn Val Thr Asn Leu Leu Ala Thr Val Leu Ile
165 170 175
Phe Leu Ile Val Ile Tyr Phe Gln Gly Phe Arg Val Val Leu Pro Val
180 185 190
Arg Ser Lys Asn Ala Arg Gly Gln Gln Gly Ser Tyr Pro Ile Lys Leu
195 200 205
Phe Tyr Thr Ser Asn Met Pro Ile Ile Leu Gln Ser Ala Leu Val Ser
210 215 220
Asn Leu Tyr Phe Ile Ser Gln Leu Leu Tyr Arg Lys Phe Ser Gly Asn
225 230 235 240
Phe Phe Val Asn Leu Leu Gly Gln Trp Lys Glu Ser Glu Tyr Ser Gly
245 250 255
Gln Ser Ile Pro Val Ser Gly Leu Ala Tyr Leu Ile Thr Ala Pro Ala
260 265 270
Ser Phe Ser Asp Met Ala Ala His Pro Phe His Ala Leu Phe Tyr Ile
275 280 285
Val Phe Met Leu Thr Ala Cys Ala Leu Phe Ser Lys Thr Trp Ile Glu
290 295 300
Val Ser Gly Ser Ser Ala Arg Asp Val Ala Lys Gln Leu Lys Glu Gln
305 310 315 320
Gln Met Val Met Pro Gly His Arg Glu Ser Asn Leu Gln Lys Glu Leu
325 330 335
Asn Arg Tyr Ile Pro Thr Ala Ala Ala Phe Gly Gly Val Cys Ile Gly
340 345 350
Ala Leu Thr Val Leu Ala Asp Phe Met Gly Ala Ile Gly Ser Gly Thr
355 360 365
Gly Ile Leu Leu Ala Val Thr Ile Ile Tyr Gln Tyr Phe Glu Thr Phe
370 375 380
Glu Lys Glu Lys Ala Ser Glu Leu Gly Phe Phe Gly Phe
385 390 395

(2) INFORMATION FOR SEQ ID NO:1399:
(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1853 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..1853
(D) OTHER INFORMATION: / Ceres Seq. ID 1569834
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1399:

```

attccttgat  attctttttg  tcacctatgc  cgcttttact  tcttgcgata  tctctgaggt  60
aattctggag  cagcataaac  aatcaattga  ttcatctctc  ttgataccaa  gttgtggaaa  120
ctctaggatt  gtttctgtga  tatctccaga  attgctgttt  tgattgaatt  taggtcgctt  180
agctcagttg  atagagcacc  acattttttg  tggtagaata  cgatttgatt  gacagctctt  240
aaccatgggt  aaagagaatt  ttcacatcaa  catttggtgc  attggccacg  tcgattctcg  300
aaagtgcacc  accactggag  acttgatcta  caagtggggt  ggtattgaca  agcgtgtcat  360
tgagaggttc  gagaaggagg  ctgctgagat  gaacaaggag  tccttcaagt  acgcatgggt  420
tttggacaaa  cttaaggctg  agcgtgagcg  tggatatcacc  attgacattg  ctctctggaa  480
gttcgagacc  accaagtact  actgcactgt  cattgatgct  cctggccattg  gtgatttcat  540
caagaacatg  atcactggta  cctcccagcg  tgatttgtct  gtccttatca  tcgactccac  600
cactgttggt  tttgaggtgc  gtatctccaa  ggaagggtcag  acccgtgagc  acgctctcct  660
tgcttttacc  ttgtgtgtga  aacagatgat  ctgctgttgt  aacaagatgg  atgccactac  720
cccacaatga  tccaaggcca  ggtacgatga  aattatcaag  gaggtgtctt  cctacttgaa  780
gaaggttggt  tacaaccccc  acaaaatccc  atttgtgccc  atctctggat  tcgagggtga  840
caacatgatt  gagagggtca  ccaaacctaga  ctggtacaag  ggaccaactc  ttcttgaggc  900
tcttgaccag  atcaacgagc  ccaagaggcc  atcagacaag  ccccttcgtc  tcccacttca  960
ggatgtctac  aagattgggt  gtattgggac  ggtgccagtg  ggacgtgttg  agactgggat  1020
gatcaagctc  ggtatgggtg  tgacotttgc  tcccaacagg  ttgaccaact  agctgcaagt  1080
tgttgagatg  caccacaggt  ctcttcttga  ggcacttcca  ggtgacaacg  ttgggttcaa  1140
gtttaagaat  gttgctgtca  aggatcttaa  gagagggtac  gtgcattcca  acctcaagga  1200
tgaccctgcc  aagggtgtcg  ctaacttca  ctcccagctc  atcatcaTda  accaccctgg  1260
tcagattggt  aacggttacg  cccagtcct  ggaatgccac  actctcaca  ttgcagtcaa  1320
gttctctgag  atcttgacca  agattgacag  cggttctggt  aaggagatgt  agaaggagcc  1380
caagttcttg  aagaatgggt  atgctggtat  ggtgaagatg  actccaacca  agcccatggt  1440
tgttgagacc  ttctctgagt  acccaccact  tggacgttgc  gctgtgaggg  acatgaggca  1500
gactgttgca  tgcggtgtta  tcaagatgt  tgacaagaag  gaccacaacc  gagccaaggt  1560
taccaggct  gccgtcaaga  aggtgtcgaa  gtgaaccatc  ctcaaaactc  tatctgccgc  1620
aggtgaatca  aaggacagtg  ttagttttat  tacaatagtt  tggtaatttg  tcgcgtgtct  1680
gtgtctctgt  ttcgttttct  ccccgtaaga  cggttgttct  cgtaattggg  tcttctgatc  1740
gaggtggcgg  atctacacac  acattcttcc  tgttttttgc  tttttatttg  ttttctcatt  1800
tgaaactgtt  taaaatttct  gttatatgaa  tgaatgtttt  ccttcgggtt  att

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(2) INFORMATION FOR SEQ ID NO:1400:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 449 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..449
(D) OTHER INFORMATION: / Ceres Seq. ID 1569835

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1400:

```

Met Gly Lys Glu Asn Phe His Ile Asn Ile Val Val Ile Gly His Val
1           5           10           15
Asp Ser Gly Lys Ser Thr Thr Thr Gly His Leu Ile Tyr Lys Leu Gly
20          25          30
Gly Ile Asp Lys Arg Val Ile Glu Arg Phe Glu Lys Glu Ala Ala Glu
35          40          45
Met Asn Lys Arg Ser Phe Lys Tyr Ala Trp Val Leu Asp Lys Leu Lys
50          55          60

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Ala Glu Arg Glu Arg Gly Ile Thr Ile Asp Ile Ala Leu Trp Lys Phe
65 70 75 80
Glu Thr Thr Lys Tyr Cys Thr Val Ile Asp Ala Pro Gly His Arg
85 90 95
Asp Phe Ile Lys Asn Met Ile Thr Gly Thr Ser Gln Ala Asp Cys Ala
100 105 110
Val Leu Ile Ile Asp Ser Thr Thr Gly Gly Phe Glu Ala Gly Ile Ser
115 120 125
Lys Asp Gly Gln Thr Arg Glu His Ala Leu Leu Ala Phe Thr Leu Gly
130 135 140
Val Lys Gln Met Ile Cys Cys Cys Asn Lys Met Asp Ala Thr Thr Pro
145 150 155 160
Lys Tyr Ser Lys Ala Arg Tyr Asp Glu Ile Ile Lys Glu Val Ser Ser
165 170 175
Tyr Leu Lys Lys Val Gly Tyr Asn Pro Asp Lys Ile Pro Phe Val Pro
180 185 190
Ile Ser Gly Phe Glu Gly Asp Asn Met Ile Glu Arg Ser Thr Asn Leu
195 200 205
Asp Trp Tyr Lys Gly Pro Thr Leu Leu Glu Ala Leu Asp Gln Ile Asn
210 215 220
Glu Pro Lys Arg Pro Ser Asp Lys Pro Leu Arg Leu Pro Leu Gln Asp
225 230 235 240
Val Tyr Lys Ile Gly Gly Ile Gly Thr Val Pro Val Gly Arg Val Glu
245 250 255
Thr Gly Met Ile Lys Pro Gly Met Val Val Thr Phe Ala Pro Thr Gly
260 265 270
Leu Thr Thr Glu Val Lys Ser Val Glu Met His His Glu Ser Leu Leu
275 280 285
Glu Ala Leu Pro Gly Asp Asn Val Gly Phe Asn Val Lys Asn Val Ala
290 295 300
Val Lys Asp Leu Lys Arg Gly Tyr Val Ala Ser Asn Ser Lys Asp Asp
305 310 315 320
Pro Ala Lys Gly Ala Ala Asn Phe Thr Ser Gln Val Ile Ile Xaa Asn
325 330 335
His Pro Gly Gln Ile Gly Asn Gly Tyr Ala Pro Val Leu Asp Cys His
340 345 350
Thr Ser His Ile Ala Val Lys Phe Ser Glu Ile Leu Thr Lys Ile Asp
355 360 365
Arg Arg Ser Gly Lys Glu Ile Glu Lys Glu Pro Lys Phe Leu Lys Asn
370 375 380
Gly Asp Ala Gly Met Val Lys Met Thr Pro Thr Lys Pro Met Val Val
385 390 395 400
Glu Thr Phe Ser Glu Tyr Pro Pro Leu Gly Arg Phe Ala Val Arg Asp
405 410 415
Met Arg Gln Thr Val Ala Val Gly Val Ile Lys Ser Val Asp Lys Lys
420 425 430
Asp Pro Thr Gly Ala Lys Val Thr Lys Ala Ala Val Lys Lys Gly Ala
435 440 445
Lys

(2) INFORMATION FOR SEQ ID NO:1401:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 401 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..401
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569836

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1401:

Met	Asn	Lys	Arg	Ser	Phe	Lys	Tyr	Ala	Trp	Val	Leu	Asp	Lys	Leu	Lys
1			5						10					15	
Ala	Glu	Arg	Glu	Arg	Gly	Ile	Thr	Ile	Asp	Ile	Ala	Leu	Trp	Lys	Phe
			20					25					30		
Glu	Thr	Thr	Lys	Tyr	Tyr	Cys	Thr	Val	Ile	Asp	Ala	Pro	Gly	His	Arg
		35					40					45			
Asp	Phe	Ile	Lys	Asn	Met	Ile	Thr	Gly	Thr	Ser	Gln	Ala	Asp	Cys	Ala
	50				55						60				
Val	Leu	Ile	Ile	Asp	Ser	Thr	Thr	Gly	Gly	Phe	Glu	Ala	Gly	Ile	Ser
	65				70					75				80	
Lys	Asp	Gly	Gln	Thr	Arg	Glu	His	Ala	Leu	Ala	Phe	Thr	Leu	Gly	
			85					90					95		
Val	Lys	Gln	Met	Ile	Cys	Cys	Cys	Asn	Lys	Met	Asp	Ala	Thr	Thr	Pro
		100						105					110		
Lys	Tyr	Ser	Lys	Ala	Arg	Tyr	Asp	Glu	Ile	Ile	Lys	Glu	Val	Ser	Ser
		115					120					125			
Tyr	Leu	Lys	Lys	Val	Gly	Tyr	Asn	Pro	Asp	Lys	Ile	Pro	Phe	Val	Pro
	130					135					140				
Ile	Ser	Gly	Phe	Glu	Gly	Asp	Asn	Met	Ile	Glu	Arg	Ser	Thr	Asn	Leu
	145				150					155				160	
Asp	Trp	Tyr	Lys	Gly	Pro	Thr	Leu	Leu	Glu	Ala	Leu	Asp	Gln	Ile	Asn
			165						170					175	
Glu	Pro	Lys	Arg	Pro	Ser	Asp	Lys	Pro	Leu	Arg	Leu	Pro	Leu	Gln	Asp
			180					185					190		
Val	Tyr	Lys	Ile	Gly	Gly	Ile	Gly	Thr	Val	Pro	Val	Gly	Arg	Val	Glu
		195					200					205			
Thr	Gly	Met	Ile	Lys	Pro	Gly	Met	Val	Val	Thr	Phe	Ala	Pro	Thr	Gly
	210					215					220				
Leu	Thr	Thr	Glu	Val	Lys	Ser	Val	Glu	Met	His	His	Glu	Ser	Leu	Leu
	225				230					235				240	
Glu	Ala	Leu	Pro	Gly	Asp	Asn	Val	Gly	Phe	Asn	Val	Lys	Asn	Val	Ala
			245						250					255	
Val	Lys	Asp	Leu	Lys	Arg	Gly	Tyr	Val	Ala	Ser	Asn	Ser	Lys	Asp	Asp
		260					265						270		
Pro	Ala	Lys	Gly	Ala	Ala	Asn	Phe	Thr	Ser	Gln	Val	Ile	Ile	Xaa	Asn
		275					280					285			
His	Pro	Gly	Gln	Ile	Gly	Asn	Gly	Tyr	Ala	Pro	Val	Leu	Asp	Cys	His
	290					295						300			
Thr	Ser	His	Ile	Ala	Val	Lys	Phe	Ser	Glu	Ile	Leu	Thr	Lys	Ile	Asp
	305				310					315				320	
Arg	Arg	Ser	Gly	Lys	Glu	Ile	Glu	Lys	Glu	Pro	Lys	Phe	Leu	Lys	Asn
			325						330					335	
Gly	Asp	Ala	Gly	Met	Val	Lys	Met	Thr	Pro	Thr	Lys	Pro	Met	Val	Val
		340						345					350		
Glu	Thr	Phe	Ser	Glu	Tyr	Pro	Pro	Leu	Gly	Arg	Phe	Ala	Val	Arg	Asp
		355					360					365			
Met	Arg	Gln	Thr	Val	Ala	Val	Gly	Val	Ile	Lys	Ser	Val	Asp	Lys	Lys
	370					375					380				
Asp	Pro	Thr	Gly	Ala	Lys	Val	Thr	Lys	Ala	Ala	Val	Lys	Lys	Gly	Ala
					390					395				400	
Lys															

(2) INFORMATION FOR SEQ ID NO:1402:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 348 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1..348
(D) OTHER INFORMATION: / Ceres Seq. ID 1569837

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1402:

```
Met Ile Thr Gly Thr Ser Gln Ala Asp Cys Ala Val Leu Ile Ile Asp
1      5      10      15
Ser Thr Thr Gly Gly Phe Glu Ala Gly Ile Ser Lys Asp Gly Gln Thr
20      25      30
Arg Glu His Ala Leu Leu Ala Phe Thr Leu Gly Val Lys Gln Met Ile
35      40      45
Cys Cys Cys Asn Lys Met Asp Ala Thr Thr Pro Lys Tyr Ser Lys Ala
50      55      60
Arg Tyr Asp Glu Ile Ile Lys Glu Val Ser Ser Tyr Leu Lys Lys Val
65      70      75      80
Gly Tyr Asn Pro Asp Lys Ile Pro Phe Val Pro Ile Ser Gly Phe Glu
85      90      95
Gly Asp Asn Met Ile Glu Arg Ser Thr Asn Leu Asp Trp Tyr Lys Gly
100      105      110
Pro Thr Leu Leu Glu Ala Leu Asp Gln Ile Asn Glu Pro Lys Arg Pro
115      120      125
Ser Asp Lys Pro Leu Arg Leu Pro Leu Gln Asp Val Tyr Lys Ile Gly
130      135      140
Gly Ile Gly Thr Val Pro Val Gly Arg Val Glu Thr Gly Met Ile Lys
145      150      155      160
Pro Gly Met Val Val Thr Phe Ala Pro Thr Gly Leu Thr Thr Glu Val
165      170      175
Lys Ser Val Glu Met His His Glu Ser Leu Leu Glu Ala Leu Pro Gly
180      185      190
Asp Asn Val Gly Phe Asn Val Lys Asn Val Ala Val Lys Asp Leu Lys
195      200      205
Arg Gly Tyr Val Ala Ser Asn Ser Lys Asp Asp Pro Ala Lys Gly Ala
210      215      220
Ala Asn Phe Thr Ser Gln Val Ile Ile Xaa Asn His Pro Gly Gln Ile
225      230      235      240
Gly Asn Gly Tyr Ala Pro Val Leu Asp Cys His Thr Ser His Ile Ala
245      250      255
Val Lys Phe Ser Glu Ile Leu Thr Lys Ile Asp Arg Arg Ser Gly Lys
260      265      270
Glu Ile Glu Lys Glu Pro Lys Phe Leu Lys Asn Gly Asp Ala Gly Met
275      280      285
Val Lys Met Thr Pro Thr Lys Pro Met Val Val Glu Thr Phe Ser Glu
290      295      300
Tyr Pro Pro Leu Gly Arg Phe Ala Val Arg Asp Met Arg Gln Thr Val
305      310      315      320
Ala Val Gly Val Ile Lys Ser Val Asp Lys Lys Asp Pro Thr Gly Ala
325      330      335
Lys Val Thr Lys Ala Ala Val Lys Lys Gly Ala Lys
340      345
```

(2) INFORMATION FOR SEQ ID NO:1403:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1442 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -
(B) LOCATION: 1..1442
(D) OTHER INFORMATION: / Ceres Seq. ID 1569846

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1403:

gccaatTTta aaccgagact gatgattgag aagaaactgt cgaagatgaa gatgagaacc

aaatcgattc	cggtttaggtc	ttcgcgcgaaa	tcctctgatt	cgctttctgga	tgatgaagct	120
aatgaaaaca	cacaatgtga	tgaagagat	gtgccacaca	agaagcgtcg	ttgtcttggg	180
actagttaga	ctactgatag	aggaggatct	gtagagccgc	tgctggactt	ggatccttgt	240
attgtatgtg	aagtttcaga	cgagcgggta	tctcgttgtt	cgcggggtga	ctgtcttctt	300
tcgttttcacg	gcgagtggtt	gtatgctgat	ttgggttagta	ctagttagta	tagtagtagt	360
agtagtgagg	atgttttcgaa	tcatttttgt	ccttatttgt	ggctcaagat	tgttgcaactg	420
aaatccaaaa	cattgagaga	aaagaccctt	gagggcgga	aggcggctcg	caagtatcta	480
gataaagaga	tgaamAgcAg	ggatgaggat	ataaccttat	ctgtgttagta	aattgggaaac	540
caagagcaga	gtacagacat	tgtaatgtat	catgagttac	aaggagagaa	ggatggctgt	600
tcatacaaac	cagatgcgga	tcaagggaaa	gtgggtactg	gtaaagtgtat	tgcagaaagt	660
ggagcatcag	agaaggtagc	tacagaaaaa	tttcaagacg	ctgaagtga	tgaacacagt	720
aaagatcaag	gtacaagaat	ctcgaatata	gggtgcaggga	aaaagagaga	ggtttctctg	780
tttttgccta	tgcagaatc	gttttcagca	aaagaacagg	accaggtcca	gcagaatgag	840
aagcgaagaa	ggagaggagt	gaaaattatc	gatagtga	tctcatcaaa	gggatacaat	900
aacgaacgaa	atggagaaga	tgtaaactgag	caggtaactt	catcggttca	agtaacctcc	960
ccgtcaggga	gaatgaggaa	ccagcaggga	acaaccaaa	tggctaagtc	aaagacagt	1020
agggacattt	ctttctttaa	gatggatcaa	agaaggaggc	tactttggac	gtacgaagaa	1080
gaagagatgc	taaaagtggt	agtgaggaaa	tttgagcagc	aagcaaacaa	gaacatgcc	1140
tggaggaaaa	ttctggaat	gggagagaag	gtgttccacg	aaacacgtac	tccagctgat	1200
ctcaaggaaa	atgtggaggag	catgggtcaag	attatgaaca	aaaacgaaca	aggcagcaca	1260
ctaaccctca	ctgctatgta	atcaaatagt	agtgtagact	attgagatga	agccagactt	1320
ggtgaactaa	tgtgggagtt	gatctgtgta	atagacaaaa	gttcctcctt	tacaagaact	1380
gactctact	ttttgtgtat	cttcgacatc	tttagatttt	cagtatagat	aatatatggc	1440
tc						

(2) INFORMATION FOR SEQ ID NO:1404:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 426 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..426

(D) OTHER INFORMATION: / Ceres Seq. ID 1569847

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1404:

Ala	Asn	Phe	Lys	Pro	Arg	Leu	Met	Ile	Glu	Lys	Lys	Leu	Ser	Lys	Met
1				5				10					15		
Lys	Met	Arg	Thr	Lys	Ser	Ile	Pro	Val	Arg	Ser	Ser	Arg	Lys	Ser	Leu
			20					25					30		
Asp	Ser	Leu	Leu	Asp	Asp	Glu	Ala	Asn	Glu	Asn	Thr	Gln	Cys	Asp	Glu
			35					40					45		
Arg	Asp	Val	Pro	His	Lys	Lys	Arg	Arg	Cys	Leu	Gly	Thr	Ser	Glu	Thr
			50					55					60		
Thr	Asp	Arg	Gly	Gly	Ser	Val	Glu	Pro	Leu	Leu	Asp	Leu	Asp	Ala	Cys
			65					70					75		
Ile	Val	Cys	Glu	Val	Ser	Asp	Glu	Arg	Val	Ser	Arg	Cys	Cys	Gly	Val
			85					90					95		
Asp	Cys	Leu	Leu	Ser	Phe	His	Gly	Glu	Cys	Leu	Tyr	Ala	Asp	Leu	Gly
			100					105					110		
Ser	Thr	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Glu	Asp	Val	Ser	Asn	Pro
			115					120					125		
Phe	Cys	Pro	Tyr	Cys	Trp	Leu	Lys	Ile	Val	Ala	Leu	Lys	Ser	Lys	Thr
			130					135					140		
Leu	Arg	Glu	Lys	Thr	Leu	Glu	Ala	Glu	Lys	Ala	Val	Cys	Lys	Tyr	Leu
			145					150					155		
Asp	Lys	Glu	Met	Xaa	Ser	Arg	Asp	Glu	Asp	Ile	Thr	Leu	Ser	Gly	Asp
			165					170					175		
Glu	Ile	Gly	Asn	Gln	Glu	Gln	Ser	Thr	Asp	Ile	Val	Ser	Asp	His	Glu
			180					185					190		
Leu	Gln	Gly	Glu	Lys	Asp	Gly	Cys	Ser	Ser	Lys	Pro	Asp	Ala	Asp	Gln

195 200 205
Gly Lys Val Gly Thr Gly Lys Val Ile Asp Glu Val Gly Ala Ser Glu
210 215 220
Lys Val Ala Thr Glu Lys Phe Gln Asp Ala Glu Asp Asp Glu Thr Ala
225 230 240
Lys Asp Gln Gly Thr Arg Ile Leu Asn Thr Gly Ala Gly Lys Lys Arg
245 250 255
Glu Val Ser Ser Phe Leu Ser Met Gln Glu Ser Phe Ser Ala Lys Glu
260 265 270
Gln Asp Gln Val Gln Gln Asn Glu Lys Arg Arg Arg Arg Gly Leu Lys
275 280 285
Ile Ile Asp Ser Asp Ile Ser Ser Lys Gly Ser Ser Asn Glu Arg Asn
290 295 300
Gly Glu Asp Val Thr Glu Gln Val Thr Ser Ser Val Gln Val Thr Ser
305 310 315 320
Pro Ser Gly Arg Met Arg Asn Gln Gln Ala Thr Thr Lys Val Ala Lys
325 330 335
Ser Lys Thr Val Arg Asp Ile Ser Phe Phe Lys Met Asp Gln Arg Arg
340 345 350
Arg Leu Leu Trp Thr Tyr Glu Glu Glu Glu Met Leu Lys Val Gly Val
355 360 365
Glu Lys Phe Ala Ala Glu Ala Asn Lys Asn Met Pro Trp Arg Lys Ile
370 375 380
Leu Glu Met Gly Glu Lys Val Phe His Glu Thr Arg Thr Pro Ala Asp
385 390 395 400
Leu Lys Asp Lys Trp Arg Ser Met Val Lys Ile Met Asn Lys Asn Glu
405 410 415
Gln Gly Ser Thr Leu Thr Pro Thr Ala Met
420 425

(2) INFORMATION FOR SEQ ID NO:1405:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 419 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..419
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569848

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1405:

Met Ile Glu Lys Lys Leu Ser Lys Met Lys Met Arg Thr Lys Ser Ile
1 5 10 15
Pro Val Arg Ser Ser Arg Lys Ser Leu Asp Ser Leu Leu Asp Asp Glu
20 25 30
Ala Asn Glu Asn Thr Gln Cys Asp Glu Arg Asp Val Pro His Lys Lys
35 40 45
Arg Arg Cys Leu Gly Thr Ser Glu Thr Thr Asp Arg Gly Gly Ser Val
50 55 60
Glu Pro Leu Leu Asp Leu Asp Ala Cys Ile Val Cys Glu Val Ser Asp
65 70 75 80
Glu Arg Val Ser Arg Cys Cys Gly Val Asp Cys Leu Leu Ser Phe His
85 90 95
Gly Glu Cys Leu Tyr Ala Asp Leu Gly Ser Thr Ser Ser Ser Ser
100 105 110
Ser Ser Ser Glu Asp Val Ser Asn Pro Phe Cys Pro Tyr Cys Trp Leu
115 120 125
Lys Ile Val Ala Leu Lys Ser Lys Thr Leu Arg Glu Lys Thr Leu Glu
130 135 140
Ala Glu Lys Ala Val Cys Lys Tyr Leu Asp Lys Glu Met Xaa Ser Arg
145 150 155 160

Asp Glu Asp Ile Thr Leu Ser Gly Asp Glu Ile Gly Asn Gln Glu Gln
165 170 175
Ser Thr Asp Ile Val Ser Asp His Glu Leu Gln Gly Glu Lys Asp Gly
180 185 190
Cys Ser Ser Lys Pro Asp Ala Asp Gln Gly Lys Val Gly Thr Gly Lys
195 200 205
Val Ile Asp Glu Val Gly Ala Ser Glu Lys Val Ala Thr Glu Lys Phe
210 215 220
Gln Asp Ala Glu Asp Asp Glu Thr Ala Lys Asp Gln Gly Thr Arg Ile
225 230 235 240
Leu Asn Thr Gly Ala Gly Lys Lys Arg Glu Val Ser Ser Phe Leu Ser
245 250 255
Met Gln Glu Ser Phe Ser Ala Lys Glu Gln Asp Gln Val Gln Gln Asn
260 265 270
Glu Lys Arg Arg Arg Arg Gly Leu Lys Ile Ile Asp Ser Asp Ile Ser
275 280 285
Ser Lys Gly Ser Ser Asn Glu Arg Asn Gly Glu Asp Val Thr Glu Gln
290 295 300
Val Thr Ser Ser Val Gln Val Thr Ser Pro Ser Gly Arg Met Arg Asn
305 310 315 320
Gln Gln Ala Thr Thr Lys Val Ala Lys Ser Lys Thr Val Arg Asp Ile
325 330 335
Ser Phe Phe Lys Met Asp Gln Arg Arg Arg Leu Leu Trp Thr Tyr Glu
340 345 350
Glu Glu Glu Met Leu Lys Val Gly Val Glu Lys Phe Ala Ala Glu Ala
355 360 365
Asn Lys Asn Met Pro Trp Arg Lys Ile Leu Glu Met Gly Glu Lys Val
370 375 380
Phe His Glu Thr Arg Thr Pro Ala Asp Leu Lys Asp Lys Trp Arg Ser
385 390 395 400
Met Val Lys Ile Met Asn Lys Asn Glu Gln Gly Ser Thr Leu Thr Pro
405 410 415
Thr Ala Met

(2) INFORMATION FOR SEQ ID NO:1406:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 411 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..411

(D) OTHER INFORMATION: / Ceres Seq. ID 1569849

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1406:

Met Lys Met Arg Thr Lys Ser Ile Pro Val Arg Ser Ser Arg Lys Ser
1 5 10
Leu Asp Ser Leu Leu Asp Asp Glu Ala Asn Glu Asn Thr Gln Cys Asp
20 25 30
Glu Arg Asp Val Pro His Lys Lys Arg Arg Cys Leu Gly Thr Ser Glu
35 40 45
Thr Thr Asp Arg Gly Gly Ser Val Glu Pro Leu Leu Asp Leu Asp Ala
50 55 60
Cys Ile Val Cys Glu Val Ser Asp Glu Arg Val Ser Arg Cys Cys Gly
65 70 75 80
Val Asp Cys Leu Leu Ser Phe His Gly Glu Cys Leu Tyr Ala Asp Leu
85 90 95
Gly Ser Thr Ser Ser Ser Ser Ser Ser Ser Glu Asp Val Ser Asn
100 105 110
Pro Phe Cys Pro Tyr Cys Trp Leu Lys Ile Val Ala Leu Lys Ser Lys

115	120	125
Thr Leu Arg Glu Lys	Thr Leu Glu Ala Glu Lys	Ala Val Cys Lys Tyr
130	135	140
Leu Asp Lys Glu Met	Xaa Ser Arg Asp	Glu Asp Ile Thr Leu Ser Gly
145	150	155
Asp Glu Ile Gly Asn	Gln Glu Gln Ser	Thr Asp Ile Val Ser Asp His
165	170	175
Glu Leu Gln Gly Glu	Lys Asp Gly Cys Ser	Ser Lys Pro Asp Ala Asp
180	185	190
Gln Gly Lys Val Gly	Thr Gly Lys Val Ile	Asp Glu Val Gly Ala Ser
195	200	205
Glu Lys Val Ala Thr	Glu Lys Phe Gln Asp	Ala Glu Asp Asp Glu Thr
210	215	220
Ala Lys Asp Gln Gly	Thr Arg Ile Leu Asn	Thr Gly Ala Gly Lys Lys
225	230	235
Arg Glu Val Ser Ser	Phe Leu Ser Met	Gln Glu Ser Phe Ser Ala Lys
245	250	255
Glu Gln Asp Gln Val	Gln Gln Asn Glu Lys	Arg Arg Arg Arg Gly Leu
260	265	270
Lys Ile Ile Asp Ser	Asp Ile Ser Ser	Lys Gly Ser Ser Asn Glu Arg
275	280	285
Asn Gly Glu Asp Val	Thr Glu Gln Val Thr	Ser Ser Val Gln Val Thr
290	295	300
Ser Pro Ser Gly Arg	Met Arg Asn Gln Gln	Ala Thr Thr Lys Val Ala
305	310	315
Lys Ser Lys Thr Val	Arg Asp Ile Ser Phe	Phe Lys Met Asp Gln Arg
325	330	335
Arg Arg Leu Leu Trp	Thr Tyr Glu Glu Glu	Met Leu Lys Val Gly
340	345	350
Val Glu Lys Phe Ala	Ala Glu Ala Asn Lys	Asn Met Pro Trp Arg Lys
355	360	365
Ile Leu Glu Met Gly	Glu Lys Val Phe His	Glu Thr Arg Thr Pro Ala
370	375	380
Asp Leu Lys Asp Lys	Trp Arg Ser Met Val	Lys Ile Met Asn Lys Asn
385	390	395
Glu Gln Gly Ser Thr	Leu Thr Pro Thr Ala	Met
405	410	

(2) INFORMATION FOR SEQ ID NO:1407:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 986 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..986
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569867

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1407:

aattcacc	ctccctccc	ttaagtctgt	ttgaattctgc	tgaattgttt	tataaagagt	60
tactttgcca	aaatggaaaa	tccggcggaag	agagtgttga	tgcacatccaa	cggcgacgag	120
gtgtcccgaa	acatcgcttt	ccatctagcc	aaacacgggtt	gcaagtgtgt	aatgatggga	180
aatgagggtt	ccctaaggag	catgttagag	attccattga	gggagccttc	cotgcccgatg	240
ttatagcact	cgacatggaa	tctgactctg	aagttgcttt	tcatgcgcgt	gtccaaaagg	300
catgggaact	ttccggccat	tctgatgctt	ttctcaactc	ttatacctac	caaggaaaagg	360
tgccagacat	tcttcaagtc	tctcaagatg	agttccacag	aatcacaaaag	atcaatctca	420
ccgcctcatg	gtttctctaa	aggctgtagc	cacaaggatg	aaggaccatg	gatcaggagg	480
ctccattgtc	ttcatggcca	ctatcgccag	cggagagagg	gcgctttacc	ctggcgctga	540
tgccatagct	tcaacttctg	ccgctattca	ccagctcgtt	cgggcatcag	ccatgagtct	600
cgggaagcac	aagatcacgg	tcaacatgat	ctctagaggg	ctgcatctg	atgatgagta	660
tacagcttct	gtgggaagag	accgagcaca	gaagctggtc	aaggacgctg	caccctcgg	720

ccagtggtc aaccgggaga cagacctcta ctccactgtt atctacttga tcagcgatgg 780
Ctcacgcttc atgacaggga ccaactgtctt ggtggatgga gcgcagtc cc ttacgcgacc 840
ccgtctcaaa tcttactatgt gatcaacgcg tagtattata attctatgtt gtgtgtaaaa 900
agtgaatatg aatcaagttt gaataacttt ggagggatta ataaccatg gaatcaatga 960
ttacataactt ttgacaagta tagaag

(2) INFORMATION FOR SEQ ID NO:1408:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 144 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..144

(D) OTHER INFORMATION: / Ceres Seq. ID 1569868

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1408:

Met	Val	Ser	Leu	Lys	Ala	Val	Ala	Thr	Arg	Met	Lys	Asp	His	Gly	Ser
1			5					10						15	
Gly	Gly	Ser	Ile	Val	Phe	Met	Ala	Thr	Ile	Ala	Ser	Gly	Glu	Arg	Ala
			20				25						30		
Leu	Tyr	Pro	Gly	Ala	Asp	Ala	Tyr	Ala	Ser	Thr	Ser	Ala	Ala	Ile	His
		35					40					45			
Gln	Leu	Val	Arg	Ala	Ser	Ala	Met	Ser	Leu	Gly	Lys	His	Lys	Ile	Arg
		50				55					60				
Val	Asn	Met	Ile	Ser	Arg	Gly	Leu	His	Leu	Asp	Asp	Glu	Tyr	Thr	Ala
		65			70					75				80	
Ser	Val	Gly	Arg	Asp	Arg	Ala	Gln	Lys	Leu	Val	Lys	Asp	Ala	Ala	Pro
			85					90					95		
Leu	Gly	Gln	Trp	Leu	Asn	Pro	Glu	Thr	Asp	Leu	Tyr	Ser	Thr	Val	Ile
			100				105						110		
Tyr	Leu	Ile	Ser	Asp	Gly	Ser	Arg	Phe	Met	Thr	Gly	Thr	Thr	Val	Leu
		115					120					125			
Val	Asp	Gly	Ala	Gln	Ser	Leu	Thr	Arg	Pro	Arg	Leu	Lys	Ser	Tyr	Met
	130					135					140				

(2) INFORMATION FOR SEQ ID NO:1409:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 134 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..134

(D) OTHER INFORMATION: / Ceres Seq. ID 1569869

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1409:

Met	Lys	Asp	His	Gly	Ser	Gly	Gly	Ser	Ile	Val	Phe	Met	Ala	Thr	Ile
1				5				10						15	
Ala	Ser	Gly	Glu	Arg	Ala	Leu	Tyr	Pro	Gly	Ala	Asp	Ala	Tyr	Ala	Ser
			20					25					30		
Thr	Ser	Ala	Ala	Ile	His	Gln	Leu	Val	Arg	Ala	Ser	Ala	Met	Ser	Leu
		35					40					45			
Gly	Lys	His	Lys	Ile	Arg	Val	Asn	Met	Ile	Ser	Arg	Gly	Leu	His	Leu
		50				55					60				
Asp	Asp	Glu	Tyr	Thr	Ala	Ser	Val	Gly	Arg	Asp	Arg	Ala	Gln	Lys	Leu
	65				70				75					80	
Val	Lys	Asp	Ala	Ala	Pro	Leu	Gly	Gln	Trp	Leu	Asn	Pro	Glu	Thr	Asp
				85					90					95	

Leu Tyr Ser Thr Val Ile Tyr Leu Ile Ser Asp Gly Ser Arg Phe Met
100 105 110
Thr Gly Thr Thr Val Leu Val Asp Gly Ala Gln Ser Leu Thr Arg Pro
115 120 125
Arg Leu Lys Ser Tyr Met
130

(2) INFORMATION FOR SEQ ID NO:1410:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 122 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..122

(D) OTHER INFORMATION: / Ceres Seq. ID 1569870

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1410:

Met Ala Thr Ile Ala Ser Gly Glu Arg Ala Leu Tyr Pro Gly Ala Asp
1 5 10 15
Ala Tyr Ala Ser Thr Ser Ala Ala Ile His Gln Leu Val Arg Ala Ser
20 25 30
Ala Met Ser Leu Gly Lys His Lys Ile Arg Val Asn Met Ile Ser Arg
35 40
Gly Leu His Leu Asp Asp Glu Tyr Thr Ala Ser Val Gly Arg Asp Arg
50 55 60
Ala Gln Lys Leu Val Lys Asp Ala Ala Pro Leu Gly Gln Trp Leu Asn
65 70 75 80
Pro Glu Thr Asp Leu Tyr Ser Thr Val Ile Tyr Leu Ile Ser Asp Gly
85 90 95
Ser Arg Phe Met Thr Gly Thr Thr Val Leu Val Asp Gly Ala Gln Ser
100 105 110
Leu Thr Arg Pro Arg Leu Lys Ser Tyr Met
115 120

(2) INFORMATION FOR SEQ ID NO:1411:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1573 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -

- (B) LOCATION: 1..1573

(D) OTHER INFORMATION: / Ceres Seq. ID 1569871

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1411:

ctctctctct ctctctccct ctctaaactgt atctctctct tcttcttcaa ccttcagact 60
ttcttagttg caactctcat tcaattgttc aattctctctg taataaatcaa agcttttttg 120
aatcttttctt cggcgagata ttctttcacc ggcgcaagct tctcttgagc gtgattcatc 180
actgggtttg cattttttcc tgggtgggtat tcttcaaatg gtccaaagct ccgacctttt 240
cttctcttaga atctgattac tggaaatcttg aagctggaga gactcagatt tatatggttt 300
caagactcgt tgagctcaatc attgagttgt gtagaagaaa ggtttggttt tcttctccgt 360
ttaagtgggt ttgggttttg taggatttgg tgtaactcgg gagataaaga aagatgaata 420
tgagtgattt aggttgggat gatgaagata aatcgggtgt tagtgcgtgt ttaggcatt 480
tagcttctga ttttctctga gcaaacctcta attcgaatca gaatctcttt cttgttatgg 540
gaactcatga tactctgaat aagaagctct ctagtctcgt tgatttggcca aactcggaga 600
atttcagctg gaactacgct attttctggc aacaaacctat gtctagatcc ggacaaacag 660
tcttaggttg gggagatggg tgttgcgcag agcctaataa ggaagaggaa tcaaaagtgt 720
ttaggtctta taattttaac aacatggggg cagaggaaga gacatggcaa gatatgagga 780
agagagtggt gcagaagctt cataggttgt ttggtggatc tgatgaagac aattatgctt 840
tgagcttaga gaaagtact gctactgaga ttttctctt agcttccatg tattttctt 900

tcaatcacgg	tgaaggcgg	cctggggaggt	gttattcttc	agggaacat	gtgtggctct	960
ctgatcggt	taactctgag	tctgactatt	gtttcaggtc	ttttatggcg	aaatctgcgg	1020
gaatcagaga	gatcggtatg	gttctctactg	atgctgggtg	tcttgagcgt	ggttctgttt	1080
ggctcttggc	tgaaaacatt	ggctgtgtta	agtctgttca	agctttgttc	atgaggagag	1140
ttacgcaacc	agtaatgggtg	acttcaaaca	ctaacatgac	tggaggggatt	cacaagcctt	1200
tcggggcagg	tttgagtgga	gCtcacgggt	atcctaagaa	gctcgaagtg	agaagaaact	1260
tggatgagag	atcactcct	caaagttggg	aaggctataa	taacaataaa	gggtccaacat	1320
ttgggttacac	acctcagagg	gatgatgtga	aagtgcctaga	gaatgtgaat	atggttgtag	1380
ataataacaa	ttacaagacg	cagattgagt	ttgcgggatc	atcagttgct	gcttcttcga	1440
atccatctac	aaacactcag	caagaaaaat	cagaatcttg	tacagagaaa	agaccagtga	1500
gcttgtagc	aggagcagga	atagtttctg	ttgttgatga	gaagagaccg	agaaaagagag	1560
ggagaaagcc	tgc					

(2) INFORMATION FOR SEQ ID NO:1412:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 386 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..386
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569872

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1412:

Met	Asn	Met	Ser	Asp	Leu	Gly	Trp	Asp	Asp	Glu	Asp	Lys	Ser	Val	Val
1			5					10						15	
Ser	Ala	Val	Leu	Gly	His	Leu	Ala	Ser	Asp	Phe	Leu	Arg	Ala	Asn	Ser
			20					25					30		
Asn	Ser	Asn	Gln	Asn	Leu	Phe	Leu	Val	Met	Gly	Thr	Asp	Asp	Thr	Leu
		35				40						45			
Asn	Lys	Lys	Leu	Ser	Ser	Leu	Val	Asp	Trp	Pro	Asn	Ser	Glu	Asn	Phe
		50				55					60				
Ser	Trp	Asn	Tyr	Ala	Ile	Phe	Trp	Gln	Gln	Thr	Met	Ser	Arg	Ser	Gly
65			70							75				80	
Gln	Gln	Val	Leu	Gly	Trp	Gly	Asp	Gly	Cys	Cys	Arg	Glu	Pro	Asn	Glu
			85						90					95	
Glu	Glu	Glu	Ser	Lys	Val	Val	Arg	Ser	Tyr	Asn	Phe	Asn	Asn	Met	Gly
			100					105					110		
Ala	Glu	Glu	Glu	Thr	Trp	Gln	Asp	Met	Arg	Lys	Arg	Val	Leu	Gln	Lys
			115					120				125			
Leu	His	Arg	Leu	Phe	Gly	Gly	Ser	Asp	Glu	Asp	Asn	Tyr	Ala	Leu	Ser
			130			135					140				
Leu	Glu	Lys	Val	Thr	Ala	Thr	Glu	Ile	Phe	Phe	Leu	Ala	Ser	Met	Tyr
145					150				155					160	
Phe	Phe	Phe	Asn	His	Gly	Glu	Gly	Gly	Pro	Gly	Arg	Cys	Tyr	Ser	Ser
			165						170					175	
Gly	Lys	His	Val	Trp	Leu	Ser	Asp	Ala	Val	Asn	Ser	Glu	Ser	Asp	Tyr
			180					185					190		
Cys	Phe	Arg	Ser	Phe	Met	Ala	Lys	Ser	Ala	Gly	Ile	Arg	Thr	Ile	Val
			195				200					205			
Met	Val	Pro	Thr	Asp	Ala	Gly	Val	Leu	Glu	Leu	Gly	Ser	Val	Trp	Ser
			210			215						220			
Leu	Pro	Glu	Asn	Ile	Gly	Leu	Val	Lys	Ser	Val	Gln	Ala	Leu	Phe	Met
225					230					235				240	
Arg	Arg	Val	Thr	Gln	Pro	Val	Met	Val	Thr	Ser	Asn	Thr	Asn	Met	Thr
			245						250					255	
Gly	Gly	Ile	His	Lys	Leu	Phe	Gly	Gln	Asp	Leu	Ser	Gly	Ala	His	Ala
			260					265					270		
Tyr	Pro	Lys	Lys	Leu	Glu	Val	Arg	Arg	Asn	Leu	Asp	Glu	Arg	Phe	Thr
			275				280					285			
Pro	Gln	Ser	Trp	Glu	Gly	Tyr	Asn	Asn	Lys	Gly	Pro	Thr	Phe	Gly	

(2) INFORMATION FOR SEQ ID NO:1413:

(A) LENGTH: 384 amino acids

(C) STRANDEDNESS:

(D) TOPOLOGY: lin

MOLECULE TYPE: peptide

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(11) MOLECULE TYPE: peptide
(12) FEATURE:
```

(A) NAME/KEY: peptide
(B) LOCATION: 1 384

(B) LOCATION: 1..384
(D) OTHER INFORMATION:

SEQUENCE DESCRIPTION: SEQ ID NO:1413:

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:1413:
Ser Asp Lys Gly Trp Asp Asp Glu Asp Lys Se

Met	Ser	Asp	Leu	Gly	Trp	Asp	Asp	Glu	Asp	Lys	Ser	Val	Val	Asn	Ala
1			5					10					15		
Val	Leu	Gly	20	Leu	Ala	Ser	Asp	Phe	Leu	Arg	Ala	Asn	Ser	Asn	Ser
			His					25				30			
Asn	Gln	Asn	Leu	Phe	Leu	Val	Met	Gly	Thr	Asp	Asp	Thr	Leu	Asn	Lys
		35					40					45			
Lys	Leu	Ser	Ser	Leu	Val	Asp	Trp	Pro	Asn	Ser	Glu	Asn	Phe	Ser	Trp
	50					55					60				
Asn	Tyr	Ala	Ile	Phe	Trp	Gln	Gln	Thr	Met	Ser	Arg	Ser	Gly	Gln	Gln
65					70					75					80
Val	Leu	Gly	Trp	Gly	Asp	Gly	Cys	Cys	Arg	Glu	Pro	Asn	Glu	Glu	Glu
				85					90				95		
Glu	Ser	Lys	Val	Val	Arg	Ser	Tyr	Asn	Phe	Asn	Asn	Met	Gly	Ala	Glu
			100					105					110		
Glu	Glu	Thr	Trp	Gln	Asp	Met	Arg	Lys	Arg	Val	Leu	Gln	Lys	Leu	His
			115				120					125			
Arg	Leu	Phe	Gly	Gly	Ser	Asp	Glu	Asp	Asn	Tyr	Ala	Leu	Ser	Leu	Glu
	130					135					140				
Lys	Val	Thr	Ala	Thr	Glu	Ile	Phe	Phe	Leu	Ala	Ser	Met	Tyr	Phe	Phe
145					150					155					160
Phe	Asn	His	Gly	Glu	Gly	Gly	Pro	Gly	Arg	Cys	Tyr	Ser	Ser	Gly	Lys
				165					170					175	
His	Val	Trp	Leu	Ser	Asp	Ala	Val	Asn	Ser	Ser	Glu	Ser	Asp	Tyr	Cys
			180					185						190	
Arg	Ser	Phe	Met	Ala	Lys	Ser	Ala	Gly	Ile	Arg	Thr	Ile	Val	Met	Val
		195					200					205			
Pro	Thr	Asp	Ala	Gly	Val	Leu	Glu	Leu	Gly	Ser	Val	Trp	Ser	Leu	Pro
	210					215						220			
Glu	Asn	Ile	Gly	Leu	Val	Lys	Ser	Val	Gln	Ala	Leu	Phe	Met	Arg	Arg
225					230					235					240
Val	Thr	Gln	Pro	Val	Met	Val	Thr	Ser	Asn	Thr	Asn	Met	Thr	Gly	Gly
				245					250					255	
Ile	His	Lys	Leu	Phe	Gly	Gln	Asp	Leu	Ser	Gly	Ala	His	Ala	Tyr	Pro
		260						265					270		
Lys	Lys	Leu	Glu	Val	Arg	Arg	Asn	Leu	Asp	Glu	Arg	Phe	Thr	Pro	Gln
		275					280					285			

Ser	Trp	Glu	Gly	Tyr	Asn	Asn	Asn	Lys	Gly	Pro	Thr	Phe	Gly	Tyr	Thr
290					295						300				
Pro	Gln	Arg	Asp	Asp	Val	Lys	Val	Leu	Glu	Asn	Val	Asn	Met	Val	Val
305					310					315				320	
Asp	Asn	Asn	Asn	Tyr	Lys	Thr	Gln	Ile	Glu	Phe	Ala	Gly	Ser	Ser	Val
				325					330					335	
Ala	Ala	Ser	Ser	Asn	Pro	Ser	Thr	Asn	Thr	Gln	Gln	Glu	Lys	Ser	Glu
				340					345				350		
Ser	Cys	Thr	Glu	Lys	Arg	Pro	Val	Ser	Leu	Leu	Ala	Gly	Ala	Gly	Ile
		355					360					365			
Val	Ser	Val	Val	Asp	Glu	Lys	Arg	Pro	Arg	Lys	Arg	Gly	Arg	Lys	Pro
370					375						380				

(2) INFORMATION FOR SEQ ID NO:1414:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 345 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..345

(D) OTHER INFORMATION: / Ceres Seq. ID 1569874

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1414:

Met	Gly	Thr	Asp	Asp	Thr	Leu	Asn	Lys	Lys	Leu	Ser	Ser	Leu	Val	Asp
1			5					10					15		
Trp	Pro	Asn	Ser	Glu	Asn	Phe	Ser	Trp	Asn	Tyr	Ala	Ile	Phe	Trp	Gln
			20					25					30		
Gln	Thr	Met	Ser	Arg	Ser	Gly	Gln	Gln	Val	Leu	Gly	Trp	Gly	Asp	Gly
		35					40					45			
Cys	Cys	Arg	Glu	Pro	Asn	Glu	Glu	Glu	Ser	Lys	Val	Val	Arg	Ser	
	50					55				60					
Tyr	Asn	Phe	Asn	Asn	Met	Gly	Ala	Glu	Glu	Glu	Thr	Trp	Gln	Asp	Met
	65				70					75				80	
Arg	Lys	Arg	Val	Leu	Gln	Lys	Leu	His	Arg	Leu	Phe	Gly	Gly	Ser	Asp
			85						90				95		
Glu	Asp	Asn	Tyr	Ala	Leu	Ser	Leu	Glu	Lys	Val	Thr	Ala	Thr	Glu	Ile
			100					105					110		
Phe	Phe	Leu	Ala	Ser	Met	Tyr	Phe	Phe	Phe	Asn	His	Gly	Glu	Gly	Gly
		115					120					125			
Pro	Gly	Arg	Cys	Tyr	Ser	Ser	Gly	Lys	His	Val	Trp	Leu	Ser	Asp	Ala
	130					135					140				
Val	Asn	Ser	Glu	Ser	Asp	Tyr	Cys	Phe	Arg	Ser	Phe	Met	Ala	Lys	Ser
	145				150				155					160	
Ala	Gly	Ile	Arg	Thr	Ile	Val	Met	Val	Pro	Thr	Asp	Ala	Gly	Val	Leu
			165						170					175	
Glu	Leu	Gly	Ser	Val	Trp	Ser	Leu	Pro	Glu	Asn	Ile	Gly	Leu	Val	Lys
			180					185					190		
Ser	Val	Gln	Ala	Leu	Phe	Met	Arg	Arg	Val	Thr	Gln	Pro	Val	Met	Val
		195					200					205			
Thr	Ser	Asn	Thr	Asn	Met	Thr	Gly	Gly	Ile	His	Lys	Leu	Phe	Gly	Gln
	210					215					220				
Asp	Leu	Ser	Gly	Ala	His	Ala	Tyr	Pro	Lys	Lys	Leu	Glu	Val	Arg	Arg
	225				230					235					240
Asn	Leu	Asp	Glu	Arg	Phe	Thr	Pro	Gln	Ser	Trp	Glu	Gly	Tyr	Asn	Asn
			245						250					255	
Asn	Lys	Gly	Pro	Thr	Phe	Gly	Tyr	Thr	Pro	Gln	Arg	Asp	Asp	Val	Lys
			260				265						270		
Val	Leu	Glu	Asn	Val	Asn	Met	Val	Val	Asp	Asn	Asn	Asn	Tyr	Lys	Thr

	275		280		285
Gln Ile Glu Phe Ala Gly Ser Ser Val Ala Ala Ser Ser Asn Pro Ser					
290	295	300			
Thr Asn Thr Gln Gln Glu Lys Ser Glu Ser Cys Thr Glu Lys Arg Pro					
305	310	315	320		
Val Ser Leu Leu Ala Gly Ala Gly Ile Val Ser Val Val Asp Glu Lys					
	325	330	335		
Arg Pro Arg Lys Arg Gly Arg Lys Pro					
	340	345			

(2) INFORMATION FOR SEQ ID NO:1415:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1215 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1215
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569897

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1415:

ggttaaAttt	gtttctctctg	atcgaaaagg	aatcagtttta	ggtcttttgcc	tcctctctcc	60
ggccagctca	attctcgtatc	aaaggtgacg	tgatataatg	aagcagatgt	tttggggaac	120
cagagtctctg	taaatagaaa	ccttcacgcg	acgttgaaag	gttttttgaga	cgaatatagg	180
aggagaagat	gggatgtgtt	tcttcttctg	tccgggttga	ggacattgat	gagtcacatg	240
atccaaacag	ctctgtctat	aggaactgtc	cctgcataag	atgccttctg	cataatttcc	300
ttaacctgtc	tatttcggct	ttcagaagag	gggaaactcg	ctctctccca	tcttcggctc	360
aagctactgc	atcgataact	tctctctctt	cacacgataa	ctttttgtct	gaagcattcc	420
gttctactcc	aaagcctctg	ccttatgatg	ctgatcctag	atacttcocg	tcactcgtct	480
caaggcgagg	gaagggttca	agtcattctc	atgaggaagt	tgaaccttta	agaagcgata	540
cgatgcgaga	tcttgaatct	tccgggttag	gaggggtcaa	atgggctaat	aataagtcga	600
ccctctctga	taaaagtctc	aaagaagagt	actctagtta	atccagtctc	aggattttga	660
gatcaaggtc	caagtcata	atggccgact	ctgaaaaaat	gtatatattg	tctgaagacg	720
aaagtgtctg	cccaacttgt	cttgaagaat	atcacatcga	gaaccocaa	attgtgacaa	780
aatgttcaca	ccatttccac	cttagttgca	tttatgatgt	gatggagaga	agtgtaaaact	840
gtccagctcg	cggaaaaggt	atggaaattca	acgaaacacc	gtgatcatcg	accattgatc	900
cgtgtccctg	atctgaactg	aaaccgggga	agatgacaag	gcaatgcaag	gaatataatt	960
tgtaaatatt	gctttgtttg	tttgtgaata	ttttcattta	caatggtaaa	tatatgaagc	1020
agaaaaggag	aaactgtttc	tctgcacacg	tttaagtttc	tgagaaattt	taacttccat	1080
gaacaagaaa	gcaatgtttc	ttcttttaag	gactttttct	catgaaatgc	ctctgtgttt	1140
gtattctcta	gtcagtcata	aaaactctta	catcattgtc	gttatataaa	taaatttttc	1200
tttttttatg	tggttc					

(2) INFORMATION FOR SEQ ID NO:1416:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 231 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..231
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569898

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1416:

Met Gly Cys Val Ser Ser Cys Phe Arg Val Glu Asp Ile Asp Glu Tyr					
1	5	10	15		
Met Asn Pro Asn Ser Ser Val Tyr Arg Asn Cys Pro Cys Ile Arg Cys					
	20	25	30		
Leu Ala His Asn Phe Leu Asn Leu Tyr Ile Ser Val Phe Arg Arg Gly					
	35	40	45		
Glu Thr Arg Ser Leu Pro Ser Ser Val Gln Ala Thr Ala Ser Ile Thr					

(2) INFORMATION FOR SEQ ID NO:1417:

(A) LENGTH: 215 amino acids

(A) LENGTH: 215 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(A) NAME/KEY: peptide

(B) LOCATION: 1..215

(D) OTHER INFORMATION: / Ceres Seq. ID 1569899

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1417:

Met	Asn	Pro	Asn	Ser	Ser	Val	Tyr	Arg	Asn	Cys	Pro	Cys	Ile	Arg	Cys
1			5						10					15	
Leu	Ala	His	Asn	Phe	Leu	Asn	Leu	Tyr	Ile	Ser	Val	Phe	Arg	Arg	Gly
			20					25					30		
Glu	Thr	Arg	Ser	Leu	Pro	Ser	Ser	Val	Gln	Ala	Thr	Ala	Ser	Ile	Thr
		35					40					45			
Ser	Ser	Ser	Ser	His	Asp	Asn	Phe	Leu	Ser	Glu	Ala	Phe	Arg	Ser	Thr
		50				55					60				
Pro	Arg	Pro	Leu	Pro	Tyr	Asp	Ala	Asp	Pro	Arg	Tyr	Phe	Arg	Ser	Leu
65					70					75					80
Val	Ser	Arg	Arg	Glu	Lys	Gly	Ser	Ser	His	Ser	His	Glu	Glu	Val	Glu
				85					90					95	
Pro	Leu	Arg	Ser	Asp	Ser	Asp	Ala	Asp	Ser	Glu	Ser	Phe	Gly	Val	Gly
				100				105					110		
Gly	Cys	Lys	Trp	Ala	Asn	Asn	Lys	Ser	Thr	Leu	Ser	Asp	Lys	Asp	Ser
		115					120					125			
Lys	Glu	Glu	Tyr	Ser	Ser	Lys	Ser	Ser	Leu	Arg	Ile	Leu	Arg	Ser	Arg
		130				135					140				
Ser	Lys	Ser	Ile	Met	Ala	Asp	Ser	Glu	Asn	Met	Tyr	Ile	Leu	Ser	Glu
145					150					155					160
Asp	Glu	Asp	Val	Cys	Pro	Thr	Cys	Leu	Glu	Glu	Tyr	Thr	Ser	Glu	Asn
				165					170					175	
Pro	Lys	Ile	Val	Thr	Lys	Cys	Ser	His	His	Phe	His	Leu	Ser	Cys	Ile
			180					185					190		
Tyr	Glu	Trp	Met	Glu	Arg	Ser	Glu	Asn	Cys	Pro	Val	Cys	Gly	Lys	Val
		195					200					205			

Met Glu Phe Asn Glu Thr Pro
210 215

(2) INFORMATION FOR SEQ ID NO:1418:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1253 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1253
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569932

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1418:

aaacacatga	cccttaaatc	gagaggcttc	gttaggagaa	ggagaagcag	aagagtgttg	60
gttctcgatt	gtcgaatcga	acaatggcgt	agtcctccca	aaatgcgtca	acctcgagct	120
tctcctgcgc	cgtatgttaa	ggatgggtctg	atcattgtga	ttggaggttg	caggtcccaa	180
aatatcgaga	cttggggaga	gatttatgat	ctaaagacca	atacttgggg	gcgaataactg	240
ctccaatcac	atgatcccac	agttcaaaat	gcttacttga	atcgctttaa	acctaaactgt	300
cagacgaatg	cttgcatagt	agagattgac	aaggtgtcgt	gctcgatatt	tttatccgat	360
gggaagactat	tttggcgtga	aacaaagcaa	ggttttgaga	ggtgtagtgt	tatatgtgga	420
gatgatgagc	aagtgtcctc	ttatcaactt	gttctcgttg	caaacgcgcg	cggaggagga	480
agagtgcacg	tttgggtgaa	gtcgggggta	aaagtctctgg	atctcttaag	tggcactgag	540
acttgggaa	gttacacaaa	tagtcggtgt	gcagagattt	cgtttgagag	aagaggttta	600
agagagcttt	ggggattcgt	tgaatggctc	agagaggtgt	ttaccgttga	tggatatgac	660
gataacttaag	atttcttttt	aaattctgct	attgtgacct	attgatcagt	gggactttat	720
cttaacttga	ctgtgggaat	tttgagtatg	attttaaatg	ataaataaat	gtgatttctg	780
aacaacatta	caacatagat	ctaagcatto	aaggtgtTtg	tggtgcctga	tggcttttga	840
tgaaggggag	gttttctact	ttgtatcaga	cttttgcctg	ctagtgaag	agagaataat	900
gggcacaaca	tttttggttac	tccatgggaa	agataatgta	gagtggtctc	aaggaaaaaa	960
tggtgtggag	agtggtcaag	ggacttggat	tgccaaacat	tgtgtttcag	tttgtgtgtg	1020
tacaatgttg	gatcacccct	atggctcgtaa	agtgacagatt	tcgcagagct	ttccaagggg	1080
atcatagaat	cgtcaacgga	gttgtgtttc	gaaccaaagg	atgtatatatt	cgttccactt	1140
tctctettgca	cttgtctata	gtaacacatg	gattgtatg	ctctcatggg	agtgtaacaaa	1200
tctctagtga	tcttctgtttt	tatttgcctt	ttggaatgct	taaagaatga	tat	

(2) INFORMATION FOR SEQ ID NO:1419:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 234 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..234
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569933

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1419:

Lys	His	Met	Thr	Pro	Lys	Ser	Arg	Gly	Phe	Val	Arg	Arg	Arg	Arg	Ser	
1					5			10						15		
Arg	Arg	Val	Leu	Val	Leu	Asp	Cys	Arg	Ser	Gln	Gln	Trp	Arg	Ser	Leu	
					20			25					30			
Pro	Lys	Met	Arg	Gln	Pro	Arg	Ala	Ser	Pro	Ala	Ala	Tyr	Val	Lys	Asp	
					35			40				45				
Gly	Leu	Ile	Ile	Val	Ile	Gly	Cys	Arg	Ser	Lys	Asn	Ile	Glu	Thr		
					50			55				60				
Trp	Gly	Glu	Ile	Tyr	Asp	Leu	Lys	Thr	Asn	Thr	Trp	Gly	Arg	Ile	Leu	
					65			70				75			80	
Leu	Gln	Ser	His	Asp	Pro	Thr	Val	Gln	Asn	Ala	Tyr	Leu	Asn	Arg	Phe	
					85			90				95				
Lys	Pro	Asn	Leu	Gln	Thr	Asn	Ala	Cys	Tyr	Val	Glu	Ile	Asp	Lys	Val	
					100			105				110				

Ser Cys Leu Ile Phe Leu Ser Asp Gly Lys Leu Phe Trp Arg Glu Thr
115 120 125
Lys Gln Gly Phe Glu Arg Cys Ser Val Ile Leu Gly Asp Asp Glu Gln
130 135 140
Val Ser Ser Tyr Gln Leu Val Ser Val Ala Asn Ala Ala Gly Gly Gly
145 150 155 160
Arg Val Thr Val Trp Trp Lys Ser Gly Leu Lys Val Leu Asp Leu Leu
165 170 175
Ser Gly Thr Glu Thr Trp Glu Cys Tyr Thr Asn Ser Arg Cys Ala Glu
180 185 190
Ile Ser Phe Glu Arg Arg Gly Leu Arg Glu Leu Trp Gly Phe Val Glu
195 200 205
Trp Ser Arg Glu Val Phe Thr Val Asp Gly Tyr Asp Asp Thr Tyr Asp
210 215 220
Phe Phe Leu Asn Ser Ala Ile Val Thr Tyr
225 230

(2) INFORMATION FOR SEQ ID NO:1420:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 232 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..232

(D) OTHER INFORMATION: / Ceres Seq. ID 1569934

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1420:

Met Thr Pro Lys Ser Arg Gly Phe Val Arg Arg Arg Arg Ser Arg Arg
1 5 10 15
Val Leu Val Leu Asp Cys Arg Ser Gln Gln Trp Arg Ser Leu Pro Lys
20 25 30
Met Arg Gln Pro Arg Ala Ser Pro Ala Ala Tyr Val Lys Asp Gly Leu
35 40 45
Ile Ile Val Ile Gly Gly Cys Arg Ser Lys Asn Ile Glu Thr Trp Gly
50 55 60
Glu Ile Tyr Asp Leu Lys Thr Asn Thr Trp Gly Arg Ile Leu Leu Gln
65 70 75 80
Ser His Asp Pro Thr Val Gln Asn Ala Tyr Leu Asn Arg Phe Lys Pro
85 90 95
Asn Leu Gln Thr Asn Ala Cys Tyr Val Glu Ile Asp Lys Val Ser Cys
100 105 110
Leu Ile Phe Leu Ser Asp Gly Lys Leu Phe Trp Arg Glu Thr Lys Gln
115 120 125
Gly Phe Glu Arg Cys Ser Val Ile Leu Gly Asp Asp Glu Gln Val Ser
130 135 140
Ser Tyr Gln Leu Val Ser Val Ala Asn Ala Ala Gly Gly Gly Arg Val
145 150 155 160
Thr Val Trp Trp Lys Ser Gly Leu Lys Val Leu Asp Leu Leu Ser Gly
165 170 175
Thr Glu Thr Trp Glu Cys Tyr Thr Asn Ser Arg Cys Ala Glu Ile Ser
180 185 190
Phe Glu Arg Arg Gly Leu Arg Glu Leu Trp Gly Phe Val Glu Trp Ser
195 200 205
Arg Glu Val Phe Thr Val Asp Gly Tyr Asp Asp Thr Tyr Asp Phe Phe
210 215 220
Leu Asn Ser Ala Ile Val Thr Tyr
225 230

(2) INFORMATION FOR SEQ ID NO:1421:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 200 amino acids

(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..200
 (D) OTHER INFORMATION: / Ceres Seq. ID 1569935
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1421:
Met Arg Gln Pro Arg Ala Ser Pro Ala Ala Tyr Val Lys Asp Gly Leu
1 5 10 15
Ile Ile Val Ile Gly Gly Cys Arg Ser Lys Asn Ile Glu Thr Trp Gly
20 25 30
Glu Ile Tyr Asp Leu Lys Thr Asn Thr Trp Gly Arg Ile Leu Leu Gln
35 40 45
Ser His Asp Pro Thr Val Gln Asn Ala Tyr Leu Asn Arg Phe Lys Pro
50 55 60
Asn Leu Gln Thr Asn Ala Cys Tyr Val Glu Ile Asp Lys Val Ser Cys
65 70 75 80
Leu Ile Phe Leu Ser Asp Gly Lys Leu Phe Trp Arg Glu Thr Lys Gln
85 90 95
Gly Phe Glu Arg Cys Ser Val Ile Leu Gly Asp Asp Glu Gln Val Ser
100 105 110
Ser Tyr Gln Leu Val Ser Val Ala Asn Ala Ala Gly Gly Gly Arg Val
115 120 125
Thr Val Trp Trp Lys Ser Gly Leu Lys Val Leu Asp Leu Leu Ser Gly
130 135 140
Thr Glu Thr Trp Glu Cys Tyr Thr Asn Ser Arg Cys Ala Glu Ile Ser
145 150 155 160
Phe Glu Arg Arg Gly Leu Arg Glu Leu Trp Gly Phe Val Glu Trp Ser
165 170 175
Arg Glu Val Phe Thr Val Asp Gly Tyr Asp Asp Thr Tyr Asp Phe Phe
180 185 190
Leu Asn Ser Ala Ile Val Thr Tyr
195 200

(2) INFORMATION FOR SEQ ID NO:1422:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 715 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..715
(D) OTHER INFORMATION: / Ceres Seq. ID 1569942

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1422:

aatggattat ctaggaatcg acttgagctg cgcaatcgGa tctctcCgta acggtgagtt 60
TccgGcgaaa gattgtctTc tTcctctcat tTcaaAgcta ctcggtTact tctctgctgc 120
tgcttcaatg accggttaagc ttctctcagat aatgaaaatc gtggacaaca agagtgtaaa 180
agggctaagt gttgtagcat ttgagcttga agtgattggt Tacacaatct cacttgctta 240
ctgtcttaac aaagaccttc ctttttcagc ttttggtgaa tttagctttt ttttgatcca 300
agctttaatc ttggtggcctt gtatctacta tttctcacia cctctctctg taacaacttg 360
ggtcaaaagca attctttatt ttgctatagc accaactgtg ttgctgtaat ccctcagatt 420
tggaagaact tcagaaacaa aagcaactgga caacttagtt tcttgacttg tctcatgaac 480
tttggtggag cttttggcgag agttttcacc agcattcaag agaaggctcc acttagcatg 540
cttttggata ttgtcttttc tatcttcacc aatTggaatc attatgagtc agatTctttt 600
gtatagaagc aaagGaaacg aagataagct agtgaaaAgt aaaaAgattT catgatatat 660
tgtaaaagtg attcaaacga tgttcacatt cattgaataa agtaaagctt ttttc

(2) INFORMATION FOR SEQ ID NO:1423:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 154 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..154
(D) OTHER INFORMATION: / Ceres Seq. ID 1569943
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1423:

Met	Asp	Tyr	Leu	Gly	Ile	Asp	Leu	Ser	Cys	Ala	Ile	Gly	Ser	Leu	Arg
1			5					10					15		
Asn	Gly	Glu	Phe	Pro	Ala	Lys	Asp	Cys	Leu	Leu	Pro	Leu	Ile	Ser	Lys
			20				25					30			
Leu	Leu	Gly	Tyr	Phe	Leu	Val	Ala	Ala	Ser	Met	Thr	Val	Lys	Leu	Pro
		35					40					45			
Gln	Ile	Met	Lys	Ile	Val	Asp	Asn	Lys	Ser	Val	Lys	Gly	Leu	Ser	Val
	50					55				60					
Val	Ala	Phe	Glu	Leu	Glu	Val	Ile	Gly	Tyr	Thr	Ile	Ser	Leu	Ala	Tyr
	65			70				75				80			
Cys	Leu	Asn	Lys	Asp	Leu	Pro	Phe	Ser	Ala	Phe	Gly	Glu	Leu	Ala	Phe
			85					90				95			
Leu	Leu	Ile	Gln	Ala	Leu	Ile	Leu	Val	Ala	Cys	Ile	Tyr	Tyr	Phe	Ser
		100					105					110			
Gln	Pro	Leu	Ser	Val	Thr	Thr	Trp	Val	Lys	Ala	Ile	Leu	Tyr	Phe	Ala
		115					120					125			
Ile	Ala	Pro	Thr	Val	Phe	Ala	Glu	Ser	Leu	Arg	Phe	Gly	Arg	Thr	Ser
	130				135					140					
Glu	Thr	Lys	Ala	Leu	Asp	Asn	Leu	Val	Ser						
	145				150										

(2) INFORMATION FOR SEQ ID NO:1424:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 112 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..112
(D) OTHER INFORMATION: / Ceres Seq. ID 1569945
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1424:

Met	Thr	Val	Lys	Leu	Pro	Gln	Ile	Met	Lys	Ile	Val	Asp	Asn	Lys	Ser
1			5					10					15		
Val	Lys	Gly	Leu	Ser	Val	Val	Ala	Phe	Glu	Leu	Glu	Val	Ile	Gly	Tyr
		20					25					30			
Thr	Ile	Ser	Leu	Ala	Tyr	Cys	Leu	Asn	Lys	Asp	Leu	Pro	Phe	Ser	Ala
		35				40					45				
Phe	Gly	Glu	Leu	Ala	Phe	Leu	Leu	Ile	Gln	Ala	Leu	Ile	Leu	Val	Ala
	50				55					60					
Cys	Ile	Tyr	Tyr	Phe	Ser	Gln	Pro	Leu	Ser	Val	Thr	Thr	Trp	Val	Lys
	65			70				75				80			
Ala	Ile	Leu	Tyr	Phe	Ala	Ile	Ala	Pro	Thr	Val	Phe	Ala	Glu	Ser	Leu
		85					90					95			
Arg	Phe	Gly	Arg	Thr	Ser	Glu	Thr	Lys	Ala	Leu	Asp	Asn	Leu	Val	Ser
		100				105						110			

(2) INFORMATION FOR SEQ ID NO:1425:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 496 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
 (A) NAME/KEY: -
 (B) LOCATION: 1..496
 (D) OTHER INFORMATION: / Ceres Seq. ID 1569946
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1425:
atgacgaag cttcttggtc tctgttgctc tctcagtcgt gttagatctt cgtcttctca 60
cgtatcatat ggatagtgac attgtttcca cgttagatcg atctcagaca gcaatgcctg 120
atgcttttagc attcaagagt atcaatgato ctatcaagaa ccagatcaat agttgtgctg 180
caatctgtgt taagcaagat gatccatgcc atttcttgcc tgtcctgtat gagtctttga 240
taacaggagg gttagctggt gttgtgggtg aagctgctct gtatccaatt gatacaatca 300
aaactcgagt acaggttagca cgggatgggt gaaagataat gtgaaggagg ctatactctg 360
gtcttggtgc aaatcttgct ggtgtcttcc ctgcttcggc tctatttttt ggtgtatatg 420
aaccaccaa acagaagctg Gcactaagat tttctggtaa aaccttttagc agcttctggt 480
tggttggttc atatac

(2) INFORMATION FOR SEQ ID NO:1426:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 164 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..164
 (D) OTHER INFORMATION: / Ceres Seq. ID 1569947
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1426:
Asp Glu Ser Ser Leu Ala Ser Val Ala Leu Ser Val Trp Leu Asp Leu
1 5 10 15
Arg Leu Leu Thr Tyr His Met Asp Ser Asp Ile Val Ser Ser Val Asp
20 25 30
Arg Ser Gln Thr Ala Met Pro Asp Ala Leu Ala Phe Lys Ser Ile Asn
35 40 45
Asp Pro Ile Lys Asn Gln Ile Asn Ser Cys Ala Ala Ile Cys Val Lys
50 55 60
Gln Asp Asp Pro Cys His Phe Leu Arg Val Leu Tyr Glu Ser Leu Ile
65 70 75 80
Thr Gly Gly Leu Ala Gly Val Val Val Glu Ala Ala Leu Tyr Pro Ile
85 90 95
Asp Thr Ile Lys Thr Arg Val Gln Val Ala Arg Asp Gly Gly Lys Ile
100 105 110
Ile Trp Lys Gly Leu Tyr Ser Gly Leu Gly Ala Asn Leu Val Gly Val
115 120 125
Leu Pro Ala Ser Ala Leu Phe Phe Gly Val Tyr Glu Pro Thr Lys Gln
130 135 140
Lys Leu Ala Leu Arg Phe Ser Gly Lys Thr Phe Ser Ser Phe Cys Leu
145 150 155 160
Val Gly Ser Tyr

(2) INFORMATION FOR SEQ ID NO:1427:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 142 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide

(B) LOCATION: 1..142

(D) OTHER INFORMATION: / Ceres Seq. ID 1569948

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1427:

Met Asp Ser Asp Ile Val Ser Ser Val Asp Arg Ser Gln Thr Ala Met
1 5 10 15
Pro Asp Ala Leu Ala Phe Lys Ser Ile Asn Asp Pro Ile Lys Asn Gln
20 25 30
Ile Asn Ser Cys Ala Ala Ile Cys Val Lys Gln Asp Asp Pro Cys His
35 40 45
Phe Leu Arg Val Leu Tyr Glu Ser Leu Ile Thr Gly Gly Leu Ala Gly
50 55 60
Val Val Val Glu Ala Ala Leu Tyr Pro Ile Asp Thr Ile Lys Thr Arg
65 70 75 80
Val Gln Val Ala Arg Asp Gly Gly Lys Ile Ile Trp Lys Gly Leu Tyr
85 90 95
Ser Gly Leu Gly Ala Asn Leu Val Gly Val Leu Pro Ala Ser Ala Leu
100 105 110
Phe Phe Gly Val Tyr Glu Pro Thr Lys Gln Lys Leu Ala Leu Arg Phe
115 120 125
Ser Gly Lys Thr Phe Ser Ser Phe Cys Leu Val Gly Ser Tyr
130 135 140

(2) INFORMATION FOR SEQ ID NO:1428:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 127 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..127

(D) OTHER INFORMATION: / Ceres Seq. ID 1569949

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1428:

Met Pro Asp Ala Leu Ala Phe Lys Ser Ile Asn Asp Pro Ile Lys Asn
1 5 10 15
Gln Ile Asn Ser Cys Ala Ala Ile Cys Val Lys Gln Asp Asp Pro Cys
20 25 30
His Phe Leu Arg Val Leu Tyr Glu Ser Leu Ile Thr Gly Gly Leu Ala
35 40 45
Gly Val Val Val Glu Ala Ala Leu Tyr Pro Ile Asp Thr Ile Lys Thr
50 55 60
Arg Val Gln Val Ala Arg Asp Gly Gly Lys Ile Ile Trp Lys Gly Leu
65 70 75 80
Tyr Ser Gly Leu Gly Ala Asn Leu Val Gly Val Leu Pro Ala Ser Ala
85 90 95
Leu Phe Phe Gly Val Tyr Glu Pro Thr Lys Gln Lys Leu Ala Leu Arg
100 105 110
Phe Ser Gly Lys Thr Phe Ser Ser Phe Cys Leu Val Gly Ser Tyr
115 120 125

(2) INFORMATION FOR SEQ ID NO:1429:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1368 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1368

(D) OTHER INFORMATION: / Ceres Seq. ID 1569950

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1429:

Cys Pro Asn Trp Pro Gly Asp Ser Ser Asp Gly Ser Thr Gly Thr Leu
210 215 220
Met Leu Ser His Ile Gly Cys Gly Thr Trp Thr Lys Lys Leu Gln Asn
225 230 235 240
Val Ser Gly Asn Val Ala Gly Asp Trp Ile Arg Cys Phe Val Asp Ala
245 250 255
Cys Val Leu Met Asn Lys Ala Arg Phe Cys Ile Gln Glu Ser Gln Thr
260 265 270
Trp Glu Ser Leu Pro Leu Ser Gly Phe Phe Asp Ala Ser Thr Val Ser
275 280 285
Glu Asp Leu Lys His Lys Glu Ile Leu Leu Leu Pro Thr Cys Cys Gly
290 295 300
Ser Leu Cys Lys Tyr Leu Met Val Ala Ser Gly Arg Ala Ser Val Phe
305 310 315 320
Leu Leu Arg Ala Lys Thr Gln Arg Thr Ile Lys Ser Trp Asp His Ala
325 330 335
Val Gly Ile Ile Cys Val His Glu Ala Gly Gly Lys Val Thr Asp Trp
340 345 350
Glu Gly Asp Glu Ile Asn Leu Glu Glu Asp Gln Ser Glu Arg Arg Leu
355 360 365
Ile Phe Pro Ala Gly Gly Val Val Val Ser Asn Gly Ser Leu His Asn
370 375 380
Gln Ile Leu Glu Met Ile Ser Ser Ala Ser Pro Thr Leu
385 390 395

(2) INFORMATION FOR SEQ ID NO:1431:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 976 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..976
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569972

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1431:

acgtctgacg	gaagtcggtt	cacttccacc	tgtgcgctgg	ggatgttctg	tcgtcacagt	60
cggtcaagag	atgtatgtaa	tgtgtggact	ccctagacata	agacgtttac	aggtaatgac	120
ttctatcgat	tgcagaactc	acaaatttcc	ctcgtctccg	agtatgaaaa	gaggtcggtt	180
caaaagcagcc	gcggaggttg	tcgacggaaa	gatttacgta	atcggaggtt	tcaggatgag	240
aaaaccggat	gctgaatgga	ttgaagtgtt	tgatctaaag	acacagattt	gggaatcttt	300
gccttggtccg	taccctaaaa	ctagttctgt	ttgcgagttg	gacgcttatg	tgtgtatgga	360
agagaagtta	tacatgttgt	gttctaaatt	ttgttttggt	tacgaaccac	aaagaaacgg	420
tgaatgggac	gcacccgtcg	gagcaacccc	attaaaaaat	ttgtgggaca	agacttgttg	480
tgtgtgatag	gatatgttgt	atacagactg	tctctggcgt	actcttgagg	atccaaatag	540
cgtgtatcat	ccaaaggaca	agacttggag	acctgtgaaa	ggtgaatcct	tggggagttt	600
gcctagtatt	ttcttttcta	agtcctgaaa	tggcgaaatt	tgttgggaaa	ttggtgattt	660
tgggcagaaa	caagagctat	gttactgggt	attgcattgg	agaaaaagtt	attttggtgc	720
taatgatcga	gttggaaaaa	cgtgaaggag	gtgagatttg	ggggaaggtt	gaatcactcg	780
actgtgtgtt	tggatacata	gacattgtgt	cggttgggct	ttgtcgatct	ctgaccattt	840
gatgatacat	gggatgttat	cttgacagta	cggtgatgtg	aatgagtatg	acttttttgt	900
tgtttatgcc	ttttctttag	cctcaagact	tacttgtctt	tttcatgac	ttattactac	960
acottaacct	ttgtgc					

(2) INFORMATION FOR SEQ ID NO:1432:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 229 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1..229
(D) OTHER INFORMATION: / Ceres Seq. ID 1569973

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1432:

Arg	Leu	Thr	Glu	Val	Gly	Ser	Leu	Pro	Pro	Val	Pro	Trp	Gly	Cys	Ser
1			5						10					15	
Val	Val	Thr	Val	Gly	Gln	Glu	Met	Tyr	Val	Ile	Gly	Gly	Leu	Leu	Asp
			20				25						30		
Ile	Arg	Arg	Leu	Gln	Val	Met	Thr	Leu	Ile	Asp	Cys	Arg	Thr	His	Lys
			35				40					45			
Phe	Arg	Ser	Leu	Pro	Ser	Met	Lys	Arg	Gly	Arg	Cys	Lys	Ala	Ala	Ala
			50				55				60				
Gly	Val	Val	Asp	Gly	Lys	Ile	Tyr	Val	Ile	Gly	Gly	Phe	Arg	Met	Arg
			65				70				75			80	
Lys	Pro	Asp	Ala	Glu	Trp	Ile	Glu	Val	Phe	Asp	Leu	Lys	Thr	Gln	Ile
				85					90					95	
Trp	Glu	Ser	Leu	Pro	Gly	Pro	Tyr	Pro	Lys	Thr	Ser	Ser	Cys	Cys	Glu
			100					105					110		
Leu	Asp	Ala	Tyr	Val	Val	Met	Glu	Glu	Lys	Leu	Tyr	Met	Leu	Gly	Ser
			115				120					125			
Lys	Phe	Cys	Leu	Val	Tyr	Glu	Pro	Lys	Arg	Asn	Gly	Glu	Trp	Asp	Ala
			130				135				140				
Ser	Val	Gly	Ala	Thr	Pro	Leu	Lys	Asp	Leu	Trp	Asp	Lys	Thr	Cys	Cys
					150					155				160	
Val	Val	Asp	Asp	Met	Leu	Tyr	Thr	Thr	Asp	Pro	Arg	Arg	Thr	Leu	Gly
				165					170					175	
His	Pro	Ile	Val	Val	Tyr	His	Pro	Lys	Asp	Lys	Thr	Trp	Arg	Pro	Val
				180				185					190		
Lys	Gly	Glu	Ser	Leu	Gly	Ser	Leu	Pro	Ser	Tyr	Phe	Phe	Ser	Lys	Ser
				195			200					205			
Glu	Asn	Gly	Glu	Phe	Trp	Trp	Lys	Val	Gly	Asp	Phe	Gly	Gln	Lys	Gln
				210			215				220				
Glu	Leu	Cys	Tyr	Trp											
225															

(2) INFORMATION FOR SEQ ID NO:1433:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 206 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1..206
(D) OTHER INFORMATION: / Ceres Seq. ID 1569974

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1433:

Met	Tyr	Val	Ile	Gly	Gly	Leu	Leu	Asp	Ile	Arg	Arg	Leu	Gln	Val	Met
1			5						10					15	
Thr	Leu	Ile	Asp	Cys	Arg	Thr	His	Lys	Phe	Arg	Ser	Leu	Pro	Ser	Met
			20					25					30		
Lys	Arg	Gly	Arg	Cys	Lys	Ala	Ala	Ala	Gly	Val	Val	Asp	Gly	Lys	Ile
			35				40					45			
Tyr	Val	Ile	Gly	Gly	Phe	Arg	Met	Arg	Lys	Pro	Asp	Ala	Glu	Trp	Ile
			50				55				60				
Glu	Val	Phe	Asp	Leu	Lys	Thr	Gln	Ile	Trp	Glu	Ser	Leu	Pro	Gly	Pro
				65			70				75			80	
Tyr	Pro	Lys	Thr	Ser	Ser	Cys	Cys	Glu	Leu	Asp	Ala	Tyr	Val	Val	Met
				85					90					95	
Glu	Glu	Lys	Leu	Tyr	Met	Leu	Gly	Ser	Lys	Phe	Cys	Leu	Val	Tyr	Glu
				100			105					110			
Pro	Lys	Arg	Asn	Gly	Glu	Trp	Asp	Ala	Ser	Val	Gly	Ala	Thr	Pro	Leu

115	120	125
Lys Asp Leu Trp Asp Lys Thr Cys Cys Val Val Asp Asp Met Leu Tyr		
130	135	140
Thr Thr Asp Pro Arg Arg Thr Leu Gly His Pro Ile Val Val Tyr His		
145	150	155
Pro Lys Asp Lys Thr Trp Arg Pro Val Lys Gly Glu Ser Leu Gly Ser		
165	170	175
Leu Pro Ser Tyr Phe Phe Ser Lys Ser Glu Asn Gly Glu Phe Trp Trp		
180	185	190
Lys Val Gly Asp Phe Gly Gln Lys Gln Glu Leu Cys Tyr Trp		
195	200	205

(2) INFORMATION FOR SEQ ID NO:1434:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 191 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..191
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569975

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1434:

Met Thr Leu Ile Asp Cys Arg Thr His Lys Phe Arg Ser Leu Pro Ser	
1	5
Met Lys Arg Gly Arg Cys Lys Ala Ala Ala Gly Val Val Asp Gly Lys	
20	25
Ile Tyr Val Ile Gly Gly Phe Arg Met Arg Lys Pro Asp Ala Glu Trp	
35	40
Ile Glu Val Phe Asp Leu Lys Thr Gln Ile Trp Glu Ser Leu Pro Gly	
50	55
Pro Tyr Pro Lys Thr Ser Cys Cys Glu Leu Asp Ala Tyr Val Val	
65	70
Met Glu Glu Lys Leu Tyr Met Leu Gly Ser Lys Phe Cys Leu Val Tyr	
85	90
Glu Pro Lys Arg Asn Gly Glu Trp Asp Ala Ser Val Gly Ala Thr Pro	
100	105
Leu Lys Asp Leu Trp Asp Lys Thr Cys Cys Val Val Asp Asp Met Leu	
115	120
Tyr Thr Thr Asp Pro Arg Arg Thr Leu Gly His Pro Ile Val Val Tyr	
130	135
His Pro Lys Asp Lys Thr Trp Arg Pro Val Lys Gly Glu Ser Leu Gly	
145	150
Ser Leu Pro Ser Tyr Phe Phe Ser Lys Ser Glu Asn Gly Glu Phe Trp	
165	170
Trp Lys Val Gly Asp Phe Gly Gln Lys Gln Glu Leu Cys Tyr Trp	
180	185
	190

(2) INFORMATION FOR SEQ ID NO:1435:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1663 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1663
- (D) OTHER INFORMATION: / Ceres Seq. ID 1569986

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1435:

aagcaaaaat gctacaaatt aaaaagtgtc tccaacatgt gcatattcac acacaagttg	60
gtgtcaacgc tcagacaaga aaggcgtgtg ttcattgttg aatcttccca ttctctcatc	120

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caaatccga cataactatc ctagccgcc tttgtcttc acattacaaa accctcagca 180
gcttcaaaa tcttcgcgat tctccctcac gctcgcaatt ctctcgtctc ctttttaata 240
gtttttcttc tcggaatcac aaactctcgg cttctgtgtc cttggcgtgt gtgtgtgtgt 300
ttgaatggct ctgtgtcagc ggattccaat tctctcctcc agtattcggg attggcaaca 360
agcggaggacc aatttgactc ctatttgttg tttacattac aatactgcac ctctctcttc 420
ttcacccctt acagagaagc actctgtgga gagataccaa agggatcaat ggctgtacaa 480
agcgtgttaa ccaacgcgac catcgactcc atctccatcg ccatttgaag atgaagtctt 540
tgttaggaaa aacgacattg catcgagctt gacctgagct aagaagcttt tggcagtgct 600
gaaagagaag agagttaaa gatgcaaaag tgggtattgt ggaccaggag atgtgtatct 660
tgttgggaca gggccaggag atcctgagct tttgactctt aaagctgtca gagtattca 720
aagtgcgcat cttttgtctt acgacaggct tgtctccaat gatgtcttgg agttggtgtc 780
tctgtagctc agactcttt atgtcggcaa aactgctgtg tatcatagca gaactcaagg 840
agagattcat gaactactcc taaattttgc tgaagctgtg gccactgttg tcaggcttaa 900
aggtggagat cctctggtct ttggacgggg cggcgaaaga atggactttc tgcaacagca 960
agggattcga gttcaagtta taccagggat aactgcggcg tcggggatag cagcagagtt 1020
ggggattcca ctaacacatc gagggtgttc aactagtgtg aggtttctca ctgtgcttc 1080
aaggaaagga gggacagacc ctctgtttgt tgcagagaat gcagctgacc cggatataac 1140
actttgcgtt tataatgggt ttggaaactt accctctctt gcacaaaaac taatggacca 1200
tggtctcctt tctgatacac cagctgttgc ggttgaacgt ggaaccactc ctctacagcg 1260
tacagttttt ctgtagcatc aagattttgc aactgagatt cagtcagctg gattggtgtc 1320
accaacatct atcatcatag ggaagtcgt tgagctctca cttttatgac cacattgacc 1380
gaaagaatcc tcttcgcttg tagagaccg gtatgatatt cactcttatt ttacggcgct 1440
gtggcttcca tcgacattac ggtgaagttt taggagctat ggagctatga aggttgagac 1500
ttgagagatg taataaacaa aaaggaaagc tgatagtttc ttatgacgtg tcttcaatt 1560
gttttgggac aatggtaatg gcaatgttaa tgtaataaac aagttAtcaa tcagtgccac 1620
tgtgactaat tttttccaca caagatgatg tctttaaaac ttt

```

(2) INFORMATION FOR SEQ ID NO:1436:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 369 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..369

(D) OTHER INFORMATION: / Ceres Seq. ID 1569987

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1436:

```

Met Ala Leu Val Gln Arg Ile Pro Ile Ser Ser Ser Ile Arg Asn
1 5 10 15
Trp Gln Gln Ala Arg Thr Asn Leu Thr Pro Ile Cys Cys Leu His Tyr
20 25 30
Asn Thr Ala Ser Ser Ser Ser Pro Phe Thr Glu Lys His Ser Val
35 40 45
Glu Arg Tyr Gln Arg Asp Gln Trp Leu Tyr Lys Ala Val Glu Pro Thr
50 55 60
Pro Pro Ser Thr Pro Ser Pro Ser Pro Phe Glu Asp Glu Val Phe Val
65 70 75 80
Arg Glu Asn Asp Ile Ala Ser Gln Leu Pro Glu Leu Lys Lys Leu Leu
85 90 95
Ala Val Leu Lys Glu Lys Arg Val Lys Gly Cys Lys Gly Gly Asp Cys
100 105 110
Gly Pro Gly Asp Val Tyr Leu Val Gly Thr Gly Pro Gly Asp Pro Glu
115 120 125
Leu Leu Thr Leu Lys Ala Val Arg Val Ile Gln Ser Ala Asp Leu Leu
130 135 140
Leu Tyr Asp Arg Leu Val Ser Asn Asp Val Leu Glu Leu Val Ala Pro
145 150 155 160
Asp Ala Arg Leu Leu Tyr Val Gly Lys Thr Ala Gly Tyr His Ser Arg
165 170 175
Thr Gln Glu Glu Ile His Glu Leu Leu Asn Phe Ala Glu Ala Gly

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Ala	Thr	Val	Val	Arg	Leu	Lys	Gly	Gly	Asp	Pro	Leu	Val	Phe	Gly	Arg
195							200					205			
Gly	Gly	Glu	Glu	Met	Asp	Phe	Leu	Gln	Gln	Gln	Gly	Ile	Arg	Val	Gln
210							215				220				
Val	Ile	Pro	Gly	Ile	Thr	Ala	Ala	Ser	Gly	Ile	Ala	Ala	Glu	Leu	Gly
225						230					235				240
Ile	Pro	Leu	Thr	His	Arg	Gly	Val	Ala	Thr	Ser	Val	Arg	Phe	Leu	Thr
						245					250				255
Gly	His	Ser	Arg	Lys	Gly	Gly	Thr	Asp	Pro	Leu	Phe	Val	Ala	Glu	Asn
						260									270
Ala	Ala	Asp	Pro	Asp	Thr	Thr	Leu	Val	Val	Tyr	Met	Gly	Leu	Gly	Thr
275							280								285
Leu	Pro	Ser	Leu	Ala	Gln	Lys	Leu	Met	Asp	His	Gly	Leu	Pro	Ser	Asp
290						295					300				
Thr	Pro	Ala	Val	Ala	Val	Glu	Arg	Gly	Thr	Thr	Pro	Leu	Gln	Arg	Thr
305						310					315				320
Val	Phe	Ala	Glu	Leu	Lys	Asp	Phe	Ala	Thr	Glu	Ile	Gln	Ser	Ala	Gly
						325									335
Leu	Val	Ser	Pro	Thr	Leu	Ile	Ile	Ile	Gly	Lys	Val	Val	Glu	Leu	Ser
						340									350
Pro	Leu	Trp	Pro	His	Cys	Thr	Lys	Glu	Ser	Ser	Cys	Leu	Val	Glu	Thr
355							360								365

(2) INFORMATION FOR SEQ ID NO:1437:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1409 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1409
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570000

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1437:

acgaatcaaa	attcaattaa	aaaaaacctt	togatctctc	tcatccaatc	gaatcgaaaa	60
tctttgtatc	tctttctctc	taactctact	gcactcagaa	tctctctgta	tagaaaaaac	120
ctaaagttagt	tgtgatgttg	cgagctttag	cacggcctct	cgaacgctgt	ttgggaagca	180
gagctagtgg	tgatgttita	ctctggcaat	cgaattgag	acctcacgct	ggcggtgatt	240
attcgatcgc	gggtgttcaa	gccaatcca	ggcttgaaga	tcagagtcag	gttttcacat	300
cttctctcgc	tacttaacgtc	ggtgtatagc	atggtcatgg	tggacctgaa	gctctagat	360
tcgttaacag	acatctcttt	ccttatatgc	acaaatttgc	aagagaacat	ggcggattat	420
ctgtgatgtg	tatcaaaaag	gcattcaaag	aaacagaaga	agagttttgt	ggtagtggtta	480
aacgatccct	tcccatgaaa	cgcgaatagg	ctactgtag	atctgtcgtg	cttgttggtg	540
caatctctaa	tgacacactg	tatgttgcga	atcttgggga	ctcgagagcc	gttcttgtaa	600
gcgttgtttc	aggggttgat	agtaataaag	gtgcctgagc	tgaacggtta	tcactgac	660
ataatgttgc	tgttgaagaa	gtgagaaagg	aggttaaggc	acttaaccct	gatgactcac	720
aaatcgtctt	atacacacgt	ggagtttggc	ggattaaagg	cattattcag	gtatcgagat	780
caattggggg	tgtatatttg	aaaaaacccg	agtattacag	ggaccocgat	ttccagcgac	840
atggaaatcc	cattctctttg	aggagaccgc	cgatgacagc	cgaacccctc	attatagttaa	900
ggaagcttaa	gccacagcag	tgttttctga	tatttgcctc	agatggtctc	tgggaacatc	960
ttagtgatga	aacgacgcga	gaatatcttc	tcaaaacacc	agaactggtg	attgcacgaa	1020
gacttgtaa	agctgctctg	gaagaagcgg	caaagaagag	agaatagaga	tatggagata	1080
taaaagaaat	agccaaagga	attcgcagac	attccatgat	cgcataaagc	gttatgtgat	1140
tttatctaga	tcaaaaacaa	accagttcat	cgaatagttaa	attggtagta	caaggaggtta	1200
tcaccgcgtc	accggatatt	tactcattac	actctgatga	agcagagcaa	cgacggttac	1260
tcaatgtgtt	atactgactg	tgtgattatg	gtaaaaatgc	tgtctgggaa	agatccgaat	1320
agggagaaaa	cttgtttaca	tatttgttta	tttgttttct	tacgaagaac	tgtttttttt	1380
ttttttttca	atattggagt	tggatttggc				

(2) INFORMATION FOR SEQ ID NO:1438:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 380 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..380

(D) OTHER INFORMATION: / Ceres Seq. ID 1570001

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1438:

Met Leu Arg Ala Leu Ala Arg Pro Leu Glu Arg Cys Leu Gly Ser Arg
1 5 10 15
Ala Ser Gly Asp Gly Leu Leu Trp Gln Ser Glu Leu Arg Pro His Ala
20 25 30
Gly Gly Asp Tyr Ser Ile Ala Val Val Gln Ala Asn Ser Arg Leu Glu
35 40 45
Asp Gln Ser Gln Val Phe Thr Ser Ser Ala Thr Tyr Val Gly Val
50 55 60
Tyr Asp Gly His Gly Gly Pro Glu Ala Ser Arg Phe Val Asn Arg His
65 70 75 80
Leu Phe Pro Tyr Met His Lys Phe Ala Arg Glu His Gly Gly Leu Ser
85 90 95
Val Asp Val Ile Lys Lys Ala Phe Lys Glu Thr Glu Glu Glu Phe Cys
100 105 110
Gly Met Val Lys Arg Ser Leu Pro Met Lys Pro Gln Met Ala Thr Val
115 120 125
Gly Ser Cys Cys Leu Val Gly Ala Ile Ser Asn Asp Thr Leu Tyr Val
130 135 140
Ala Asn Leu Gly Asp Ser Arg Ala Val Leu Gly Ser Val Val Ser Gly
145 150 155 160
Val Asp Ser Asn Lys Gly Ala Val Ala Glu Arg Leu Ser Thr Asp His
165 170 175
Asn Val Ala Val Glu Glu Val Arg Lys Glu Val Lys Ala Leu Asn Pro
180 185 190
Asp Asp Ser Gln Ile Val Leu Tyr Thr Arg Gly Val Trp Arg Ile Lys
195 200 205
Gly Ile Ile Gln Val Ser Arg Ser Ile Gly Asp Val Tyr Leu Lys Lys
210 215 220
Pro Glu Tyr Tyr Arg Asp Pro Ile Phe Gln Arg His Gly Asn Pro Ile
225 230 235 240
Pro Leu Arg Arg Pro Ala Met Thr Ala Glu Pro Ser Ile Ile Val Arg
245 250 255
Lys Leu Lys Pro Gln Asp Leu Phe Leu Ile Phe Ala Ser Asp Gly Leu
260 265 270
Trp Glu His Leu Ser Asp Glu Thr Ala Val Glu Ile Val Leu Lys His
275 280 285
Pro Arg Thr Gly Ile Ala Arg Arg Leu Val Arg Ala Ala Leu Glu Glu
290 295 300
Ala Ala Lys Lys Arg Glu Met Arg Tyr Gly Asp Ile Lys Lys Ile Ala
305 310 315 320
Lys Gly Ile Arg Arg His Phe His Asp Asp Ile Ser Val Ile Val Val
325 330 335
Tyr Leu Asp Gln Asn Lys Thr Ser Ser Ser Asn Ser Lys Leu Val Lys
340 345 350
Gln Gly Gly Ile Thr Ala Pro Pro Asp Ile Tyr Ser Leu His Ser Asp
355 360 365
Glu Ala Glu Gln Arg Arg Leu Leu Asn Val Leu Tyr
370 375 380

(2) INFORMATION FOR SEQ ID NO:1439:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 296 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..296
 (D) OTHER INFORMATION: / Ceres Seq. ID 1570002
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1439:

Met	His	Lys	Phe	Ala	Arg	Glu	His	Gly	Gly	Leu	Ser	Val	Asp	Val	Ile
1			5						10					15	
Lys	Lys	Ala	Phe	Lys	Glu	Thr	Glu	Glu	Glu	Phe	Cys	Gly	Met	Val	Lys
		20						25					30		
Arg	Ser	Leu	Pro	Met	Lys	Pro	Gln	Met	Ala	Thr	Val	Gly	Ser	Cys	Cys
		35					40					45			
Leu	Val	Gly	Ala	Ile	Ser	Asn	Asp	Thr	Leu	Tyr	Val	Ala	Asn	Leu	Gly
	50					55					60				
Asp	Ser	Arg	Ala	Val	Leu	Gly	Ser	Val	Val	Ser	Gly	Val	Asp	Ser	Asn
65					70					75				80	
Lys	Gly	Ala	Val	Ala	Glu	Arg	Leu	Ser	Thr	Asp	His	Asn	Val	Ala	Val
				85					90				95		
Glu	Glu	Val	Arg	Lys	Glu	Val	Lys	Ala	Leu	Asn	Pro	Asp	Asp	Ser	Gln
			100					105					110		
Ile	Val	Leu	Tyr	Thr	Arg	Gly	Val	Trp	Arg	Ile	Lys	Gly	Ile	Ile	Gln
		115					120					125			
Val	Ser	Arg	Ser	Ile	Gly	Asp	Val	Tyr	Leu	Lys	Lys	Pro	Glu	Tyr	Tyr
	130					135					140				
Arg	Asp	Pro	Ile	Phe	Gln	Arg	His	Gly	Asn	Pro	Ile	Pro	Leu	Arg	Arg
145					150					155				160	
Pro	Ala	Met	Thr	Ala	Glu	Pro	Ser	Ile	Ile	Val	Arg	Lys	Leu	Lys	Pro
			165						170					175	
Gln	Asp	Leu	Phe	Leu	Ile	Phe	Ala	Ser	Asp	Gly	Leu	Trp	Glu	His	Leu
		180						185					190		
Ser	Asp	Glu	Thr	Ala	Val	Glu	Ile	Val	Leu	Lys	His	Pro	Arg	Thr	Gly
		195					200					205			
Ile	Ala	Arg	Arg	Leu	Val	Arg	Ala	Ala	Leu	Glu	Glu	Ala	Ala	Lys	Lys
	210						215					220			
Arg	Glu	Met	Arg	Tyr	Gly	Asp	Ile	Lys	Lys	Ile	Ala	Lys	Gly	Ile	Arg
225					230					235				240	
Arg	His	Phe	His	Asp	Asp	Ile	Ser	Val	Ile	Val	Val	Tyr	Leu	Asp	Gln
				245					250					255	
Asn	Lys	Thr	Ser	Ser	Ser	Asn	Ser	Lys	Leu	Val	Lys	Gln	Gly	Gly	Ile
			260					265						270	
Thr	Ala	Pro	Pro	Asp	Ile	Tyr	Ser	Leu	His	Ser	Asp	Glu	Ala	Glu	Gln
		275						280					285		
Arg	Arg	Leu	Leu	Asn	Val	Leu	Tyr								
	290						295								

(2) INFORMATION FOR SEQ ID NO:1440:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 267 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..267
 (D) OTHER INFORMATION: / Ceres Seq. ID 1570003
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1440:

```

Met Val Lys Arg Ser Leu Pro Met Lys Pro Gln Met Ala Thr Val Gly
1          5          10          15
Ser Cys Cys Leu Val Gly Ala Ile Ser Asn Asp Thr Leu Tyr Val Ala
20          25          30
Asn Leu Gly Asp Ser Arg Ala Val Leu Gly Ser Val Val Ser Gly Val
35          40          45
Asp Ser Asn Lys Gly Ala Val Ala Glu Arg Leu Ser Thr Asp His Asn
50          55          60
Val Ala Val Glu Glu Val Arg Lys Glu Val Lys Ala Leu Asn Pro Asp
65          70          75          80
Asp Ser Gln Ile Val Leu Tyr Thr Arg Gly Val Trp Arg Ile Lys Gly
85          90          95
Ile Ile Gln Val Ser Arg Ser Ile Gly Asp Val Tyr Leu Lys Lys Pro
100          105          110
Glu Tyr Tyr Arg Asp Pro Ile Phe Gln Arg His Gly Asn Pro Ile Pro
115          120          125
Leu Arg Arg Pro Ala Met Thr Ala Glu Pro Ser Ile Ile Val Arg Lys
130          135          140
Leu Lys Pro Gln Asp Leu Phe Leu Ile Phe Ala Ser Asp Gly Leu Trp
145          150          155          160
Glu His Leu Ser Asp Glu Thr Ala Val Glu Ile Val Leu Lys His Pro
165          170          175
Arg Thr Gly Ile Ala Arg Arg Leu Val Arg Ala Ala Leu Glu Ala
180          185          190
Ala Lys Lys Arg Glu Met Arg Tyr Gly Asp Ile Lys Lys Ile Ala Lys
195          200          205
Gly Ile Arg Arg His Phe His Asp Asp Ile Ser Val Ile Val Val Tyr
210          215          220
Leu Asp Gln Asn Lys Thr Ser Ser Ser Asn Ser Lys Leu Val Lys Gln
225          230          235          240
Gly Gly Ile Thr Ala Pro Pro Asp Ile Tyr Ser Leu His Ser Asp Glu
245          250          255
Ala Glu Gln Arg Arg Leu Leu Asn Val Leu Tyr
260          265

```

(2) INFORMATION FOR SEQ ID NO:1441:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1649 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1649
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570004

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1441:

```

aattttctctt gaaaaccctt aaatctccgg atttcgattc ccgaggctcg aaaaaaccct      60
aaatctcttc tcggttcaact catccaacgg aagatgcgtg agattcttca catccagggt      120
ggtcgaatgcg gtaaccagat cgggcgccaag ttctgggaag tggtttgcgc cgagcacggc      180
atcgatccaa ccggaaggta caccggagac tcagatctgc aacttgagcg catcaacggt      240
tactacaagt aagcgagatt cggtagattc gttcctcgtg cagtgcctat ggatttgagg      300
ctcggggacta tggatagttc cagatctgga cgtacgggtc agacctttcg acctgataac      360
ttcgtctttg gccaatccgg tgctggttaac aactgggcca agggacacta caccgaagga      420
gtcgaaactaa tgcattccgt tctcgtattg gttcgttaagg aagctgGaga actgtgactg      480
ttccaagggt ttccagggtt gtcactcgtt gggaggagga actggatctg gtatgggaac      540
attgttgatc tetaagatcc gtgaagagta cccagatcgc atgatgctta cttcttcggt      600
gttcctctca ccaaagggtt ctgatactgt ggttgagcct tacaacgcta cctctgtctg      660
ccatcagctt gttgagaatt ctgatgagtg catggttctt gataatgagg ccttgtacga      720
tatttgcttc aggactctca aactcactac cccacgcttt ggtgatttga accacttgat      780
ttctgctact atgtctggtg tgacttgctg tctgaggttc cctgggtaac tcaactctga      840
ctcccgaaag ctgtcgtgtga atctcatccc attccccggt cttcacttct tcatgggtgg      900

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ttttgctcct	ctcacctcaa	gaggttctca	gcagtagcgt	tcctctacag	tccttgagct	960
caccagcaca	atgtgggact	ccaagaacat	gatgtgtgct	gcagacccaa	ggcagcgagc	1020
ctacctcaca	gocctctgcca	tggtccgtgg	caagatgagc	acaaaggaag	ttgacagaga	1080
gatgctgaat	gtgcagaaaca	agaactcgtc	ctactttgtg	gagtgagatcc	ccaacaacgt	1140
gaatcgaca	gtctgtgaca	tcccacctac	tggtctgaag	atggcatcaa	ctttcattgg	1200
aaactcaaca	tcaatccaag	agatgttcag	gcgagtgaat	gagcagttca	cagctatgtt	1260
caggagaaag	gottttcttg	attggtacac	agtgaggaga	atggacagaga	tggaaatcac	1320
agaagcggag	agcaacatga	acgatcttgt	gtcagagtac	cagcaatacc	aagatgcaac	1380
tgccgatgaa	gaagggtgact	acgaggatga	ggaagaaggt	gaatatcaac	aggaggaaga	1440
gtactgagaa	taattttagt	ataactgctt	taaaaacaaa	aacaatttag	tcgtttgcta	1500
ctttttcttt	ttttaaaagg	aacacctcaa	ctaccagtgt	tagttttttt	ctctgcttgt	1560
atttgacata	ctgggttgat	gtttctgtac	ttttgttctt	aatcttgta	ttgcctgtga	1620
gtttcttatt	aatattttcc	agttgtact				

(2) INFORMATION FOR SEQ ID NO:1442:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 333 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..333

- (D) OTHER INFORMATION: / Ceres Seq. ID 1570005

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1442:

Met	Leu	Phe	Val	Arg	Lys	Leu	Glu	Asn	Cys	Asp	Cys	Leu	Gln	Gly	Phe
1			5						10					15	
Gln	Val	Cys	His	Ser	Leu	Gly	Gly	Gly	Thr	Gly	Ser	Gly	Met	Gly	Thr
			20					25					30		
Leu	Leu	Ile	Ser	Lys	Ile	Arg	Glu	Glu	Tyr	Pro	Asp	Arg	Met	Met	Leu
			35				40					45			
Thr	Phe	Ser	Val	Phe	Pro	Ser	Pro	Lys	Val	Ser	Asp	Thr	Val	Val	Glu
			50				55				60				
Pro	Tyr	Asn	Ala	Thr	Leu	Ser	Val	His	Gln	Leu	Val	Glu	Asn	Ala	Asp
			65				70				75			80	
Glu	Cys	Met	Val	Leu	Asp	Asn	Glu	Ala	Leu	Tyr	Asp	Ile	Cys	Phe	Arg
			85						90					95	
Thr	Leu	Lys	Leu	Thr	Thr	Pro	Ser	Phe	Gly	Asp	Leu	Asn	His	Leu	Ile
			100					105					110		
Ser	Ala	Thr	Met	Ser	Gly	Val	Thr	Cys	Cys	Leu	Arg	Phe	Pro	Gly	Gln
			115				120					125			
Leu	Asn	Ser	Asp	Leu	Arg	Lys	Leu	Ala	Val	Asn	Leu	Ile	Pro	Phe	Pro
			130				135					140			
Arg	Leu	His	Phe	Phe	Met	Val	Gly	Phe	Ala	Pro	Leu	Thr	Ser	Arg	Gly
			145				150				155			160	
Ser	Gln	Gln	Tyr	Arg	Ser	Leu	Thr	Val	Pro	Glu	Leu	Thr	Gln	Gln	Met
			165						170					175	
Trp	Asp	Ser	Lys	Asn	Met	Met	Cys	Ala	Ala	Asp	Pro	Arg	His	Gly	Arg
			180					185					190		
Tyr	Leu	Thr	Ala	Ser	Ala	Met	Phe	Arg	Gly	Lys	Met	Ser	Thr	Lys	Glu
			195				200					205			
Val	Asp	Glu	Gln	Met	Leu	Asn	Val	Gln	Asn	Lys	Asn	Ser	Ser	Tyr	Phe
			210				215				220				
Val	Glu	Trp	Ile	Pro	Asn	Asn	Val	Lys	Ser	Thr	Val	Cys	Asp	Ile	Pro
			225				230				235			240	
Pro	Thr	Gly	Leu	Lys	Met	Ala	Ser	Thr	Phe	Ile	Gly	Asn	Ser	Thr	Ser
			245						250					255	
Ile	Gln	Glu	Met	Phe	Arg	Arg	Val	Ser	Glu	Gln	Phe	Thr	Ala	Met	Phe
			260					265					270		
Arg	Arg	Lys	Ala	Phe	Leu	His	Trp	Tyr	Thr	Gly	Glu	Gly	Met	Asp	Glu
			275				280					285			

Met Glu Phe Thr Glu Ala Glu Ser Asn Met Asn Asp Leu Val Ser Glu
290 295 300
Tyr Gln Gln Tyr Gln Asp Ala Thr Ala Asp Glu Gly Asp Tyr Glu
305 310 315 320
Asp Glu Glu Glu Gly Glu Tyr Gln Gln Glu Glu Tyr
325 330

(2) INFORMATION FOR SEQ ID NO:1443:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 304 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..304

(D) OTHER INFORMATION: / Ceres Seq. ID 1570006

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1443:

Met Gly Thr Leu Leu Ile Ser Lys Ile Arg Glu Glu Tyr Pro Asp Arg
1 5 10 15
Met Met Leu Thr Phe Ser Val Phe Pro Ser Pro Lys Val Ser Asp Thr
20 25 30
Val Val Glu Pro Tyr Asn Ala Thr Leu Ser Val His Gln Leu Val Glu
35 40 45
Asn Ala Asp Glu Cys Met Val Leu Asp Asn Glu Ala Leu Tyr Asp Ile
50 55 60
Cys Phe Arg Thr Leu Lys Leu Thr Thr Pro Ser Phe Gly Asp Leu Asn
65 70 75 80
His Leu Ile Ser Ala Thr Met Ser Gly Val Thr Cys Cys Leu Arg Phe
85 90 95
Pro Gly Gln Leu Asn Ser Asp Leu Arg Lys Leu Ala Val Asn Leu Ile
100 105 110
Pro Phe Pro Arg Leu His Phe Phe Met Val Gly Phe Ala Pro Leu Thr
115 120 125
Ser Arg Gly Ser Gln Gln Tyr Arg Ser Leu Thr Val Pro Glu Leu Thr
130 135 140
Gln Gln Met Trp Asp Ser Lys Asn Met Met Cys Ala Ala Asp Pro Arg
145 150 155 160
His Gly Arg Tyr Leu Thr Ala Ser Ala Met Phe Arg Gly Lys Met Ser
165 170 175
Thr Lys Glu Val Asp Glu Gln Met Leu Asn Val Gln Asn Lys Asn Ser
180 185 190
Ser Tyr Phe Val Glu Trp Ile Pro Asn Asn Val Lys Ser Thr Val Cys
195 200 205
Asp Ile Pro Pro Thr Gly Leu Lys Met Ala Ser Thr Phe Ile Gly Asn
210 215 220
Ser Thr Ser Ile Gln Glu Met Phe Arg Arg Val Ser Glu Gln Phe Thr
225 230 235 240
Ala Met Phe Arg Arg Lys Ala Phe Leu His Trp Tyr Thr Gly Glu Gly
245 250 255
Met Asp Glu Met Glu Phe Thr Glu Ala Glu Ser Asn Met Asn Asp Leu
260 265 270
Val Ser Glu Tyr Gln Gln Tyr Gln Asp Ala Thr Ala Asp Glu Glu Gly
275 280 285
Asp Tyr Glu Asp Glu Glu Glu Gly Glu Tyr Gln Gln Glu Glu Glu Tyr
290 295 300

(2) INFORMATION FOR SEQ ID NO:1444:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 288 amino acids

(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..288
(D) OTHER INFORMATION: / Ceres Seq. ID 1570007
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1444:

Met	Met	Leu	Thr	Phe	Ser	Val	Phe	Pro	Ser	Pro	Lys	Val	Ser	Asp	Thr
1				5				10						15	
Val	Val	Glu	Pro	Tyr	Asn	Ala	Thr	Leu	Ser	Val	His	Gln	Leu	Val	Glu
			20					25					30		
Asn	Ala	Asp	Glu	Cys	Met	Val	Leu	Asp	Asn	Glu	Ala	Leu	Tyr	Asp	Ile
		35					40					45			
Cys	Phe	Arg	Thr	Leu	Lys	Leu	Thr	Thr	Pro	Ser	Phe	Gly	Asp	Leu	Asn
	50				55						60				
His	Leu	Ile	Ser	Ala	Thr	Met	Ser	Gly	Val	Thr	Cys	Cys	Leu	Arg	Phe
65				70				75							80
Pro	Gly	Gln	Leu	Asn	Ser	Asp	Leu	Arg	Lys	Leu	Ala	Val	Asn	Leu	Ile
			85					90					95		
Pro	Phe	Pro	Arg	Leu	His	Phe	Phe	Met	Val	Gly	Phe	Ala	Pro	Leu	Thr
			100					105					110		
Ser	Arg	Gly	Ser	Gln	Gln	Tyr	Arg	Ser	Leu	Thr	Val	Pro	Glu	Leu	Thr
		115				120						125			
Gln	Gln	Met	Trp	Asp	Ser	Lys	Asn	Met	Met	Cys	Ala	Ala	Asp	Pro	Arg
		130				135					140				
His	Gly	Arg	Tyr	Leu	Thr	Ala	Ser	Ala	Met	Phe	Arg	Gly	Lys	Met	Ser
145				150					155						160
Thr	Lys	Glu	Val	Asp	Glu	Gln	Met	Leu	Asn	Val	Gln	Asn	Lys	Asn	Ser
			165					170					175		
Ser	Tyr	Phe	Val	Glu	Trp	Ile	Pro	Asn	Asn	Val	Lys	Ser	Thr	Val	Cys
			180				185						190		
Asp	Ile	Pro	Pro	Thr	Gly	Leu	Lys	Met	Ala	Ser	Thr	Phe	Ile	Gly	Asn
		195				200						205			
Ser	Thr	Ser	Ile	Gln	Glu	Met	Phe	Arg	Arg	Val	Ser	Glu	Gln	Phe	Thr
		210				215					220				
Ala	Met	Phe	Arg	Arg	Lys	Ala	Phe	Leu	His	Trp	Tyr	Thr	Gly	Glu	Gly
225				230						235					240
Met	Asp	Glu	Met	Glu	Phe	Thr	Glu	Ala	Glu	Ser	Asn	Met	Asn	Asp	Leu
			245						250				255		
Val	Ser	Glu	Tyr	Gln	Gln	Tyr	Gln	Asp	Ala	Thr	Ala	Asp	Glu	Glu	Gly
			260				265						270		
Asp	Tyr	Glu	Asp	Glu	Glu	Glu	Gly	Glu	Tyr	Gln	Gln	Glu	Glu	Glu	Tyr
		275					280						285		

(2) INFORMATION FOR SEQ ID NO:1445:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 503 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..503
(D) OTHER INFORMATION: / Ceres Seq. ID 1570008

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1445:

attttttttt gaacagaaMH atcTCagaaa gatcaatcta gagagaccaa aaagagatcg
gaagagatgg cttctacctc cgcgatgtca ttggtcacac cacttaacca gaccggttcg

60
120

tctctcttcc tcaagccatt acctctgaaa ccattccaagg ctttggttgc aactggaggc 180
agagcacaga ggcttcaagt taaggccctc aagatggaca aggcctttgac cggtatctcc 240
gcggctgctc ttactgtctc gatggtgatt ccggagatag ctgaagctgc tggttctgga 300
atctctcctt cctccaagaa tttcttgctc agcattgctt ctggtggcct cgtctcact 360
gtcatcattg gtgtcgtcgt cggtgtctcc aactttgacc ctgtcaagag aacctaaagac 420
ctatatatct ttcttacatc attattgtaa tctgttctcc ttctgtgtat tegtttcaat 480
gttgcaagaa tgaacttttg gat

(2) INFORMATION FOR SEQ ID NO:1446:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 138 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..138
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570009

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1446:

Ile Xaa Phe Arg Asn Arg Xaa Ser Gln Lys Asp Gln Ser Arg Glu Thr
1 5 10 15
Lys Lys Arg Ser Glu Glu Met Ala Ser Thr Ser Ala Met Ser Leu Val
20 25 30
Thr Pro Leu Asn Gln Thr Arg Ser Ser Pro Phe Leu Lys Pro Leu Pro
35 40 45
Leu Lys Pro Ser Lys Ala Leu Val Ala Thr Gly Gly Arg Ala Gln Arg
50 55 60
Leu Gln Val Lys Ala Leu Lys Met Asp Lys Ala Leu Thr Gly Ile Ser
65 70 75 80
Ala Ala Ala Leu Thr Ala Ser Met Val Ile Pro Glu Ile Ala Glu Ala
85 90 95
Ala Gly Ser Gly Ile Ser Pro Ser Leu Lys Asn Phe Leu Leu Ser Ile
100 105 110
Ala Ser Gly Gly Leu Val Leu Thr Val Ile Ile Gly Val Val Val Gly
115 120 125
Val Ser Asn Phe Asp Pro Val Lys Arg Thr
130 135

(2) INFORMATION FOR SEQ ID NO:1447:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 116 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..116
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570010

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1447:

Met Ala Ser Thr Ser Ala Met Ser Leu Val Thr Pro Leu Asn Gln Thr
1 5 10 15
Arg Ser Ser Pro Phe Leu Lys Pro Leu Pro Leu Lys Pro Ser Lys Ala
20 25 30
Leu Val Ala Thr Gly Gly Arg Ala Gln Arg Leu Gln Val Lys Ala Leu
35 40 45
Lys Met Asp Lys Ala Leu Thr Gly Ile Ser Ala Ala Leu Thr Ala
50 55 60
Ser Met Val Ile Pro Glu Ile Ala Glu Ala Ala Gly Ser Gly Ile Ser
65 70 75 80
Pro Ser Leu Lys Asn Phe Leu Leu Ser Ile Ala Ser Gly Gly Leu Val
85 90 95

Leu Thr Val Ile Ile Gly Val Val Val Gly Val Ser Asn Phe Asp Pro
100 105 110
Val Lys Arg Thr
115

(2) INFORMATION FOR SEQ ID NO:1448:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 110 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..110

(D) OTHER INFORMATION: / Ceres Seq. ID 1570011

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1448:

Met	Ser	Leu	Val	Thr	Pro	Leu	Asn	Gln	Thr	Arg	Ser	Ser	Pro	Phe	Leu
1			5					10						15	
Lys	Pro	Leu	Pro	Leu	Lys	Pro	Ser	Lys	Ala	Leu	Val	Ala	Thr	Gly	Gly
			20					25					30		
Arg	Ala	Gln	Arg	Leu	Gln	Val	Lys	Ala	Leu	Lys	Met	Asp	Lys	Ala	Leu
		35					40					45			
Thr	Gly	Ile	Ser	Ala	Ala	Ala	Leu	Thr	Ala	Ser	Met	Val	Ile	Pro	Glu
		50				55					60				
Ile	Ala	Glu	Ala	Ala	Gly	Ser	Gly	Ile	Ser	Pro	Ser	Leu	Lys	Asn	Phe
65				70					75					80	
Leu	Leu	Ser	Ile	Ala	Ser	Gly	Gly	Leu	Val	Leu	Thr	Val	Ile	Ile	Gly
			85					90						95	
Val	Val	Val	Gly	Val	Ser	Asn	Phe	Asp	Pro	Val	Lys	Arg	Thr		
			100					105					110		

(2) INFORMATION FOR SEQ ID NO:1449:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 691 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..691

(D) OTHER INFORMATION: / Ceres Seq. ID 1570036

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1449:

aaccttattc	tattgattaa	aattgttcg	tctcgattat	ctctgtgttt	ttgggaactg	60
agaagcatcc	actcgacaat	ggagactcgc	atttgttgga	gatttagctct	cgcaccatcc	120
tctctcttca	attctaaatc	aggggacaaa	catttagtct	caaaaggacc	atgtgtgaaat	180
cgtagcattc	tcattgacctt	gtctacatct	gctgcattgg	gtaaaaggagg	tggtgtctcta	240
gcacaaacaa	ttatagagaa	aaccactcct	ggctgtgaaat	ccgagtttga	tttaaggaaa	300
tcaaaagaaga	tagctccacc	ttacagggtg	atactacaca	atgacaactt	caacaagagg	360
gaatatgtgg	ttcaggtggt	gatgaaggta	atacccccatg	actgtagaca	acgcggttaa	420
cattatgcaa	gaagctcata	tcaacggttt	ggcagtttgt	attgttttgt	ctcaggctga	480
tcgacagcaa	cactgtatgc	agctgcgcgg	taacggcctt	ctcagttctg	ttgaacctga	540
tggtggaggc	tgctgaaact	aattaaactc	agtatagatt	ttcccacctt	ccaggactct	600
ctatttagtc	aaaaacatGt	tgttgtttta	atgtatataa	tatcagaaat	ttggtacaag	660
actgttacta	tatgcaatga	acctgtcccc	c			

(2) INFORMATION FOR SEQ ID NO:1450:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..113
(D) OTHER INFORMATION: / Ceres Seq. ID 1570037

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1450:
Met Glu Thr Ala Ile Cys Gly Arg Leu Ala Leu Ala Pro Ser Ser Leu
1 5 10 15
Phe Asn Ser Lys Ser Gly Asp Lys His Leu Val Ser Lys Gly Pro Cys
20 25 30
Val Asn Arg Ser Ile Leu Met Thr Leu Ser Thr Ser Ala Ala Leu Gly
35 40 45
Lys Gly Gly Gly Val Leu Asp Lys Pro Ile Ile Glu Lys Thr Thr Pro
50 55 60
Gly Arg Glu Ser Glu Phe Asp Leu Arg Lys Ser Lys Lys Ile Ala Pro
65 70 75 80
Pro Tyr Arg Val Ile Leu His Asn Asp Asn Phe Asn Lys Arg Glu Tyr
85 90 95
Val Val Gln Val Leu Met Lys Val Ile Pro His Asp Cys Arg Gln Arg
100 105 110
Gly

(2) INFORMATION FOR SEQ ID NO:1451:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 75 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..75
(D) OTHER INFORMATION: / Ceres Seq. ID 1570038

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1451:
Met Thr Leu Ser Thr Ser Ala Ala Leu Gly Lys Gly Gly Gly Val Leu
1 5 10 15
Asp Lys Pro Ile Ile Glu Lys Thr Thr Pro Gly Arg Glu Ser Glu Phe
20 25 30
Asp Leu Arg Lys Ser Lys Lys Ile Ala Pro Pro Tyr Arg Val Ile Leu
35 40 45
His Asn Asp Asn Phe Asn Lys Arg Glu Tyr Val Val Gln Val Leu Met
50 55 60
Lys Val Ile Pro His Asp Cys Arg Gln Arg Gly
65 70 75

(2) INFORMATION FOR SEQ ID NO:1452:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 664 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..664
(D) OTHER INFORMATION: / Ceres Seq. ID 1570039

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1452:
aacggccgat ttattaaaaa aaaactccga caaatgattc gccggccgat ctacgacttc 60
gcgcgcgttt ttgcgcactt aacttctccg ttatcgacat cctcggttt ttgtttctat 120
ttctcatctg aacatgaagc tcgaaaaccg attgtctcga accctaaatc cccaatcggtg 180
ttctcgactc ggggttcaaaa gctcatagct tcgcaatcgt atcctctcct cgccaaggag 240
attttcgatt atgctttcca acagcccaat ttccgccttt ctcatcttc tcatcctaac 300
ctcatttcca aactcggcgc tggtagatat ttcaatctta tcgacgcagt tctcgccaaa 360

cacagatcaa	gtggttatcc	attaacctga	gaaattttca	cttatctgat	caaagtctac	420
gcagaagcaa	agttaccgga	gaaagtctta	agtagctttt	acaaaatgct	ggagtccaat	480
ttcaagccgc	agccaaaaca	tctgaatcgg	attctagatg	ttctcgtaag	ccatagaggt	540
tatctccaga	aagctttttg	gcttttcaag	agtttcacgc	ttcatggagt	aatgcctaac	600
acggaaggt	acaattttat	gatgcaagct	ttttgtttga	atgatgattt	gagttatgca	660
tacc						

(2) INFORMATION FOR SEQ ID NO:1453:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 129 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..129

(D) OTHER INFORMATION: / Ceres Seq. ID 1570040

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1453:

Asn	Gly	Arg	Phe	Ile	Lys	Lys	Lys	Leu	Arg	Gln	Met	Ile	Arg	Arg	Pro
1				5					10					15	
Ile	Tyr	Asp	Phe	Ala	Ala	Val	Phe	Arg	His	Leu	Thr	Ser	Pro	Leu	Ser
			20					25					30		
Thr	Ser	Ser	Arg	Phe	Leu	Phe	Tyr	Ser	Ser	Ser	Glu	His	Glu	Ala	Arg
			35				40					45			
Lys	Pro	Ile	Val	Ser	Asn	Pro	Lys	Ser	Pro	Ile	Gly	Ser	Pro	Thr	Arg
			50				55				60				
Val	Gln	Lys	Leu	Ile	Ala	Ser	Gln	Ser	Asp	Pro	Leu	Leu	Ala	Lys	Glu
65				70					75					80	
Ile	Phe	Asp	Tyr	Ala	Ser	Gln	Gln	Pro	Asn	Phe	Arg	His	Ser	Arg	Ser
			85						90				95		
Ser	His	Leu	Ile	Leu	Ile	Leu	Lys	Leu	Gly	Arg	Gly	Arg	Tyr	Phe	Asn
			100				105						110		
Leu	Ile	Asp	Asp	Val	Leu	Ala	Lys	His	Arg	Ser	Ser	Gly	Tyr	Pro	Leu
			115				120					125			
Thr															

(2) INFORMATION FOR SEQ ID NO:1454:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 118 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..118

(D) OTHER INFORMATION: / Ceres Seq. ID 1570041

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1454:

Met	Ile	Arg	Arg	Pro	Ile	Tyr	Asp	Phe	Ala	Ala	Val	Phe	Arg	His	Leu
1				5					10					15	
Thr	Ser	Pro	Leu	Ser	Thr	Ser	Ser	Arg	Phe	Leu	Phe	Tyr	Ser	Ser	Ser
			20					25					30		
Glu	His	Glu	Ala	Arg	Lys	Pro	Ile	Val	Ser	Asn	Pro	Lys	Ser	Pro	Ile
			35				40					45			
Gly	Ser	Pro	Thr	Arg	Val	Gln	Lys	Leu	Ile	Ala	Ser	Gln	Ser	Asp	Pro
			50				55				60				
Leu	Leu	Ala	Lys	Glu	Ile	Phe	Asp	Tyr	Ala	Ser	Gln	Gln	Pro	Asn	Phe
65				70				75					80		
Arg	His	Ser	Arg	Ser	Ser	His	Leu	Ile	Leu	Ile	Leu	Lys	Leu	Gly	Arg
			85				90					95			
Gly	Arg	Tyr	Phe	Asn	Leu	Ile	Asp	Asp	Val	Leu	Ala	Lys	His	Arg	Ser

100 105 110
Ser Gly Tyr Pro Leu Thr
115

(2) INFORMATION FOR SEQ ID NO:1455:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..66
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570042

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1455:

Met	Leu	Glu	Phe	Asn	Phe	Thr	Pro	Gln	Pro	Lys	His	Leu	Asn	Arg	Ile
1		5						10				15			
Leu	Asp	Val	Leu	Val	Ser	His	Arg	Gly	Tyr	Leu	Gln	Lys	Ala	Phe	Glu
		20						25					30		
Leu	Phe	Lys	Ser	Ser	Arg	Leu	His	Gly	Val	Met	Pro	Asn	Thr	Arg	Ser
		35					40					45			
Tyr	Asn	Leu	Leu	Met	Gln	Ala	Phe	Cys	Leu	Asn	Asp	Asp	Leu	Ser	Ile
	50				55						60				
Ala	Tyr														
	65														

(2) INFORMATION FOR SEQ ID NO:1456:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 509 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..509
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570066

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1456:

acatctccca	agatcatttg	tcggttgatt	ccatacgate	tccaagtctt	gtcgttcgac	60
aatctctaag	aagctaacga	aaatggctct	tcaaaacgat	attgatctgc	ttaaccctcc	120
tgctgagctc	gagaagagga	agcacaagct	caagcgctct	gttcaatcac	ccaattcggt	180
tttcattgat	gtcaaagtgc	aagcgtgctt	taacattacg	actgtgttca	gccactctca	240
gaccgtttgt	atgtgtggaa	actgccagac	tttgctctgc	acacccacag	gagggaaggg	300
aaagctcact	gaaggatgct	ctttcaggaa	aaagtgaagc	tgaagaagaa	gatatgactc	360
cattccattc	actcaccacc	aaattttctt	ttcgtttatt	atgaattttt	gttgatattt	420
gagctagtag	taacccctct	ttgtcgatta	tcctttgttt	taatacgcga	agCtcgttcc	480
tcctttatga	atgggttatgt	attttcttg				

(2) INFORMATION FOR SEQ ID NO:1457:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 84 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..84
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570067

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1457:

Met	Val	Leu	Gln	Asn	Asp	Ile	Asp	Leu	Leu	Asn	Pro	Pro	Ala	Glu	Leu
1		5						10					15		
Glu	Lys	Arg	Lys	His	Lys	Leu	Lys	Arg	Leu	Val	Gln	Ser	Pro	Asn	Ser

	20					25						30							
Phe	Phe	Met	Asp	Val	Lys	Cys	Gln	Gly	Cys	Phe	Asn	Ile	Thr	Thr	Val				
	35						40					45							
Phe	Ser	His	Ser	Gln	Thr	Val	Val	Met	Cys	Gly	Asn	Cys	Gln	Thr	Leu				
	50						55				60								
Leu	Cys	Thr	Pro	Thr	Gly	Gly	Lys	Ala	Lys	Leu	Thr	Glu	Gly	Cys	Ser				
	65				70					75				80					
Phe	Arg	Lys	Lys																

(2) INFORMATION FOR SEQ ID NO:1458:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..50
(D) OTHER INFORMATION: / Ceres Seq. ID 1570068

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1458:

Met	Asp	Val	Lys	Cys	Gln	Gly	Cys	Phe	Asn	Ile	Thr	Thr	Val	Phe	Ser				
1			5				10				15								
His	Ser	Gln	Thr	Val	Val	Met	Cys	Gly	Asn	Cys	Gln	Thr	Leu	Leu	Cys				
		20					25				30								
Thr	Pro	Thr	Gly	Gly	Lys	Ala	Lys	Leu	Thr	Glu	Gly	Cys	Ser	Phe	Arg				
		35				40					45								
Lys	Lys																		
	50																		

(2) INFORMATION FOR SEQ ID NO:1459:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 931 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..931
(D) OTHER INFORMATION: / Ceres Seq. ID 1570069

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1459:

aaaaattctc	tgccggtgtt	gacttcaaac	tctcttgat	tagatcggcg	ccaacttcta	60
aacgcaaatg	ggaactcacg	gaaacttgat	cctgggtttg	gcttgtttag	cctttgtctc	120
cattgctaaa	gctctgcctc	atgaaccaga	acttggctcg	gctcgtgtcg	tcttccagac	180
tagttatgga	gatatcgaat	ttgggttcta	tcccactgtg	gcacccaaga	cagtggatca	240
catcttcaag	cttgttcggt	taggaggata	caacactaat	cattttctca	gggttgataa	300
aggttttgtt	gctcaagttg	cggatgtggc	gagtggaaga	tcagctccaa	tgaatgagga	360
gcaaaggaaa	gaagctgaga	agaaaattgt	gggagagttc	agtgatgtta	agcatgtcag	420
aggtactcTt	tccatgggaa	gatatgacga	tccaaacagt	gcacaaactt	cattttcgat	480
gcttcttgcc	aatgctctct	atcttgatcg	ccagtatgct	gtgtttggta	aagtacttaa	540
aggagatgaa	acattgagta	agctagaaga	agttcccact	cgccgcgag	ggatttttgt	600
tatgcgcagc	gagcggatca	cgattttgtc	gacatactat	tacgacacta	aaatggagag	660
ctgtgaagaa	gagagatctg	tcctgaaaag	aaggcttcaa	gcactctttg	tggaggtcga	720
aagacacaga	atgaagtgtc	tcctcgtgaat	gaagtttaaca	cataagaaca	tgttcaacaa	780
aagcctttaa	acgcccaggga	acacaaaggt	aaatgtatgt	ctagtaaaaa	aactcagaat	840
gctagacagt	ttttgagtg	tttatcagtg	tgagagattg	tagttaacag	tgtaaacagt	900
ttgagacatt	gaatcatgga	ttgttctctc	c			

(2) INFORMATION FOR SEQ ID NO:1460:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 226 amino acids
(B) TYPE: amino acid

(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..226
(D) OTHER INFORMATION: / Ceres Seq. ID 1570070
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1460:
Met Gly Ile Thr Arg Asn Leu Ile Leu Gly Leu Ala Cys Leu Ala Phe
1 5 10 15
Val Ser Ile Ala Lys Ala Leu Pro His Glu Pro Glu Leu Gly Ser Ala
20 25 30
Arg Val Val Phe Gln Thr Ser Tyr Gly Asp Ile Glu Phe Gly Phe Tyr
35 40 45
Pro Thr Val Ala Pro Lys Thr Val Asp His Ile Phe Lys Leu Val Arg
50 55 60
Leu Gly Gly Tyr Asn Thr Asn His Phe Phe Arg Val Asp Lys Gly Phe
65 70 75 80
Val Ala Gln Val Ala Asp Val Ala Ser Gly Arg Ser Ala Pro Met Asn
85 90 95
Glu Glu Gln Arg Lys Glu Ala Glu Lys Lys Ile Val Gly Glu Phe Ser
100 105 110
Asp Val Lys His Val Arg Gly Thr Leu Ser Met Gly Arg Tyr Asp Asp
115 120 125
Pro Asn Ser Ala Gln Ser Ser Phe Ser Met Leu Leu Gly Asn Ala Pro
130 135 140
His Leu Asp Arg Gln Tyr Ala Val Phe Gly Lys Val Thr Lys Gly Asp
145 150 155 160
Glu Thr Leu Ser Lys Leu Glu Glu Val Pro Thr Arg Arg Glu Gly Ile
165 170 175
Phe Val Met Pro Thr Glu Arg Ile Thr Ile Leu Ser Thr Tyr Tyr Tyr
180 185 190
Asp Thr Lys Met Glu Ser Cys Glu Glu Glu Arg Ser Val Leu Lys Arg
195 200 205
Arg Leu Gln Ala Ser Phe Val Glu Val Glu Arg Gln Arg Met Lys Cys
210 215 220
Phe Pro
225

(2) INFORMATION FOR SEQ ID NO:1461:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 132 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1..132
(D) OTHER INFORMATION: / Ceres Seq. ID 1570071

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1461:

Met Asn Glu Glu Gln Arg Lys Glu Ala Glu Lys Lys Ile Val Gly Glu
1 5 10 15
Phe Ser Asp Val Lys His Val Arg Gly Thr Leu Ser Met Gly Arg Tyr
20 25 30
Asp Asp Pro Asn Ser Ala Gln Ser Ser Phe Ser Met Leu Leu Gly Asn
35 40 45
Ala Pro His Leu Asp Arg Gln Tyr Ala Val Phe Gly Lys Val Thr Lys
50 55 60
Gly Asp Glu Thr Leu Ser Lys Leu Glu Glu Val Pro Thr Arg Arg Glu
65 70 75 80
Gly Ile Phe Val Met Pro Thr Glu Arg Ile Thr Ile Leu Ser Thr Tyr

	85		90		95
Tyr Tyr Asp Thr Lys Met Glu Ser Cys Glu Glu Glu Arg Ser Val Leu					
	100		105		110
Lys Arg Arg Leu Gln Ala Ser Phe Val Glu Val Glu Arg Gln Arg Met					
	115		120		125
Lys Cys Phe Pro					
	130				

(2) INFORMATION FOR SEQ ID NO:1462:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1248 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1248

(D) OTHER INFORMATION: / Ceres Seq. ID 1570072

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1462:

aatagccaca	aagacttttt	tctttcatcc	tctaaaaaaa	aatctttcta	gtgagtaacg	60
aaaaaaatgt	gtccggtgga	gaacaaatgg	ttaaagggtgg	gtcaaaaagg	agctgggtcc	120
ggggctagaa	gctcacatgc	catgaccgtc	gttgggaaca	aaattttactg	ttttggtggt	180
gagcttaagc	caacgatcca	tattgataac	gatctttacg	ttttcgatct	tgggactcaa	240
gaatgggtga	tagctcctgc	gaccggagag	gctcctttcc	ccgtgttttg	tgctcgtgat	300
gtaacgatcg	gttcaacgat	ctatgtctac	gggtggcctg	acgataaaag	gagatacaac	360
ggctcttcatt	cgtatgatac	tgagaccaat	gagtggaaat	tgttatctcc	gggtgaggaa	420
gggcttccgt	ctcgtatgata	tcattcaaat	gctggtgatg	atcggaagag	ttatgtgttt	480
cgtgggtgga	ctgctaaagg	acgtgtgaat	acgcttcatg	cgtagcatgt	tggtgatcag	540
aaatgggttg	agtatccggc	ggctggggaa	gcttgtaaa	gcagaggagc	acctgggctt	600
gtggtttggg	aaggagaaat	ttgggtttt	tttgggtttg	atggtaaatg	atgggtgat	660
attcattggt	ttgacttgcc	tagtgaacag	tggaaggctg	tggaagactc	cggggatgat	720
ccggcgggga	gaagcgtggt	tcggcggtt	tottacggga	agtaacattg	tatttatggt	780
ggggaggaga	agccgcgatg	gcttatgcac	atgggagctg	ggaagatgtc	tggaagaggt	840
tatcagcttg	atacagaagc	gttagtggtg	gagaggatgg	ttgtgtggga	tgaagaggag	900
aagccgagcc	aacgcgggtg	gtgcgcgttt	acgaaagcgg	ttaaggatgg	tgaggaaagt	960
ttgtgtgttc	atggtgggaa	ttctccgacc	aatgagcggc	ttgatgattt	gggtgttttg	1020
ggtttctctc	actttaatgt	caattaatga	ctagtgtgct	tggtgtcttc	gtgtttatga	1080
actgtttagt	gtgtgttgtt	tttaaggagt	ttaagtgtgt	atgatatgta	actgcctaag	1140
gtctgctgtt	aaggagctat	gtgtgtgtaa	actttgctac	ctattccaaa	tattttatta	1200
agtgtgtgtg	tttgtaatt	taataaaaaa	cttgttagtc	tgattctc		

(2) INFORMATION FOR SEQ ID NO:1463:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 326 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..326

(D) OTHER INFORMATION: / Ceres Seq. ID 1570073

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1463:

Met Cys Pro Val Glu Asn Lys Trp Leu Lys Val Gly Gln Lys Gly Ala	
1	5 10 15
Gly Pro Gly Ala Arg Ser Ser His Ala Met Thr Val Val Gly Asn Lys	
	20 25 30
Val Tyr Cys Phe Gly Gly Glu Leu Lys Pro Thr Ile His Ile Asp Asn	
	35 40 45
Asp Leu Tyr Val Phe Asp Leu Gly Thr Gln Glu Trp Ser Ile Ala Pro	
	50 55 60
Ala Thr Gly Glu Ala Pro Phe Pro Cys Phe Gly Val Ser Met Val Thr	

(i) SEQUENCE CHARACTERISTICS:

(i) SEQUENCE CHARACTERISTICS:

- (ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (x1) SEQUENCE DESCRIPTION: SEQ ID NO:1464:

Met	Thr	Val	Val	Gly	Asn	Lys	Val	Tyr	Cys	Phe	Gly	Gly	Glu	Leu	Lys
1				5					10					15	
Pro	Thr	Ile	His	Ile	Asp	Asn	Asp	Leu	Tyr	Val	Phe	Asp	Leu	Gly	Thr
			20					25					30		
Gln	Glu	Trp	Ser	Ile	Ala	Pro	Ala	Thr	Gly	Glu	Ala	Pro	Phe	Pro	Cys
		35					40					45			
Phe	Gly	Val	Ser	Met	Val	Thr	Ile	Gly	Ser	Thr	Ile	Tyr	Val	Tyr	Gly
	50					55					60				
Gly	Arg	Asp	Asp	Lys	Arg	Tyr	Asn	Gly	Leu	His	Ser	Tyr	Asp	Thr	
65					70				75					80	
Glu	Thr	Asn	Glu	Trp	Lys	Leu	Leu	Ser	Pro	Val	Glu	Glu	Gly	Leu	Pro
				85				90					95		
Gly	Arg	Ser	Tyr	His	Ser	Met	Ala	Gly	Asp	Asp	Arg	Lys	Val	Tyr	Val
		100						105					110		
Phe	Arg	Gly	Val	Thr	Ala	Lys	Gly	Arg	Val	Asn	Thr	Leu	His	Ala	Tyr
		115					120					125			

Asp	Val	Val	Asp	Gln	Lys	Trp	Val	Glu	Tyr	Pro	Ala	Ala	Gly	Glu	Ala	
	130					135					140					
Cys	Lys	Gly	Arg	Gly	Ala	Pro	Gly	Leu	Val	Val	Val	Glu	Gly	Arg	Ile	
145					150					155					160	
Trp	Val	Leu	Phe	Gly	Phe	Asp	Gly	Asn	Glu	Leu	Gly	Asp	Ile	His	Cys	
				165					170					175		
Phe	Asp	Leu	Ala	Ser	Glu	Gln	Trp	Lys	Ala	Val	Glu	Thr	Thr	Gly	Asp	
		180						185					190			
Val	Pro	Ala	Ala	Arg	Ser	Val	Phe	Pro	Ala	Val	Ser	Tyr	Gly	Lys	Tyr	
		195					200					205				
Ile	Val	Ile	Tyr	Gly	Gly	Glu	Glu	Glu	Pro	His	Glu	Leu	Met	His	Met	
	210						215				220					
Gly	Ala	Gly	Lys	Met	Ser	Gly	Glu	Val	Tyr	Gln	Leu	Asp	Thr	Glu	Thr	
225					230				235						240	
Leu	Val	Trp	Glu	Arg	Ile	Val	Cys	Gly	Asn	Glu	Glu	Lys	Pro	Ser		
				245					250				255			
Gln	Arg	Gly	Trp	Cys	Ala	Phe	Thr	Lys	Ala	Val	Lys	Asp	Gly	Glu	Glu	
			260					265					270			
Gly	Leu	Leu	Val	His	Gly	Gly	Asn	Ser	Pro	Thr	Asn	Glu	Arg	Leu	Asp	
	275						280						285			
Asp	Leu	Val	Phe	Trp	Gly	Phe	Ser	His	Leu	Asn	Val	Asn				
	290					295					300					

(2) INFORMATION FOR SEQ ID NO:1465:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 249 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..249

(D) OTHER INFORMATION: / Ceres Seq. ID 1570075

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1465:

Met	Val	Thr	Ile	Gly	Ser	Thr	Ile	Tyr	Val	Tyr	Gly	Gly	Arg	Asp	Asp	
1				5				10					15			
Lys	Arg	Arg	Tyr	Asn	Gly	Leu	His	Ser	Tyr	Asp	Thr	Glu	Thr	Asn	Glu	
			20					25					30			
Trp	Lys	Leu	Leu	Ser	Pro	Val	Glu	Glu	Gly	Leu	Pro	Gly	Arg	Ser	Tyr	
		35					40					45				
His	Ser	Met	Ala	Gly	Asp	Asp	Arg	Lys	Val	Tyr	Val	Phe	Arg	Gly	Val	
	50					55					60					
Thr	Ala	Lys	Gly	Arg	Val	Asn	Thr	Leu	His	Ala	Tyr	Asp	Val	Val	Asp	
65					70					75					80	
Gln	Lys	Trp	Val	Glu	Tyr	Pro	Ala	Ala	Gly	Glu	Ala	Cys	Lys	Gly	Arg	
			85					90					95			
Gly	Ala	Pro	Gly	Leu	Val	Val	Val	Glu	Gly	Arg	Ile	Trp	Val	Leu	Phe	
		100						105					110			
Gly	Phe	Asp	Gly	Asn	Glu	Leu	Gly	Asp	Ile	His	Cys	Phe	Asp	Leu	Ala	
		115					120					125				
Ser	Glu	Gln	Trp	Lys	Ala	Val	Glu	Thr	Thr	Gly	Asp	Val	Pro	Ala	Ala	
	130					135					140					
Arg	Ser	Val	Phe	Pro	Ala	Val	Ser	Tyr	Gly	Lys	Tyr	Ile	Val	Ile	Tyr	
145					150					155					160	
Gly	Gly	Glu	Glu	Glu	Pro	His	Glu	Leu	Met	His	Met	Gly	Ala	Gly	Lys	
				165					170				175			
Met	Ser	Gly	Glu	Val	Tyr	Gln	Leu	Asp	Thr	Glu	Thr	Leu	Val	Trp	Glu	
		180						185					190			
Arg	Ile	Val	Cys	Gly	Asn	Glu	Glu	Glu	Lys	Pro	Ser	Gln	Arg	Gly	Trp	
		195				200					205					
Cys	Ala	Phe	Thr	Lys	Ala	Val	Lys	Asp	Gly	Glu	Glu	Gly	Leu	Leu	Val	

210 215 220
His Gly Gly Asn Ser Pro Thr Asn Glu Arg Leu Asp Asp Leu Val Phe
225 230 235 240
Trp Gly Phe Ser His Leu Asn Val Asn

(2) INFORMATION FOR SEQ ID NO:1466:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 276 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..276
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570080

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1466:

ctcttttcgac ttcagtgaggc gcgcattcag agattcaaac tcagagaaaa tgggtggcgac 60
aggcttattc gtgggggctaa acaaaggaca cggtgttacc aaacgcgagc aacctctcgc 120
ccctaacaac agaaaaagga aaacaagcaa aaggactatt ttatcaggga atctcatcaa 180
ggaagtgtgc ggtcaagctc cctatgagaa gaggtacact gataaaaaata gtccttttgc 240
tcgtddtaat tttagctgtt taggtacttc tgggttc

(2) INFORMATION FOR SEQ ID NO:1467:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 91 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..91
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570081

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1467:

Ser Phe Asp Phe Ser Gly Gly Ala Phe Arg Asp Ser Asn Ser Glu Lys
1 5 10 15
Met Val Ala Thr Gly Leu Phe Val Gly Leu Asn Lys Gly His Val Val
20 25 30
Thr Lys Arg Glu Gln Pro Pro Arg Pro Asn Asn Arg Lys Gly Lys Thr
35 40 45
Ser Lys Arg Thr Ile Phe Ile Arg Asn Leu Ile Lys Glu Val Ala Gly
50 55 60
Gln Ala Pro Tyr Glu Lys Arg Ile Thr Asp Lys Asn Ser Pro Phe Ala
65 70 75 80
Arg Xaa Asn Phe Gln Leu Leu Gly Thr Ser Gly
85 90

(2) INFORMATION FOR SEQ ID NO:1468:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 75 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..75
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570082

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1468:

Met Val Ala Thr Gly Leu Phe Val Gly Leu Asn Lys Gly His Val Val
1 5 10 15
Thr Lys Arg Glu Gln Pro Pro Arg Pro Asn Asn Arg Lys Gly Lys Thr

	20		25		30										
Ser	Lys	Arg	Thr	Ile	Phe	Ile	Arg	Asn	Leu	Ile	Lys	Glu	Val	Ala	Gly
	35		40		45		50		55		60				
Gln	Ala	Pro	Tyr	Glu	Lys	Arg	Ile	Thr	Asp	Lys	Asn	Ser	Pro	Phe	Ala
	50		55		60										
Arg	Xaa	Asn	Phe	Gln	Leu	Leu	Gly	Thr	Ser	Gly					
	65		70		75										

(2) INFORMATION FOR SEQ ID NO:1469:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 941 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..941
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570107

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1469:

gacaaacccaa	aaaaaaagcc	taaaaaagccg	accttttttc	ttcttttttc	tcctctacct	60
ctcagctttct	gctgtgattct	tccagcagac	acgatcttgc	tcggagagat	tcgtaggggg	120
ccgatctatc	aagccttcaa	gggcaaacag	aaatggacca	cgacaagaca	ggatgccaaa	180
gcccacctga	aggtcccaag	ctatgtacta	acaactgcgg	ttcttttgaa	gcgctgccac	240
aatgaacatg	tgttctaagt	gtcacaagga	tatgtgtgtc	caacagtagc	agggcgctaa	300
gtttgcattc	gcagtgctgc	gaacatcgtc	atccagcaac	atcataaagg	aaacctttac	360
cgctgcgttg	gtcgatattg	aaaccaaact	cgttgagcgc	atgactgttt	ctgtacagcc	420
atcctctgtc	caagtcgttg	cagaggtagt	agccagcaga	aagsgtcgca	aaccaaaagg	480
accaaagcga	tgtactactt	gcaataaagc	ggttggcctg	actggattca	aatgtcgcgt	540
tggtgagctc	ttctgcggaa	AACacaccgc	tatgcagaca	tacatgactg	ctccttcaat	600
taccatgtgc	ctcgccaaga	gcgcgatagc	aaggcaaac	cggttgtaga	agcagagaag	660
cttgacaaaa	ttctgaaact	taagttaaact	tctctgtgtt	catcaggtgg	ctggtgtttt	720
ctctctctgc	ttctgtgtgc	gttcaagtat	tctcatgtta	aaaagggttt	atataaggtc	780
gaatgaaagc	gtgcttgatc	tttagcgtct	tccatctctc	tgcaatattt	gtggtgtgga	840
actttctatt	atctgtgttt	gcaagcagag	aaacgtgctc	ttaaaaaaa	tgctttgtgt	900
gtttatcttt	ctactatttt	tgagcactgt	gttattgttt	c		

(2) INFORMATION FOR SEQ ID NO:1470:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 85 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..85
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570108

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1470:

Asp	Lys	Pro	Lys	Lys	Pro	Lys	Lys	Pro	Thr	Phe	Phe	Leu	Ser	Phe
	5		10		15		20		25		30		35	
Ser	Pro	Leu	Pro	Leu	Ser	Phe	Cys	Trp	Ile	Ser	Pro	Ala	Asp	Thr
	20		25		30		35		40		45		50	
Leu	Phe	Gly	Glu	Ile	Arg	Arg	Gly	Pro	Ile	Tyr	Gln	Gly	Phe	Lys
	35		40		45		50		55		60		65	
Lys	Gln	Lys	Trp	Thr	Thr	Thr	Arg	Gln	Asp	Ala	Lys	Ala	His	Leu
	50		55		60		65		70		75		80	
Val	Pro	Ser	Tyr	Val	Leu	Thr	Thr	Ala	Val	Ser	Leu	Lys	Arg	Cys
	65		70		75		80		85		90		95	
Asn	Glu	His	Val	Phe										

(2) INFORMATION FOR SEQ ID NO:1471:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 62 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..62
(D) OTHER INFORMATION: / Ceres Seq. ID 1570109
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1471:
Thr Asn Gln Lys Lys Ser Leu Lys Ser Arg Pro Phe Phe Phe Leu Ser
1 5 10 15
Leu Leu Tyr Leu Ser Ala Ser Ala Gly Ser Leu Gln Gln Thr Arg Ser
20 25 30
Cys Ser Glu Arg Phe Val Gly Asp Arg Ser Ile Lys Ala Ser Arg Ala
35 40 45
Asn Arg Asn Gly Pro Arg Gln Asp Arg Met Pro Lys Pro Thr
50 55 60

(2) INFORMATION FOR SEQ ID NO:1472:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 75 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..75
(D) OTHER INFORMATION: / Ceres Seq. ID 1570110
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1472:
Met Thr Val Ser Val Gln Pro Ser Ser Val Gln Val Val Ala Glu Val
1 5 10 15
Val Ala Pro Glu Glu Xaa Ala Lys Pro Lys Gly Pro Ser Arg Cys Thr
20 25 30
Thr Cys Asn Lys Arg Val Gly Leu Thr Gly Phe Lys Cys Arg Cys Gly
35 40 45
Ser Leu Phe Cys Gly Lys His Thr Ala Met Gln Thr Tyr Met Thr Ala
50 55 60
Pro Ser Ile Thr Met Leu Leu Arg Lys Arg Arg
65 70 75

(2) INFORMATION FOR SEQ ID NO:1473:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 601 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..601
(D) OTHER INFORMATION: / Ceres Seq. ID 1570111
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1473:
aagacaaaagc gcagaaaatg gtgggagcga ctgtagttag taaatggact ccctatgtg 60
tgGCttcgcc gccggagaga aactcggcaa gtctcaatcc acactgtttc ccagccaggg 120
ttaattttag aacagcggtg gccgcatttc gtctcagtt cgtctctttc tctcgcaatt 180
cgcgctctcg ccgcccgtct cgcgcttcca gctccgcgga atcgggcggg agacgcggat 240
gctcaaggaa agtatccata cacaggttcg ctcgattgtg cgatgaaaac cttaaaagaa 300
ggaggacctc tgaattttta ctcaggtttc ccagtttact gtgtcaggat tgccctcatc 360
gtcatgatga catggatctt cctaaaccag attacgaaat ttcaaaagaa gatgggtgat 420
tgaggaaacg agacagcagc aaaaaataa gatgagaaga acgaaaacac aattggaatt 480
gtgttcattt accttttaat catatacata acctgcctta aaagcatatt attgtagctg 540

tttgaacttt aattttttgt ttcggtcggt gattggtccg gtgaatttta aattttcttc 600
C

(2) INFORMATION FOR SEQ ID NO:1474:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 150 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..150
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570112

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1474:

Asp	Lys	Ala	Gln	Lys	Met	Val	Gly	Ala	Thr	Val	Val	Ser	Lys	Trp	Thr
1				5					10					15	
Pro	Leu	Cys	Val	Ala	Ser	Pro	Pro	Glu	Arg	Asn	Ser	Ala	Ser	Leu	Asn
			20					25					30		
Pro	His	Cys	Ser	Pro	Ala	Arg	Val	Asn	Phe	Arg	Thr	Ala	Leu	Ala	Ala
		35					40					45			
Phe	Arg	Pro	Gln	Phe	Arg	Leu	Phe	Ser	Arg	Asn	Ser	Ala	Ser	Arg	Arg
	50					55					60				
Arg	Leu	Arg	Ala	Ser	Ser	Ala	Glu	Ser	Ala	Ala	Arg	Arg	Gly	Cys	
	65				70				75					80	
Ser	Arg	Lys	Val	Ser	Ile	His	Arg	Phe	Ala	Arg	Leu	Cys	Asp	Glu	Asn
			85						90					95	
Leu	Lys	Arg	Arg	Arg	Thr	Ser	Glu	Ile	Leu	Leu	Arg	Phe	Pro	Ser	Leu
			100					105					110		
Leu	Cys	Gln	Asp	Cys	Pro	Ser	Arg	His	Asp	Asp	Met	Asp	Leu	Pro	Lys
		115						120					125		
Pro	Asp	Tyr	Glu	Ile	Ser	Lys	Glu	Asp	Trp	Tyr	Val	Arg	Asn	Glu	Asp
	130					135					140				
Ser	Ser	Lys	Lys	Ile	Arg										
	145				150										

(2) INFORMATION FOR SEQ ID NO:1475:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 145 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..145
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570113

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1475:

Met	Val	Gly	Ala	Thr	Val	Val	Ser	Lys	Trp	Thr	Pro	Leu	Cys	Val	Ala
1									10					15	
Ser	Pro	Pro	Glu	Arg	Asn	Ser	Ala	Ser	Leu	Asn	Pro	His	Cys	Ser	Pro
			20					25					30		
Ala	Arg	Val	Asn	Phe	Arg	Thr	Ala	Leu	Ala	Ala	Phe	Arg	Pro	Gln	Phe
		35					40					45			
Arg	Leu	Phe	Ser	Arg	Asn	Ser	Ala	Ser	Arg	Arg	Arg	Leu	Arg	Ala	Ser
	50					55					60				
Ser	Ser	Ala	Glu	Ser	Ala	Ala	Arg	Arg	Gly	Cys	Ser	Arg	Lys	Val	Ser
	65				70				75					80	
Ile	His	Arg	Phe	Ala	Arg	Leu	Cys	Asp	Glu	Asn	Leu	Lys	Arg	Arg	Arg
			85						90					95	
Thr	Ser	Glu	Ile	Leu	Leu	Arg	Phe	Pro	Ser	Leu	Leu	Cys	Gln	Asp	Cys
			100					105					110		
Pro	Ser	Arg	His	Asp	Asp	Met	Asp	Leu	Pro	Lys	Pro	Asp	Tyr	Glu	Ile

115 120 125
Ser Lys Glu Asp Trp Tyr Val Arg Asn Glu Asp Ser Ser Lys Lys Ile
130 135 140

Arg
145

(2) INFORMATION FOR SEQ ID NO:1476:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 621 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..621
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570116

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1476:

accctaagcg	tatataaatc	atatagtttt	catttttttcg	tactttctot	ccatcgccgt	60
ctaaaaaaccc	taatctcact	cgcctctctg	cgagatccat	caacacttac	gcaaaaaatga	120
agggttggtgc	tgcggtttttg	cttgccgctct	tgagcgggaa	agcttcccca	accaactggcg	180
atatcaagga	tattcttgga	tcagttgggtg	ctgagacaga	ggattctcag	attgagcttt	240
tgttgaagga	agtgaagg	aaagacttgg	ctgagctaata	tgctgctgga	agggagaagt	300
tagcttcagt	accatcagga	ggtgggtgggt	gtgttcgggt	tgctctgct	acatctggag	360
gtggaggagg	tggttggtgct	cctgctgctg	agtcgaagaa	agaagagaag	aaagaagaga	420
agaagaagac	cgatgatgac	atgggtttca	gtttgttcga	gtaatgcggt	atactggca	480
tttggttttg	ctgtaccctt	tcgaaatctt	tatgtcggtg	tttagttgt	tgatttcgac	540
tatctcttta	gactttgctg	aaattctcaa	gagatttttt	Tactcaaca	tcagtoCact	600
tgtagttggc	atttatattt	c				

(2) INFORMATION FOR SEQ ID NO:1477:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..115
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570117

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1477:

Met	Lys	Val	Val	Ala	Ala	Phe	Leu	Leu	Ala	Val	Leu	Ser	Gly	Lys	Ala
1				5					10					15	
Ser	Pro	Thr	Thr	Gly	Asp	Ile	Lys	Asp	Ile	Leu	Gly	Ser	Val	Gly	Ala
			20				25						30		
Glu	Thr	Glu	Asp	Ser	Gln	Ile	Glu	Leu	Leu	Leu	Lys	Glu	Val	Lys	Gly
			35				40					45			
Lys	Asp	Leu	Ala	Glu	Leu	Ile	Ala	Ala	Gly	Arg	Glu	Lys	Leu	Ala	Ser
	50				55				60						
Val	Pro	Ser	Gly	Gly	Gly	Gly	Val	Ala	Val	Ala	Ser	Ala	Thr	Ser	
65				70			75						80		
Gly	Gly	Gly	Gly	Gly	Gly	Gly	Ala	Pro	Ala	Ala	Glu	Ser	Lys	Lys	Glu
			85				90					95			
Glu	Lys	Lys	Glu	Glu	Lys	Glu	Glu	Ser	Asp	Asp	Asp	Met	Gly	Phe	Ser
			100				105					110			
Leu	Phe	Glu													

(2) INFORMATION FOR SEQ ID NO:1478:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 534 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

- (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..534

(D) OTHER INFORMATION: / Ceres Seq. ID 1570138

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1478:

atattcaaag attagaaca ttcttgatag atacaaaaaa cattttttca gacacaaatt	60
cataaaatct ttgccttgag tagatcaaaag ttctttacat taatcgttag aagatgagcc	120
agtagcatca caaccagttct gcaggagcta acccaaccgcc accgatgtct acctgtacat	180
caccaccacc gccgatttgt taccgcacta acccaaccgcc tcatggttcg gtatgtcagc	240
gtaaaagtga aaccaagtct aagggtgacg gattcttcaa aggtgtgtct gcggccatgt	300
gttgctgttg tgccttgagc atttgcttct aagccatttg ggaattggga tggctctatt	360
atgacgagtt tatgtgaagt tgaatggaat tattattatt attctctcca gccttatgt	420
ataaaattctc tattttttgt ttattatttt ctgtgaatc tttgtgagc gaacatatta	480
tgttttgtat ttgatctct actctctagt acttaaatc atttgccttg cYtt	

- (2) INFORMATION FOR SEQ ID NO:1479:

- (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 72 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide

- (ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..72

(D) OTHER INFORMATION: / Ceres Seq. ID 1570139

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1479:

Met Ser Gln Tyr Asp His Asn Gln Ser Ala Gly Ala Asn Pro Pro Pro	
1 5 10 15	
Pro Met Ser Thr Cys Thr Ser Pro Pro Pro Pro Ile Gly Tyr Pro Thr	
20 25 30	
Asn Gln Pro Ser His Gly Ser Val Ala Gln Gly Lys Val Glu Thr Lys	
35 40 45	
Ser Lys Gly Asp Gly Phe Phe Lys Gly Cys Leu Ala Ala Met Cys Cys	
50 55 60	
Cys Cys Ala Leu Asp Ile Cys Phe	
65 70	

- (2) INFORMATION FOR SEQ ID NO:1480:

- (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 55 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide

- (ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..55

(D) OTHER INFORMATION: / Ceres Seq. ID 1570140

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1480:

Met Ser Thr Cys Thr Ser Pro Pro Pro Pro Ile Gly Tyr Pro Thr Asn	
1 5 10 15	
Gln Pro Ser His Gly Ser Val Ala Gln Gly Lys Val Glu Thr Lys Ser	
20 25 30	
Lys Gly Asp Gly Phe Phe Lys Gly Cys Leu Ala Ala Met Cys Cys Cys	
35 40 45	
Cys Ala Leu Asp Ile Cys Phe	
50 55	

- (2) INFORMATION FOR SEQ ID NO:1481:

- (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 51 amino acids

(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..51
(D) OTHER INFORMATION: / Ceres Seq. ID 1570141
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1481:
Met Thr Ser Leu Cys Glu Cys Asp Val Asn Tyr Tyr Tyr Ser Leu
1 5 10 15
Gln Pro Tyr Cys Ile Asn Ser Leu Phe Val Tyr Tyr Phe Leu Val
20 25 30
Ile Leu Cys Glu Thr Asn Ile Leu Cys Phe Val Phe Gly Ser Leu Leu
35 40 45
Ser Ser Thr
50

(2) INFORMATION FOR SEQ ID NO:1482:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 689 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..689
(D) OTHER INFORMATION: / Ceres Seq. ID 1570142
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1482:
aaccaatctc aaagcaaat aaatacacta ctactttctg agctttttaa ctacacaaac 60
aaatggctcc aagaaccccc ctgacactct tcgtttctct caacctctct ttcttcaact 120
acactctcgc aaccacaggc acttgctcta aaaattccat agagatcggt acttgtgtca 180
ctgtgctcaa tctagtggac ctaacattgg gaaaccacac tgtaaagcca tgttgctcgc 240
tcatccaagg ctggctgac cttgaggctg cggcctgcct ctgcaactgcg ctcaaagcta 300
gcattcttgg aattgtcaat attaaccttc ctatcaatct cagcgctact ctcaatgttt 360
gtagtaggaa tgcctccaaag agtttccagt gcgcgttaagt tgaataccta tgacatacct 420
atgaaacaaa cgaatcatac csmTgcttga acatgttttc ttacctactt gttgtgttct 480
taagatgttt gttttttctt tctttcttgg attgttaata atgaacgtac gacgttctga 540
tgcaaaaataa tggaaaaatg gggtgtgtgt acaatcgaca agtttgtata tactccttta 600
ctttgtgttt cctttgtttt gttgttcttc ttcttgttaa ctgtgtattt caaatgtgct 660
taataaaaaa ataaaattgat gttgtagcc

(2) INFORMATION FOR SEQ ID NO:1483:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 111 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..111
(D) OTHER INFORMATION: / Ceres Seq. ID 1570143
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1483:
Met Ala Pro Arg Thr Pro Leu Ala Leu Phe Val Ser Leu Asn Leu Leu
1 5 10 15
Phe Phe Thr Tyr Thr Ser Ala Thr Thr Gly Thr Cys Pro Lys Asn Ser
20 25 30
Ile Glu Ile Gly Thr Cys Val Thr Val Leu Asn Leu Val Asp Leu Thr
35 40 45
Leu Gly Asn Pro Pro Val Lys Pro Cys Cys Ser Leu Ile Gln Gly Leu
50 55 60

Ala Asp Leu Glu Ala Ala Ala Cys Leu Cys Thr Ala Leu Lys Ala Ser
65 70 75 80
Ile Leu Gly Ile Val Asn Ile Asn Leu Pro Ile Asn Leu Ser Val Leu
85 90 95
Leu Asn Val Cys Ser Arg Asn Ala Pro Lys Ser Phe Gln Cys Ala
100 105 110

(2) INFORMATION FOR SEQ ID NO:1484:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 716 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..716
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570159

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1484:

aatcaagcaa	tccaaagcga	ttaaacctac	tcaatctcag	atctcgtaa	acctagaaac	60
ctcgagaaaa	accgtatcaa	tggcgccgaa	agcagagaag	aagcccgctg	agaagaaacc	120
agcttcggag	aagccggtgg	aggagaaatc	aaaagccgag	aaagctccgg	cggagaagaa	180
accaaaggcc	ggaaaagaagc	tccgaagga	agctgtgtgc	ggaggcgaca	agaagaaaaa	240
gatgaagaag	aagagtgtgc	agacttacaa	gatctacatc	tcaaggtgc	ttaagcaagt	300
tcattccgat	atcggaatct	ccagcaaaagc	gatggggatc	atgaacagtt	tcattaacga	360
tatcttcgag	aagcttgctc	aagaggcgtc	gaagcttgcg	aggtacaata	agadacctac	420
gatcactctc	cggagagattc	agactgctgt	gagattgggtg	cttcctcgga	agttggcgaa	480
cgatcgcggtt	tctgagggga	ctaaagccgt	cacgaaattc	accagctctt	gaataattga	540
gttaggggttc	ttatcatatg	gatgttgctc	tgctttagggt	ttaatggatc	tttaagagtc	600
tgagttaggg	ttttagaatg	tcctttaagt	atctctgttt	cgtttggaat	ttctacgttt	660
tgtaagtact	gctgctattg	ataatgtttg	gagtcatat	ttgctctttg	tgctccc	

(2) INFORMATION FOR SEQ ID NO:1485:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 176 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..176
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570160

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1485:

Ile	Lys	Gln	Ser	Lys	Ala	Ile	Lys	Pro	Thr	Gln	Ser	Gln	Ile	Ser	Leu
1		5						10					15		
Asn	Leu	Glu	Thr	Ser	Arg	Lys	Thr	Val	Ser	Met	Ala	Pro	Lys	Ala	Glu
		20					25						30		
Lys	Lys	Pro	Ala	Glu	Lys	Lys	Pro	Ala	Ser	Glu	Lys	Pro	Val	Glu	Glu
		35				40					45				
Lys	Ser	Lys	Ala	Glu	Lys	Ala	Pro	Ala	Glu	Lys	Lys	Pro	Lys	Ala	Gly
	50				55					60					
Lys	Lys	Leu	Pro	Lys	Glu	Ala	Gly	Ala	Gly	Gly	Asp	Lys	Lys	Lys	Lys
65			70					75						80	
Met	Lys	Lys	Lys	Ser	Val	Glu	Thr	Tyr	Lys	Ile	Tyr	Ile	Phe	Lys	Val
			85					90					95		
Leu	Lys	Gln	Val	His	Pro	Asp	Ile	Gly	Ile	Ser	Ser	Lys	Ala	Met	Gly
			100				105						110		
Ile	Met	Asn	Ser	Phe	Ile	Asn	Asp	Ile	Phe	Glu	Lys	Leu	Ala	Gln	Glu
			115				120					125			
Ala	Ser	Lys	Leu	Ala	Arg	Tyr	Asn	Lys	Xaa	Pro	Thr	Ile	Thr	Ser	Arg
			130				135					140			
Glu	Ile	Gln	Thr	Ala	Val	Arg	Leu	Val	Leu	Pro	Gly	Glu	Leu	Ala	Lys

145 150 155 160
His Ala Val Ser Glu Gly Thr Lys Ala Val Thr Lys Phe Thr Ser Ser
 165 170 175

(i) SEQUENCE CHARACTERISTICS:

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: lin

MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..150

(D) OTHER INFORMATION: / Ceres Seq. ID 1570161

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1486:

Met	Ala		Pro	Lys		Ala	Glu	Lys	Lys	Pro		Ala	Ser
1					5					10			15
Glu	Lys		Pro	Val		Glu	Glu	Lys	Ser	Lys	Ala	Glu	Lys
				20					25			30	
Lys	Lys		Pro	Lys		Ala	Gly	Lys	Lys	Leu	Pro	Lys	Glu
				35					40			45	
Gly	Asp		Lys	Lys		Lys	Lys	Met	Lys	Lys	Lys	Ser	Val
50								55				60	
Ile	Tyr		Ile	Phe		Lys	Val	Leu	Lys	Gln	Val	His	Pro
65							70					75	
Ser	Ser		Lys	Ala		Met	Gly	Ile	Met	Asn	Ser	Phe	Ile
					85						90		
Glu	Lys		Leu	Ala		Gln	Glu	Ala	Ser	Lys	Leu	Ala	Arg
				100						105			
Pro	Thr		Ile	Thr		Ser	Arg	Glu	Ile	120	Gln	Thr	Ala
				115					120				
Pro	Gly		Glu	Leu		Ala	Lys	His	Ala	Val	Ser	Glu	Gly
130								135					140
Thr	Lys		Phe	Thr		Ser	Ser						
145							150						

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 96 amino aci

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: lin

MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..96

(D) OTHER INFORMATION: / Ceres Seq. ID 1570162

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1487:

Met	Lys	Lys	Lys	Ser	Val	Glu	Thr	Tyr	Lys	Ile	Tyr	Ile	Phe	Lys	Val
1				5					10					15	
Leu	Lys	Gln	Val	His	Pro	Asp	Ile	Gly	Ile	Ser	Ser	Lys	Ala	Met	Gly
			20					25					30		
Ile	Met	Asn	Ser	Phe	Ile	Asn	Asp	Ile	Phe	Glu	Lys	Leu	Ala	Gln	Glu
		35					40					45			
Ala	Ser	Lys	Leu	Ala	Arg	Tyr	Asn	Lys	Xaa	Pro	Thr	Ile	Thr	Ser	Arg
	50					55				60					
Glu	Ile	Gln	Thr	Ala	Val	Arg	Leu	Val	Leu	Pro	Gly	Glu	Leu	Ala	Lys
65					70					75				80	
His	Ala	Val	Ser	Glu	Gly	Thr	Lys	Ala	Val	Thr	Lys	Phe	Thr	Ser	Ser
				85					90					95	

(2) INFORMATION FOR SEQ ID NO:1488:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 936 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..936
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570163

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1488:

aaccttatca	cgctattctc	aaacaagcaa	agaaccttaa	ccaaaagaaa	aacgtctacg	60
gagacatatg	gagaggaaac	atcacttcgt	gttagttcac	aacgcttacc	atggagcctg	120
gattctggtag	aaagctcaagc	ccctcccttga	atcagccggc	caccgcgtta	ctgctgtcga	180
actcgccgcc	tccgggtagc	accacagacc	aatccaggcc	gttgaaacgc	tcgacgaata	240
ctccaaacgc	ttgatcgaaa	ccctcaaatc	tctccagag	aacgaagagg	taattctggt	300
tggattcagc	tccggaggca	tcaacatcgc	tctccggcc	gacatatctc	cgcggaagat	360
taaggttctt	gtgttctctc	acgccttctt	gcccgacaca	acccacgtgc	cttctcacgt	420
tctggacaag	tatatggaga	tgccctggagg	tttgggagat	tgtgagtttt	catctcatga	480
aaacaagaaa	gggacgatga	gtttattTga	agatggggacc	aaaattcatg	aaggcacgtc	540
ttaccacaaa	tgtctccata	gaggattacg	agctggcaca	aatgttgcat	aggaacgggt	600
catctttcac	agaggatcta	tcaagaagaa	aaaagttag	cgaggaaagga	tatgggtcgg	660
tgaacagagt	ttacgttatg	agttagtgaag	acaaagccat	ccctcgcat	ttcattcggt	720
ggatgattga	taatttcaac	gtctcgaaag	tctacagat	cgatggcgga	gatcacatgg	780
tgatgctctc	caaaccccaa	aaactctttg	actctctctc	tgctattgcc	acgattata	840
tgttaataatc	ttaagtcctg	ttacttttt	tctcatggt	actaataaaa	caaacccctt	900
tttcggcgca	actttcatca	aaaaacaaaa	cttatg			

(2) INFORMATION FOR SEQ ID NO:1489:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 174 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..174
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570164

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1489:

Met	Glu	Arg	Lys	His	His	Phe	Val	Leu	Val	His	Asn	Ala	Tyr	His	Gly
1			5					10					15		
Ala	Trp	Ile	Trp	Tyr	Lys	Leu	Lys	Pro	Leu	Leu	Glu	Ser	Ala	Gly	His
			20					25					30		
Arg	Val	Thr	Ala	Val	Glu	Leu	Ala	Ala	Ser	Gly	Ile	Asp	Pro	Arg	Pro
			35					40					45		
Ile	Gln	Ala	Val	Glu	Thr	Val	Asp	Glu	Tyr	Ser	Lys	Pro	Leu	Ile	Glu
			50					55					60		
Thr	Leu	Lys	Ser	Leu	Pro	Glu	Asn	Glu	Val	Ile	Leu	Val	Gly	Phe	
65								70					75		80
Ser	Phe	Gly	Gly	Ile	Asn	Ile	Ala	Leu	Ala	Ala	Asp	Ile	Phe	Pro	Ala
			85					90					95		
Lys	Ile	Lys	Val	Leu	Val	Phe	Leu	Asn	Ala	Phe	Leu	Pro	Asp	Thr	Thr
			100					105					110		
His	Val	Pro	Ser	His	Val	Leu	Asp	Lys	Tyr	Met	Glu	Met	Pro	Gly	Gly
			115					120					125		
Leu	Gly	Asp	Cys	Glu	Phe	Ser	Ser	His	Glu	Thr	Arg	Asn	Gly	Thr	Met
			130					135					140		
Ser	Leu	Phe	Glu	Asp	Gly	Thr	Lys	Ile	His	Glu	Gly	Thr	Ser	Leu	Pro

(2) INFORMATION FOR SEO ID NO:1490:

(i) SEQUENCE CHARACTERISTICS:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 110 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

```
(ix) FEATURE:
```

- ```
(A) NAME/KEY: peptide
(B) LOCATION: 1..110
```

(D) OTHER INFORMATION: / Ceres Seq. ID 1570165

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1490:

(2) INFORMATION FOR SEO ID NO:1491:

(i) SEQUENCE CHARACTERISTICS:

- SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 105 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- ```
(A) NAME/KEY: peptide
(B) LOCATION: 1..105
```

(D) OTHER INFORMATION: / Ceres Seq. ID 1570166

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1491:

(2) INFORMATION FOR SEO ID NO:1492:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1220 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:

(A) NAME/KEY: -
(B) LOCATION: 1..1220

(D) OTHER INFORMATION: / Ceres Seq. ID 1570170

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1492:

attctaatca	tcccttgtaa	ttttccaagt	tttctctctt	tgtctctctt	aactattttc	60
ccttaaaaata	aaaatccaat	ttttctttgt	ttcagtcctc	tctctctgctc	attgatcttt	120
taattaaactt	tgattctctc	cgtttatgga	ttaacatttt	gatcgagata	actctccaag	180
aaatcgactg	agttcgttaac	ttgtttgtgt	ctgatctttt	aaagattcaa	cctttttttg	240
tcgcgatcatg	ctctgttgctg	agaatgctgt	tgctaaaagt	gactctcttg	gtcagaattt	300
agacaaacaac	aacactgctg	cttcagctac	cgagacgaca	aagccgcat	gtcctgatga	360
tgatcaaaagc	cctaatactg	actcatccac	tcctcttacc	atcgattoga	ctcctgaaac	420
tgacgatogg	atcaatgaga	ctgctcaaaa	ggttcagact	ttaaaatggg	ttagtggaaa	480
tggtgagaga	gataacaatg	gagagatcaa	agatttggtc	gatgcgtttt	ctaagcttaa	540
tcgcgatgct	caggagtgtg	ttctctcttc	tcttgctcga	agtcaactctg	gggttttgag	600
aaatgggata	gggttttacta	acaattttgc	agccccacct	aaacttgctg	atgggaaatga	660
tcattttctc	agaaggagaa	ggagttttgc	ccaagggaag	cgaagaatga	acaaaaggac	720
aagcttggtc	cagaaggatg	atgtaatacag	gacaactgta	tatgtctctg	acatcgacca	780
acaggttaca	gaggagaacc	tcgcaggtgt	ctttattaac	ttgtgacagg	ttgttgattg	840
tcgtgtatgc	gggtatccaa	attctgtctc	tcgtttcgtc	tcaattgaat	ttaccaatga	900
agaggagact	agagctgctt	tgagcatgtc	gggtactgtg	ctaggttttt	acctcttaa	960
ggttctcttc	tccaaaacag	ctattgctcc	tgtaaaccg	acctttcttc	cacgatctga	1020
ggatgagcgt	gagatgtgcg	ttaggactgt	ttactgtacc	acatttgaca	agcggtcac	1080
ccaaattgac	ttgaaaggct	tccttgaaat	gctttcgagg	gaggttcaac	gtctgaggct	1140
tggagactat	caccacccaa	cccgatttgc	tttgttgtag	tttgcatgag	cggaaagcgc	1200

aaCttgCtgc gcttcactgc

(2) INFORMATION FOR SEQ ID NO:1493:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 324 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1..324

(D) OTHER INFORMATION: / Ceres Seq. ID 1570171

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1493:

Met	Ala	Val	Ala	Glu	Asn	Ala	Gly	Val	Lys	Val	Asp	Ser	Ser	Gly	Gln
1			5					10						15	
Asn	Leu	Asp	Asn	Asn	Asn	Thr	Ala	Ala	Ser	Ala	Thr	Glu	Thr	Thr	Lys
			20					25						30	
Pro	Pro	Cys	Pro	Asp	Asp	Asp	Gln	Ser	Pro	Lys	Ser	Asp	Ser	Ser	Thr
			35				40					45			
Pro	Leu	Thr	Ile	Asp	Ser	Thr	Pro	Glu	Thr	Asp	Asp	Arg	Ile	Asn	Glu
			50				55					60			
Thr	Ala	Gln	Lys	Val	Gln	Thr	Leu	Asn	Gly	Phe	Ser	Gly	Asn	Gly	Glu
			65			70			75				80		
Arg	Gsp	Asn	Asn	Gly	Glu	Ile	Lys	Asp	Leu	Ala	Asp	Ala	Phe	Ser	Lys
			85					90					95		
Leu	Asn	Pro	Met	Ala	Gln	Glu	Phe	Val	Pro	Pro	Ser	Leu	Ala	Arg	Ser
			100					105					110		
Gln	Ser	Gly	Val	Leu	Arg	Asn	Gly	Leu	Gly	Phe	Thr	Asn	Asn	Phe	Ala
			115				120					125			
Ala	Pro	Pro	Lys	Leu	Ala	Asp	Gly	Asn	Asp	His	Phe	Pro	Arg	Arg	Arg
			130				135					140			
Arg	Ser	Phe	Gly	Gln	Gly	Lys	Arg	Arg	Met	Asn	Lys	Arg	Thr	Ser	Leu
			145			150			155					160	
Ala	Gln	Lys	Asp	Asp	Val	Ile	Arg	Thr	Thr	Val	Tyr	Val	Ser	Asp	Ile
			165					170						175	

(2) INFORMATION FOR SEQ ID NO:1494:

(A) LENGTH: 225 amino acids

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

MOLECULE TYPE: peptid

(ix) FEATURE:

(B) LOCATION: 1..225

(D) OTHER INFORMATION

SEQUENCE DESCRIPTION: SEQ ID NO:1494:

Ala Gln Glu Phe Val Pro Pro Ser Leu Ala Arg

[illegible]

225

(2) INFORMATION FOR SEQ ID NO:1495:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 171 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..171
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570173

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1495:

Met	Asn	Lys	Arg	Thr	Ser	Leu	Ala	Gln	Lys	Asp	Asp	Val	Ile	Arg	Thr
1				5					10					15	
Thr	Val	Tyr	Val	Ser	Asp	Ile	Asp	Gln	Val	Thr	Glu	Glu	Asn	Leu	
			20					25				30			
Ala	Gly	Val	Phe	Ile	Asn	Cys	Gly	Gln	Val	Val	Asp	Cys	Arg	Val	Cys
			35				40					45			
Gly	Asp	Pro	Asn	Ser	Val	Leu	Arg	Phe	Ala	Phe	Ile	Glu	Phe	Thr	Asn
	50					55					60				
Glu	Glu	Gly	Ala	Arg	Ala	Ala	Leu	Ser	Met	Ser	Gly	Thr	Val	Leu	Gly
	65				70				75					80	
Phe	Tyr	Pro	Leu	Lys	Val	Leu	Pro	Ser	Lys	Thr	Ala	Ile	Ala	Pro	Val
				85					90					95	
Asn	Pro	Thr	Phe	Leu	Pro	Arg	Ser	Glu	Asp	Glu	Arg	Glu	Met	Cys	Val
				100				105					110		
Arg	Thr	Val	Tyr	Cys	Thr	Asn	Ile	Asp	Lys	Arg	Ile	Thr	Gln	Ile	Asp
				115			120					125			
Leu	Lys	Gly	Phe	Phe	Glu	Met	Leu	Cys	Gly	Glu	Val	His	Arg	Leu	Arg
						135					140				
Leu	Gly	Asp	Tyr	His	His	Gln	Thr	Arg	Ile	Ala	Phe	Val	Glu	Phe	Ala
					150				155					160	
Met	Ala	Glu	Ser	Ala	Thr	Cys	Cys	Ala	Ser	Leu					
				165					170						

(2) INFORMATION FOR SEQ ID NO:1496:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1460 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1460
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570183

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1496:

atttttgagt	tctcagattt	caaacacaaa	agtttcgtct	cogatttaat	ctttctacgt	60
cttggtttat	gagctcaaa	gagaagccca	ctctcgagg	tacgcggatt	aagaccgcga	120
aaaggaatat	tgtctctcct	ctcgaccctg	ctgcttttct	tgatgcacta	gttcagattt	180
atctggataa	tgtcgttgat	ctggaacttg	ttgccaaga	tttagagtoa	tctgatctta	240
attttcgaag	atacgttgat	attttctttg	aggttggttt	cattggagga	cgtaactcaa	300
ctgggttcagt	gaatctctgat	gaagggggaac	gccaccctta	ctctataatc	gactctgtaac	360
caaaagcgtga	agctattttta	ccatcagttg	tatacataca	gaaaattttg	cgagggaaga	420
ccttccttat	taagaacctt	gagaatgtta	cacggagatt	cttacagtaa	ctggagcttt	480
ttagggagaa	tgagaggaag	aagcttgcaa	tattcacagc	acttgcaatt	tcacagaaga	540
tctcaggatt	acctgcagag	actgtcttcc	agccattgtc	taaggataact	cttgttgcca	600
aagggatagt	tctcaatttt	gtaacagact	tcttcaatga	atatttggtt	gagaacagtc	660
ttgatgactt	gatttctatt	ctgagcgctg	gcaagatgga	tgacaaactc	ttggagtctc	720
tgccaccac	aaagcgagct	acagaaagtt	ttgccgagca	tttcaactaa	gcaggattga	780
cagctctggt	agagtacaat	gaaaggaaaa	tatttgaggt	gaagctgga	gaaatcaaga	840

```

cggtccttac gagccaagt acagaggaaa taaacgtaga tgaagtgtact gaaatgtgtga 900
agcaacaggt gaagatgtca aagctgccag agAactgagg ttgtgcatgt gatctggggt 960
aggataatga atgctgttca atggctctgg aaaaaccagc agcagaattc gaatgctgta 1020
ttacgccaaag tgaaaacatg ggcacccctt ctgaacacgc ttgttagcac cgggaacatg 1080
gagatggaac tgatgtataa agtacagatg caatgctatg aggatgcaaa gctgatgaaa 1140
gtgtttcctg aggtagtgtg atctctGTmt gTATrmAyggt atgtgcttgc ggaagacacc 1200
attctgcact ggtatcgcaa agggaccaac cctaagggca ggcacaacgtt tbtgaaggga 1260
ttggaaccgt ttgtgaattg gctcgaagag gccgaagaag aggagtgtgt gagacgtctt 1320
gcttctgttt ttctcttttt actctcttct aataaaagaa agacaatatt ttacttctct 1380
taacgcaaaa ttacagatgt ctacattgtt gtgacttggg ttgtgatctct tttttgaatt 1440
aataagtact tctttagttg

```

(2) INFORMATION FOR SEQ ID NO:1497:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 289 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..289

(D) OTHER INFORMATION: / Ceres Seq. ID 1570184

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1497:

```

Met Ser Ser Lys Glu Lys Pro Thr Leu Gly Gly Thr Arg Ile Lys Thr
1      5      10      15
Arg Lys Arg Asn Ile Ala Ala Pro Leu Asp Pro Ala Ala Phe Ser Asp
20      25      30
Ala Leu Val Gln Ile Tyr Leu Asp Asn Ala Gly Asp Leu Gly Leu Val
35      40      45
Ala Arg Ser Leu Glu Ser Ser Asp Leu Asn Phe Ser Arg Tyr Gly Asp
50      55      60
Ile Phe Phe Glu Val Val Phe Ile Gly Gly Arg Thr Gln Thr Gly Ser
65      70      75      80
Val Lys Ser Asp Glu Gly Glu Arg His Pro Tyr Ser Ile Ile Asp Cys
85      90      95
Glu Pro Lys Arg Glu Ala Ile Leu Pro Ser Val Val Tyr Ile Gln Lys
100     105     110
Ile Leu Arg Arg Lys Ala Phe Leu Ile Lys Asn Leu Glu Asn Val Thr
115     120     125
Arg Arg Phe Leu Gln Ser Leu Glu Leu Phe Glu Glu Asn Glu Arg Lys
130     135     140
Lys Leu Ala Ile Phe Thr Ala Leu Ala Phe Ser Gln Lys Leu Ser Gly
145     150     155     160
Leu Pro Ala Glu Thr Val Phe Gln Pro Leu Leu Lys Asp Thr Leu Val
165     170     175
Ala Lys Gly Ile Val Leu Asn Phe Val Thr Asp Phe Phe Asn Glu Tyr
180     185     190
Leu Val Glu Asn Ser Leu Asp Asp Leu Ile Ser Ile Leu Arg Arg Gly
195     200     205
Lys Met Asp Asp Lys Leu Leu Glu Phe Leu Pro Pro Thr Lys Arg Thr
210     215     220
Thr Glu Ser Phe Ala Glu His Phe Thr Lys Ala Gly Leu Thr Ala Leu
225     230     235     240
Val Glu Tyr Asn Glu Arg Lys Ile Phe Glu Val Lys Leu Lys Glu Ile
245     250     255
Lys Ala Val Leu Thr Ser Gln Val Thr Glu Glu Ile Asn Val Asp Glu
260     265     270
Val Thr Glu Met Val Lys Gln Glu Val Lys Asp Ala Lys Leu Pro Glu
275     280     285

```

Asn

(2) INFORMATION FOR SEQ ID NO:1498:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 557 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..557
(D) OTHER INFORMATION: / Ceres Seq. ID 1570189

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1498:

actttacttt	tcggaggaa	tagaaaattg	ggggctaggg	ttcgcaattg	tagttttcga	60
gcgaagaaga	tgatcgaggt	ggttctcaac	gatcggttag	ggaaaaaagt	taggggtgaag	120
tgtaacRgAt	gatgacacga	tcggtgatct	gaagaagctt	gtcgcggcac	aaaccggaac	180
acgagccgag	aagatcagaa	ttcagaagtg	gtacaacatc	tacaaggatc	acatcaactc	240
caaggactat	gagatccatg	acggcatggg	tcttgagctt	tactacaact	aggccaatcg	300
aaggagctaa	gctgaaggag	tggtgttgat	ttggacacct	acataaacct	atatcaacca	360
tgttacatct	aaaaaagaca	caagtatgtt	gtaagacgtg	ataacttcaa	attttgggta	420
ataataatc	attcaactgtc	aatggtttta	aacccttcca	aattgtcaga	ttgattttctg	480
gttatctcta	agtttgtagt	atattagctt	ttttggtgtg	attgatgtgc	tctttctcca	540
aatgttacc	atcttcc					

(2) INFORMATION FOR SEQ ID NO:1499:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..43
(D) OTHER INFORMATION: / Ceres Seq. ID 1570190

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1499:

Thr	Leu	Leu	Phe	Arg	Arg	Asn	Arg	Lys	Leu	Gly	Ala	Arg	Val	Arg	Asn
1			5					10					15		
Cys	Ser	Phe	Arg	Ala	Lys	Lys	Met	Ile	Glu	Val	Val	Leu	Asn	Asp	Arg
			20				25						30		
Leu	Gly	Lys	Lys	Val	Arg	Val	Lys	Cys	Asn	Xaa					
			35				40								

(2) INFORMATION FOR SEQ ID NO:1500:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1625 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..1625
(D) OTHER INFORMATION: / Ceres Seq. ID 1570201

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1500:

gagtaacatc	gagacaaaga	agaaaaagcta	aaaaaagagaa	ccccaaagaa	tcgaatatatt	60
attattttgc	cccgaaagatt	ctattttctga	tcatttacac	ccctaaaaag	agtagagctt	120
tcgtgaagcc	accatgtgtg	gaggagctat	aatctccgat	ttcatacctc	cgccgaggtc	180
ctctccgcgc	actaacgagt	ttatctggcc	ggatctgaaa	aacaaagtga	aagcttcaaa	240
gaagagatcg	aataagcgat	cgatcttgac	gatgatttcg	aatgtgattt		300
ccaaggggtt	aaggatgact	cggtttttga	ctcggaagac	gatgatgatg	tcttgctcaa	360
tgttaaagcct	ttcgctcttca	ccgcaactac	taagcccgtg	gtcttcgctt	tcgtctccac	420
tgtaggttca	gcataatgcca	agaaaactgt	agagtcgcgt	gagcaagctg	agaaatcttc	480
taagaggaag	aggaagaatc	agtaccgagg	gattaggcag	cgctcctggg	gaaaatgggc	540

tgccgagatc	cgtgatccgA	aaaaaggctc	cgcagaatgg	cttggaacat	tcgacactgc	600
tgaggaagca	gcaagagcgt	atgatgctgc	agcagcgaga	atccgtggca	cgaagactaa	660
ggtgaatttt	cccgaggaga	agaaccctag	cgtcgtatcc	cagaaaacgtc	ctaagtctaa	720
gactaataat	cttcagaaat	cagtggtctaa	accaaacaaa	agcgtaactt	tggttcagca	780
gccaacacat	ctgagtcagc	agtactgcaa	caactccttt	gacaactctt	ttgggtgat	840
gagtttcatg	gaagagaagc	ctcagatgta	caacaatcag	tttgggttaa	caaaactcgt	900
cgatgctgga	ggtaacaagt	gataccagta	tttcagttcc	gatcagggca	gtaactcctt	960
cgactgttct	gagttcgggt	ggagtgatca	cggccctaaa	acacccgaga	tctcttcaat	1020
cgcttgtcaat	aacaacgaag	catcatttgt	tgaagaaacc	aatgcagcca	agaagctcaa	1080
acctaaactc	gatgagtcag	acgatctgat	ggcatacctt	gacaacgctt	tgtgggacac	1140
ccactagtaa	gtgaaagcca	tgcttggcgc	agatgctggt	gctgtgactc	aggaagagga	1200
aaaccaggtg	gagctatgga	gcttagatga	gatcaatttc	atgctggaag	gagacttttg	1260
aatgtatcga	tgtttcctta	gtttgtaaat	aaagctgtgt	tggattttgc	tgttggggga	1320
tggtacaagt	cacacctcaa	gctctatgca	ttggtatctc	atgagocctc	cttccataga	1380
gagtttctct	tttaattttg	togaataaaa	aaaaggtgta	tgaagtataa	agaggtataa	1440
taatatctat	ctattaagtc	ttgttttgtt	ctttcatttt	tgtatttctt	ttctatttaa	1500
aagaccagtt	attagctctt	tgagctctct	ttttgatctt	tgttatagcg	tatcatcacc	1560
ctcgaaagtg	taattgtttt	tacccccaaa	cttgttttag	attataataa	agtctctttg	1620

gaacc

(2) INFORMATION FOR SEQ ID NO:1501:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 375 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..375

(D) OTHER INFORMATION: / Ceres Seq. ID 1570202

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1501:

Met	Cys	Gly	Gly	Ala	Ile	Ile	Ser	Asp	Phe	Ile	Pro	Pro	Arg	Ser
1			5							10			15	
Leu	Arg	Val	Thr	Asn	Glu	Phe	Ile	Trp	Pro	Asp	Leu	Lys	Asn	Lys
			20					25					30	Val
Lys	Ala	Ser	Lys	Lys	Arg	Ser	Asn	Lys	Arg	Ser	Asp	Phe	Phe	Asp
			35					40					45	Leu
Asp	Asp	Asp	Phe	Glu	Ala	Asp	Phe	Gln	Gly	Phe	Lys	Asp	Asp	Ser
			50				55				60			Ala
Phe	Asp	Cys	Glu	Asp	Asp	Asp	Asp	Val	Phe	Val	Asn	Val	Lys	Pro
65					70				75					80
Val	Phe	Thr	Ala	Thr	Thr	Lys	Pro	Val	Ala	Ser	Ala	Phe	Val	Ser
					85				90				95	Thr
Val	Gly	Ser	Ala	Tyr	Ala	Lys	Lys	Thr	Val	Glu	Ser	Ala	Glu	Gln
					100				105				110	Ala
Glu	Lys	Ser	Ser	Lys	Arg	Lys	Arg	Lys	Asn	Gln	Tyr	Arg	Gly	Ile
					115				120				125	Arg
Gln	Arg	Pro	Trp	Gly	Lys	Trp	Ala	Ala	Glu	Ile	Arg	Asp	Pro	Arg
					130				135				140	Lys
Gly	Ser	Arg	Glu	Trp	Leu	Gly	Thr	Phe	Asp	Thr	Ala	Glu	Glu	Ala
145					150				155					160
Arg	Ala	Tyr	Asp	Ala	Ala	Ala	Arg	Arg	Ile	Arg	Gly	Thr	Lys	Ala
					165				170				175	Lys
Val	Asn	Phe	Pro	Glu	Glu	Lys	Asn	Pro	Ser	Val	Val	Ser	Gln	Lys
					180				185				190	Arg
Pro	Ser	Ala	Lys	Thr	Asn	Asn	Leu	Gln	Lys	Ser	Val	Ala	Lys	Pro
					195				200				205	Asn
Lys	Ser	Val	Thr	Leu	Val	Gln	Gln	Pro	Thr	His	Leu	Ser	Gln	Gln
					210				215				220	Tyr
Cys	Asn	Asn	Ser	Phe	Asp	Asn	Ser	Phe	Gly	Asp	Met	Ser	Phe	Met
225					230				235					Glu

Glu Lys Pro Gln Met Tyr Asn Asn Gln Phe Gly Leu Thr Asn Ser Phe
245 250 255
Asp Ala Gly Gly Asn Asn Gly Tyr Gln Tyr Phe Ser Ser Asp Gln Gly
260 265 270
Ser Asn Ser Phe Asp Cys Ser Glu Phe Gly Trp Ser Asp His Gly Pro
275 280 285
Lys Thr Pro Glu Ile Ser Ser Met Leu Val Asn Asn Asn Glu Ala Ser
290 295 300
Phe Val Glu Glu Thr Asn Ala Ala Lys Lys Leu Lys Pro Asn Ser Asp
305 310 315 320
Glu Ser Asp Asp Leu Met Ala Tyr Leu Asp Asn Ala Leu Trp Asp Thr
325 330 335
Pro Leu Glu Val Lys Ala Met Leu Gly Ala Asp Ala Gly Ala Val Thr
340 345 350
Gln Glu Glu Glu Asn Pro Val Glu Leu Trp Ser Leu Asp Glu Ile Asn
355 360 365
Phe Met Leu Glu Gly Asp Phe
370 375

(2) INFORMATION FOR SEQ ID NO:1502:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 996 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..996
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570227

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1502:

aatcaaat	tttgcatt	ttattcaaat	tttgagaaaa	tggtgagaag	taccaaaagg	60
cgctcagaaa	tagagatgaa	aaaaaatggaa	aacgaaagca	accttcagg	tactttctca	120
aaaagaagat	tcggtctttt	caaaaaagct	agtgaacttt	gcacattaa	tggtgcagag	180
attctgttga	ttgtgttctc	tcctgtgtgg	aaagtgtttt	cttttggcca	tccaagtgtt	240
caagaactca	ttcatcgctt	ttcgaatcct	aaccataatt	ctgccattgt	ccatcatcag	300
aacaacaatc	tccaacttgt	tgaaccctgt	ccggatagaa	atatccaata	tctcaacaat	360
atactcactg	agggtgctgg	aaaccaggaa	aaggagaaac	agaagagaat	ggttttggac	420
ctattgaaag	aatccagaga	acaagtagga	aactggtatg	aaaaagatgt	gaagatcttt	480
gacatgaatg	aaaccaacca	gctgatattc	gctcttcaag	atgtgaaaaa	gaactgggta	540
agagaaatgt	ctcaatatc	tcaagtaaat	gtttcgagag	attacttttg	tcaaaagtct	600
ggcgtgattg	gtgtgtgtaa	tggttgccatt	gatctttttg	atcaagaag	aaatgcattc	660
aactataatc	caaacatggt	gtttcccaat	catacaccac	caatgttttg	atacaacaat	720
gatggagttc	tcgttccgat	atccaacatg	aactacatgt	caagttacaa	cttcaaccag	780
agctagagtc	tgaagctaga	agaacatcct	aatcaaatatt	tgcgttattt	tgctatggtt	840
tactgttagg	attgtttttg	tattgtgaga	cttaagtttg	ttttttcttt	taatttggtt	900
cagctgggtg	gtttttcaat	ttattcgctg	ttgtttttcc	tttgKttttc	ggatatatttt	960
gtatccagaa	taaatattatt	tatccttttaa	ttttac			

(2) INFORMATION FOR SEQ ID NO:1503:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 261 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..261
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570228

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1503:

Asn Gln Ile Cys His Leu Phe Ile Gln Ile Phe Glu Lys Met Val Arg
1 5 10 15

```

Ser Thr Lys Gly Arg Gln Lys Ile Glu Met Lys Lys Met Glu Asn Glu
      20      25      30
Ser Asn Leu Gln Val Thr Phe Ser Lys Arg Arg Phe Gly Leu Phe Lys
      35      40      45
Lys Ala Ser Glu Leu Cys Thr Leu Ser Gly Ala Glu Ile Leu Leu Ile
      50      55      60
Val Phe Ser Pro Gly Gly Lys Val Phe Ser Phe Gly His Pro Ser Val
      65      70      75      80
Gln Glu Leu Ile His Arg Phe Ser Asn Pro Asn His Asn Ser Ala Ile
      85      90      95
Val His His Gln Asn Asn Asn Leu Gln Leu Val Glu Thr Arg Pro Asp
      100      105      110
Arg Asn Ile Gln Tyr Leu Asn Asn Ile Leu Thr Glu Val Leu Ala Asn
      115      120      125
Gln Glu Lys Glu Lys Gln Lys Arg Met Val Leu Asp Leu Leu Lys Glu
      130      135      140
Ser Arg Glu Gln Val Gly Asn Trp Tyr Glu Lys Asp Val Lys Asp Leu
      145      150      155      160
Asp Met Asn Glu Thr Asn Gln Leu Ile Ser Ala Leu Gln Asp Val Lys
      165      170      175
Lys Lys Leu Val Arg Glu Met Ser Gln Tyr Ser Gln Val Asn Val Ser
      180      185      190
Gln Asn Tyr Phe Gly Gln Ser Ser Gly Val Ile Gly Gly Gly Asn Val
      195      200      205
Gly Ile Asp Leu Phe Asp Gln Arg Arg Asn Ala Phe Asn Tyr Asn Pro
      210      215      220
Asn Met Val Phe Pro Asn His Thr Pro Pro Met Phe Gly Tyr Asn Asn
      225      230      235      240
Asp Gly Val Leu Val Pro Ile Ser Asn Met Asn Tyr Met Ser Ser Tyr
      245      250      255
Asn Phe Asn Gln Ser
      260

```

(2) INFORMATION FOR SEQ ID NO:1504:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 248 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..248

(D) OTHER INFORMATION: / Ceres Seq. ID 1570229

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1504:

```

Met Val Arg Ser Thr Lys Gly Arg Gln Lys Ile Glu Met Lys Lys Met
1      5      10      15
Glu Asn Glu Ser Asn Leu Gln Val Thr Phe Ser Lys Arg Arg Phe Gly
      20      25      30
Leu Phe Lys Lys Ala Ser Glu Leu Cys Thr Leu Ser Gly Ala Glu Ile
      35      40      45
Leu Leu Ile Val Phe Ser Pro Gly Gly Lys Val Phe Ser Phe Gly His
      50      55      60
Pro Ser Val Gln Glu Leu Ile His Arg Phe Ser Asn Pro Asn His Asn
      65      70      75      80
Ser Ala Ile Val His His Gln Asn Asn Asn Leu Gln Leu Val Glu Thr
      85      90      95
Arg Pro Asp Arg Asn Ile Gln Tyr Leu Asn Asn Ile Leu Thr Glu Val
      100      105      110
Leu Ala Asn Gln Glu Lys Glu Lys Gln Lys Arg Met Val Leu Asp Leu
      115      120      125
Leu Lys Glu Ser Arg Glu Gln Val Gly Asn Trp Tyr Glu Lys Asp Val

```

(2) INFORMATION FOR SEQ ID NO:1505:

(A) LENGTH: 236 amino acids

(C) STRANDEDNESS:

(D) TOPOLOGY: lin

MOLECULE TYPE: pentid

(A) NAME

(B) LOCATION: 1..236

(D) OTHER INFORMATION:

SEQUENCE DESCRIPTION: SEQ ID NO:1505:

(X1) SEQUENCE DESCRIPTION: SEQ ID NO:1503:
Iys Iys Met Glu Asp Glu Ser Asp Leu Gln Val

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1062 base p

(B) TYPE: nucleic acid

1. *Journal of the American Statistical Association*, 1997, 92, 1029-1042.

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..1062
(D) OTHER INFORMATION: / Ceres Seq. ID 1570235
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1506:

```

aaaaaaaaatt gttcgtattct cattctctctt ctacacagtcg taaacccctaa aaaaaaaaaa 60
gagaaatcaa atttcaatct cgaaggatct acaagaagaac atgacgacgc gagatctcgt 120
taatatccat cctactgacg ttaaattccc ctttgagttg aagaaacaaa gttcgtgttc 180
gatgcaattg accaacaaga caactactca atgtgtcgtc ttaagagtta aaacaaccaa 240
tcctcgcaaa tactgtgttc gtcctaacac tgggtgtgtc ttgcccggtg attctcgtca 300
tgttacagtg acgatgcaag cccagaaaga ggcaccactt gatatgcaat gcaaaagacaa 360
gttccttgtt cagactgtgt ttgtctctga tggctactact tccaaagaag tctcgtctga 420
aatgttcaac aaggaggctg gtatagatgt tgaggatttc aaactgcgag ttgtttacat 480
cctctgctaact cctccttcac ctgtcctctga aggttctgaa gaaggcaact cctcatgtgc 540
ttcctcaaac gatattgcct ctcaatctgc ctcaactctt gatgacgtgt caaaaacgtt 600
tgaagaaaca agtgagaaat cttcabaggc atggtctatg atttccaaat tgacggagga 660
gaagactctt gctactcaac aaagtacaga gctcgtcttc gaactggaaa tgcgtaggaa 720
agaaacAaag caagaagcag tcgggtgggtc attcctgtct cttgatgctg ctggtgggtc 780
tgctcgtgtt cgtgatgtgc tactatttga accggatata aacgccatgg ggtagcttc 840
atcatccttt taatcatcaa atcttgcaaa gttcttaaga tttttgacca gattttcgta 900
aaayggcgtt ggtttttttt taaaagttc atatttaagc tgtaaaatca gtatcgttag 960
cacaggaaca ggtgtgattt tgtggcaggt tctctgttat tgatttaaac acactttcga 1020
gtctgtagta agatctcaag agtcgttctt atgattggaa tt
```

(2) INFORMATION FOR SEQ ID NO:1507:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 250 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1..250

(D) OTHER INFORMATION: / Ceres Seq. ID 1570236

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1507:

```

Met Thr Thr Gly Asp Leu Val Asn Ile His Pro Thr Glu Leu Lys Phe
1      5      10      15
Pro Phe Glu Leu Lys Lys Gln Ser Ser Cys Ser Met Gln Leu Thr Asn
20     25     30
Lys Thr Thr Thr Gln Cys Val Ala Phe Lys Val Lys Thr Thr Asn Pro
35     40     45
Arg Lys Tyr Cys Val Arg Pro Asn Thr Gly Val Val Leu Pro Gly Asp
50     55     60
Ser Cys Asn Val Thr Val Thr Met Gln Ala Gln Lys Glu Ala Pro Leu
65     70     75     80
Asp Met Gln Cys Lys Asp Lys Phe Leu Val Gln Thr Val Val Val Ser
85     90     95
Asp Gly Thr Thr Ser Lys Glu Val Leu Ala Glu Met Phe Asn Lys Glu
100    105    110
Ala Gly Arg Val Ile Glu Asp Phe Lys Leu Arg Val Val Tyr Ile Pro
115    120    125
Ala Asn Pro Pro Ser Pro Val Pro Glu Gly Ser Glu Gly Asn Ser
130    135    140
Pro Met Ala Ser Leu Asn Asp Ile Ala Ser Gln Ser Ala Ser Leu Phe
145    150    155    160
Asp Asp Val Ser Lys Thr Phe Glu Glu Thr Ser Glu Lys Ser Ser Xaa
165    170    175
Ala Trp Ser Met Ile Ser Lys Leu Thr Glu Lys Thr Ser Ala Thr
```

	180		185		190										
Gln	Gln	Ser	Gln	Lys	Leu	Arg	Leu	Glu	Met	Leu	Arg	Lys	Glu		
	195				200					205					
Thr	Lys	Gln	Glu	Ala	Val	Gly	Trp	Ser	Phe	Leu	Ala	Leu	Asp	Ala	Ala
	210				215					220					
Gly	Gly	Ser	Ala	Arg	Leu	Arg	Asp	Trp	Leu	Leu	Ile	Glu	Pro	Asp	Ile
	225				230					235				240	
Asn	Ala	Met	Gly	Leu	Ala	Ser	Ser	Ser	Phe						
			245						250						

(2) INFORMATION FOR SEQ ID NO:1508:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 223 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..223

(D) OTHER INFORMATION: / Ceres Seq. ID 1570237

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1508:

Met	Gln	Leu	Thr	Asn	Lys	Thr	Thr	Thr	Gln	Cys	Val	Ala	Phe	Lys	Val
1				5					10					15	
Lys	Thr	Thr	Asn	Pro	Arg	Lys	Tyr	Cys	Val	Arg	Pro	Asn	Thr	Gly	Val
			20					25					30		
Val	Leu	Pro	Gly	Asp	Ser	Cys	Asn	Val	Thr	Val	Thr	Met	Gln	Ala	Gln
		35				40						45			
Lys	Glu	Ala	Pro	Leu	Asp	Met	Gln	Cys	Lys	Asp	Lys	Phe	Leu	Val	Gln
	50				55					60					
Thr	Val	Val	Val	Ser	Asp	Gly	Thr	Thr	Ser	Lys	Glu	Val	Leu	Ala	Glu
	65			70					75				80		
Met	Phe	Asn	Lys	Glu	Ala	Gly	Arg	Val	Ile	Glu	Asp	Phe	Lys	Leu	Arg
		85						90					95		
Val	Val	Tyr	Ile	Pro	Ala	Asn	Pro	Pro	Ser	Pro	Val	Pro	Glu	Gly	Ser
		100					105						110		
Glu	Glu	Gly	Asn	Ser	Pro	Met	Ala	Ser	Leu	Asn	Asp	Ile	Ala	Ser	Gln
		115				120						125			
Ser	Ala	Ser	Leu	Phe	Asp	Asp	Val	Ser	Lys	Thr	Phe	Glu	Glu	Thr	Ser
	130					135					140				
Glu	Lys	Ser	Ser	Xaa	Ala	Trp	Ser	Met	Ile	Ser	Lys	Leu	Thr	Glu	Glu
	145			150					155					160	
Lys	Thr	Ser	Ala	Thr	Gln	Gln	Ser	Gln	Lys	Leu	Arg	Leu	Glu	Leu	Glu
			165					170					175		
Met	Leu	Arg	Lys	Glu	Thr	Lys	Gln	Glu	Ala	Val	Gly	Trp	Ser	Phe	Leu
		180						185					190		
Ala	Leu	Asp	Ala	Ala	Gly	Gly	Ser	Ala	Arg	Leu	Arg	Asp	Trp	Leu	Leu
		195					200					205			
Ile	Glu	Pro	Asp	Ile	Asn	Ala	Met	Gly	Leu	Ala	Ser	Ser	Ser	Phe	
	210					215					220				

(2) INFORMATION FOR SEQ ID NO:1509:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 179 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..179

(D) OTHER INFORMATION: / Ceres Seq. ID 1570238

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1509:

Met Gln Ala Gln Lys Glu Ala Pro Leu Asp Met Gln Cys Lys Asp Lys
1 5 10 15
Phe Leu Val Gln Thr Val Val Val Ser Asp Gly Thr Thr Ser Lys Glu
20 25 30
Val Leu Ala Glu Met Phe Asn Lys Glu Ala Gly Arg Val Ile Glu Asp
35 40 45
Phe Lys Leu Arg Val Val Tyr Ile Pro Ala Asn Pro Pro Ser Pro Val
50 55 60
Pro Glu Gly Ser Glu Glu Gly Asn Ser Pro Met Ala Ser Leu Asn Asp
65 70 75 80
Ile Ala Ser Gln Ser Ala Ser Leu Phe Asp Asp Val Ser Lys Thr Phe
85 90 95
Glu Glu Thr Ser Glu Lys Ser Ser Xaa Ala Trp Ser Met Ile Ser Lys
100 105 110
Leu Thr Glu Glu Lys Thr Ser Ala Thr Gln Gln Ser Gln Lys Leu Arg
115 120 125
Leu Glu Leu Glu Met Leu Arg Lys Glu Thr Lys Gln Glu Ala Val Gly
130 135 140
Trp Ser Phe Leu Ala Leu Asp Ala Ala Gly Gly Ser Ala Arg Leu Arg
145 150 155 160
Asp Trp Leu Leu Ile Glu Pro Asp Ile Asn Ala Met Gly Leu Ala Ser
165 170 175
Ser Ser Phe

(2) INFORMATION FOR SEQ ID NO:1510:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1224 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1224

(D) OTHER INFORMATION: / Ceres Seq. ID 1570239

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1510:

atcaagtttaa	aaaaaaaaa	gaaggagaaa	tggcaataag	ttttagaact	ctagctcttt	60
tgacctctc	ggtgttacta	atttccatat	ctctcggcgt	cgctcacagca	acagagtcgc	120
agaggaatga	aggggggggt	cttacaatgt	acgagcaatg	gcttgtagag	aatgggaagt	180
aactataacg	gtcttggaga	gaaggagaga	cggttcaaga	tcttcaaga	caacttgaag	240
cgcatcgaga	aacacaattc	agatccaac	cgagtttatg	aacgcgggtt	gaacaagttt	300
tcggtactaa	cggtcgatga	gtttcaagct	agttacttag	gtgggaagat	ggaaaagaaa	360
agccatcag	atgtagcgga	gaggtatcag	tacaaagaag	gagatgtttt	acctgatgaa	420
gttgattgga	gggagagagg	agcagttggt	ccaagagtca	aaagacaagg	agagtgtgga	480
agttgtggg	cgtttgcgcg	gactgagcgg	tggaaaggtat	aaaccagatc	acaaccggag	540
aattagtaac	tttatcgga	caagaactca	ttgactgcga	tagagggaac	gacaactttg	600
gatgtgctgg	tggtggagca	gtatgggcct	ttgagttcat	taaggagaac	ggtgtattg	660
tatccatcag	agtttatggt	tataccgggt	aagatactgc	cgcatgcaag	gccattgaga	720
tgaaaaccac	tcgggttggt	accattaatg	gtcatgaggt	tgttctctga	aacgatgaga	780
tgcttttgaa	gaagctggtt	gcttatcaac	ctattagtgt	tatgatatac	gctgcaaaac	840
tgagcgacta	caaatctggt	gtgtataaag	gagcatgtag	taattttgtg	ggagatcaca	900
atgtgcta	tggtgggtat	ggaacatcat	cagatgaagg	agactactgg	cttattcgtga	960
attcttgggg	vccagagtg	ggagaaggcg	ggatccttag	gcttcaacgt	aacttccatg	1020
aaccacacgg	gaatgtgca	gtcgctgtag	ctctctgata	cccaatcaag	tcgaactctt	1080
catctcat	gttctctcca	agtgtgttta	aattggtgtg	tttatttgtt	tttcagttgt	1140
ttagtttggc	cttgccttga	aataactttt	tatcggtgtt	caagttcgtt	ggtttttggt	1200
ttataaaagg	aaacaagatt	cgctc				

(2) INFORMATION FOR SEQ ID NO:1511:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 116 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..126
(D) OTHER INFORMATION: / Ceres Seq. ID 1570242

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1513:

Met	Ser	Leu	Lys	Lys	Ala	Val	Ala	Tyr	Gln	Pro	Ile	Ile	Ser	Val	Met	Ile
1			5						10					15		
Ser	Ala	Ala	Asn	Met	Ser	Asp	Tyr	Lys	Ser	Gly	Val	Tyr	Lys	Gly	Ala	
		20						25					30			
Cys	Ser	Asn	Leu	Trp	Gly	Asp	His	Asn	Val	Leu	Ile	Val	Gly	Tyr	Gly	
		35					40					45				
Thr	Ser	Ser	Asp	Glu	Gly	Asp	Tyr	Trp	Leu	Ile	Arg	Asn	Ser	Trp	Xaa	
		50				55					60					
Pro	Glu	Trp	Gly	Glu	Gly	Gly	Tyr	Leu	Arg	Leu	Gln	Arg	Asn	Phe	His	
	65				70				75					80		
Glu	Pro	Thr	Gly	Lys	Cys	Ala	Val	Ala	Val	Ala	Pro	Val	Tyr	Pro	Ile	
			85						90				95			
Lys	Ser	Asn	Ser	Ser	Ser	His	Leu	Leu	Ser	Pro	Ser	Val	Phe	Lys	Leu	
		100						105					110			
Val	Val	Leu	Phe	Val	Phe	Gln	Leu	Ile	Ser	Leu	Ala	Leu	Leu			
		115					120									

(2) INFORMATION FOR SEQ ID NO:1514:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1387 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1387

(D) OTHER INFORMATION: / Ceres Seq. ID 1570247

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1514:

acgttctcag	agttagttac	acagcttttca	acgatgaatc	agctcgcgct	ttcaagatcc	60
ggttacaccg	ccgcggtgag	gtttctccct	atgctttccg	cagctgttcc	gaagatctta	120
tcatctctcg	ccgcgcgcac	caccgtccgc	aacttcagct	ctaccggaag	tcctctcacc	180
agctacaaaa	tcaataaaac	tgcgcgtca	aaatccttca	cttccaggct	ttccaccaa	240
tcctctctcc	ccggtactcc	tccgcaacaa	cttttcggcg	cccgtagctt	ctcatctccc	300
agcagtgaat	tcaacagcta	caacattaat	ccgcggtcta	actgggtaac	ccgaatcgct	360
ccggagagga	aagcttgtgt	gattgagcgg	tttggtaaa	tccacacgac	ttgcccgcgc	420
gggattcaact	tccttgttcc	gtttgtggat	cgtatcgctt	atgttcattc	ttcaaaaggaa	480
gaagcgattc	ctattgttaa	tcagactcgc	attacaaagg	ataacgcttg	catccacatc	540
gatgtgtttc	tctacgttaa	gattgtggat	cctaagtgtg	cttcttatgg	cggtgagaa	600
ccgatctatg	ctgttatgca	gttggctcag	actacaatgc	gtagtgaagt	cggtaaaatt	660
actctttgca	agacttttga	ggaacgggac	actctcaatg	agaagattgt	ggaagccatc	720
aatgttgttg	caaaagattg	gggtcttcag	tgccttagtt	atgagatcag	ggatatcatg	780
ctctctaatg	gagtgagagt	tgctatggaa	atgcaagctg	aagctgaacg	taaaaagaga	840
gccacagatt	ttgagttctg	aggagaacct	caagcccata	tcaatagagc	tgatgtgaag	900
aaaagtcttg	taatcttgga	atcagaagct	gcaatgatgg	accaagtcaa	tcgtgcacaa	960
ggtgagctcg	aagcaatatt	agctagagca	caagcaacag	ccaaRgggac	tgccataggt	1020
atctcaatcc	ctcaagggaag	ctgggtggaga	ggaggtgcgc	agtttgagag	ttcgggagta	1080
atacattcaa	gcttttggca	aaattgctaa	ggagggtaca	acaatcgtcg	ttYccgagta	1140
atgtcgacaa	tctgtctagc	atgatcgctc	aAgcttttag	aatgtacaaa	ggcttgtcaa	1200
caaaaggtccc	aacagtgtgt	tcagggaaac	ttctggagta	gaatcctcta	ctaacgtggt	1260
tgttgccaaa	cttgaaatga	agctataatg	tagctgaacc	tagggaacaa	ctattctttt	1320
gattgtgcc	ggcttttagc	caatttcagt	ttgtttattt	cttcatatga	gaaacagtta	1380
tcttacc						

(2) INFORMATION FOR SEQ ID NO:1515:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 369 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..369
(D) OTHER INFORMATION: / Ceres Seq. ID 1570248

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1515:

Thr	Phe	Ser	Glu	Leu	Val	Thr	Gln	Leu	Ser	Thr	Met	Asn	Gln	Leu	Ala
1			5					10					15		
Leu	Ser	Arg	Ser	Gly	Tyr	Thr	Ala	Ala	Val	Arg	Phe	Leu	Pro	Met	Leu
			20					25					30		
Ser	Ala	Ala	Val	Pro	Lys	Ile	Leu	Ser	Ser	Leu	Ala	Ala	Ala	Ser	Thr
			35				40					45			
Val	Arg	Asn	Phe	Ser	Ser	Thr	Gly	Ser	Pro	Leu	Thr	Ser	Tyr	Gln	Ile
			50			55					60				
Asn	Lys	Pro	Ser	Pro	Ser	Lys	Ser	Phe	Thr	Ser	Arg	Leu	Leu	His	Gln
65					70				75					80	
Ser	Ser	Ser	Ala	Gly	Thr	Pro	Pro	Gln	Gln	Leu	Phe	Gly	Ala	Arg	Ser
			85					90						95	
Phe	Ser	Ser	Pro	Ser	Ser	Asp	Phe	Asn	Ser	Tyr	His	Ile	Asn	Pro	Pro
			100				105						110		
Ser	Asn	Trp	Gly	Ile	Arg	Ile	Val	Pro	Glu	Arg	Lys	Ala	Cys	Val	Ile
			115				120					125			
Glu	Arg	Phe	Gly	Lys	Phe	His	Thr	Thr	Leu	Pro	Ala	Gly	Ile	His	Phe
			130			135					140				
Leu	Val	Pro	Phe	Val	Asp	Arg	Ile	Ala	Tyr	Val	His	Ser	Leu	Lys	Glu
145				150						155				160	
Glu	Ala	Ile	Pro	Ile	Gly	Asn	Gln	Thr	Ala	Ile	Thr	Lys	Asp	Asn	Val
				165				170						175	
Ser	Ile	His	Ile	Asp	Gly	Phe	Leu	Tyr	Val	Lys	Ile	Val	Asp	Pro	Lys
			180				185						190		
Leu	Ala	Ser	Tyr	Gly	Val	Glu	Asn	Pro	Ile	Tyr	Ala	Val	Met	Gln	Leu
			195				200					205			
Ala	Gln	Thr	Thr	Met	Arg	Ser	Glu	Leu	Gly	Lys	Ile	Thr	Leu	Asp	Lys
			210			215					220				
Thr	Phe	Glu	Glu	Arg	Asp	Thr	Leu	Asn	Glu	Lys	Ile	Val	Glu	Ala	Ile
225				230					235					240	
Asn	Val	Ala	Ala	Lys	Asp	Trp	Gly	Leu	Gln	Cys	Leu	Ser	Tyr	Glu	Ile
			245					250						255	
Arg	Asp	Ile	Met	Pro	Pro	Asn	Gly	Val	Arg	Val	Ala	Met	Glu	Met	Gln
			260				265						270		
Ala	Glu	Ala	Glu	Arg	Lys	Lys	Arg	Ala	Gln	Ile	Leu	Glu	Ser	Glu	Gly
			275				280					285			
Glu	Arg	Gln	Ala	His	Ile	Asn	Arg	Ala	Asp	Gly	Lys	Lys	Ser	Ser	Val
			290			295					300				
Ile	Leu	Glu	Ser	Glu	Ala	Ala	Met	Met	Asp	Gln	Val	Asn	Arg	Ala	Gln
305				310					315					320	
Gly	Glu	Ala	Glu	Ala	Ile	Leu	Ala	Arg	Ala	Gln	Ala	Thr	Ala	Xaa	Gly
			325					330						335	
Thr	Gly	His	Gly	Ile	Ser	Ile	Pro	Gln	Gly	Ser	Trp	Trp	Arg	Gly	Gly
			340				345						350		
Cys	Glu	Phe	Glu	Ser	Cys	Gly	Ala	Ile	His	Ser	Ser	Phe	Trp	Gln	Asn
			355				360						365		

Cys

(2) INFORMATION FOR SEQ ID NO:1516:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 358 amino acids

(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..358
 (D) OTHER INFORMATION: / Ceres Seq. ID 1570249
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1516:
Met Asn Gln Leu Ala Leu Ser Arg Ser Gly Tyr Thr Ala Ala Val Arg
1 5 10 15
Phe Leu Pro Met Leu Ser Ala Ala Val Pro Lys Ile Leu Ser Ser Leu
 20 25 30
Ala Ala Ala Ser Thr Val Arg Asn Phe Ser Ser Thr Gly Ser Pro Leu
 35 40 45
Thr Ser Tyr Gln Ile Asn Lys Pro Ser Pro Ser Lys Ser Phe Thr Ser
 50 55 60
Arg Leu Leu His Gln Ser Ser Ser Ala Gly Thr Pro Pro Gln Gln Leu
65 70 75 80
Phe Gly Ala Arg Ser Phe Ser Ser Pro Ser Ser Asp Phe Asn Ser Tyr
 85 90 95
His Ile Asn Pro Pro Ser Asn Trp Gly Ile Arg Ile Val Pro Glu Arg
 100 105 110
Lys Ala Cys Val Ile Glu Arg Phe Gly Lys Phe His Thr Thr Leu Pro
 115 120 125
Ala Gly Ile His Phe Leu Val Pro Phe Val Asp Arg Ile Ala Tyr Val
 130 135 140
His Ser Leu Lys Glu Glu Ala Ile Pro Ile Gly Asn Gln Thr Ala Ile
145 150 155 160
Thr Lys Asp Asn Val Ser Ile His Ile Asp Gly Phe Leu Tyr Val Lys
 165 170 175
Ile Val Asp Pro Lys Leu Ala Ser Tyr Gly Val Glu Asn Pro Ile Tyr
 180 185 190
Ala Val Met Gln Leu Ala Gln Thr Thr Met Arg Ser Glu Leu Gly Lys
 195 200 205
Ile Thr Leu Asp Lys Thr Phe Glu Glu Arg Asp Thr Leu Asn Glu Lys
 210 215 220
Ile Val Glu Ala Ile Asn Val Ala Ala Lys Asp Trp Gly Leu Gln Cys
225 230 235 240
Leu Ser Tyr Glu Ile Arg Asp Ile Met Pro Pro Asn Gly Val Arg Val
 245 250 255
Ala Met Glu Met Gln Ala Glu Ala Glu Arg Lys Lys Arg Ala Gln Ile
 260 265 270
Leu Glu Ser Glu Gly Glu Arg Gln Ala His Ile Asn Arg Ala Asp Gly
 275 280 285
Lys Lys Ser Ser Val Ile Leu Glu Ser Glu Ala Ala Met Met Asp Gln
 290 295 300
Val Asn Arg Ala Gln Gly Glu Ala Glu Ala Ile Leu Ala Arg Ala Gln
305 310 315 320
Ala Thr Ala Xaa Gly Thr Gly His Gly Ile Ser Ile Pro Gln Gly Ser
 325 330 335
Trp Trp Arg Gly Gly Cys Glu Phe Glu Ser Cys Gly Ala Ile His Ser
 340 345 350
Ser Phe Trp Gln Asn Cys
 355
(2) INFORMATION FOR SEQ ID NO:1517:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 339 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..339

(D) OTHER INFORMATION: / Ceres Seq. ID 1570250

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1517:

Met Leu Ser Ala Ala Val Pro Lys Ile Leu Ser Ser Leu Ala Ala Ala
1 5 10 15
Ser Thr Val Arg Asn Phe Ser Ser Thr Gly Ser Pro Leu Thr Ser Tyr
20 25 30
Gln Ile Asn Lys Pro Ser Pro Ser Lys Ser Phe Thr Ser Arg Leu Leu
35 40 45
His Gln Ser Ser Ser Ala Gly Thr Pro Pro Gln Gln Leu Phe Gly Ala
50 55 60
Arg Ser Phe Ser Ser Pro Ser Ser Asp Phe Asn Ser Tyr His Ile Asn
65 70 75 80
Pro Pro Ser Asn Trp Gly Ile Arg Ile Val Pro Glu Arg Lys Ala Cys
85 90 95
Val Ile Glu Arg Phe Gly Lys Phe His Thr Thr Leu Pro Ala Gly Ile
100 105 110
His Phe Leu Val Pro Phe Val Asp Arg Ile Ala Tyr Val His Ser Leu
115 120 125
Lys Glu Glu Ala Ile Pro Ile Gly Asn Gln Thr Ala Ile Thr Lys Asp
130 135 140
Asn Val Ser Ile His Ile Asp Gly Phe Leu Tyr Val Lys Ile Val Asp
145 150 155 160
Pro Lys Leu Ala Ser Tyr Gly Val Glu Asn Pro Ile Tyr Ala Val Met
165 170 175
Gln Leu Ala Gln Thr Thr Met Arg Ser Glu Leu Gly Lys Ile Thr Leu
180 185 190
Asp Lys Thr Phe Glu Glu Arg Asp Thr Leu Asn Glu Lys Ile Val Glu
195 200 205
Ala Ile Asn Val Ala Ala Lys Asp Trp Gly Leu Gln Cys Leu Ser Tyr
210 215 220
Glu Ile Arg Asp Ile Met Pro Pro Asn Gly Val Arg Val Ala Met Glu
225 230 235 240
Met Gln Ala Glu Ala Glu Arg Lys Lys Arg Ala Gln Ile Leu Glu Ser
245 250 255
Glu Gly Glu Arg Gln Ala His Ile Asn Arg Ala Asp Gly Lys Lys Ser
260 265 270
Ser Val Ile Leu Glu Ser Glu Ala Ala Met Met Asp Gln Val Asn Arg
275 280 285
Ala Gln Gly Glu Ala Glu Ala Ile Leu Ala Arg Ala Gln Ala Thr Ala
290 295 300
Xaa Gly Thr Gly His Gly Ile Ser Ile Pro Gln Gly Ser Trp Trp Arg
305 310 315 320
Gly Gly Cys Glu Phe Glu Ser Cys Gly Ala Ile His Ser Ser Phe Trp
325 330 335
Gln Asn Cys

(2) INFORMATION FOR SEQ ID NO:1518:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1412 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1412

(D) OTHER INFORMATION: / Ceres Seq. ID 1570265

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1518:

actccgagcg	ttctctttct	cacaagccaa	tgggcgcaatt	tactaattcc	atcaattatc	60
tcttttctgt	ttctctctta	tattttgtat	cgttccactg	cttatgtttt	cggttttcat	120
tggttgacgc	ttgttcaaac	tcaccgcagc	accaacagat	tcaacaccat	caccaccgga	180
aatgggttgg	tcctctcagc	cacaaagtca	tcaccgtctc	acttaacggc	cacgctcagt	240
ttcgctccgt	ccaagacgct	gtggattcca	taccaaaagv	caataaacaag	agcatcaca	300
tcaagattgc	tcctcggtatt	tcacagagaga	aagtgtgtgt	tccagctaca	aaaccgtaca	360
tAaacgttca	aaggagctgg	tagggatgtg	accgctatag	agtggcagca	cagctgcgtcc	420
gaccttggcg	ctaacggtca	acagttacgt	acctatcaaa	ccgcttccgt	caccgtctac	480
gctaattatt	tcaccgctag	aaacattagc	ttcacggtag	tctattcaat	tctaacgcga	540
tatatatat	agggaaactt	tcaaaaaaat	gcgagtcttt	ctttatttta	ttttaaattg	600
tgaagaatac	tgccgcggct	ccattgcccg	ggatgcgaag	gtggcgaagc	gtggcgttta	660
ggatctccgg	cgacaaagct	ttcttttccg	gctgcgggtt	ttacggtgca	caagacactt	720
tatgcgacga	tgctggccgt	cattacttca	aggagtgtta	cattgaaggc	tctatcgact	780
ttatctttgg	taatggccgc	tccatgtata	aagattgtga	gttgcatcgc	atagcgtcaa	840
gattcgggtg	gatagccggc	catggttaga	catgcccgga	agagaaaaag	ggttctcgct	900
tcgtgggttg	tcgggttaaca	ggtagcggtc	catgtacgt	gggcccggcc	atgggaCcaa	960
tactcacgtg	tcgtttacgc	ctacacttac	tttgatgctc	tcgtcgctca	cggtggttgg	1020
gacgattggg	accacaactc	caacaaaagc	aagacggcat	ttttcgaggt	gtacaattgc	1080
tatgggccaag	gagcagcagc	gacgagagcg	gtgtcttggg	ctagagcttt	ggactatgaa	1140
tcggcccatc	catttatcgc	gttaagcttc	gttaaatggga	gacattggat	cgcctcctga	1200
gatgctttaa	caacttcaaa	ccttggccgg	gtttcttttc	ctaattctct	ggttcctccc	1260
agtcocaaag	ctcaaaagct	tactatatt	ttatcattcg	tttattcttt	tattgtttta	1320
ttttttccaa	tttatttata	cattgtgtga	tagtacaaca	aagtattgct	tcttcttcat	1380

ctgtatccat ttcaggttaa tgttttgagc tt

(2) INFORMATION FOR SEQ ID NO:1519:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 126 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..126

(D) OTHER INFORMATION: / Ceres Seq. ID 1570266

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1519:

Ser	Glu	Arg	Phe	Leu	Ser	His	Lys	Pro	Met	Ala	Gln	Phe	Thr	Asn	Ser
1				5					10					15	
Ile	Asn	Tyr	Leu	Phe	Ser	Val	Ser	Leu	Leu	Phe	Val	Ser	Phe	His	
				20				25					30		
Cys	Leu	Cys	Phe	Arg	Phe	Ser	Leu	Val	Ala	Ala	Cys	Ser	Asn	Ser	Thr
		35						40				45			
Asp	Asp	Gln	Gln	Ile	Gln	His	His	His	Arg	Lys	Trp	Val	Gly	Pro	
		50				55					60				
Ser	Gly	His	Lys	Val	Ile	Thr	Val	Ser	Leu	Asn	Gly	His	Ala	Gln	Phe
		65			70				75					80	
Arg	Ser	Val	Gln	Asp	Ala	Val	Asp	Ser	Ile	Pro	Lys	Xaa	Asn	Asn	Lys
			85					90					95		
Ser	Ile	Thr	Ile	Lys	Ile	Ala	Pro	Gly	Phe	Tyr	Arg	Glu	Lys	Val	Val
			100				105						110		
Val	Pro	Ala	Thr	Lys	Pro	Tyr	Ile	Asn	Val	Gln	Arg	Ser	Trp		
			115				120						125		

(2) INFORMATION FOR SEQ ID NO:1520:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 175 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..175
(D) OTHER INFORMATION: / Ceres Seq. ID 1570267

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1520:

Met Pro Gly Arg Glu Asn Gly Phe Arg Val Arg Gly Leu Ser Gly Asn
1 5 10 15
Arg Tyr Gly Ser Ile Val Arg Gly Pro Gly His Gly Thr Asn Thr His
20 25 30
Val Ser Phe Thr Pro Thr Leu Thr Leu Met Leu Ser Ser Leu Thr Val
35 40 45
Val Gly Thr Ile Gly Thr Thr Asn Pro Thr Lys Ala Arg Arg His Phe
50 55 60
Ser Glu Cys Thr Ile Ala Met Gly Gln Glu Gln Arg Arg Glu Ala
65 70 75 80
Cys Leu Gly Leu Glu Leu Trp Thr Met Asn Arg Pro Ile His Leu Ser
85 90 95
Leu Arg Ala Ser Leu Met Gly Asp Ile Gly Ser Leu Leu Glu Met Leu
100 105 110
Asn Gln Leu Gln Thr Leu Ala Gly Phe Leu Phe Leu Ile Pro Arg Phe
115 120 125
Leu Pro Val Pro Ser Pro Lys Ser Leu Leu Tyr Phe Tyr His Ser Phe
130 135 140
Ile Ser Phe Ile Val Tyr Phe Phe Gln Phe Ile Tyr Thr Leu Cys Asp
145 150 155 160
Ser Thr Thr Lys Tyr Cys Phe Phe Phe Ile Cys Ile His Phe Ser
165 170 175

(2) INFORMATION FOR SEQ ID NO:1521:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 134 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

- (ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..134

(D) OTHER INFORMATION: / Ceres Seq. ID 1570268

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1521:

Met Leu Ser Ser Leu Thr Val Val Gly Thr Thr Asn Pro
1 5 10 15
Thr Lys Ala Arg Arg His Phe Ser Glu Cys Thr Ile Ala Met Gly Gln
20 25 30
Glu Gln Gln Arg Arg Glu Ala Cys Leu Gly Leu Glu Leu Trp Thr Met
35 40 45
Asn Arg Pro Ile His Leu Ser Leu Arg Ala Ser Leu Met Gly Asp Ile
50 55 60
Gly Ser Leu Leu Glu Met Leu Asn Gln Leu Gln Thr Leu Ala Gly Phe
65 70 75 80
Leu Phe Leu Ile Pro Arg Phe Leu Pro Val Pro Ser Pro Lys Ser Leu
85 90 95
Leu Tyr Phe Tyr His Ser Phe Ile Ser Phe Ile Val Tyr Phe Phe Gln
100 105 110
Phe Ile Tyr Thr Leu Cys Asp Ser Thr Thr Lys Tyr Cys Phe Phe Phe
115 120 125
Ile Cys Ile His Phe Ser
130

(2) INFORMATION FOR SEQ ID NO:1522:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 973 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single

000001-00000300

(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..973

(D) OTHER INFORMATION: / Ceres Seq. ID 1570289

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1522:

gaacaatatt	cacagagatt	ttcgatctta	accgagaaaa	ggaagaaatg	gctgtgtccat	60
cgacaacttc	aaacgcacca	aagcagagga	agagagtcga	agccgagact	agcagcaaca	120
ctctactact	cttactgcgc	gctaaagacg	gaagcgcttt	cgctctctgt	gaaggatgta	180
acaagatgtg	agctgtagcg	cttataagca	tgcacaattg	cagttctcgt	gctaagatca	240
gagtgaaatc	cgaagcaca	gttgtggaga	cacaagcaga	ggctaagaag	aagcctgcag	300
agaagaagaa	gacaacatct	gatggacctt	agccaaagag	acttaagaaa	accaatgatg	360
agaagaagag	ctcttcaact	tcaaaacaagc	ccaagcgacc	tctcactgcc	ttctttatct	420
tcatgagtga	tttccgtaaa	acgttttaagt	cagagcataa	tggttcatta	gctaaggatg	480
ctgcaaaagt	cggtggtgag	aagtggaaagt	ctttgactga	ggaagagaag	aaagtttatc	540
tggtataaag	tgctgaactt	aaggcagagt	ataAcaagtc	actggaagc	aatgatgctg	600
atgaggaaga	ggaagatgag	gagaagcaat	ctgatgatgt	tgatgatgct	gaggagaaac	660
aagttgacga	tgatgatgaa	gttgaggaga	aagaagttga	gaacacagat	gatgacaaga	720
aagaagctga	aggttaagaa	gaggagggaag	aagagatgtt	ggatgactac	tagaaatggt	780
atgtcgcttc	ttgtgggtct	agtcttactg	aaatcggttt	atctctaact	gttgcgatgc	840
attgtaaatg	aagcctttat	tagtgaagag	agtttatatt	aagtttaagt	gtgagcaagt	900
ggtttttttg	tatttactg	aaatggtaat	gccttttgtt	taaacaagta	atgaagctta	960
tgtttttcgt	ttt					

(2) INFORMATION FOR SEQ ID NO:1523:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 256 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..256

(D) OTHER INFORMATION: / Ceres Seq. ID 1570290

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1523:

Thr	Ile	Phe	Thr	Glu	Ile	Phe	Asp	Leu	Asn	Arg	Glu	Lys	Glu	Glu	Met
1			5								10			15	
Ala	Gly	Pro	Ser	Thr	Thr	Ser	Asn	Ala	Pro	Lys	Gln	Arg	Lys	Arg	Val
			20					25					30		
Glu	Ala	Glu	Thr	Ser	Ser	Asn	Thr	Ser	Thr	Thr	Leu	Arg	Arg	Ala	Lys
			35				40					45			
Asp	Gly	Ser	Ala	Phe	Ala	Leu	Cys	Glu	Gly	Cys	Asn	Lys	Ser	Val	Ala
			50				55					60			
Val	Ala	Leu	Ile	Ser	Met	His	Asn	Cys	Ser	Leu	Asp	Ala	Lys	Ile	Arg
			65			70					75			80	
Val	Asn	Leu	Glu	Ala	Gln	Val	Val	Glu	Thr	Gln	Ala	Glu	Ala	Lys	Lys
			85						90				95		
Lys	Pro	Ala	Glu	Lys	Lys	Lys	Thr	Thr	Ser	Asp	Gly	Pro	Lys	Pro	Lys
			100				105						110		
Arg	Leu	Lys	Lys	Thr	Asn	Asp	Glu	Lys	Lys	Ser	Ser	Ser	Thr	Ser	Asn
			115				120						125		
Lys	Pro	Lys	Arg	Pro	Leu	Thr	Ala	Phe	Phe	Ile	Phe	Met	Ser	Asp	Phe
			130			135						140			
Arg	Lys	Thr	Phe	Lys	Ser	Glu	His	Asn	Gly	Ser	Leu	Ala	Lys	Asp	Ala
			145			150				155				160	
Ala	Lys	Ile	Gly	Gly	Glu	Lys	Trp	Lys	Ser	Leu	Thr	Glu	Glu	Glu	Lys
			165						170				175		
Lys	Val	Tyr	Leu	Asp	Lys	Ala	Ala	Glu	Leu	Lys	Ala	Glu	Tyr	Asn	Lys
			180				185					190			
Ser	Leu	Glu	Ser	Asn	Asp	Ala	Asp	Glu	Glu	Glu	Asp	Glu	Glu	Lys	

195					200					205				
Gln	Ser	Asp	Asp	Val	Asp	Asp	Glu	Glu	Lys	Gln	Val	Asp	Asp	Asp
	210				215					220				
Asp	Glu	Val	Glu	Glu	Lys	Glu	Val	Glu	Asn	Thr	Asp	Asp	Asp	Lys
225					230					235				240
Glu	Ala	Glu	Gly	Lys	Glu	Glu	Glu	Glu	Glu	Ile	Leu	Asp	Asp	Tyr
				245					250				255	

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 241 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(1x) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..241

(D) OTHER INFORMATION: / Ceres Seq. ID 1570291

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1524:

[illegible]

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 187 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..187

(D) OTHER INFORMATION: / Ceres Seq. ID 1570292

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1525:

```
Met His Asn Cys Ser Leu Asp Ala Lys Ile Arg Val Asn Leu Glu Ala
1          5          10          15
Gln Val Val Glu Thr Gln Ala Glu Ala Lys Lys Lys Pro Ala Glu Lys
20          25          30
Lys Lys Thr Thr Ser Asp Gly Pro Lys Pro Lys Arg Leu Lys Lys Thr
35          40          45
Asn Asp Glu Lys Lys Ser Ser Ser Thr Ser Asn Lys Pro Lys Arg Pro
50          55          60
Leu Thr Ala Phe Phe Ile Phe Met Ser Asp Phe Arg Lys Thr Phe Lys
65          70          75
Ser Glu His Asn Gly Ser Leu Ala Lys Asp Ala Ala Lys Ile Gly Gly
85          90          95
Glu Lys Trp Lys Ser Leu Thr Glu Glu Glu Lys Lys Val Tyr Leu Asp
100         105         110
Lys Ala Ala Glu Leu Lys Ala Glu Tyr Asn Lys Ser Leu Glu Ser Asn
115         120         125
Asp Ala Asp Glu Glu Glu Glu Asp Glu Glu Lys Gln Ser Asp Asp Val
130         135         140
Asp Asp Ala Glu Glu Lys Gln Val Asp Asp Asp Glu Val Glu Glu
145         150         155
Lys Glu Val Glu Asn Thr Asp Asp Asp Lys Lys Glu Ala Glu Gly Lys
165         170         175
Glu Glu Glu Glu Glu Glu Ile Leu Asp Asp Tyr
180         185
```

(2) INFORMATION FOR SEQ ID NO:1526:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 795 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..795

(D) OTHER INFORMATION: / Ceres Seq. ID 1570301

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1526:

```
gttcccaact ccttaacgccc tctctctcta tctcttttagc ttctcttttc tagcggcgcaa      60
catTgggttta tccggtggggg tacactgagc tctctctccc aagaatcttc cttaactttac      120
tctctctcttt aggccttaata cgaacactca tagacacggg ttctcggata ttgggtctac      180
cgaactttct cgaatccgac ccggttttat cgtcatcgtc atggctggaa ccacgtata      240
tgtccacggc ggcgcatacat caccaagaaa gtcctatttt ctccccagtg gcggcgaggc      300
tagctggaga aatctttgcc gtcatacagat tctcggaact aactcgacc ggattcggat      360
cggtatccga ttgtgcgcgc gtgtgcctcc acgagttcga gaacgaagac gagatccgac      420
ggctgacgaa ttgtcaaacac atatctcacc ggagctgttt agaccgttgg atgatggggt      480
ataatcagat gaactgtcca cttgttagaa cgcgcgttat ttctgatgag ttacaagttg      540
cttttaacca acgagtttgg tctgaatctg aacttctcgc agaatacaaat tagaatcttt      600
cttgttttgg tggaaattagt ttctactaat gagaaaaatta atttctatct tttttttttt      660
tttgtttaat ctttagctga gtggttgata tatgtaaaaa taaaaattat aggtggtgat      720
gcttagtaaaa ttgaagaagt gaaatttgta ttatccgttg agggaaaaaa agaatgaat      780
ggaaatctta atttt
```

(2) INFORMATION FOR SEQ ID NO:1527:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 87 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(D) OTHER INFORMATION: / Ceres Seq. ID 1570302

cgctcgtggt ggacgtgtca cagccatggc tacatacaag gtcaagttca tcacaccaga 240

aggtgagcta gaggttgagt gtgacgacga cgtctacggt cttgatgctg ctgaggaagc 300
tggaatcgat ttgccttact attgccgtgc tggttcttgt tcgagctgtg ctggtaaaagt 360
tgtgtctgga tctgttgatc agtctgacca gagtttccct gatgatgaac agattggtga 420
agggtttgtt ctcacttgtg ctgcttacct tacctctgat gttaccattg aaaCccacaa 480
agaagaagac attgtttaag cctcacctac tcaccagctt ttgatgggtt aaaaatcatg 540
ctttataat tgagtttgtt gttacaaaac tattgttacc tgttgttatt gttcctggtt 600
gggtccacca tcaatcgatg acatttt

(2) INFORMATION FOR SEQ ID NO:1530:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 165 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..165
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570309

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1530:

Ile Ile Leu Lys Asn Leu Asn Phe Ile Ser Gln Asn Thr Lys Gln Lys
1 5 10 15
Lys Met Ala Ser Thr Ala Leu Ser Ser Ala Ile Val Gly Thr Ser Phe
20 25 30
Ile Arg Arg Ser Pro Ala Pro Ile Ser Leu Arg Ser Leu Pro Ser Ala
35 40 45
Asn Thr Gln Ser Leu Phe Gly Leu Lys Ser Gly Thr Ala Arg Gly Gly
50 55 60
Arg Val Thr Ala Met Ala Thr Tyr Lys Val Lys Phe Ile Thr Pro Glu
65 70 75 80
Gly Glu Leu Glu Val Glu Cys Asp Asp Asp Val Tyr Val Leu Asp Ala
85 90 95
Ala Glu Glu Ala Gly Ile Asp Leu Pro Tyr Ser Cys Arg Ala Gly Ser
100 105 110
Cys Ser Ser Cys Ala Gly Lys Val Ser Gly Ser Val Asp Gln Ser
115 120 125
Asp Gln Ser Phe Leu Asp Asp Glu Gln Ile Gly Glu Gly Phe Val Leu
130 135 140
Thr Cys Ala Ala Tyr Pro Thr Ser Asp Val Thr Ile Glu Thr His Lys
145 150 155 160
Glu Glu Asp Ile Val
165

(2) INFORMATION FOR SEQ ID NO:1531:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 148 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..148
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570310

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1531:

Met Ala Ser Thr Ala Leu Ser Ser Ala Ile Val Gly Thr Ser Phe Ile
1 5 10 15
Arg Arg Ser Pro Ala Pro Ile Ser Leu Arg Ser Leu Pro Ser Ala Asn
20 25 30
Thr Gln Ser Leu Phe Gly Leu Lys Ser Gly Thr Ala Arg Gly Gly Arg
35 40 45
Val Thr Ala Met Ala Thr Tyr Lys Val Lys Phe Ile Thr Pro Glu Gly
50 55 60

Glu Leu Glu Val Glu Cys Asp Asp Asp Val Tyr Val Leu Asp Ala Ala
65 70 75 80
Glu Glu Ala Gly Ile Asp Leu Pro Tyr Ser Cys Arg Ala Gly Ser Cys
85 90 95
Ser Ser Cys Ala Gly Lys Val Val Ser Gly Ser Val Asp Gln Ser Asp
100 105 110
Gln Ser Phe Leu Asp Asp Glu Gln Ile Gly Glu Gly Phe Val Leu Thr
115 120 125
Cys Ala Ala Tyr Pro Thr Ser Asp Val Thr Ile Glu Thr His Lys Glu
130 135 140
Glu Asp Ile Val
145

(2) INFORMATION FOR SEQ ID NO:1532:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 97 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..97

(D) OTHER INFORMATION: / Ceres Seq. ID 1570311

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1532:

Met Ala Thr Tyr Lys Val Lys Phe Ile Thr Pro Glu Gly Glu Leu Glu
1 5 10 15
Val Glu Cys Asp Asp Asp Val Tyr Val Leu Asp Ala Ala Glu Glu Ala
20 25 30
Gly Ile Asp Leu Pro Tyr Ser Cys Arg Ala Gly Ser Cys Ser Ser Cys
35 40 45
Ala Gly Lys Val Val Ser Gly Ser Val Asp Gln Ser Asp Gln Ser Phe
50 55 60
Leu Asp Asp Glu Gln Ile Gly Glu Gly Phe Val Leu Thr Cys Ala Ala
65 70 75 80
Tyr Pro Thr Ser Asp Val Thr Ile Glu Thr Lys Glu Glu Asp Ile
85 90 95
Val

(2) INFORMATION FOR SEQ ID NO:1533:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 637 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -

(B) LOCATION: 1..637

(D) OTHER INFORMATION: / Ceres Seq. ID 1570315

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1533:

tyttctctct CtCtctcacac acttcacact ttaaatatac actctcatta tgactaccga 60
agagaagag atcctcgccg ccaaatgga agaacagaag atcgatctcg ataagccoga 120
agttgaggac gatgatgata acgaagacga tgactctgat gacgatgata aggatgatga 180
cgaggctgat ggactagatg gagaggcagg aggtaagtca aaacaaagca gaagtgaaga 240
gaagagtgc aaagccatgc tcaagcttgg catgaaaccc atcacttggt ttgcccaggt 300
cacggtcaaa aagagcaaga atatcttgg ttgtcatatca aagcctgatg tgtccaagag 360
tccagcatca gacacatatg tgatctttgg agaggcggaag atcgaggatt tgactctca 420
gatccagtcg caagcagcag agcaattcaa ggcaccagat ctgagcaatg tgatctcaaa 480
gggtgagtcg tcgagccctg cagtggttca ggatgatgag gaggttgacg aggaaggtgt 540
tgagccaaag gacattgagt tggatgatgac tcaagcagga gtgtctaggc caaatgctgt 600
gaaggctctc aaggctcgac atggagatat tgtctct

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 212 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ix) FEATURE:

(B) LOCATION: 1..21

(D) OTHER INFORMATION

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1534:

[illegible]

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 196 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..196

(D) OTHER INFORMATION: / Ceres Seq. ID 1570317

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1535:

Met	Thr	Thr	Glu	Glu	Lys	Glu	Ile	Leu	Ala	Ala	Lys	Leu	Glu	Glu	Gln
1				5					10					15	
Lys	Ile	Asp	Leu	Asp	Lys	Pro	Glu	Val	Glu	Asp	Asp	Asp	Asp	Asn	Glu
			20					25					30		
Asp	Asp	Asp	Ser	Asp	Asp	Asp	Asp	Lys	Asp	Asp	Asp	Glu	Ala	Asp	Gly
		35					40					45			
Leu	Asp	Gly	Glu	Ala	Gly	Gly	Lys	Ser	Lys	Gln	Ser	Arg	Ser	Glu	Lys
		50				55					60				
Lys	Ser	Arg	Lys	Ala	Met	Leu	Lys	Leu	Gly	Met	Lys	Pro	Ile	Thr	Gly

65				70				75						80
Val	Ser	Arg	Val	Thr	Val	Lys	Lys	Ser	Lys	Asn	Ile	Leu	Phe	Val
				85					90					95
Ser	Lys	Pro	Asp	Val	Phe	Lys	Ser	Pro	Ala	Ser	Asp	Thr	Tyr	Val
			100						105				110	
Phe	Gly	Glu	Ala	Lys	Ile	Glu	Asp	Leu	Ser	Ser	Gln	Ile	Gln	Ser
			115				120				125			
Ala	Ala	Glu	Gln	Phe	Lys	Ala	Pro	Asp	Leu	Ser	Asn	Val	Ile	Ser
			130			135					140			
Gly	Glu	Ser	Ser	Ser	Ala	Ala	Val	Val	Gln	Asp	Asp	Glu	Glu	Val
			145			150				155				160
Glu	Glu	Gly	Val	Glu	Pro	Lys	Asp	Ile	Glu	Leu	Val	Met	Thr	Gln
			165					170						175
Gly	Val	Ser	Arg	Pro	Asn	Ala	Val	Lys	Ala	Leu	Lys	Ala	Ala	Asp
			180				185					190		
Asp	Ile	Val	Ser											
			195											

(2) INFORMATION FOR SEQ ID NO:1536:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 127 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..127

(D) OTHER INFORMATION: / Ceres Seq. ID 1570318

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1536:

Met	Leu	Lys	Leu	Gly	Met	Lys	Pro	Ile	Thr	Gly	Val	Ser	Arg	Val	Thr
1				5				10						15	
Val	Lys	Lys	Ser	Lys	Asn	Ile	Leu	Phe	Val	Ile	Ser	Lys	Pro	Asp	Val
			20				25						30		
Phe	Lys	Ser	Pro	Ala	Ser	Asp	Thr	Tyr	Val	Ile	Phe	Gly	Glu	Ala	Lys
			35				40					45			
Ile	Glu	Asp	Leu	Ser	Ser	Gln	Ile	Gln	Ser	Gln	Ala	Ala	Glu	Gln	Phe
			50			55					60				
Lys	Ala	Pro	Asp	Leu	Ser	Asn	Val	Ile	Ser	Lys	Gly	Glu	Ser	Ser	Ser
			65			70				75				80	
Ala	Ala	Val	Val	Gln	Asp	Asp	Glu	Glu	Val	Asp	Glu	Glu	Gly	Val	Glu
			85						90				95		
Pro	Lys	Asp	Ile	Glu	Leu	Val	Met	Thr	Gln	Ala	Gly	Val	Ser	Arg	Pro
			100				105						110		
Asn	Ala	Val	Lys	Ala	Leu	Lys	Ala	Ala	Asp	Gly	Asp	Ile	Val	Ser	
			115			120									

(2) INFORMATION FOR SEQ ID NO:1537:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1131 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1131

(D) OTHER INFORMATION: / Ceres Seq. ID 1570339

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1537:

aaccaaatac	aaacccatgc	cgccttatcc	gtctctcttcg	tctctctagtt	ttttctctcag	60
tctctgttct	tagatccctt	gtagtttcca	aattcttcga	taaaaaatgc	gggtaaaagga	120
gaaggaccag	ctatccgtat	cgatcttggt	accacttact	cttgcgtcgg	agtatggcaa	180
cacgaccgtg	ttgagatcat	tgctaattgat	caaggaaaaca	gaaccacgcc	attctacgtt	240

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gttttcaccg actccgagag gttgatcggt gacgcagcta agaatacagg cgccatgaac    300
cccgtaataca ccggttttcga cgctaagagg ttgatcggtc gtcggttttc tgacagctct    360
gttcagaggtg acatgaaatt gtggccattc aaagattcaag cggagacctg cgataagcca    420
atgatctaacg tcgaatacaa ggggtaagag aaagagttcg cagctgagga gattttcttc    480
atggttcttta ttaagatgcg tgagattgct gaggtctacc ttatgtgcac aatcaagaac    540
gcccgttgtaa ccgttccagc ttacttcaac gactctcagc gtcagggtac aaaggatgct    600
gggtgcatcg ctggtttgaa cgttatgcga atcatcaacg agctacacgc cgccgctatt    660
gCctacgggtc ttgacaaaaa ggctaccagc gttggagaga agaattgtct tatcttcgat    720
cttggtgggtg gcaacttttg tgctctctct cttaccattg aagagggtat ctttgagggtg    780
aaggcaactg ctggtgacac ccatcttggt gggaagattt ttgacaacag aatgggttaac    840
cactttgtcc aagagttcaa gaggaagagt aagaaggata tcaccggtaa cccaagagct    900
cttagagaggt tgagaacttc ctgtgagaga gcgaagagga ctcttctctc caactgtctc    960
accaccatcg agattgactc tctatacagc ggtatcgact tctactccac catcaccctg   1020
gctagatttg aggagctcaa catggatctc ttcagggaagt gtatggagcc agttgagaag   1080
tgtctctgtg atgctaagat ggacaagagc actgttcgat atgttgctct t

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(2) INFORMATION FOR SEQ ID NO:1538:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 342 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..342

(D) OTHER INFORMATION: / Ceres Seq. ID 1570340

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1538:

```

Met Ser Gly Lys Gly Glu Gly Pro Ala Ile Gly Ile Asp Leu Gly Thr
1      5      10      15
Thr Tyr Ser Cys Val Gly Val Trp Gln His Asp Arg Val Glu Ile Ile
20      25      30
Ala Asn Asp Gln Gly Asn Arg Thr Thr Pro Ser Tyr Val Ala Phe Thr
35      40      45
Asp Ser Glu Arg Leu Ile Gly Asp Ala Ala Lys Asn Gln Val Ala Met
50      55      60
Asn Pro Val Asn Thr Val Phe Asp Ala Lys Arg Leu Ile Gly Arg Arg
65      70      75      80
Phe Ser Asp Ser Ser Val Gln Ser Asp Met Lys Leu Trp Pro Phe Lys
85      90      95
Ile Gln Ala Gly Pro Ala Asp Lys Pro Met Ile Tyr Val Glu Tyr Lys
100      105      110
Gly Glu Glu Lys Glu Phe Ala Ala Glu Glu Ile Ser Ser Met Val Leu
115      120      125
Ile Lys Met Arg Glu Ile Ala Glu Ala Tyr Leu Ser Val Thr Ile Lys
130      135      140
Asn Ala Val Val Thr Val Pro Ala Tyr Phe Asn Asp Ser Gln Arg Gln
145      150      155      160
Ala Thr Lys Asp Ala Gly Val Ile Ala Gly Leu Asn Val Met Arg Ile
165      170      175
Ile Asn Glu Pro Thr Ala Ala Ala Ile Ala Tyr Gly Leu Asp Lys Lys
180      185      190
Ala Thr Ser Val Gly Glu Lys Asn Val Leu Ile Phe Asp Leu Gly Gly
195      200      205
Gly Thr Phe Asp Val Ser Leu Leu Thr Ile Glu Glu Gly Ile Phe Glu
210      215      220
Val Lys Ala Thr Ala Gly Asp Thr His Leu Gly Gly Glu Asp Phe Asp
225      230      235      240
Asn Arg Met Val Asn His Phe Val Gln Glu Phe Lys Arg Lys Ser Lys
245      250      255
Lys Asp Ile Thr Gly Asn Pro Arg Ala Leu Arg Arg Leu Arg Thr Ser
260      265      270

```

Cys Glu Arg Ala Lys Arg Thr Leu Ser Ser Thr Ala Gln Thr Thr Ile
275 280 285
Glu Ile Asp Ser Leu Tyr Glu Gly Ile Asp Phe Tyr Ser Thr Ile Thr
290 295 300
Arg Ala Arg Phe Glu Glu Leu Asn Met Asp Leu Phe Arg Lys Cys Met
305 310 315 320
Glu Pro Val Glu Lys Cys Leu Arg Asp Ala Lys Met Asp Lys Ser Thr
325 330 335
Val His Asp Val Val Leu
340

(2) INFORMATION FOR SEQ ID NO:1539:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 279 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..279

(D) OTHER INFORMATION: / Ceres Seq. ID 1570341

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1539:

Met Asn Pro Val Asn Thr Val Phe Asp Ala Lys Arg Leu Ile Gly Arg
1 5 10 15
Arg Phe Ser Asp Ser Ser Val Gln Ser Asp Met Lys Leu Trp Pro Phe
20 25 30
Lys Ile Gln Ala Gly Pro Ala Asp Lys Pro Met Ile Tyr Val Glu Tyr
35 40 45
Lys Gly Glu Glu Lys Glu Phe Ala Ala Glu Glu Ile Ser Ser Met Val
50 55 60
Leu Ile Lys Met Arg Glu Ile Ala Glu Ala Tyr Leu Ser Val Thr Ile
65 70 75 80
Lys Asn Ala Val Val Thr Val Pro Ala Tyr Phe Asn Asp Ser Gln Arg
85 90 95
Gln Ala Thr Lys Asp Ala Gly Val Ile Ala Gly Leu Asn Val Met Arg
100 105 110
Ile Ile Asn Glu Pro Thr Ala Ala Ala Ile Ala Tyr Gly Leu Asp Lys
115 120 125
Lys Ala Thr Ser Val Gly Glu Lys Asn Val Leu Ile Phe Asp Leu Gly
130 135 140
Gly Gly Thr Phe Asp Val Ser Leu Leu Thr Ile Glu Glu Gly Ile Phe
145 150 155 160
Glu Val Lys Ala Thr Ala Gly Asp Thr His Leu Gly Gly Glu Asp Phe
165 170 175
Asp Asn Arg Met Val Asn His Phe Val Gln Glu Phe Lys Arg Lys Ser
180 185 190
Lys Lys Asp Ile Thr Gly Asn Pro Arg Ala Leu Arg Arg Leu Arg Thr
195 200 205
Ser Cys Glu Arg Ala Lys Arg Thr Leu Ser Ser Thr Ala Gln Thr Thr
210 215 220
Ile Glu Ile Asp Ser Leu Tyr Glu Gly Ile Asp Phe Tyr Ser Thr Ile
225 230 235 240
Thr Arg Ala Arg Phe Glu Glu Leu Asn Met Asp Leu Phe Arg Lys Cys
245 250 255
Met Glu Pro Val Glu Lys Cys Leu Arg Asp Ala Lys Met Asp Lys Ser
260 265 270
Thr Val His Asp Val Val Leu
275

(2) INFORMATION FOR SEQ ID NO:1540:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 253 amino acids

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1540:

(2) INFORMATION FOR SEQ ID NO:1541:

(ii) MOLECULE TYPE: DNA (genomic)

(A) NAME/KEY: -

(B) LOCATION: 1..921

(D) OTHER INFORMATION: / Ceres Seq. ID 1570343

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1541:

tatccaatata	tatcctcttc	cattagotgtt	tgttctctctg	tcccaacttc	aattcctcttc	60
gaatatattca	tcgcgaattcg	tatcoggtttt	aagtaaaaaa	gcgaatggag	gtgtgaaaga	120
caagcatcat	gatgagcaag	agaaaaaggt	tcatgtgttt	ccaggaggtg	gacattaccc	180
ccctctceta	ggaggtttacc	ctccacaagg	tattccacca	caacaagggt	attctccagc	240
tggagagtcac	coacctccgc	gatatctctc	tgggtgtttac	ctctgtcgcc	ccgggtggtta	300
tcctctctctc	ctcgagggtt	acctctctgc	tggctattctc	gcacctggag	ctcacattac	360
aggacattct	ggtgtgtggac	ctcgaggcat	gatagcaggt	gcagctctgt	cagcccgacg	420
agcttatgga	gtctcacattg	ttgtgcacgc	ctctcacacg	ctactcggg	ctatctgtagg	480

acatggaggagg tatggccatg cccctgctca tggctttggc catggtgggc atggtaaaatt 540
caagcacgga aagcatggag gcaaaattcaa gcacggaaaag catggaaaagc acggggaacaa 600
tggcatgttt ggaggaggag gcaaaattcaa gaagtggag taatctcaaa aacccacact 660
ttgatctctc cctccagatg agtctcatta cctgaccgat gtttctaata atcccccttc 720
aaacataatt cattttaact atgtcggttt agagattact ggttgaggaa ataattggag 780
agtgtctagta taaaccttat ggtatctgca gcagagggtt ctttaacttc tcaatagtag 840
atgctttgaa acttatctat aattttNgga ttgtaatgac agtttgtgtt tggGtttttt 900
cttcagatc tctcttgttt g

(2) INFORMATION FOR SEQ ID NO:1542:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 179 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..179

(D) OTHER INFORMATION: / Ceres Seq. ID 1570344

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1542:

Met Gly Gly Lys Asp Lys His His Asp Glu Lys Gly Phe
1 5 10 15
His Gly Phe Pro Gly Gly His Tyr Pro Pro Ala Gln Gly Tyr
20 25 30
Pro Pro Gln Gly Tyr Pro Pro Gln Gly Tyr Pro Pro Ala Gly Gly
35 40 45
Tyr Pro Pro Ala Gly Tyr Pro Pro Gly Ala Tyr Pro Ala Ala Pro Gly
50 55 60
Gly Tyr Pro Pro Ala Pro Gly Gly Tyr Pro Pro Ala Gly Tyr Pro Ala
65 70 75 80
Pro Gly Ala His His Ser Gly His Ser Gly Gly Gly Leu Gly Gly Met
85 90 95
Ile Ala Gly Ala Ala Gly Ala Ala Ala Ala Tyr Gly Ala His His
100 105 110
Val Gly His Ala Ser His Asn Pro Tyr Gly His Ala Val Gly His Gly
115 120 125
Gly Tyr Gly His Ala Pro Ala His Gly Phe Gly His Gly Gly His Gly
130 135 140
Lys Phe Lys His Gly Lys His Gly Gly Lys Phe Lys His Gly Lys His
145 150 155 160
Gly Lys His Gly Lys His Gly Met Phe Gly Gly Gly Lys Phe Lys
165 170 175
Lys Trp Lys

(2) INFORMATION FOR SEQ ID NO:1543:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2432 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..2432

(D) OTHER INFORMATION: / Ceres Seq. ID 1570349

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1543:

acctattctc actaacaac tctgaacaaa ccaaaaaaaaa cttctttttt ttctatcttt 60
cacgcgttga agattcttga ttttctttct tctctcttct tacacgacca ctgatgtgt 120
tccgtgaactg aaaccatctg ttctcttttg cctctgattt atcgatatgt tttaaagaaa 180
aacggtgttt gaaacttttg taatttaagg ttcatcaaat actcagatct tgtctgagaa 240
attaagctga aatctgataa atgggtttgt ttaaattcat cttcttgtaa tctcttctat 300

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ggagttttcta cagtttaggc tcatctcagc tacaagcttc acaagcacia gttcttcttc 360
agctgaaaaa acacttagaa tatccacaac agctagaatc ttggtatgat cacagaacca 420
attcttgcta tctacaagca accactatga tgaacatcac ttgtttctct aatcagctct 480
cagagctaaa catcttcggt gataagtcac cagaaaaaagc caaaagcttt gatggttttg 540
ctatctcttaa tgttacttta tctgatggat tctccattga atcattttgc actacactgt 600
caaggctaaa atctcttagg gtctcttact tggctttctc agggatttgg ggtcgtctcc 660
ctgagaaact tcatcggttta tctctcacttg agtattttga tttagacaaat aactttctgt 720
ttggttcagt accacctaa gttctcacia ttgttaaagct tgaacctttH cagattttgat 780
cataactctt tcaatggcac attacctagc tgggtttgatt cgtatttgga tctcaaaagt 840
cttagcttta aaagtaataa gactatcagg gagctacatt ctctactact ctggttgta 900
acaactcgat atatcgattt gagagcaaat tctctgagtg gttcactttcc ggaatgatctg 960
aaatgtgaaa gcaaaactctg gtttatcgac atttccgaca ataagttaac cgaaaaaactt 1020
cctcgttgct taagcagcaa gcaagatatt gcgttgagat tcaatggaaa ctgtttatct 1080
ctagagaaac agcaacatct agaactcttt tgtgttaaa aagttcgcgc tgcggctaaa 1140
gctgaagcaa aagcagaagc agaggctgca aatgaatcag gaaaaagaaa atgggaagaa 1200
ggagctttta tcggttaaat cgttggtata tcaatggcgg tattggtttt agtctgctgt 1260
gtatttatct tgcctcagaag aaaaggagta acaaaagaac atgtccacca taatactgtc 1320
caagataatc atccaactac tggattttct tccgagatac tctcaaaagc aaggtacatt 1380
tctgaacctc caaagtttgg ttcagaggac ttacgggtat gtgacagtt tagcttagaa 1440
gagatagtta aagctacaaa gaactctgat aagactatga tactcgggtg aagctcctta 1500
tatggcacgc tttacaagg aaactcttgg aatggaaaca aagtggaact aagatgctta 1560
cctctatcga agaaatactc gataaggaa cttaaaactgc ggttgattt gctccgaaag 1620
cttagaaccc ogaattctgt ctgcttgggt ggtcattgca tagattgtgg aggaataaag 1680
gattacagcg ttgagaaagt ctttttgatt tattagatata ttccaaatgg aaacttccaa 1740
tctgttctct cagataaatg ttcaggtaag ggtatgaatt ggtcagagag gcttaagtgt 1800
ctcacaggtg ttgcaaaagc tgttctattt ctccacactg gatgtatttc tggatttttc 1860
agcaatagac tcaagactaa caacgttttg cttaaccaac atcgggtttg gaaactaggt 1920
gttatgtgtt tghccattgt ctctgaagca accagaaaat acacagaaaat cgcagaaata 1980
tggcaaatgt caaggctaga agacagtggt tacagctttg gattgattct tctacaatca 2040
atcgtttggc catctgtatc cgcgaagaaa gaagcatttc taccgagaga actgcatcgc 2100
ttggagagcg aagaaggagg gagaagaatg gtgaatccga cagtacaagc cactgtgtca 2160
aacggatcac tgataaagct gataaactct atgaacaaat gtgttttcc tgaattctta 2220
agccgacctg ccttcgaaga tatcttgttg aatttacagt atgcttctca gtgccaagt 2280
gctctgatg gtgaccagtg ttaataatct catagcttct tcttctctta gtaaaaaact 2340
caaacgaact ttaaatgtc ttaaaagatt gtgtaatggt ttgtacgaaa aatccccctg 2400
tatttatgta acgattggga aaaatggaaa tt

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(2) INFORMATION FOR SEQ ID NO:1544:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 356 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..356
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570350

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1544:

```

Met Ala Val Leu Val Leu Val Cys Cys Val Phe Ile Leu Leu Arg Arg
1      5      10      15
Lys Gly Val Thr Lys Lys His Val His Asn Thr Val Gln Asp Asn
20     25     30
His Pro Thr Thr Gly Phe Ser Ser Glu Ile Leu Ser Asn Ala Arg Tyr
35     40     45     50
Ile Ser Glu Thr Ser Lys Phe Gly Ser Glu Asp Leu Pro Val Cys Arg
55     60
Gln Phe Ser Leu Glu Glu Ile Val Lys Ala Thr Lys Asn Phe Asp Lys
65     70     75     80
Thr Met Ile Leu Gly Glu Ser Ser Leu Tyr Gly Thr Leu Tyr Lys Gly
85     90     95
Asn Leu Glu Asn Gly Thr Lys Val Ala Ile Arg Cys Leu Pro Ser Ser

```

100 105 110
Lys Lys Tyr Ser Ile Arg Asn Leu Lys Leu Arg Leu Asp Leu Leu Ala
115 120 125
Lys Leu Arg His Pro Asn Leu Val Cys Leu Leu Gly His Cys Ile Asp
130 135 140
Cys Gly Gly Lys Asp Asp Tyr Ser Val Glu Lys Val Phe Leu Ile Tyr
145 150 155 160
Glu Tyr Ile Pro Asn Gly Asn Phe Gln Ser Cys Leu Ser Asp Asn Ser
165 170 175
Ser Gly Lys Gly Met Asn Trp Ser Glu Arg Leu Asn Val Leu Thr Gly
180 185 190
Val Ala Lys Ala Val His Phe Leu His Thr Gly Val Ile Pro Gly Phe
195 200 205
Phe Ser Asn Arg Leu Lys Thr Asn Asn Val Leu Leu Asn Gln His Arg
210 215 220
Phe Val Lys Leu Ser Asp Tyr Gly Leu Xaa Ile Val Ser Glu Ala Thr
225 230 235 240
Arg His Asn Thr Glu Ile Ala Lys Ser Trp Gln Met Ser Arg Leu Glu
245 250 255
Asp Asp Val Tyr Ser Phe Gly Leu Ile Leu Leu Gln Ser Ile Val Gly
260 265 270
Pro Ser Val Ser Ala Arg Glu Glu Ala Phe Leu Arg Asp Glu Leu Ala
275 280 285
Ser Leu Glu Ser Glu Glu Gly Arg Arg Arg Met Val Asn Pro Thr Val
290 295 300
Gln Ala Thr Cys Arg Asn Gly Ser Leu Ile Arg Val Ile Thr Leu Met
305 310 315 320
Asn Lys Cys Val Ser Pro Glu Ser Leu Ser Arg Pro Ser Phe Glu Asp
325 330 335
Ile Leu Trp Asn Leu Gln Tyr Ala Ser Gln Leu Gln Ala Ala Ser Asp
340 345 350
Gly Asp Gln Cys
355

(2) INFORMATION FOR SEQ ID NO:1545:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 275 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..275
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570351

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1545:

Met Ile Leu Gly Glu Ser Ser Leu Tyr Gly Thr Leu Tyr Lys Gly Asn
1 5 10 15
Leu Glu Asn Gly Thr Lys Val Ala Ile Arg Cys Leu Pro Ser Ser Lys
20 25 30
Lys Tyr Ser Ile Arg Asn Leu Lys Leu Arg Leu Asp Leu Leu Ala Lys
35 40 45
Leu Arg His Pro Asn Leu Val Cys Leu Leu Gly His Cys Ile Asp Cys
50 55 60
Gly Gly Lys Asp Asp Tyr Ser Val Glu Lys Val Phe Leu Ile Tyr Glu
65 70 75 80
Tyr Ile Pro Asn Gly Asn Phe Gln Ser Cys Leu Ser Asp Asn Ser Ser
85 90 95
Gly Lys Gly Met Asn Trp Ser Glu Arg Leu Asn Val Leu Thr Gly Val
100 105 110
Ala Lys Ala Val His Phe Leu His Thr Gly Val Ile Pro Gly Phe Phe
115 120 125

Ser Asn Arg Leu Lys Thr Asn Asn Val Leu Leu Asn Gln His Arg Phe
130 135 140
Val Lys Leu Ser Asp Tyr Gly Leu Xaa Ile Val Ser Glu Ala Thr Arg
145 150 155 160
His Asn Thr Glu Ile Ala Lys Ser Trp Gln Met Ser Arg Leu Glu Asp
165 170 175
Asp Val Tyr Ser Phe Gly Leu Ile Leu Leu Gln Ser Ile Val Gly Pro
180 185 190
Ser Val Ser Ala Arg Glu Glu Ala Phe Leu Arg Asp Glu Leu Ala Ser
195 200 205
Leu Glu Ser Glu Glu Gly Arg Arg Arg Met Val Asn Pro Thr Val Gln
210 215 220
Ala Thr Cys Arg Asn Gly Ser Leu Ile Arg Val Ile Thr Leu Met Asn
225 230 235 240
Lys Cys Val Ser Pro Glu Ser Leu Ser Arg Pro Ser Phe Glu Asp Ile
245 250 255
Leu Trp Asn Leu Gln Tyr Ala Ser Gln Leu Gln Ala Ala Ser Asp Gly
260 265 270
Asp Gln Cys
275

(2) INFORMATION FOR SEQ ID NO:1546:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 780 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..780
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570356

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1546:

acagtaataa	tcaagtcaga	gccggcgaas	ttgccgtttc	cgccgttgga	gaggaattat	60
agtcatgaag	cttatttcac	ttgtcagaaa	cgttcgtttc	cgccaatgac	aaccggaagt	120
tatctgggtc	ttgcaagttc	gtttcttgca	gcaagattct	gtctcgaaag	ctaaacccaa	180
gaaatacaaa	taccgcgcag	tttatgatcc	gtatggtctc	agaccccagc	cttcaagcaa	240
aatcatggag	ctagctgagc	gtatagctgc	tttatctcca	gaagaaagaa	aacagattgg	300
tcctgcactc	aatgaacacc	tgaggcttcc	aaaaacaacg	atgatttcat	cggacggcat	360
tggaataaaa	caagataccg	gagctgggaa	agtagaggag	aagaaggaga	agacggcttt	420
cgatgtgaag	ttggagaagt	ttaatgcac	tgataagatc	aaagtataa	aagaagtgg	480
aacgtttaca	agtttgggtc	tgaaggaagc	gaaagagctt	gtggagaaag	tcccgctcat	540
tccttaacaa	ggtgtgcaca	aggaagaagc	taatgaaatc	atagccaaga	tcaaaagctgt	600
tggtggagtc	gcagttatgg	agtaggtgac	ttttgacact	tcaattgttt	ttttgtttga	660
ttcactattt	ggtattgtga	tcacatcttg	gtacttaagg	tagatgtttt	gtaataacaa	720
atcgattact	tgacattgag	ttttcaagaa	ctttggDtca	attgtttgcc	ttctctttgc	780

(2) INFORMATION FOR SEQ ID NO:1547:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 186 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..186
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570357

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1547:

Met Lys Leu Ile Ser Leu Val Arg Asn Val Arg Ser Arg Gln Cys Gln						
1	5	10	15			
Pro Glu Val Ile Trp Ser Leu Gln Val Arg Phe Leu Gln Gln Asp Ser						

20										25										30																		
Val	Ser	Lys	Ala	Lys	Pro	Lys	Lys	Tyr	Lys	Tyr	Pro	Ser	Lys	Ile	Met	Glu	Leu	Ala	Asp	Val	Ser	Lys	Ala	Lys	Pro	Lys	Lys	Tyr	Lys	Tyr	Pro	Ser	Lys	Ile	Met	Glu	Leu	Ala
35										40										45																		
Pro	Tyr	Gly	Pro	Arg	Pro	Gln	Pro	Ser	Ser	Lys	Ile	Met	Glu	Leu	Ala	Asp	Val	Ser	Lys	Ala	Lys	Pro	Lys	Lys	Tyr	Lys	Tyr	Pro	Ser	Lys	Ile	Met	Glu	Leu	Ala			
50										55										60																		
Glu	Arg	Ile	Ala	Ala	Leu	Ser	Pro	Glu	Glu	Arg	Lys	Gln	Ile	Gly	Pro	Asp	Val	Ser	Lys	Ala	Lys	Pro	Lys	Lys	Tyr	Lys	Tyr	Pro	Ser	Lys	Ile	Met	Glu	Leu	Ala			
65										70										75																		
Ala	Leu	Asn	Glu	His	Leu	Arg	Leu	Pro	Lys	Gln	Ile	Met	Glu	Leu	Ala	Asp	Val	Ser	Lys	Ala	Lys	Pro	Lys	Lys	Tyr	Lys	Tyr	Pro	Ser	Lys	Ile	Met	Glu	Leu	Ala			
85										90										95																		
Asp	Gly	Ile	Gly	Ala	Lys	Gln	Asp	Thr	Gly	Ala	Gly	Lys	Val	Glu	Glu	Asp	Val	Ser	Lys	Ala	Lys	Pro	Lys	Lys	Tyr	Lys	Tyr	Pro	Ser	Lys	Ile	Met	Glu	Leu	Ala			
100										105										110																		
Lys	Lys	Glu	Lys	Thr	Ala	Phe	Asp	Val	Lys	Leu	Glu	Lys	Phe	Asn	Ala	Asp	Val	Ser	Lys	Ala	Lys	Pro	Lys	Lys	Tyr	Lys	Tyr	Pro	Ser	Lys	Ile	Met	Glu	Leu	Ala			
115										120										125																		
Ser	Asp	Lys	Ile	Lys	Val	Ile	Lys	Glu	Val	Arg	Thr	Phe	Thr	Ser	Leu	Asp	Val	Ser	Lys	Ala	Lys	Pro	Lys	Lys	Tyr	Lys	Tyr	Pro	Ser	Lys	Ile	Met	Glu	Leu	Ala			
130										135										140																		
Gly	Leu	Lys	Glu	Ala	Lys	Glu	Leu	Val	Glu	Lys	Val	Pro	Ala	Ile	Leu	Asp	Val	Ser	Lys	Ala	Lys	Pro	Lys	Lys	Tyr	Lys	Tyr	Pro	Ser	Lys	Ile	Met	Glu	Leu	Ala			
145										150										155																		
Lys	Gln	Gly	Val	Thr	Lys	Glu	Glu	Ala	Asn	Glu	Ile	Ile	Ala	Lys	Ile	Asp	Val	Ser	Lys	Ala	Lys	Pro	Lys	Lys	Tyr	Lys	Tyr	Pro	Ser	Lys	Ile	Met	Glu	Leu	Ala			
165										170										175																		
Lys	Ala	Val	Gly	Gly	Val	Ala	Val	Met	Glu																													
180										185																												

(2) INFORMATION FOR SEQ ID NO:1548:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 126 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..126

(D) OTHER INFORMATION: / Ceres Seq. ID 1570358

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1548:

Met	Glu	Leu	Ala	Glu	Arg	Ile	Ala	Ala	Leu	Ser	Pro	Glu	Glu	Arg	Lys	1	5	10	15
Gln	Ile	Gly	Pro	Ala	Leu	Asn	Glu	His	Leu	Arg	Leu	Pro	Lys	Gln	Gln	20	25	30	
Met	Ile	Ser	Ser	Asp	Gly	Ile	Gly	Ala	Lys	Gln	Asp	Thr	Gly	Ala	Gly	35	40	45	
Lys	Val	Glu	Glu	Lys	Lys	Glu	Lys	Thr	Ala	Phe	Asp	Val	Lys	Leu	Glu	50	55	60	
Lys	Phe	Asn	Ala	Ser	Asp	Lys	Ile	Lys	Val	Ile	Lys	Glu	Val	Arg	Thr	65	70	75	80
Phe	Thr	Ser	Leu	Gly	Leu	Lys	Glu	Ala	Lys	Glu	Leu	Val	Glu	Lys	Val	85	90	95	
Pro	Ala	Ile	Leu	Lys	Gln	Gly	Val	Thr	Lys	Glu	Glu	Ala	Asn	Glu	Ile	100	105	110	
Ile	Ala	Lys	Ile	Lys	Ala	Val	Gly	Gly	Val	Ala	Val	Met	Glu			115	120	125	

(2) INFORMATION FOR SEQ ID NO:1549:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 94 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..94

(D) OTHER INFORMATION: / Ceres Seq. ID 1570359

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1549:

Met Ile Ser Ser Asp Gly Ile Gly Ala Lys Gln Asp Thr Gly Ala Gly
1 5 10 15
Lys Val Glu Glu Lys Lys Glu Lys Thr Ala Phe Asp Val Lys Leu Glu
20 25 30
Lys Phe Asn Ala Ser Asp Lys Ile Lys Val Ile Lys Glu Val Arg Thr
35 40 45
Phe Thr Ser Leu Gly Leu Lys Glu Ala Lys Glu Leu Val Glu Lys Val
50 55 60
Pro Ala Ile Leu Lys Gln Gly Val Thr Lys Glu Glu Ala Asn Glu Ile
65 70 75 80
Ile Ala Lys Ile Lys Ala Val Gly Gly Val Ala Val Met Glu
85 90

(2) INFORMATION FOR SEQ ID NO:1550:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1147 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1147
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570366

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1550:

ctttttctct	ttcacatcgt	tctttctctc	gcaaaacccaa	attctctcag	cgccgggtcaa	60
atactgtgct	ctctctctct	ctctctttca	ctcttgctct	gtctctcttg	aagctgtgttg	120
ttctgttaaga	aagatggaag	caggtggcgc	gtaccaatcca	cgactctgtg	aagaggtgtt	180
tagggattttt	aagggtcgta	gagctggcat	gattaaggct	ttaccactgt	atgttcagga	240
gttttttcoga	ctttgtgatc	ccgaaaagga	gaaccttttg	ctttacggac	atccaaatga	300
gcactgggaaa	gtgaatttgc	cagctgaaga	ggttctctct	gagctccag	agcctgtctt	360
gggtatcaat	tttgcagag	acgggatgag	ggaaaaggat	tgtttgtccc	ttgtgtgctg	420
ccacagtgtg	gcttggcttc	ttgtgtgttc	tttctttttt	ggagccagggt	ttgatttga	480
caaaagctgat	aggaagaggg	ttttcaatat	ggtgaatgac	ctcccaacaa	cttttgaggt	540
tgtagtggc	actgctaaga	aacaaggaaa	agataagfcc	ctctgtttcca	acaacagcag	600
caacagatcc	aaatcaagct	ccaagcgagg	atctgaatcc	cgtgccagt	tctcaaaagcc	660
ggagccgaaa	gatgatgagg	aggaggaaga	ggaaggtgtg	gaagaggagg	atgaggatga	720
gcaaggtgaa	acacagtggt	gagcatgtgg	tgagagctat	gcagctgatg	agttctggat	780
ttgtctgtac	ctctgtgaga	tgtgttttca	tggaaaagtgt	gttaagataa	caccagcaag	840
agctgagcac	atcaagcaat	acaagtgccc	ttctgtcagc	aaAcaaaagg	gctcgtttctt	900
aaatttgggt	accgtctcgt	tctgtgtatc	tacctttgca	tatgatgatg	aacagcttaa	960
ctgttttggt	tagatcagat	tgttcatatg	gatttggtaa	ttttaggaag	acatttttga	1020
tttttcattg	ttacattttg	gcgattgaag	ggataactct	ttgttttaggg	gtaatgatct	1080
ttgtctctgt	tttatgtttg	tttattaaca	ttcttcaaac	tcaatcaaaa	gtattttgggt	1140
tagtctt						

(2) INFORMATION FOR SEQ ID NO:1551:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 323 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..323
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570367

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1551:

Phe Phe Ser Phe Thr Ser Phe Phe Leu Ser Gln Thr Gln Ile Leu Ser	5	10	15
Ala Pro Val Lys Tyr Leu Ser Leu Ser Leu Ser Leu Phe His Ser Cys	20	25	30
Leu Val Ser Phe Glu Ala Val Cys Ser Val Arg Lys Met Glu Ala Gly			

Met	Glu	Ala	Gly	Gly	Ala	Tyr	Asn	Pro	Arg	Thr	Val	Glu	Glu	Val	Phe
1				5					10					15	
Arg	Asp	Phe	Lys	Gly	Arg	Arg	Ala	Gly	Met	Ile	Lys	Ala	Leu	Thr	Thr
			20					25					30		
Asp	Val	Gln	Glu	Phe	Phe	Arg	Leu	Cys	Asp	Pro	Glu	Lys	Glu	Asn	Leu
		35					40					45			
Cys	Leu	Tyr	Gly	His	Pro	Asn	Glu	His	Trp	Glu	Val	Asn	Leu	Pro	Ala
	50					55					60				
Glu	Glu	Val	Pro	Pro	Glu	Leu	Pro	Glu	Pro	Val	Leu	Gly	Ile	Asn	Phe
65					70					75				80	
Ala	Arg	Asp	Gly	Met	Ala	Glu	Lys	Asp	Trp	Leu	Ser	Leu	Val	Ala	Val
				85					90					95	

His Ser Asp Ala Trp Leu Leu Ala Val Ala Phe Phe Phe Gly Ala Arg
100 105 110
Phe Gly Phe Asp Lys Ala Asp Arg Lys Arg Leu Phe Asn Met Val Asn
115 120 125
Asp Leu Pro Thr Ile Phe Glu Val Val Ala Gly Thr Ala Lys Lys Gln
130 135 140
Gly Lys Asp Lys Ser Ser Val Ser Asn Asn Ser Ser Asn Arg Ser Lys
145 150 155 160
Ser Ser Ser Lys Arg Gly Ser Glu Ser Arg Ala Lys Phe Ser Lys Pro
165 170 175
Glu Pro Lys Asp Asp Glu Glu Glu Glu Glu Gly Val Glu Glu Glu
180 185 190
Asp Glu Asp Glu Gln Gly Glu Thr Gln Cys Gly Ala Cys Gly Glu Ser
195 200 205
Tyr Ala Ala Asp Glu Phe Trp Ile Cys Cys Asp Leu Cys Glu Met Trp
210 215 220
Phe His Gly Lys Cys Val Lys Ile Thr Pro Ala Arg Ala Glu His Ile
225 230 235 240
Lys Gln Tyr Lys Cys Pro Ser Cys Ser Lys Gln Lys Gly Ser Phe Leu
245 250 255
Asn Leu Leu Thr Ala Arg Phe Cys Val Ser Thr Phe Ala Tyr Asp Asp
260 265 270
Glu Gln Leu Asn Cys Leu Val
275

(2) INFORMATION FOR SEQ ID NO:1553:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 254 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..254

(D) OTHER INFORMATION: / Ceres Seq. ID 1570369

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1553:

Met Ile Lys Ala Leu Thr Thr Asp Val Gln Glu Phe Phe Arg Leu Cys
1 5 10 15
Asp Pro Glu Lys Glu Asn Leu Cys Leu Tyr Gly His Pro Asn Glu His
20 25 30
Trp Glu Val Asn Leu Pro Ala Glu Glu Val Pro Pro Glu Leu Pro Glu
35 40 45
Pro Val Leu Gly Ile Asn Phe Ala Arg Asp Gly Met Ala Glu Lys Asp
50 55 60
Trp Leu Ser Leu Val Ala Val His Ser Asp Ala Trp Leu Leu Ala Val
65 70 75 80
Ala Phe Phe Phe Gly Ala Arg Phe Gly Phe Asp Lys Ala Asp Arg Lys
85 90 95
Arg Leu Phe Asn Met Val Asn Asp Leu Pro Thr Ile Phe Glu Val Val
100 105 110
Ala Gly Thr Ala Lys Lys Gln Gly Lys Asp Lys Ser Ser Val Ser Asn
115 120 125
Asn Ser Ser Asn Arg Ser Lys Ser Ser Ser Lys Arg Gly Ser Glu Ser
130 135 140
Arg Ala Lys Phe Ser Lys Pro Glu Pro Lys Asp Asp Glu Glu Glu Glu
145 150 155 160
Glu Glu Gly Val Glu Glu Glu Asp Glu Asp Glu Gln Gly Glu Thr Gln
165 170 175
Cys Gly Ala Cys Gly Glu Ser Tyr Ala Ala Asp Glu Phe Trp Ile Cys
180 185 190
Cys Asp Leu Cys Glu Met Trp Phe His Gly Lys Cys Val Lys Ile Thr

195	200	205
Pro Ala Arg Ala Glu His Ile Lys Gln Tyr Lys Cys Pro Ser Cys Ser		
210	215	220
Lys Gln Lys Gly Ser Phe Leu Asn Leu Leu Thr Ala Arg Phe Cys Val		
225	230	235
Ser Thr Phe Ala Tyr Asp Asp Glu Gln Leu Asn Cys Leu Val		
245	250	

(2) INFORMATION FOR SEQ ID NO:1554:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1386 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1386
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570370

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1554:

gtaattttctt	aggaagtgca	ttttgataga	gcgcacgata	aacacagcac	cgcaaaaagc	60
acagagacag	agaaagcgca	agacaaaaca	aaaaagcttc	ccccaagaac	aaaaagttag	120
catagatgaa	gagttctcgg	gtttttgtagt	ttttgtaaaa	cagaaaaaaa	aaaaagagaa	180
gaagagatgg	gaggtttgctg	ttgttttctt	tcttcacgaa	gagctgatgt	agataatgga	240
cctgcgtaact	actactacc	aagggcaaca	gaagagcgtg	tgccctttatc	ttccgcctcat	300
aacaggactct	cctctgcaat	ctctactggt	gtttgtagtag	tagacmcaaa	cttagagacaa	360
tcatctctcgt	atgctttatat	accaccgccca	ctgcctaccc	ctttcgatgt	gcctataggg	420
attctctcaaa	caccagctag	tggtgaagag	gctacttggt	ttgatataag	agaggtttctg	480
gtggactctg	ctaataccgca	gtctgctcaa	gaacacagttg	atggtattac	tctcgggggtt	540
ccaactacat	gctcacatcaa	agagacagat	agcaaaaatcc	aaacagagat	tgatcttgaa	600
tctactgaag	aaatagacc	gaagctatca	aaagctgttt	ttataccaat	agaggaagag	660
gaggattgtg	ccatatgttt	ggaagaatat	gatatcgaga	accgaaaact	tgtagccaaa	720
tgtgatcacc	attttcacct	tgcatgcatt	ctagaatgga	tggagagaga	tgaacacctgc	780
cccgctctgca	acaaggaaat	ggtatttgac	tctactcttg	actagcaacc	cgcaaatgcc	840
gcactcttga	aggtctcaat	ctctctgtat	cagaagaaag	aaattggagW	acaagagaaaa	900
aacttaaaaa	gaaaaaatgg	gtaagaatac	actaatagct	gatcacaaag	tgggatttacc	960
gaaacatgct	agtgttgata	tatatatggt	tgtgtacaga	cgttttcaaat	cgtctacaaa	1020
aaaaacggga	ttaagaatta	gagttttgtgc	tttagattca	ctctctgtgaa	taaaaaacga	1080
gacaaaactg	ataatttttc	ttctagatgt	tttaattttg	gtaattctctg	tttataggtt	1140
atttttagag	tggttttaaa	ctgggggttgc	aattttgggtt	tgatttcagtt	ttttcttgag	1200
tttaagaaaa	atattaatca	aactgaaatt	gagagtttgt	tatgtatgga	tgggttttat	1260
tacgggttga	tttttagttg	tttttagtgc	tattttattt	ctttatattt	ttttgtgata	1320
tgtaatatga	aaattgttta	tacttactag	ttttagtgtt	ttatgtttta	gattttottag	1380
ttcttc						

(2) INFORMATION FOR SEQ ID NO:1555:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 212 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..212
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570371

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1555:

Met Gly Gly Cys Cys Cys Ser Ser Ser Arg Arg Ala Asp Val Asp	
1	10
Asn Gly Pro Ala Tyr Tyr Tyr Tyr Pro Arg Ala Thr Glu Glu Arg Val	
20	30
Pro Leu Ser Ser Ala His Asn Arg Thr Ser Ser Ala Ile Ser Thr Gly	
35	45

Val	Val	Val	Val	Asp	Xaa	Asn	Leu	Glu	Thr	Ser	Ser	Pro	Asp	Ala	Tyr
50					55					60					
Ile	Pro	Pro	Pro	Leu	Pro	Thr	Pro	Phe	Asp	Val	Pro	Ile	Gly	Ile	Pro
65				70					75					80	
Gln	Thr	Pro	Ala	Ser	Gly	Glu	Glu	Ala	Thr	Cys	Val	Asp	Ile	Arg	Glu
			85						90					95	
Val	Ser	Val	Asp	Ser	Ala	Asn	Thr	Glu	Ser	Ala	Gln	Glu	Thr	Val	Asp
			100					105					110		
Gly	Ile	Thr	Leu	Gly	Val	Pro	Thr	Thr	Cys	Ser	His	Lys	Glu	Thr	Asp
			115				120					125			
Ser	Lys	Ile	Gln	Thr	Glu	Ile	Asp	Leu	Glu	Ser	Thr	Glu	Glu	Ile	Asp
			130				135				140				
Pro	Lys	Leu	Ser	Lys	Ala	Val	Phe	Ile	Pro	Ile	Glu	Glu	Glu	Glu	Asp
145					150					155				160	
Cys	Pro	Ile	Cys	Leu	Glu	Glu	Tyr	Asp	Ile	Glu	Asn	Pro	Lys	Leu	Val
			165					170						175	
Ala	Lys	Cys	Asp	His	His	Phe	His	Leu	Ala	Cys	Ile	Leu	Glu	Trp	Met
			180					185					190		
Glu	Arg	Ser	Glu	Thr	Cys	Pro	Val	Cys	Asn	Lys	Glu	Met	Val	Phe	Asp
			195			200						205			
Ser	Thr	Leu	Asp												
210															

(2) INFORMATION FOR SEQ ID NO:1556:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1247 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1247
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570372

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1556:

ctcttgcttc	tcttcactca	caatctcaca	gcaaaagctc	tcgttgctag	aggaatcaaa	60
caatgtggtt	tgtgaagtcc	accaagtcca	atgcttactt	caagagggtac	caagtgaagt	120
tcaggagaag	aagagatgga	aagactgact	acagggcaag	gatccgtctt	atcaaccaag	180
acaagaacaa	gtacaatata	cctaagtatc	gttttggtgt	ccggtttacc	aacaagaaca	240
tagtggcaca	gattgtatct	gcaagcattg	ctggtgacat	tgttaaagct	tctgtctaac	300
cacatgaact	gcctcagtat	ggctctcactg	ttggtcttac	aaactatgct	gcagcttaact	360
gtactggcct	tcttttggct	cgccgtgtgt	taaaagatgt	ggaaaatggat	gacgagtatg	420
agggaacgt	tgaggccact	ggagaggact	tttccgttga	gccaaactgat	tcaaggagac	480
ctttccgtgc	tcttcttgat	tttggaacta	tcaggaccac	aacaggaaac	cgtgtgttgc	540
gtgctcttaa	gggtgctttg	gatggtgggt	ttgatatacc	tcacagtgc	aagagatttg	600
ctgggttcca	caaggagaac	aagcaacttg	atgctgaaat	ccacaggaaac	tacatctatg	660
gtggccatgt	ctcaaaactac	atgaagctgt	tgggagaaga	tgagccagag	aagttacaaa	720
ctcacttcag	tgtttacatc	aagaaaaggag	ttgaagtgtg	gagcattgag	gagttgtaca	780
agaaggttca	cgcagctatt	ctgctgtgrc	ccaaCcsaag	gaaaaccctg	aaacctgtct	840
ccaagcaaca	caagagggtac	aacttgaaga	aaacttactta	cgaggagagg	aagaacaagt	900
tgatcgagag	agtcaggcat	tgaatggagc	aggtgggtgat	gatgatgatg	aggacgatga	960
asagtaaatc	agtcacagct	tctttatctc	atgcctcttg	tagttttttt	tcttttgagc	1020
taaagtcctc	aaattttctg	ttttcagact	aaaaactcoa	gcttttgggt	tcacatttta	1080
attgtgttgc	aggattttga	tattgaggat	acattttctt	tgaagtatca	ttatcttatt	1140
attacctcca	tcataatttt	caagaatttt	tatgacaata	gtttgatgat	ttgattttat	1200
ctgtagtttg	ctattgttaa	gttaagaac	tgtagactt	catctat		

(2) INFORMATION FOR SEQ ID NO:1557:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 286 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..286

(D) OTHER INFORMATION: / Ceres Seq. ID 1570373

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1557:

Met	Val	Phe	Val	Lys	Ser	Thr	Lys	Ser	Asn	Ala	Tyr	Phe	Lys	Arg	Tyr
1			5					10					15		
Gln	Val	Lys	Phe	Arg	Arg	Arg	Arg	Asp	Gly	Lys	Thr	Asp	Tyr	Arg	Ala
			20					25					30		
Arg	Ile	Arg	Leu	Ile	Asn	Gln	Asp	Lys	Asn	Lys	Tyr	Asn	Thr	Pro	Lys
			35				40					45			
Tyr	Arg	Phe	Val	Val	Arg	Phe	Thr	Asn	Lys	Asp	Ile	Val	Ala	Gln	Ile
			50			55					60				
Val	Ser	Ala	Ser	Ile	Ala	Gly	Asp	Ile	Val	Lys	Ala	Ser	Ala	Tyr	Ala
					70					75				80	
His	Glu	Leu	Pro	Gln	Tyr	Gly	Leu	Thr	Val	Gly	Leu	Thr	Asn	Tyr	Ala
				85					90				95		
Ala	Ala	Tyr	Cys	Thr	Gly	Leu	Leu	Leu	Ala	Arg	Arg	Val	Leu	Lys	Met
			100					105					110		
Leu	Glu	Met	Asp	Asp	Glu	Tyr	Glu	Gly	Asn	Val	Glu	Ala	Thr	Gly	Glu
			115				120					125			
Asp	Phe	Ser	Val	Glu	Pro	Thr	Asp	Ser	Arg	Arg	Pro	Phe	Arg	Ala	Leu
			130			135					140				
Leu	Asp	Val	Gly	Leu	Ile	Arg	Thr	Thr	Gly	Asn	Arg	Val	Phe	Gly	
			145			150			155					160	
Ala	Leu	Lys	Gly	Ala	Leu	Asp	Gly	Gly	Leu	Asp	Ile	Pro	His	Ser	Asp
			165						170					175	
Lys	Arg	Phe	Ala	Gly	Phe	His	Lys	Glu	Asn	Lys	Gln	Leu	Asp	Ala	Glu
			180					185					190		
Ile	His	Arg	Asn	Tyr	Ile	Tyr	Gly	Gly	His	Val	Ser	Asn	Tyr	Met	Lys
			195			200						205			
Leu	Leu	Gly	Glu	Asp	Glu	Pro	Glu	Lys	Leu	Gln	Thr	His	Phe	Ser	Ala
			210			215					220				
Tyr	Ile	Lys	Lys	Gly	Val	Glu	Ala	Glu	Ser	Ile	Glu	Glu	Leu	Tyr	Lys
			225			230			235					240	
Lys	Val	His	Ala	Ala	Ile	Arg	Ala	Xaa	Pro	Asn	Xaa	Arg	Lys	Thr	Val
			245					250					255		
Lys	Pro	Ala	Pro	Lys	Gln	His	Lys	Arg	Tyr	Asn	Leu	Lys	Lys	Leu	Thr
			260				265					270			
Tyr	Glu	Glu	Arg	Lys	Asn	Lys	Leu	Ile	Glu	Arg	Val	Arg	His		
			275			280						285			

(2) INFORMATION FOR SEQ ID NO:1558:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 175 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..175

(D) OTHER INFORMATION: / Ceres Seq. ID 1570374

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1558:

Met	Leu	Glu	Met	Asp	Asp	Glu	Tyr	Glu	Gly	Asn	Val	Glu	Ala	Thr	Gly
1			5					10					15		
Glu	Asp	Phe	Ser	Val	Glu	Pro	Thr	Asp	Ser	Arg	Arg	Pro	Phe	Arg	Ala
			20					25					30		
Leu	Leu	Asp	Val	Gly	Leu	Ile	Arg	Thr	Thr	Gly	Asn	Arg	Val	Phe	
			35			40				45					
Gly	Ala	Leu	Lys	Gly	Ala	Leu	Asp	Gly	Gly	Leu	Asp	Ile	Pro	His	Ser

50 55 60
Asp Lys Arg Phe Ala Gly Phe His Lys Glu Asn Lys Gln Leu Asp Ala
65 70 75 80
Glu Ile His Arg Asn Tyr Ile Tyr Gly Gly His Val Ser Asn Tyr Met
85 90 95
Lys Leu Leu Gly Glu Asp Glu Pro Glu Lys Leu Gln Thr His Phe Ser
100 105 110
Ala Tyr Ile Lys Lys Gly Val Glu Ala Glu Ser Ile Glu Glu Leu Tyr
115 120 125
Lys Lys Val His Ala Ala Ile Arg Ala Xaa Pro Asn Xaa Arg Lys Thr
130 135 140
Val Lys Pro Ala Pro Lys Gln His Lys Arg Tyr Asn Leu Lys Lys Leu
145 150 155 160
Thr Tyr Glu Glu Arg Lys Asn Lys Leu Ile Glu Arg Val Arg His
165 170 175

(2) INFORMATION FOR SEQ ID NO:1559:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 172 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..172

(D) OTHER INFORMATION: / Ceres Seq. ID 1570375

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1559:

Met Asp Asp Glu Tyr Glu Gly Asn Val Glu Ala Thr Gly Glu Asp Phe
1 5 10 15
Ser Val Glu Pro Thr Asp Ser Arg Arg Pro Phe Arg Ala Leu Leu Asp
20 25 30
Val Gly Leu Ile Arg Thr Thr Thr Gly Asn Arg Val Phe Gly Ala Leu
35 40 45
Lys Gly Ala Leu Asp Gly Gly Leu Asp Ile Pro His Ser Asp Lys Arg
50 55 60
Phe Ala Gly Phe His Lys Glu Asn Lys Gln Leu Asp Ala Glu Ile His
65 70 75 80
Arg Asn Tyr Ile Tyr Gly Gly His Val Ser Asn Tyr Met Lys Leu Leu
85 90 95
Gly Glu Asp Glu Pro Glu Lys Leu Gln Thr His Phe Ser Ala Tyr Ile
100 105 110
Lys Lys Gly Val Glu Ala Glu Ser Ile Glu Glu Leu Tyr Lys Lys Val
115 120 125
His Ala Ala Ile Arg Ala Xaa Pro Asn Xaa Arg Lys Thr Val Lys Pro
130 135 140
Ala Pro Lys Gln His Lys Arg Tyr Asn Leu Lys Lys Leu Thr Tyr Glu
145 150 155 160
Glu Arg Lys Asn Lys Leu Ile Glu Arg Val Arg His
165 170

(2) INFORMATION FOR SEQ ID NO:1560:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1724 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1724

(D) OTHER INFORMATION: / Ceres Seq. ID 1570376

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1560:

aatttttagt	ctccctccgc	gtagaagcgt	ctccgagact	tgtctctgct	tgtattgaag	60
aagacgcttg	atcgaaaaatt	cccttagatt	tcgtaaatag	gggttttacg	aaggtgagat	120
tacacagaga	tcggtatttc	gaaaaaaaaa	aatgggaagt	ccaaagaaga	acgagaacaa	180
aggctctctc	gccgccatga	cttctggcgt	ctccatgttc	ggtaaccgcc	gtctcgagatc	240
cgttaaacgc	gtgcaagcta	atgaaggagt	tgaggtcata	aatccagaag	gtggcaagga	300
agatgctgaa	gaggaagcgt	agaaaaggac	gtggaaggac	gaggaacgag	atagttacta	360
gaagatgatg	cagaaaatata	taggttcgga	tattacgtca	atggtgactc	ttcctgttgt	420
tatatattgag	cctatgacta	gtgtccagaa	gatggctgag	ataatggagt	attctcattt	480
gttggtatcaa	gcagatgaat	gcgaagatcc	atacttgctg	ttagtatatg	cttcacatgt	540
ggctatatct	gtttactatg	ccttccaacg	aacttggaaag	cttttcaatc	ctattcttgg	600
ggagacatat	gagatgtgtca	accatgggtg	gattttcttt	atttctgagc	aggtttagcca	660
tcataccacca	gatagtgctg	gtcatgccga	gaacgacgac	ttcattttacg	acatcacatc	720
aaagtgtgaaa	actRaacttt	tgggtaactc	tgttgatgtt	taccctgtgg	gaagaacgcg	780
tgtaaccctc	aagaaaagct	gtgtggttct	ggatttgggt	cgcctctcca	ctaagattca	840
caatctaata	tttggacgaa	cctgggttga	ctcacctggg	gaaatggcta	tgacaaatct	900
aaccactgga	gacaaaagt	tgctttattt	ccagccatgt	ggctgggtcg	gttctggccc	960
ctatgaagtt	gatggctacg	tttacagcgc	agctgaagaa	ccgaaaaatca	tgatgacagg	1020
aaaatggaa	gagaaaaatga	gctaccaacc	ttgtgatgcc	gaagggggaac	cccttccagg	1080
aacagagctg	aaagaggtgt	ggcatttggc	tgatgtcccc	aaaaacgcga	aatttcagta	1140
cactcacttt	gtctcacaga	taaacagcgt	cgacacagcg	cctgctaagc	tccttgcttc	1200
agactcacgt	atccgtcctg	atagatatcc	ccttgagcag	ggtagacctt	ctaaaagctgg	1260
ttccgagaaa	cacagccttg	aggagagaca	aagccgaaaa	gaggaccaga	gagacaagaag	1320
gacaaaaagt	cactccaaga	tggttcgcac	taacggtgat	gacacacct	actccatggg	1380
gagatatattga	agtatatac	tacaacggga	agtaacaatga	acaccgagac	acggcagaga	1440
gctcaagtag	tgcttccaac	gaaacggacc	ctaaatcgat	cgagttttaa	ccttgccaat	1500
atggtaatat	ctcaaacgaa	tgaagtaact	cttatagttt	aatttggatt	ctctatatac	1560
gaatgctgtg	attcatgttc	acttggaa	gagtcacatg	tgttttttaa	ctttgtttca	1620
gactgaaaaa	tctgattatg	tgatttggat	gataaaacat	aagtttttgg	ttctctgtct	1680
attgtatctt	tgtccattt	cgatcaatag	taattatggt	tgttt		

(2) INFORMATION FOR SEQ ID NO:1561:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 331 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..331

(D) OTHER INFORMATION: / Ceres Seq. ID 1570377

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1561:

Met	Met	Gln	Lys	Tyr	Ile	Gly	Ser	Asp	Ile	Thr	Ser	Met	Val	Thr	Leu
1			5				10					15			
Pro	Val	Val	Ile	Phe	Glu	Pro	Met	Thr	Met	Leu	Gln	Lys	Met	Ala	Glu
			20				25					30			
Ile	Met	Glu	Tyr	Ser	His	Leu	Leu	Asp	Gln	Ala	Asp	Glu	Cys	Glu	Asp
			35				40					45			
Pro	Tyr	Leu	Arg	Leu	Val	Tyr	Ala	Ser	Ser	Trp	Ala	Ile	Ser	Val	Tyr
			50				55				60				
Tyr	Ala	Phe	Gln	Arg	Thr	Trp	Lys	Pro	Phe	Asn	Pro	Ile	Leu	Gly	Glu
			65				70			75				80	
Thr	Tyr	Glu	Met	Val	Asn	His	Gly	Gly	Ile	Ser	Phe	Ile	Ser	Glu	Gln
			85				90					95			
Val	Ser	His	His	Pro	Pro	Met	Ser	Ala	Gly	His	Ala	Glu	Asn	Glu	His
			100				105					110			
Phe	Ile	Tyr	Asp	Ile	Thr	Ser	Lys	Leu	Lys	Thr	Xaa	Leu	Leu	Gly	Asn
			115				120					125			
Ser	Val	Asp	Val	Tyr	Pro	Val	Gly	Arg	Thr	Arg	Val	Thr	Leu	Lys	Lys
			130				135				140				
Asp	Gly	Val	Val	Leu	Asp	Leu	Val	Pro	Pro	Leu	Thr	Lys	Ile	His	Asn
			145				150				155				

Leu Ile Phe Gly Arg Thr Trp Val Asp Ser Pro Gly Glu Met Val Met
165 170 175
Thr Asn Leu Thr Thr Gly Asp Lys Val Val Leu Tyr Phe Gln Pro Cys
180 185 190
Gly Trp Phe Gly Ser Gly Arg Tyr Glu Val Asp Gly Tyr Val Tyr Ser
195 200 205
Ala Ala Glu Glu Pro Lys Ile Met Met Thr Gly Lys Trp Asn Glu Lys
210 215 220
Met Ser Tyr Gln Pro Cys Asp Ala Glu Gly Glu Pro Leu Pro Gly Thr
225 230 235 240
Glu Leu Lys Glu Val Trp His Leu Ala Asp Val Pro Lys Asn Asp Lys
245 250 255
Phe Gln Tyr Thr His Phe Ala His Lys Ile Asn Ser Phe Asp Thr Ala
260 265 270
Pro Ala Lys Leu Leu Ala Ser Asp Ser Arg Ile Arg Pro Asp Arg Tyr
275 280 285
Ser Leu Glu Gln Gly Asp Leu Ser Lys Ala Gly Ser Glu Lys His Ser
290 295 300
Leu Glu Glu Arg Gln Ser Arg Lys Glu Asp Gln Arg Asp Lys Gly Thr
305 310 315 320
Lys Val His Ser Lys Met Val Arg Ser Asn Gly
325 330

(2) INFORMATION FOR SEQ ID NO:1562:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 330 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..330

(D) OTHER INFORMATION: / Ceres Seq. ID 1570378

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1562:

Met Gln Lys Tyr Ile Gly Ser Asp Ile Thr Ser Met Val Thr Leu Pro
1 5 10 15
Val Val Ile Phe Glu Pro Met Thr Met Leu Gln Lys Met Ala Glu Ile
20 25 30
Met Glu Tyr Ser His Leu Leu Asp Gln Ala Asp Glu Cys Glu Asp Pro
35 40 45
Tyr Leu Arg Leu Val Tyr Ala Ser Ser Trp Ala Ile Ser Val Tyr Tyr
50 55 60
Ala Phe Gln Arg Thr Trp Lys Pro Phe Asn Pro Ile Leu Gly Glu Thr
65 70 75 80
Tyr Glu Met Val Asn His Gly Gly Ile Ser Phe Ile Ser Glu Gln Val
85 90 95
Ser His His Pro Pro Met Ser Ala Gly His Ala Glu Asn Glu His Phe
100 105 110
Ile Tyr Asp Ile Thr Ser Lys Leu Lys Thr Xaa Leu Leu Gly Asn Ser
115 120 125
Val Asp Val Tyr Pro Val Gly Arg Thr Arg Val Thr Leu Lys Lys Asp
130 135 140
Gly Val Val Leu Asp Leu Val Pro Pro Leu Thr Lys Ile His Asn Leu
145 150 155 160
Ile Phe Gly Arg Thr Trp Val Asp Ser Pro Gly Glu Met Val Met Thr
165 170 175
Asn Leu Thr Thr Gly Asp Lys Val Val Leu Tyr Phe Gln Pro Cys Gly
180 185 190
Trp Phe Gly Ser Gly Arg Tyr Glu Val Asp Gly Tyr Val Tyr Ser Ala
195 200 205
Ala Glu Glu Pro Lys Ile Met Met Thr Gly Lys Trp Asn Glu Lys Met

Met	Val	Thr	Leu	Pro	Val	Val	Ile	Phe	Glu	Pro	Met	Thr	Met	Leu	Gln
1	Lys	Met	Ala	Glu	Ile	Met	Glu	Tyr	Ser	His	Leu	Leu	Asp	Gln	Ala
			20					25					30		
Glu	Cys	Glu	Asp	Pro	Tyr	Leu	Arg	Leu	Val	Tyr	Ala	Ser	Ser	Trp	Ala
		35					40					45			
Ile	Ser	Val	Tyr	Tyr	Ala	Phe	Glu	Arg	Thr	Trp	Lys	Pro	Phe	Asn	Pro
	50					55					60				
Ile	Leu	Gly	Glu	Thr	Tyr	Glu	Met	Val	Asn	His	Gly	Gly	Ile	Ser	Phe
65					70					75					80
Ile	Ser	Glu	Gln	Val	Ser	His	His	Pro	Pro	Met	Ser	Ala	Gly	His	Ala
			85						90					95	
Glu	Asn	Glu	His	Phe	Ile	Tyr	Asp	Ile	Thr	Ser	Lys	Leu	Lys	Thr	Xaa
			100					105					110		
Leu	Leu	Gly	Asn	Ser	Val	Asp	Val	Tyr	Pro	Val	Gly	Arg	Thr	Arg	Val
		115					120					125			
Thr	Leu	Lys	Lys	Asp	Gly	Val	Val	Leu	Asp	Leu	Val	Pro	Pro	Leu	Thr
	130					135					140				
Lys	Ile	His	Asn	Leu	Ile	Phe	Gly	Arg	Thr	Trp	Val	Asp	Ser	Pro	Gly
145					150					155					160
Glu	Met	Val	Met	Thr	Asn	Leu	Thr	Ser	Gly	Asp	Lys	Val	Val	Leu	Tyr
			165						170					175	
Phe	Gln	Pro	Cys	Gly	Trp	Phe	Gly	Ser	Gly	Arg	Tyr	Glu	Val	Asp	Gly
			180					185					190		
Tyr	Val	Tyr	Ser	Ala	Ala	Glu	Glu	Pro	Lys	Ile	Met	Met	Thr	Gly	Lys
		195					200					205			
Trp	Asn	Glu	Lys	Met	Ser	Tyr	Gln	Pro	Cys	Asp	Ala	Glu	Gly	Glu	Pro
	210					215					220				
Leu	Pro	Gly	Thr	Glu	Leu	Lys	Glu	Val	Trp	His	Leu	Ala	Asp	Val	Pro
225					230					235				240	
Lys	Asn	Asp	Lys	Phe	Gln	Tyr	Thr	His	Phe	Ala	His	Lys	Ile	Asn	Ser
			245						250					255	
Phe	Asp	Thr	Ala	Pro	Ala	Lys	Leu	Leu	Ala	Ser	Asp	Ser	Arg	Ile	Arg
		260						265					270		

Pro Asp Arg Tyr Ser Leu Glu Gln Gly Asp Leu Ser Lys Ala Gly Ser
275 280 285
Glu Lys His Ser Leu Glu Glu Arg Gln Ser Arg Lys Glu Asp Gln Arg
290 295 300
Asp Lys Gly Thr Lys Val His Ser Lys Met Val Arg Ser Asn Gly
305 310 315

(2) INFORMATION FOR SEQ ID NO:1564:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1195 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1195

(D) OTHER INFORMATION: / Ceres Seq. ID 1570380

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1564:

ataagatcca	aaaccataaa	actaggtttc	acactttctc	tctaaacact	gtctcttttc	60
tccgatacat	atccccccgc	ttccccctgt	tttttcttcg	ccgtccgtcg	ttctttttcaa	120
ctccctagct	ggcatattaa	agcttagaca	caatgagagg	aaggagctac	acgccatcac	180
caccaagggg	ttatggaagg	aggggcccga	gccctagccc	tcggggccgg	tttgatggga	240
gtcgtgacag	tgatctccca	accagttctt	tggttcgcaa	ctacgtcat	gattgcaggc	300
aagaagacct	caggaggcca	tttgagcagt	ttggtccogt	caaggacatc	taccttctta	360
gggattacta	tactggagat	ccaagggggt	ttggattcat	tcagtttatg	gatccctgct	420
atgctgctga	ggctaaacat	caaatggatg	gttatcttct	tcttggtcgt	gagtgactgt	480
tcgtatttgc	tgaagaaaaa	cggaagaagc	caactgagat	gagaacaagg	gatcgagggt	540
gaaggagcaa	cagattccag	gacagaagac	gttctcctcc	tcggtactct	cggctccttc	600
ctcgccgtgg	tcgtagatca	cgatcacgta	gctgcggcta	taattctcct	cccgtaaaaa	660
gacatcaatc	taggtctgtc	tcacctcagg	atagacgata	tgagaaggag	agggtcatac	720
ctcgctcacc	accccataat	ggctcaaggg	ttcgagtggt	aagtcctggg	agagtgaaga	780
gccacagcag	aagcccaaga	agaagcgtga	gcccaagaaa	aaacaggagc	tacacgccag	840
aacaagcaag	gagccaaagc	cctgtcccta	ggcagagcag	gagcccgacc	ccagtccttc	900
gtggagcaca	aaatggagac	cgttctccaa	gccagtattt	tAacaccagt	tatctctcta	960
ctcttcagtt	tttcagttct	gttctgtttg	atcagatatt	ttgtttgctc	cagatttgata	1020
tttccctact	tagacagata	ttgtagtgct	tattggtatt	ttgctttatg	tttgatccat	1080
ggatgatctt	gagacagtat	ttgaagtag	catgtgttat	ttgtcatctt	atcttttagt	1140
atctcatcta	acattgttat	ggtgaaaaag	atggtcctat	tacggggagct	ttttt	

(2) INFORMATION FOR SEQ ID NO:1565:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 261 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..261

(D) OTHER INFORMATION: / Ceres Seq. ID 1570381

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1565:

Met	Arg	Gly	Arg	Ser	Tyr	Thr	Pro	Ser	Pro	Pro	Arg	Gly	Tyr	Gly	Arg
1				5					10					15	
Arg	Gly	Arg	Ser	Pro	Ser	Pro	Arg	Gly	Arg	Phe	Gly	Gly	Ser	Arg	Asp
				20					25					30	
Ser	Asp	Leu	Pro	Thr	Ser	Leu	Leu	Val	Arg	Asn	Leu	Arg	His	Asp	Cys
				35					40					45	
Arg	Gln	Glu	Asp	Leu	Arg	Arg	Pro	Phe	Glu	Gln	Phe	Gly	Pro	Val	Lys
				50					55					60	
Asp	Ile	Tyr	Leu	Pro	Arg	Asp	Asp	Tyr	Tyr	Thr	Gly	Asp	Pro	Arg	Gly
				65					70					75	80
Gly	Phe	Ile	Gln	Phe	Met	Asp	Pro	Ala	Asp	Ala	Glu	Ala	Lys	His	

[illegible]

(2) INFORMATION FOR SEQ ID NO:1566:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 176 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..176

(D) OTHER INFORMATION: / Ceres Seq. ID 1570382

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1566:

Met	Asp	Pro	Ala	Asp	Ala	Ala	Glu	Ala	Lys	His	Gln	Met	Asp	Gly	Tyr
1				5					10					15	
Leu	Leu	Leu	Gly	Arg	Glu	Leu	Thr	Val	Val	Phe	Ala	Glu	Glu	Asn	Arg
			20					25					30		
Lys	Lys	Pro	Thr	Glu	Met	Arg	Thr	Arg	Asp	Arg	Gly	Gly	Arg	Ser	Asn
		35					40					45			
Arg	Phe	Gln	Asp	Arg	Arg	Arg	Ser	Pro	Pro	Arg	Tyr	Ser	Arg	Ser	Pro
	50					55					60				
Pro	Arg	Arg	Gly	Arg	Arg	Ser	Arg	Ser	Arg	Ser	Cys	Gly	Tyr	Asn	Ser
65				70						75				80	
Pro	Pro	Ala	Lys	Arg	His	Gln	Ser	Arg	Ser	Val	Ser	Pro	Gln	Asp	Arg
				85					90					95	
Arg	Tyr	Glu	Lys	Glu	Arg	Ser	Tyr	Ser	Arg	Ser	Pro	Pro	His	Asn	Gly
			100					105					110		
Ser	Arg	Val	Arg	Ser	Gly	Ser	Pro	Gly	Arg	Val	Lys	Ser	His	Ser	Arg
		115					120					125			
Ser	Pro	Arg	Arg	Ser	Val	Ser	Pro	Arg	Lys	Asn	Arg	Ser	Tyr	Thr	Pro
		130				135					140				
Glu	Gln	Ala	Arg	Ser	Gln	Ser	Pro	Val	Pro	Arg	Gln	Ser	Arg	Ser	Pro
145					150					155				160	
Thr	Pro	Val	Pro	Arg	Gly	Ala	Gln	Asn	Gly	Asp	Arg	Ser	Pro	Ser	Gln
				165					170					175	

(2) INFORMATION FOR SEQ ID NO:1567:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 164 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..164
(D) OTHER INFORMATION: / Ceres Seq. ID 1570383
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1567:
Met Asp Gly Tyr Leu Leu Leu Gly Arg Glu Leu Thr Val Val Phe Ala
1 5 10 15
Glu Glu Asn Arg Lys Lys Pro Thr Glu Met Arg Thr Arg Asp Arg Gly
20 25 30
Gly Arg Ser Asn Arg Phe Gln Asp Arg Arg Ser Pro Pro Arg Tyr
35 40 45
Ser Arg Ser Pro Pro Arg Arg Gly Arg Arg Ser Arg Ser Arg Ser Cys
50 55 60
Gly Tyr Asn Ser Pro Pro Ala Lys Arg His Gln Ser Arg Ser Val Ser
65 70 75 80
Pro Gln Asp Arg Arg Tyr Glu Lys Glu Arg Ser Tyr Ser Arg Ser Pro
85 90 95
Pro His Asn Gly Ser Arg Val Arg Ser Gly Ser Pro Gly Arg Val Lys
100 105 110
Ser His Ser Arg Ser Pro Arg Arg Ser Val Ser Pro Arg Lys Asn Arg
115 120 125
Ser Tyr Thr Pro Glu Gln Ala Arg Ser Gln Ser Pro Val Pro Arg Gln
130 135 140
Ser Arg Ser Pro Thr Pro Val Pro Arg Gly Ala Gln Asn Gly Asp Arg
145 150 155 160
Ser Pro Ser Gln

(2) INFORMATION FOR SEQ ID NO:1568:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1358 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1358

(D) OTHER INFORMATION: / Ceres Seq. ID 1570384

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1568:

aatcgcttcc acgaaaacaa gtagagagag tgattcgagt ttcccaatca taaaatcag 60
cgaagaagat cttcgttctt gttcattctg tgagggtttca ttgttataaa cgaaacgaat 120
ctcagggttg agtaaatcct gggagagatc cgatttccgt ttccatggcg attcgggtgt 180
cggagctgtg tatcgtactg ttgcgtcttt cctacgccat vtgcgtcctt gccgggaaga 240
gttactacga tgtgttgcaa gtccccaag gtgcatctga tgaacagatc aagagagcct 300
ataggaaact agccttgaag tatcatcccg ataagaatca aggaatgag gaagcgactc 360
gaaatttcgc tgagatcaac aatgcttatg aagtgttato ggaatgaggag aagaggggag 420
tatataacaa gtatggtgaa gagggaacta aacagttttc tgcaaatgga ggaagaggag 480
gagKaggagg cggcatgaat atgcaggaca tcttcagctc atttttttgt ggaggttcga 540
tgagggaaga agagaaggtt gtcaaggggg atgacgtaat tgtggaactt gaggcaactc 600
tagaagattt gtacatggga ggctctatga aggtatggag ggaaaaaatg gtgataaaac 660
cagctcctgg aaagagaaag tgtaactgca ggaacgaggt ctatcacaga caaatgtgtc 720
ctggaatggt ccaacagagt acagagcagg tctgtgacaa atgccctaag tccaataacg 780
aacgggaggt atactttgtg acagttgata tcgagaaagg aatgaaagat ggagaagaag 840
tgtctttcta tgaagacggc gaaAcccCat tcttgacggt gaccctggT gaccttaagt 900
tcogaatcag aactgcacca catgcccggt Tcagaagggt atggcaacga tctacacatg 960
aacgtgaaca ttacactggt tgaggcgcta gttggttttg agaaatcatt caaacacttg 1020

gatgatcagc	aagttgacat	cagttccaag	ggaattacaa	agccgaagga	agtaaagaag	1080
ttcaaaggag	aagggatgcc	acttcactac	agcacaaga	aaggcaacot	ctttgtcact	1140
tttgaggttt	tgtttccgtc	ttctctcact	gacgatcaga	agaagaagat	taaagaagtc	1200
tttgcttagt	gctcttctct	cgctttcgct	ctctctctct	ttagaagttt	ggggattaaa	1260
gagaagaaca	tgtgatggtc	ctaagtata	acatgattac	gttttaatat	agaaagaaaa	1320
aagatatggg gagacaaagt cggaaggagc ttttgacc						

(2) INFORMATION FOR SEQ ID NO:1569:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 272 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..272

(D) OTHER INFORMATION: / Ceres Seq. ID 1570385

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1569:

Met	Ala	Ile	Arg	Trp	Ser	Glu	Leu	Cys	Ile	Val	Leu	Phe	Ala	Leu	Ser	
1				5					10					15		
Tyr	Ala	Xaa	Cys	Val	Leu	Ala	Gly	Lys	Ser	Tyr	Tyr	Asp	Val	Leu	Gln	
			20					25					30			
Val	Pro	Lys	Gly	Ala	Ser	Asp	Glu	Gln	Ile	Lys	Arg	Ala	Tyr	Arg	Lys	
			35					40				45				
Leu	Ala	Leu	Lys	Tyr	His	Pro	Asp	Lys	Asn	Gln	Gly	Asn	Glu	Glu	Ala	
			50					55				60				
Thr	Arg	Lys	Phe	Ala	Glu	Ile	Asn	Asn	Ala	Tyr	Glu	Val	Leu	Ser	Asp	
			65					70				75				
Glu	Glu	Lys	Arg	Glu	Ile	Tyr	Asn	Lys	Tyr	Gly	Glu	Glu	Gly	Leu	Lys	
			85					90					95			
Gln	Phe	Ser	Ala	Asn	Gly	Gly	Arg	Gly	Gly	Xaa	Gly	Gly	Gly	Met	Asn	
			100					105					110			
Met	Gln	Asp	Ile	Phe	Ser	Ser	Phe	Phe	Gly	Gly	Gly	Ser	Met	Glu	Glu	
			115					120					125			
Glu	Glu	Lys	Val	Val	Lys	Gly	Asp	Val	Ile	Val	Glu	Leu	Glu	Ala		
			130					135					140			
Thr	Leu	Glu	Asp	Leu	Tyr	Met	Gly	Gly	Ser	Met	Lys	Val	Trp	Arg	Glu	
			145					150				155			160	
Lys	Asn	Val	Ile	Lys	Pro	Ala	Pro	Gly	Lys	Arg	Lys	Cys	Asn	Cys	Arg	
			165					170					175			
Asn	Glu	Val	Tyr	His	Arg	Gln	Ile	Gly	Pro	Gly	Met	Phe	Gln	Gln	Met	
			180					185					190			
Thr	Glu	Gln	Val	Cys	Asp	Lys	Cys	Pro	Asn	Val	Lys	Tyr	Glu	Arg	Glu	
			195					200					205			
Gly	Tyr	Phe	Val	Thr	Val	Asp	Ile	Glu	Lys	Gly	Met	Lys	Asp	Gly	Glu	
			210					215					220			
Glu	Val	Ser	Phe	Tyr	Glu	Asp	Gly	Glu	Thr	Pro	Phe	Leu	Thr	Val	Thr	
			225					230					235			
Leu	Val	Asp	Leu	Lys	Phe	Arg	Ile	Arg	Thr	Ala	Pro	His	Ala	Arg	Phe	
			245					250					255			
Gln	Lys	Gly	Trp	Gln	Arg	Ser	Thr	His	Glu	Arg	Glu	His	Tyr	Thr	Gly	
			260					265					270			

(2) INFORMATION FOR SEQ ID NO:1570:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 162 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..162

(D) OTHER INFORMATION: / Ceres Seq. ID 1570386

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1570:

Met	Asn	Met	Gln	Asp	Ile	Phe	Ser	Ser	Phe	Phe	Gly	Gly	Ser	Met
1				5					10				15	
Glu	Glu	Glu	Glu	Lys	Val	Val	Lys	Gly	Asp	Asp	Val	Ile	Val	Glu
			20					25					30	Leu
Glu	Ala	Thr	Leu	Glu	Asp	Leu	Tyr	Met	Gly	Gly	Ser	Met	Lys	Val
	35						40					45		Trp
Arg	Glu	Lys	Asn	Val	Ile	Lys	Pro	Ala	Pro	Gly	Lys	Arg	Lys	Cys
	50					55					60			Asn
Cys	Arg	Asn	Glu	Val	Tyr	His	Arg	Gln	Ile	Gly	Pro	Gly	Met	Phe
	65				70				75					80
Gln	Met	Thr	Glu	Gln	Val	Cys	Asp	Lys	Cys	Pro	Asn	Val	Lys	Tyr
			85						90				95	Glu
Arg	Glu	Gly	Tyr	Phe	Val	Thr	Val	Asp	Ile	Glu	Lys	Gly	Met	Lys
			100					105					110	Asp
Gly	Glu	Glu	Val	Ser	Phe	Tyr	Glu	Asp	Gly	Glu	Thr	Pro	Phe	Leu
		115					120					125		Thr
Val	Thr	Leu	Val	Asp	Leu	Lys	Phe	Arg	Ile	Arg	Thr	Ala	Pro	His
	130					135						140		Ala
Arg	Phe	Gln	Lys	Gly	Trp	Gln	Arg	Ser	Thr	His	Glu	Arg	Glu	His
	145				150					155				160
Thr	Gly													

(2) INFORMATION FOR SEQ ID NO:1571:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 160 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..160

(D) OTHER INFORMATION: / Ceres Seq. ID 1570387

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1571:

Met	Gln	Asp	Ile	Phe	Ser	Ser	Phe	Phe	Gly	Gly	Ser	Met	Glu	Glu
1				5					10			15		
Glu	Glu	Lys	Val	Val	Lys	Gly	Asp	Asp	Val	Ile	Val	Glu	Leu	Glu
			20					25						Ala
Thr	Leu	Glu	Asp	Leu	Tyr	Met	Gly	Gly	Ser	Met	Lys	Val	Trp	Arg
		35					40					45		Glu
Lys	Asn	Val	Ile	Lys	Pro	Ala	Pro	Gly	Lys	Arg	Lys	Cys	Asn	Cys
	50					55					60			Arg
Asn	Glu	Val	Tyr	His	Arg	Gln	Ile	Gly	Pro	Gly	Met	Phe	Gln	Gln
	65				70				75					80
Thr	Glu	Gln	Val	Cys	Asp	Lys	Cys	Pro	Asn	Val	Lys	Tyr	Glu	Arg
			85						90				95	Glu
Gly	Tyr	Phe	Val	Thr	Val	Asp	Ile	Glu	Lys	Gly	Met	Lys	Asp	Gly
		100					105					110		Glu
Glu	Val	Ser	Phe	Tyr	Glu	Asp	Gly	Glu	Thr	Pro	Phe	Leu	Thr	Val
		115					120					125		Thr
Leu	Val	Asp	Leu	Lys	Phe	Arg	Ile	Arg	Thr	Ala	Pro	His	Ala	Arg
	130					135					140			Phe
Gln	Lys	Gly	Trp	Gln	Arg	Ser	Thr	His	Glu	Arg	Glu	His	Tyr	Thr
	145				150					155				Gly

(2) INFORMATION FOR SEQ ID NO:1572:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1879 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1879

(D) OTHER INFORMATION: / Ceres Seq. ID 1570388

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1572:

```
acagcaaaaa gccactctcc ttctctctc tctctgttc ctctgcatcc atggccacca      60
agctcgacac cagtagetta cttttggccc tcttgtccaa atgtagcctc cttaactcaaa    120
ccaatctctgc tctctctctc ctctgagcct ccctagcttc tctcgctctt tctctctctt    180
tcttggtctca tcccggagga cccgcatggg gaaagtaact cctccaccgc cgcggtcaaa    240
ccaccgtgat acccgggcca agagggttac cttttgtcgg aagcatgtct ctcatgtcaa    300
acactctggc tcaccgttgc atagccgcaa ccgcagagaa atttagagcc gaacgggttaa    360
tgcggttttag tttagggaaa actgcgctga tgcgtcaoctg caatcctgat ctgagctaaa    420
agattctaaa cagtcctggg ttgcgtgacc gcccggttaa ggaatcagct tattccotca    480
tggttaacgc tgcatacgtt tctgcctctt acggcggttta ctggcgaacc ttgagaaaaa    540
tcgcgtctaa tcatcttttc agcccgaaac agattaaacg ttccgaaacg cagagaaagcg    600
tgatcgcgaa tcaaatcgtg aagtgtctca caaaacagag taacacaaaa ggctctctgt    660
tcgcacgtga cttgatcaaa accgcatcgc ttaataacat gatgtgctct gttttcggaa    720
aagaatacga gcttgaggaa gagcatgaag aagtgaagta gctacgtgaa ttggtggaag    780
aaggttatga tttactcgat acactgaatt ggaccgatca tctcccatgc ctctctgaat    840
ttgatctcca aagaatccgg tctagatgct ctaatctcgt cccaaaaagta aacccggtttg    900
tgaaacggat tatctctgac caccgtgaac ctacacgtga ctccacagag gactcgtgtg    960
acgtattgct ctctctcgat ggtcctgata aattatccga cctcgatata atcgccgttg    1020
tatgggaaat gatattcaga ggaactgaca cggtggtcgt ttgtagctag ttgattcttg    1080
ctaggatggt ctctctatcca gatattcaat cgacgggttca caatgagttg gatcaaatcg    1140
tgggacgatc aagggtctgc gaagagtcgt acgtgggtgc ttgagcttat ctgaagcgctg    1200
tggtgaaaga agtcttgagg ctctcaccgc caggcccaact actctcatgg gcccgcttag    1260
caatcacaga cagcatcatc gacggtcgtc gtgttccggc ggggaacacc gcaatgggtga    1320
acatgtgggc tattgcacac gatccacacg tgtggggaga tccgttgtag tttaaaccgc    1380
aacgttttgt agccaaggaa ggtgaggttg agttctcgtt tcttggtctc gattttgaggc    1440
ttgcaccggt cgggtccggt cgtcggtgtt gccccgggaa gaatcttggg ttgaccaccg    1500
tgacgttttg gactgcgacg cttttgcata agtttgaanT Ggctgacgcc gtccgatgag    1560
aagaccggtt accttgcaga gaaactgagg ctctcgtgtg agatggctaa tcctcttgct    1620
gcataattac gccccaggcg cagttttagt gtatgataag ggtaaggcta tacacagata    1680
cagtggtaac taaagcgag gaaaattagt gtgaatttaa agcaaaaagaa taaaataaag    1740
aacaagaaga gtaaaagaaa caaaaaaaa gaatcatata aaaaatacta ataagaatgg    1800
taatgaagct tttatattaa actaacatct tgatcagtgt tgtatatatg atgaaacat    1860
taatgtcaca aagaaaaagc
```

(2) INFORMATION FOR SEQ ID NO:1573:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 518 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..518

(D) OTHER INFORMATION: / Ceres Seq. ID 1570389

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1573:

```
Ser Lys Lys Pro Leu Ser Phe Leu Ser Leu Ser Cys Ser Ser Ala Ser
1          5          10          15
Met Ala Thr Lys Leu Asp Thr Ser Ser Leu Leu Leu Ala Leu Leu Ser
20          25          30
Lys Cys Ser Leu Leu Thr Gln Thr Asn Leu Ala Leu Ser Leu Leu Val
```

35			40			45		
Ala Ser	Leu Ala	Ser	Leu Ala	Leu Ser	Leu Phe	Phe Trp	Ser His	Pro
50 Gly Gly	Pro Ala	Trp Gly	55 Gly Lys	Tyr Phe	Leu His	60 Arg Arg	Arg Gln	Thr
65 Thr Val	Ile Pro	Gly 85	Pro Arg	Gly Leu	70 Phe Pro	75 Val Gly	Ser Met	Ser
Leu Met	Ser Asn	Thr 100	Leu Ala	His Arg	105 Cys Ile	Ala Ala	Thr Ala	Glu
Lys Phe	Arg Ala	Glu 115	Arg Leu	Met Ala	Phe Ser	Leu Gly	110 Thr Arg	
Val Ile	Val Thr	Cys 130	Asn Pro	Asp Asp	Val Ala	Lys Glu	Ile Leu	Asn Ser
Pro Val	Phe Ala	Asp 145	Arg Pro	Val Lys	Glu Ser	Ala Tyr	Ser Leu	Met
Phe Asn	Arg Ala	Ile 165	Gly Phe	Ala Pro	Tyr 170	Gly Val	Tyr Trp	Arg Thr
Leu Arg	Lys Ile	Ala 180	Ser Asn	His Leu	Phe 185	Ser Pro	Lys Gln	Ile Lys
Arg Ser	Glu Thr	Gln 195	Arg Ser	Val Ile	Ala Asn	Gln Ile	Val Lys	Cys
Leu Thr	Lys Gln	Ser 210	Asn Thr	Lys 200	Gly Leu	Cys Phe	Ala Arg	Asp Leu
Ile Lys	Thr Ala	Ser 225	Leu Asn	Asn Met	Met Cys	220 Ser Val	Phe Gly	Lys
Glu Tyr	Glu Leu	Glu 240	Glu Glu	His Leu	Glu 250	Val Ser	Glu Leu	Arg Glu
Leu Val	Glu Glu	Gly 260	Tyr Asp	Leu Leu	Gly Thr	Leu Asn	Trp Thr	Asp
His Leu	Pro Trp	Leu 275	Ser Glu	Phe 280	Phe Asp	Pro Gln	Arg Ile	Arg Ser
Cys Ser	Asn Leu	Val 290	Pro Lys	Val Asn	Arg Phe	Val Asn	Arg Ile	Ile
Ser Asp	His Arg	Glu 305	Gln Thr	Arg Asp	Ser Pro	Ser Asp	Phe Val	Asp
Val Leu	Leu Ser	Leu 320	Asp Gly	Pro Asp	Lys 330	Leu Ser	Asp Pro	Asp Ile
Ile Ala	Val Leu	Trp 340	Glu Met	Ile Phe	Arg 345	Gly Thr	Asp Thr	Val Ala
Val Leu	Ile Glu	Trp 355	Ile Leu	Ala Arg	Met Val	Leu His	Pro Asp	Ile
Gln Ser	Thr Val	His 370	Asn Glu	Leu Leu	Asp Gln	Ile Val	Gly Arg	Ser Arg
Ala Val	Glu Glu	Ser 385	Asp Val	Val Ser	Leu Val	380 Trp Leu	Thr Thr	Ala Val
Val Lys	Glu Val	Leu 405	Arg Leu	His Pro	Pro Gly	Pro Leu	Leu Ser	Thr
Ala Arg	Leu Ala	Ile 420	Thr Asp	Thr Ile	410 Asp Gly	Arg Arg	Arg Val	Pro
Ala Gly	Thr Thr	Ala 435	Met Val	Asn Met	Trp Ala	Ile Ala	His Asp	Pro
His Val	Trp Glu	Asn 450	Pro Leu	Glu Phe	Lys Pro	Glu Arg	Phe Val	Ala
Lys Glu	Gly Glu	Val 465	Glu Phe	Ser Val	Leu Gly	470 Ser Asp	Arg Leu	Arg
Ala Pro	Phe Gly	Ser 485	Gly Arg	Arg Val	Cys 490	Pro Gly	Lys Asn	Leu Gly
Leu Thr	Thr Val	Thr 500	Phe Trp	Thr Ala	Thr 505	Leu Leu	His Glu	Phe Glu
Xaa Ala	Asp Ala	Val Arg						
	515							

(2) INFORMATION FOR SEQ ID NO:1574:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 502 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..502

(D) OTHER INFORMATION: / Ceres Seq. ID 1570390

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1574:

```
Met Ala Thr Lys Leu Asp Thr Ser Ser Leu Leu Leu Ala Leu Leu Ser
1      5      10
Lys Cys Ser Leu Leu Thr Gln Thr Asn Leu Ala Leu Ser Leu Leu Val
20      25      30
Ala Ser Leu Ala Ser Leu Ala Leu Ser Leu Phe Phe Trp Ser His Pro
35      40      45
Gly Gly Pro Ala Trp Gly Lys Tyr Phe Leu His Arg Arg Arg Gln Thr
50      55      60
Thr Val Ile Pro Gly Pro Arg Gly Leu Pro Phe Val Gly Ser Met Ser
65      70      75      80
Leu Met Ser Asn Thr Leu Ala His Arg Cys Ile Ala Ala Thr Ala Glu
85      90      95
Lys Phe Arg Ala Glu Arg Leu Met Ala Phe Ser Leu Gly Glu Thr Arg
100      105      110
Val Ile Val Thr Cys Asn Pro Asp Val Ala Lys Glu Ile Leu Asn Ser
115      120      125
Pro Val Phe Ala Asp Arg Pro Val Lys Glu Ser Ala Tyr Ser Leu Met
130      135      140
Phe Asn Arg Ala Ile Gly Phe Ala Pro Tyr Gly Val Tyr Trp Arg Thr
145      150      155      160
Leu Arg Lys Ile Ala Ser Asn His Leu Phe Ser Pro Lys Gln Ile Lys
165      170      175
Arg Ser Glu Thr Gln Arg Ser Val Ile Ala Asn Gln Ile Val Lys Cys
180      185      190
Leu Thr Lys Lys Gln Ser Asn Thr Lys Gly Leu Cys Phe Ala Arg Asp Leu
195      200      205
Ile Lys Thr Ala Ser Leu Asn Asn Met Met Cys Ser Val Phe Gly Lys
210      215      220
Glu Tyr Glu Leu Glu Glu Glu His Glu Glu Val Ser Glu Leu Arg Glu
225      230      235      240
Leu Val Glu Glu Gly Tyr Asp Leu Leu Gly Thr Leu Asn Trp Thr Asp
245      250      255
His Leu Pro Trp Leu Ser Glu Phe Asp Pro Gln Arg Ile Arg Ser Arg
260      265      270
Cys Ser Asn Leu Val Pro Lys Val Asn Arg Phe Val Asn Arg Ile Ile
275      280      285
Ser Asp His Arg Glu Gln Thr Arg Asp Ser Pro Ser Asp Phe Val Asp
290      295      300
Val Leu Leu Ser Leu Asp Gly Pro Asp Lys Leu Ser Asp Pro Asp Ile
305      310      315      320
Ile Ala Val Leu Trp Glu Met Ile Phe Arg Gly Thr Asp Thr Val Ala
325      330      335
Val Leu Ile Glu Trp Ile Leu Ala Arg Met Val Leu His Pro Asp Ile
340      345      350
Gln Ser Thr Val His Asn Glu Leu Asp Gln Ile Val Gly Arg Ser Arg
355      360      365
Ala Val Glu Glu Ser Asp Val Val Ser Leu Val Tyr Leu Thr Ala Val
370      375      380
Val Lys Glu Val Leu Arg Leu His Pro Pro Gly Pro Leu Leu Ser Trp
```

385	390	395	400
Ala Arg Leu Ala	Ile Thr Asp Thr Ile	Ile Asp Gly Arg Arg	Val Pro
	405	410	415
Ala Gly Thr Thr	Ala Met Val Asn Met	Trp Ala Ile Ala His	Asp Pro
	420	425	430
His Val Trp Glu	Asn Pro Leu Glu Phe	Lys Pro Glu Arg Phe	Val Ala
	435	440	445
Lys Glu Gly Glu	Val Glu Phe Ser Val	Leu Gly Ser Asp Leu	Arg Leu
	450	455	460
Ala Pro Phe Gly	Ser Gly Arg Arg Val	Cys Pro Gly Lys Asn	Leu Gly
	465	470	475
Leu Thr Thr Val	Thr Phe Trp Thr Ala	Thr Leu Leu His Glu	Phe Glu
	485	490	495
Xaa Ala Asp Ala	Val Arg		
	500		

(2) INFORMATION FOR SEQ ID NO:1575:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 424 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..424

(D) OTHER INFORMATION: / Ceres Seq. ID 1570391

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1575:

Met Ser Leu Met Ser Asn Thr Leu Ala His Arg Cys Ile Ala Ala Thr	
1	5 10 15
Ala Glu Lys Phe Arg Ala Glu Arg Leu Met Ala Phe Ser Leu Gly Glu	
	20 25 30
Thr Arg Val Ile Val Thr Cys Asn Pro Asp Val Ala Lys Glu Ile Leu	
	35 40 45
Asn Ser Pro Val Phe Ala Asp Arg Pro Val Lys Glu Ser Ala Tyr Ser	
	50 55 60
Leu Met Phe Asn Arg Ala Ile Gly Phe Ala Pro Tyr Gly Val Tyr Trp	
	65 70 75 80
Arg Thr Leu Arg Lys Ile Ala Ser Asn His Leu Phe Ser Pro Lys Gln	
	85 90 95
Ile Lys Arg Ser Glu Thr Gln Arg Ser Val Ile Ala Asn Gln Ile Val	
	100 105 110
Lys Cys Leu Thr Lys Gln Ser Asn Thr Lys Gly Leu Cys Phe Ala Arg	
	115 120 125
Asp Leu Ile Lys Thr Ala Ser Leu Asn Asn Met Met Cys Ser Val Phe	
	130 135 140
Gly Lys Glu Tyr Glu Leu Glu Glu His Glu Glu Val Ser Glu Leu	
	145 150 155 160
Arg Glu Leu Val Glu Glu Gly Tyr Asp Leu Leu Gly Thr Leu Asn Trp	
	165 170 175
Thr Asp His Leu Pro Trp Leu Ser Glu Phe Asp Pro Gln Arg Ile Arg	
	180 185 190
Ser Arg Cys Ser Asn Leu Val Pro Lys Val Asn Arg Phe Val Asn Arg	
	195 200 205
Ile Ile Ser Asp His Arg Glu Gln Thr Arg Asp Ser Pro Ser Asp Phe	
	210 215 220
Val Asp Val Leu Leu Ser Leu Asp Gly Pro Asp Lys Leu Ser Asp Pro	
	225 230 235 240
Asp Ile Ile Ala Val Leu Trp Glu Met Ile Phe Arg Gly Thr Asp Thr	
	245 250 255
Val Ala Val Leu Ile Glu Trp Ile Leu Ala Arg Met Val Leu His Pro	
	260 265 270


```

Asp Ile Gln Ser Thr Val His Asn Glu Leu Asp Gln Ile Val Gly Arg
    275                280                285
Ser Arg Ala Val Glu Glu Ser Asp Val Val Ser Leu Val Tyr Leu Thr
    290                295                300
Ala Val Val Lys Glu Val Leu Arg Leu His Pro Pro Gly Pro Leu Leu
    305                310                315                320
Ser Trp Ala Arg Leu Ala Ile Thr Asp Thr Ile Ile Asp Gly Arg Arg
    325                330                335
Val Pro Ala Gly Thr Thr Ala Met Val Asn Met Trp Ala Ile Ala His
    340                345                350
Asp Pro His Val Trp Glu Asn Pro Leu Glu Phe Lys Pro Glu Arg Phe
    355                360                365
Val Ala Lys Glu Gly Glu Val Glu Phe Ser Val Leu Gly Ser Asp Leu
    370                375                380
Arg Leu Ala Pro Phe Gly Ser Gly Arg Arg Val Cys Pro Gly Lys Asn
    385                390                395                400
Leu Gly Leu Thr Thr Val Thr Phe Trp Thr Ala Thr Leu Leu His Glu
    405                410                415
Phe Glu Xaa Ala Asp Ala Val Arg
    420

```

(2) INFORMATION FOR SEQ ID NO:1576:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1443 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1443
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570412

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1576:

```

gtcctaggaa gagcacaagc ctccacaagt ggtgttgccct ctctgttccct aactcccttc      60
tcttatataa aattgtgtat cctccatata tacaacaaga agagaaaact ttgatatggg      120
gttaaagatg tcaagaatcag ccaagcctta ctttgcaatg gtttgtcttc aattcggata      180
cgccggcatg aacctcgtga cgaaggtgtg gctagaccgc ggcctatgac attacgtcct      240
tgtgtgttac cgtaatgcct ttgccacggc tgctatcgca ccttttgctc tactctccga      300
gaggaaagtg aggcgaaga tgacatttcc aatattcatg cagatttttg ttctagctct      360
tctcgggcct ttgatcgatc aaaacttata ttacgcctgt ctcaaaacta ctccaaccaac      420
ttttgcggcg cgactcacaa atactgttcc agctttgacc ttatcatatt ccataatttg      480
caggatggag aaggtggaga tgagaaaagt aagattccaa gcaaaagtgg tggggacatt      540
agtgatagtg gttggagcca tgttgatgat ttattccaaa attcctctaa tccactcttc      600
tccgatctca cctcaaccgc catgtctttg cgccggcagg tgaggactac ctcaaaagca      660
ccgtcttccct cctcatcgcc tcattttctt gggcttccct ttctgttctt caggcggcta      720
cgttgaagag atactcatct cacttttcat tatcgacgat ggtgtgtttc atggggcaagt      780
tacagttcac agctctaacg ttgtgatgg agccaaacct ttctgcctgg aacattggct      840
ttgacatgaa cctcttctgc tctgttctat cgggcataat tgctgcgagc atagcgtact      900
acgttcaagg aatgatgacg aagcaaaaga gtgttatctt tgttaactgt tttaactctc      960
ttgtttgcat aatcggatcc atcattggct tcctcatcct caaccaaact ttaaacctgt      1020
gcggggcttc tggaaatggca attttagtgg tgggagtttg cactgttctt tggggaaagg      1080
aaggagatat cgatgaagaa gagaacattg aggagaagtt tgtagaaatt gtcgaagtgt      1140
gcaaccgctg cgatatcaag gttctctcga tgaatgcaag aatcgatgag gaagtatgac      1200
ttgaaatgca atccgcaggc acagctaaag tggcgggtggg ttctctcgtaa cctctcgtgt      1260
gtggaaaaag atgttcacga ccttaattag atcttttcaa gtcttttttt ttaacaaaaa      1320
ttttgatagc aggaacaact ttttctttgt tctatatcat tgcctcaact tttttatttc      1380
ttttgatggt ttgttttata atcttctata gaagggtaat tattattatt aaataaatgt      1440
tcc

```

(2) INFORMATION FOR SEQ ID NO:1577:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 175 amino acids
- (B) TYPE: amino acid

(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..175
(D) OTHER INFORMATION: / Ceres Seq. ID 1570413
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1577:
Met Gly Leu Lys Met Ser Glu Ser Ala Lys Pro Tyr Phe Ala Met Val
1 5 10 15
Cys Leu Gln Phe Gly Tyr Ala Gly Met Asn Leu Val Thr Lys Val Val
20 25 30
Leu Asp Arg Gly Met Ser His Tyr Val Leu Val Ala Tyr Arg Asn Ala
35 40 45
Phe Ala Thr Ala Ala Ile Ala Pro Phe Ala Leu Leu Ser Glu Arg Lys
50 55 60
Val Arg Pro Lys Met Thr Phe Pro Ile Phe Met Gln Ile Phe Val Leu
65 70 75 80
Ala Leu Leu Gly Pro Leu Ile Asp Gln Asn Leu Tyr Tyr Ala Cys Leu
85 90 95
Lys Leu Thr Ser Pro Thr Phe Ala Gly Ala Val Thr Asn Ile Val Pro
100 105 110
Ala Leu Thr Phe Ile Ile Ser Ile Ile Cys Arg Met Glu Lys Val Glu
115 120 125
Met Arg Lys Val Arg Phe Gln Ala Lys Val Val Gly Thr Leu Val Ile
130 135 140
Val Val Gly Ala Met Leu Met Ile Leu Phe Lys Ile Pro Leu Met His
145 150 155 160
Leu Ser Pro Ile Ser Pro His Arg Pro Cys Phe Val Ala Gly Arg
165 170 175

(2) INFORMATION FOR SEQ ID NO:1578:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 171 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide
(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..171
(D) OTHER INFORMATION: / Ceres Seq. ID 1570414

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1578:

Met Ser Glu Ser Ala Lys Pro Tyr Phe Ala Met Val Cys Leu Gln Phe
1 5 10 15
Gly Tyr Ala Gly Met Asn Leu Val Thr Lys Val Val Leu Asp Arg Gly
20 25 30
Met Ser His Tyr Val Leu Val Ala Tyr Arg Asn Ala Phe Ala Thr Ala
35 40 45
Ala Ile Ala Pro Phe Ala Leu Leu Ser Glu Arg Lys Val Arg Pro Lys
50 55 60
Met Thr Phe Pro Ile Phe Met Gln Ile Phe Val Leu Ala Leu Leu Gly
65 70 75 80
Pro Leu Ile Asp Gln Asn Leu Tyr Tyr Ala Cys Leu Lys Leu Thr Ser
85 90 95
Pro Thr Phe Ala Gly Ala Val Thr Asn Ile Val Pro Ala Leu Thr Phe
100 105 110
Ile Ile Ser Ile Ile Cys Arg Met Glu Lys Val Glu Met Arg Lys Val
115 120 125
Arg Phe Gln Ala Lys Val Val Gly Thr Leu Val Ile Val Val Gly Ala
130 135 140
Met Leu Met Ile Leu Phe Lys Ile Pro Leu Met His Leu Ser Pro Ile

145 150 155 160
Ser Pro His Arg Pro Cys Phe Val Ala Gly Arg
165 170

(2) INFORMATION FOR SEQ ID NO:1579:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 163 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..163
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570415

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1579:

Met	Val	Cys	Phe	Met	Gly	Thr	Leu	Gln	Ser	Thr	Ala	Leu	Thr	Phe	Val
1				5						10				15	
Met	Glu	Pro	Asn	Leu	Ser	Ala	Trp	Asn	Ile	Gly	Phe	Asp	Met	Asn	Leu
			20					25					30		
Leu	Ala	Ser	Ala	Tyr	Ala	Gly	Ile	Met	Ser	Ser	Ser	Ile	Ala	Tyr	Tyr
			35				40					45			
Val	Gln	Gly	Met	Met	Thr	Lys	Gln	Lys	Ser	Val	Ile	Phe	Val	Thr	Ala
			50			55					60				
Phe	Asn	Pro	Leu	Val	Val	Ile	Ile	Gly	Ser	Ile	Ile	Gly	Phe	Leu	Ile
					70				75				80		
Leu	Asn	Gln	Thr	Leu	Asn	Leu	Gly	Gly	Val	Leu	Gly	Met	Ala	Ile	Leu
					85				90				95		
Val	Val	Gly	Val	Cys	Thr	Val	Leu	Trp	Gly	Lys	Glu	Gly	Asp	Ile	Asp
Glu	Glu	Glu	Asn	Ile	Glu	Glu	Lys	Phe	Val	Glu	Ile	Val	Lys	Cys	Cys
			115				120					125			
Asn	Arg	Cys	Asp	Ile	Lys	Val	Leu	Ser	Met	Met	Pro	Arg	Ile	Asp	Glu
			130				135					140			
Glu	Val	Asp	Val	Glu	Met	Gln	Ser	Ala	Gly	Thr	Ala	Lys	Val	Ala	Val
					150					155				160	
Gly	Phe	Ser													

(2) INFORMATION FOR SEQ ID NO:1580:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 916 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..916
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570422

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1580:

aaagcgaaagC	tttattcggt	tgccttgagct	ccgaagagtg	gaaacaaaaa	tggaggaaaga	60
agagcacgag	gtttacgggt	gagaaatccc	tgaagtcggc	gatacggatg	ttcccgatcc	120
ggatatcgat	atgctctgag	ccgatgagga	cgccgttacg	gagcttgcgt	agatgaagag	180
gagattaaag	gagatggagg	aagaagctcg	tgcgctacga	gagatgcaag	caaaaagtcga	240
aaaagaaatg	ggagctactc	aagatcctgc	tagtatggct	gcaaatcaag	aaggaaagga	300
ggagggtggat	gctcgatcag	tttatgttgg	caatgtcgac	tatgcctgta	cacctgaaga	360
agtgcacaat	catttccaaa	catgcggaaac	agtcacacgg	gtaaccattc	taatggacaa	420
gtttggacag	ccaaagggat	ttgcttatgt	ggagtttgta	gaagtggaaag	ccgtgcaaga	480
agctctgcag	ctgaatgaat	cagagcttca	tggtcgctcaa	ctgaagggtct	cgcctaagcg	540
aaccaatggt	ctgggaatga	aacagtatca	ttcctggcgt	ttcaaccctt	caatgggata	600
ccgcttttcg	agaccctttg	tgcctccgta	tttttattcc	ccatatggat	acgggaaggc	660
tcctagggtc	agaaggccaa	tgcggtacat	gccttaccaa	tagaaacctg	accggaataa	720

gaagaactat gacagagatg atgccgaggt cgtccctcca ttctgagctt tatatatgaa 780
tatgactttg ctgcacchg aacttaattt tgaatctgtc atgtacggat gagattataa 840
gcttttgttt ctttagatta tgattatatt tggctgatat tactttcagt ttatatcttt 900
gttagtactt tcttcc

(2) INFORMATION FOR SEQ ID NO:1581:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 233 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..233
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570423

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1581:

Lys Arg Ser Phe Ile Arg Leu Leu Glu Leu Arg Arg Val Glu Thr Lys
1 5 10 15
Met Glu Glu Glu Glu His Glu Val Tyr Gly Gly Glu Ile Pro Glu Val
20 25 30
Gly Asp Thr Asp Val Pro Asp Pro Asp Ile Asp Met Ser Ala Ala Asp
35 40 45
Glu Asp Ala Val Thr Glu Leu Ala Glu Met Lys Arg Arg Leu Lys Glu
50 55 60
Met Glu Glu Glu Ala Ala Leu Arg Glu Met Gln Ala Lys Val Glu
65 70 75 80
Lys Glu Met Gly Ala Thr Gln Asp Pro Ala Ser Met Ala Ala Asn Gln
85 90 95
Glu Gly Lys Glu Glu Val Asp Ala Arg Ser Val Tyr Val Gly Asn Val
100 105 110
Asp Tyr Ala Cys Thr Pro Glu Glu Val Gln Leu His Phe Gln Thr Cys
115 120 125
Gly Thr Val Asn Arg Val Thr Ile Leu Met Asp Lys Phe Gly Gln Pro
130 135 140
Lys Gly Phe Ala Tyr Val Glu Phe Val Glu Val Glu Ala Val Gln Glu
145 150 155 160
Ala Leu Gln Leu Asn Glu Ser Glu Leu His Gly Arg Gln Leu Lys Val
165 170 175
Ser Pro Lys Arg Thr Asn Val Pro Gly Met Lys Gln Tyr His Pro Gly
180 185 190
Arg Phe Asn Pro Ser Met Gly Tyr Arg Phe Arg Arg Pro Phe Val Pro
195 200 205
Pro Tyr Phe Tyr Ser Pro Tyr Gly Tyr Gly Lys Ala Pro Arg Phe Arg
210 215 220
Arg Pro Met Arg Tyr Met Pro Tyr Gln
225 230

(2) INFORMATION FOR SEQ ID NO:1582:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 217 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..217
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570424

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1582:

Met Glu Glu Glu Glu His Glu Val Tyr Gly Gly Glu Ile Pro Glu Val
1 5 10 15
Gly Asp Thr Asp Val Pro Asp Pro Asp Ile Asp Met Ser Ala Ala Asp

1	Ser	Ala	Ala	Asp	Glu	Asp	Ala	Val	Thr	Glu	Leu	Ala	Glu	Met	Lys
1	Arg	Arg	Leu	Lys	Glu	Met	Glu	Glu	Glu	Ala	Ala	Ala	Leu	Arg	Glu
			20						25					30	
	Gln	Ala	Lys	Val	Glu	Lys	Glu	Met	Gly	Ala	Thr	Gln	Asp	Pro	Ala
			35						40				45		
	Met	Ala	Ala	Asn	Gln	Glu	Gly	Lys	Glu	Glu	Val	Asp	Ala	Arg	Ser
			50					55				60			
	Tyr	Val	Gly	Asn	Val	Asp	Tyr	Ala	Cys	Thr	Pro	Glu	Glu	Val	Gln
65						70					75				80
	His	Phe	Gln	Thr	Cys	Gly	Thr	Val	Asn	Arg	Val	Thr	Ile	Leu	Met
					85					90					95
	Lys	Phe	Gly	Gln	Pro	Lys	Gly	Phe	Ala	Tyr	Val	Glu	Phe	Val	Glu
					100				105					110	
	Glu	Ala	Val	Gln	Glu	Ala	Leu	Gln	Leu	Asn	Glu	Ser	Glu	Leu	His
			115					120					125		Gly
	Arg	Gln	Leu	Lys	Val	Ser	Pro	Lys	Arg	Thr	Asn	Val	Pro	Gly	Met
			130					135				140			Lys
	Gln	Tyr	His	Pro	Gly	Arg	Phe	Asn	Pro	Ser	Met	Gly	Tyr	Arg	Phe
145						150					155				160
	Arg	Pro	Phe	Val	Pro	Pro	Tyr	Phe	Tyr	Ser	Pro	Tyr	Gly	Tyr	Gly
					165					170					175
	Ala	Pro	Arg	Phe	Arg	Arg	Pro	Met	Arg	Tyr	Met	Pro	Tyr	Gln	
				180						185				190	

(2) INFORMATION FOR SEQ ID NO:1584:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 617 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..617
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570437

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1584:

aatatataac	tttaaaacat	tgaagctaac	ttctcacaag	tcaccaccat	ttctctctag	60
aaaaaatctg	aaaaaacaaa	ccatctcaaa	gtttcttgag	aagaaaaaaa	gggtcaagaa	120
agatgcctaa	agacaggaat	atcggaatcg	ccatgggattt	ctcagagagc	agcaagaacg	180
ctctgaaatg	ggcgatcgag	aacttagcag	acaaaggaga	cacgatttac	atcatccaca	240
ctctaccact	ctctggcgat	gaatctcgta	actccctctg	gttcaaatcc	gggtctcctc	300
tcataccggt	ggcagagttt	agggaaacgg	agattatgga	gaaatacggg	gtcaaaacgg	360
acatcgcatg	tcttgatatg	ctcgacactg	gttcgaggca	gaaagaggtg	catgtagtga	420
ccaagtata	ctggggagat	gcaagagaga	agcttgttga	tgctgttaaa	gatcttaaac	480
tcgattctat	tgctatggga	agcagaggac	tcagtgctct	tcaaaggata	ataatgggaa	540
gcgtgaGcag	ctttgtgtgc	caacacgcgc	cttgccctgt	caccgttgtc	aaggataacg	600
aataaacgat	ttctact					

(2) INFORMATION FOR SEQ ID NO:1585:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 160 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..160
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570438

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1585:

Met	Pro	Lys	Asp	Arg	Asn	Ile	Gly	Ile	Ala	Met	Asp	Phe	Ser	Glu	Ser	
1			5					10					15			
Ser	Lys	Asn	Ala	Leu	Lys	Trp	Ala	Ile	Glu	Asn	Leu	Ala	Asp	Lys	Gly	
			20				25					30				
Asp	Thr	Ile	Tyr	Ile	Ile	His	Thr	Leu	Pro	Leu	Ser	Gly	Asp	Glu	Ser	
			35				40					45				
Arg	Asn	Ser	Leu	Trp	Phe	Lys	Ser	Gly	Ser	Pro	Leu	Ile	Pro	Leu	Ala	
			50			55					60					
Glu	Phe	Arg	Glu	Pro	Glu	Ile	Met	Glu	Lys	Tyr	Gly	Val	Lys	Thr	Asp	
			65			70				75			80			
Ile	Ala	Cys	Leu	Asp	Met	Leu	Asp	Thr	Gly	Ser	Arg	Gln	Lys	Glu	Val	
			85					90					95			
His	Val	Val	Thr	Lys	Leu	Tyr	Trp	Gly	Asp	Ala	Arg	Glu	Lys	Leu	Val	
			100					105					110			
Asp	Ala	Val	Lys	Asp	Leu	Lys	Leu	Asp	Ser	Ile	Val	Met	Gly	Ser	Arg	
			115				120					125				
Gly	Leu	Ser	Ala	Leu	Gln	Arg	Ile	Ile	Met	Gly	Ser	Val	Ser	Ser	Phe	
			130			135					140					
Val	Ile	Gln	His	Ala	Pro	Cys	Pro	Val	Thr	Val	Val	Lys	Asp	Asn	Glu	
			145			150				155					160	

(2) INFORMATION FOR SEQ ID NO:1586:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 150 amino acids
- (B) TYPE: amino acid

(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..150
 (D) OTHER INFORMATION: / Ceres Seq. ID 1570439
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1586:
Met Asp Phe Ser Glu Ser Ser Lys Asn Ala Leu Lys Trp Ala Ile Glu
1 5 10 15
Asn Leu Ala Asp Lys Gly Asp Thr Ile Tyr Ile Ile His Thr Leu Pro
 20 25 30
Leu Ser Gly Asp Glu Ser Arg Asn Ser Leu Trp Phe Lys Ser Gly Ser
 35 40 45
Pro Leu Ile Pro Leu Ala Glu Phe Arg Glu Pro Glu Ile Met Glu Lys
 50 55 60
Tyr Gly Val Lys Thr Asp Ile Ala Cys Leu Asp Met Leu Asp Thr Gly
 65 70 75 80
Ser Arg Gln Lys Glu Val His Val Val Thr Lys Leu Tyr Trp Gly Asp
 85 90 95
Ala Arg Glu Lys Leu Val Asp Ala Val Lys Asp Leu Lys Leu Asp Ser
 100 105 110
Ile Val Met Gly Ser Arg Gly Leu Ser Ala Leu Gln Arg Ile Ile Met
 115 120 125
Gly Ser Val Ser Ser Phe Val Ile Gln His Ala Pro Cys Pro Val Thr
 130 135 140
Val Val Lys Asp Asn Glu
145 150

(2) INFORMATION FOR SEQ ID NO:1587:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 89 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..89
 (D) OTHER INFORMATION: / Ceres Seq. ID 1570440
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1587:
Met Glu Lys Tyr Gly Val Lys Thr Asp Ile Ala Cys Leu Asp Met Leu
1 5 10 15
Asp Thr Gly Ser Arg Gln Lys Glu Val His Val Val Thr Lys Leu Tyr
 20 25 30
Trp Gly Asp Ala Arg Glu Lys Leu Val Asp Ala Val Lys Asp Leu Lys
 35 40 45
Leu Asp Ser Ile Val Met Gly Ser Arg Gly Leu Ser Ala Leu Gln Arg
 50 55 60
Ile Ile Met Gly Ser Val Ser Ser Phe Val Ile Gln His Ala Pro Cys
 65 70 75 80
Pro Val Thr Val Val Lys Asp Asn Glu
 85

(2) INFORMATION FOR SEQ ID NO:1588:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 641 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: DNA (genomic)
 (ix) FEATURE:
 (A) NAME/KEY: -

(B) LOCATION: 1..641

(D) OTHER INFORMATION: / Ceres Seq. ID 1570446

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1588:

aatattatttg	tgttttggtcc	tatttattac	tctctgctct	cttcctgaag	cttcttcac	60
tttttgtttg	acaagaagag	gtagagaaga	agatgtctca	atcaatctcc	tccagcacaa	120
aggcagaaga	agttgttagt	gtagatgtga	gccaagccaa	gactctctc	cagttctggc	180
atcaatatct	tgacgttagg	actcaggacg	agtttaggag	aggccattgt	gaggcagcta	240
agatcgtcaa	cattccctac	atgctcaaca	cacctcaagg	tagagtgaag	aatcgagagt	300
tcttgtagca	agtatctctt	cttctaaacc	cagctgatga	tatccttggt	gggtgtcaga	360
gtggagccag	atccttaaaa	gccacaactg	aacttggttc	tgccaggttac	aagaaagtga	420
gaaacgtggg	aggtggctac	ttggcttggg	tagatcacag	cttcccctac	aacaaggagg	480
aggagggacc	actctgcta	taataatctt	aagattctct	ctttttstta	atcaaatMat	540
ataactgcct	gtgtgatgta	gtaatcattt	tcaatttaaa	attccagttt	cttgtaataca	600
aaactctcgt	gtaccaaat	caataaaagc	tgtgtttctc	t		

(2) INFORMATION FOR SEQ ID NO:1589:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 136 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..136

(D) OTHER INFORMATION: / Ceres Seq. ID 1570447

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1589:

Met	Ser	Gln	Ser	Ile	Ser	Ser	Ser	Thr	Lys	Ala	Glu	Glu	Val	Val	Ser	
1			5						10					15		
Val	Asp	Val	Ser	Gln	Ala	Lys	Thr	Leu	Leu	Gln	Ser	Gly	His	Gln	Tyr	
			20					25					30			
Leu	Asp	Val	Arg	Thr	Gln	Asp	Glu	Phe	Arg	Arg	Gly	His	Cys	Glu	Ala	
			35					40								
Ala	Lys	Ile	Val	Asn	Ile	Pro	Tyr	Met	Leu	Asn	Thr	Pro	Gln	Gly	Arg	
			50					55				60				
Val	Lys	Asn	Arg	Glu	Phe	Leu	Glu	Gln	Val	Ser	Ser	Leu	Leu	Asn	Pro	
			65					70			75			80		
Ala	Asp	Asp	Ile	Leu	Val	Gly	Cys	Gln	Ser	Gly	Ala	Arg	Ser	Leu	Lys	
			85					90						95		
Ala	Thr	Thr	Glu	Leu	Val	Ala	Ala	Gly	Tyr	Lys	Lys	Val	Arg	Asn	Val	
			100					105					110			
Gly	Gly	Gly	Tyr	Leu	Ala	Trp	Val	Asp	His	Ser	Phe	Pro	Ile	Asn	Lys	
			115					120					125			
Glu	Glu	Glu	Glu	Pro	Ser	Ala	Asn									
			130				135									

(2) INFORMATION FOR SEQ ID NO:1590:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 80 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..80

(D) OTHER INFORMATION: / Ceres Seq. ID 1570448

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1590:

Met	Leu	Asn	Thr	Pro	Gln	Gly	Arg	Val	Lys	Asn	Arg	Glu	Phe	Leu	Glu	
1				5					10					15		
Gln	Val	Ser	Ser	Leu	Leu	Asn	Pro	Ala	Asp	Asp	Ile	Leu	Val	Gly	Cys	
				20				25					30			
Gln	Ser	Gly	Ala	Arg	Ser	Leu	Lys	Ala	Thr	Thr	Glu	Leu	Val	Ala	Ala	

(2) INFORMATION FOR SEQ ID NO:1591:

(A) LENGTH: 702 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

MOLECULE TYPE: DNA (a

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..702

(D) OTHER INFORMATION: / Ceres Seq. ID 1570449

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1591:

aacaaacaat	cgaaacacc	atgagggtta	tctcaaaact	gttcgatctc	gacagaagac	60
gaatacacga	atcgccgaag	cattttgatt	cgcggcgaag	cgccacacgt	ctctctctcac	120
tcagcagcga	aaccacgcgc	ctcaagcagc	tctatagcag	tctctctctc	caaacgctct	180
ctctcagttc	ctctctcttag	aaaataccat	ccaccacgtg	acgcgtctcN	CTCactcggt	240
acctctctgt	ttaaaactcg	tgaaagcgat	ctctctgtaa	cttgtctctc	cgtaacgctg	300
ggcatatctc	tcgcgcgttc	tggacacgaa	Gtaagtatct	acgatcgcga	catgtgttgt	360
catctcgcga	cattcaacgc	ccaagatctc	tcttcagcaa	cgtggaactc	ctgcggtctc	420
tcgcggtgga	aaatctctac	ggcgcatcaa	gacggtaaaa	tcggagtttg	gaaactaacg	480
gttaaaacgc	gttataaaac	gtttaaagcg	cttccaactt	taaaacacgc	tttaacagct	540
tttgctctct	ctataaaacta	cgttcacaga	cgcgcgtata	gaaacgctc	ctggatcgaa	600
catgCtagct	cggttaactgc	tcttcgcggt	aatgacggat	ctatttaact	gtttctctgg	660
gagaagactg	ttaagaatatg	gaagacgtcc	gacttctggt	gc		

(2) INFORMATION FOR SEQ ID NO:1592:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 83 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) **FEATURE:**

(A) NAME/KEY: peptide

(B) LOCATION: 1..83

(D) OTHER INFORMATION: / Ceres Seq. ID 1570450

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1592:

[illegible]

(2) INFORMATION FOR SEO ID NO:1593:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 77 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..77

(D) OTHER INFORMATION: / Ceres Seq. ID 1570451

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1593:

Met	Arg	Val	Ile	Ser	Lys	Leu	Phe	Asp	Ser	Asp	Arg	Arg	Arg	Ile	Pro	
1				5					10					15		
Lys	Ser	Pro	Lys	His	Leu	Asp	Ser	Gly	Glu	Ser	Ala	Thr	Ser	Ser	Ser	
			20					25					30			
Ser	Leu	Ser	Asp	Val	Thr	Thr	Gly	Ser	Ser	Ser	Leu	His	Ser	Ser	Leu	
		35					40				45					
Ser	Leu	Gln	Thr	Leu	Pro	Ser	Val	Pro	Ser	Leu	Gln	Lys	Ile	Pro	Ser	
		50				55					60					
Thr	Thr	Val	Thr	Val	Xaa	Ser	Leu	Arg	Tyr	Leu	Leu	Val				
65				70					75							

(2) INFORMATION FOR SEQ ID NO:1594:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 117 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..117

(D) OTHER INFORMATION: / Ceres Seq. ID 1570452

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1594:

Met	Cys	Ala	His	Leu	Asp	Thr	Phe	Asn	Gly	Gln	Asp	Pro	Phe	Ser	Gly	
1				5					10					15		
Thr	Val	Lys	Ser	Val	Gly	Phe	Ser	Gly	Glu	Lys	Ile	Phe	Thr	Ala	His	
			20					25					30			
Gln	Asp	Gly	Lys	Ile	Gly	Val	Trp	Lys	Leu	Thr	Ala	Lys	Ser	Gly	Tyr	
		35				40					45					
Lys	Gln	Leu	Thr	Thr	Leu	Pro	Thr	Leu	Asn	Asp	Arg	Leu	Arg	Arg	Phe	
		50				55					60					
Ala	Leu	Pro	Lys	Asn	Tyr	Val	Gln	Val	Arg	Arg	His	Lys	Lys	Arg	Leu	
65				70					75					80		
Trp	Ile	Glu	His	Ala	Asp	Ala	Val	Thr	Ala	Leu	Ala	Val	Asn	Asp	Gly	
		85						90					95			
Phe	Ile	Tyr	Ser	Val	Ser	Trp	Asp	Lys	Thr	Leu	Lys	Ile	Trp	Arg	Ala	
		100					105						110			
Ser	Asp	Leu	Arg	Cys												
		115														

(2) INFORMATION FOR SEQ ID NO:1595:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 751 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..751

(D) OTHER INFORMATION: / Ceres Seq. ID 1570474

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1595:

atccaccaca	tatttatgtt	tgatccaaaa	gccaacacaa	gcaaagaaat	taaaagtgtt	60
cttgttgctg	tagaacacaa	acagaacaaa	caaaaaatca	attgaagagt	ctctcagtcg	120
ttaggggaag	caaatagaga	aatggctagc	tttactgcct	ccgcttccac	cgtctccgcc	180
gctcgtccgg	ctctcctctc	caagcctacc	gtcgccatct	ctgctcctgt	tcttggtttg	240
cttccaatgg	gtaagaagaa	gggaggagtg	agatgttcaa	tggagacaaa	gcaaggaaac	300

gtctcagtc tgggggctgg agtttcagct gcagcaacag ctgtctttgac ggcgggtgatg 360
agcaatcccg cgaatggcttt ggttgatgag aggatgtcaa cagaaggaaac aggattaccc 420
tttgggtctaa gcaacaacct ctggggttgg attctgtttg gagtctttgg ttgtatctgg 480
actttctctt tegtctacac ttcattcttc gaggaggatg aagaatctgg tcttctactc 540
tgaaggaaga atcaatcttt cgtcttctca ttccatttt catgtgagaa catgaatcaa 600
gtgttcaccc ttctagtttc ttgtaattgt taagtaaaga ctaaaaacta ttttcatgtg 660
gttttacttt ccccatcttc ctttatcttg tcataacatt gataaggagg agattatSgt 720
gattattaaa tatcatgcat gacatgttca t

(2) INFORMATION FOR SEQ ID NO:1596:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 133 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..133

(D) OTHER INFORMATION: / Ceres Seq. ID 1570475

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1596:

Met Ala Ser Phe Thr Ala Ser Ala Ser Thr Val Ser Ala Ala Arg Pro
1 5 10 15
Ala Leu Leu Leu Lys Pro Thr Val Ala Ile Ser Ala Pro Val Leu Gly
20 25 30
Leu Pro Pro Met Gly Lys Lys Lys Gly Gly Val Arg Cys Ser Met Glu
35 40 45
Thr Lys Gln Gly Asn Val Ser Val Met Gly Ala Gly Val Ser Ala Ala
50 55 60
Ala Thr Ala Ala Leu Thr Ala Val Met Ser Asn Pro Ala Met Ala Leu
65 70 75 80
Val Asp Glu Arg Met Ser Thr Glu Gly Thr Gly Leu Pro Phe Gly Leu
85 90 95
Ser Asn Asn Leu Leu Gly Trp Ile Leu Phe Gly Val Phe Gly Leu Ile
100 105 110
Trp Thr Phe Phe Phe Val Tyr Thr Ser Ser Leu Glu Glu Asp Glu Glu
115 120 125
Ser Gly Leu Ser Leu
130

(2) INFORMATION FOR SEQ ID NO:1597:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 98 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..98

(D) OTHER INFORMATION: / Ceres Seq. ID 1570476

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1597:

Met Gly Lys Lys Lys Gly Gly Val Arg Cys Ser Met Glu Thr Lys Gln
1 5 10 15
Gly Asn Val Ser Val Met Gly Ala Gly Val Ser Ala Ala Ala Thr Ala
20 25 30
Ala Leu Thr Ala Val Met Ser Asn Pro Ala Met Ala Leu Val Asp Glu
35 40 45
Arg Met Ser Thr Glu Gly Thr Gly Leu Pro Phe Gly Leu Ser Asn Asn
50 55 60
Leu Leu Gly Trp Ile Leu Phe Gly Val Phe Gly Leu Ile Trp Thr Phe
65 70 75 80
Phe Phe Val Tyr Thr Ser Ser Leu Glu Glu Asp Glu Glu Ser Gly Leu

85

90

95

Ser Leu

(2) INFORMATION FOR SEQ ID NO:1598:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 87 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..87

(D) OTHER INFORMATION: / Ceres Seq. ID 1570477

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1598:

Met	Glu	Thr	Lys	Gln	Gly	Asn	Val	Ser	Val	Met	Gly	Ala	Gly	Val	Ser
1			5					10					15		
Ala	Ala	Ala	Thr	Ala	Ala	Leu	Thr	Ala	Val	Met	Ser	Asn	Pro	Ala	Met
			20					25					30		
Ala	Leu	Val	Asp	Glu	Arg	Met	Ser	Thr	Glu	Gly	Thr	Gly	Leu	Pro	Phe
		35					40					45			
Gly	Leu	Ser	Asn	Asn	Leu	Leu	Gly	Trp	Ile	Leu	Phe	Gly	Val	Phe	Gly
		50				55					60				
Leu	Ile	Trp	Thr	Phe	Phe	Phe	Val	Tyr	Thr	Ser	Ser	Leu	Glu	Glu	Asp
		65				70				75				80	
Glu	Glu	Ser	Gly	Leu	Ser	Leu									
						85									

(2) INFORMATION FOR SEQ ID NO:1599:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 782 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..782

(D) OTHER INFORMATION: / Ceres Seq. ID 1570478

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1599:

taaaggaggc	tactctagtc	acattgttgt	tcatgaaagg	tactgtctaca	agataccctgt	60
ggactatccc	ttggaatcag	ctgcaccatt	actctgtgct	ggaatcacgg	tttatgcacc	120
tatgatcgct	cacaatatga	atcaacctgg	taaatctctt	ggggtgatcg	ggctaggtgg	180
tcttgagcac	atggcgcgtta	agttgttgca	ggcttttgga	cttagtgtta	cggtttttag	240
caccagcatt	tccaagaaga	aagaagcttt	gaatctgcta	ggagctgaga	atttcggtat	300
ctcatctgac	catgaccaga	tgaaggcact	agagaaatct	ctagactttc	tagttgacac	360
agcatctggg	gatcacgcgt	tgtatcctta	catgtctctc	ttgaagattg	ctggaactta	420
tgtattgggt	ggtttcccaa	gtgaaattaa	aatcagtcct	gccaatctca	atcttggtat	480
gagaatgctc	gctggaagcg	taaccggggg	gaccaaaata	acacagcaaa	tggttagattt	540
ctgtgcagct	cataagattt	atccaaacat	agaggtgatt	cccatctcaa	agataaacga	600
agctctcgaa	agagttagta	agaaggacat	caagtaccgt	ttcgtgattg	acatcaagaa	660
ctccctcaaa	tagatgttgc	tcaaaggaga	gaataatgga	gtctgtataa	agagaataat	720
actcactgtc	acaaatttta	ttacgtattt	tctcgTtttt	bcattagtaa	agcaataata	780
tt						

(2) INFORMATION FOR SEQ ID NO:1600:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 223 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1..223
(D) OTHER INFORMATION: / Ceres Seq. ID 1570479

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1600:

Lys Gly Gly Tyr Ser Ser His Ile Val Val His Glu Arg Tyr Cys Tyr
1 5 10 15
Lys Ile Pro Val Asp Tyr Pro Leu Glu Ser Ala Ala Pro Leu Leu Cys
20 25 30
Ala Gly Ile Thr Val Tyr Ala Pro Met Met Arg His Asn Met Asn Gln
35 40 45
Pro Gly Lys Ser Leu Gly Val Ile Gly Leu Gly Gly Leu Gly His Met
50 55 60
Ala Val Lys Phe Gly Lys Ala Phe Gly Leu Ser Val Thr Val Phe Ser
65 70 75 80
Thr Ser Ile Ser Lys Lys Glu Glu Ala Leu Asn Leu Leu Gly Ala Glu
85 90 95
Asn Phe Val Ile Ser Ser Asp His Asp Gln Met Lys Ala Leu Glu Lys
100 105 110
Ser Leu Asp Phe Leu Val Asp Thr Ala Ser Gly Asp His Ala Phe Asp
115 120 125
Pro Tyr Met Ser Leu Leu Lys Ile Ala Gly Thr Tyr Val Leu Val Gly
130 135 140
Phe Pro Ser Glu Ile Lys Ile Ser Pro Ala Asn Leu Asn Leu Gly Met
145 150 155 160
Arg Met Leu Ala Gly Ser Val Thr Gly Gly Thr Lys Ile Thr Gln Gln
165 170 175
Met Leu Asp Phe Cys Ala Ala His Lys Ile Tyr Pro Asn Ile Glu Val
180 185 190
Ile Pro Ile Gln Lys Ile Asn Glu Ala Leu Glu Arg Val Val Lys Lys
195 200 205
Asp Ile Lys Tyr Arg Phe Val Ile Asp Ile Lys Asn Ser Leu Lys
210 215 220

(2) INFORMATION FOR SEQ ID NO:1601:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 183 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1..183
(D) OTHER INFORMATION: / Ceres Seq. ID 1570480

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1601:

Met Met Arg His Asn Met Asn Gln Pro Gly Lys Ser Leu Gly Val Ile
1 5 10 15
Gly Leu Gly Gly Leu Gly His Met Ala Val Lys Phe Gly Lys Ala Phe
20 25 30
Gly Leu Ser Val Thr Val Phe Ser Thr Ser Ile Ser Lys Lys Glu Glu
35 40 45
Ala Leu Asn Leu Leu Gly Ala Glu Asn Phe Val Ile Ser Ser Asp His
50 55 60
Asp Gln Met Lys Ala Leu Glu Lys Ser Leu Asp Phe Leu Val Asp Thr
65 70 75 80
Ala Ser Gly Asp His Ala Phe Asp Pro Tyr Met Ser Leu Leu Lys Ile
85 90 95
Ala Gly Thr Tyr Val Leu Val Gly Phe Pro Ser Glu Ile Lys Ile Ser
100 105 110
Pro Ala Asn Leu Asn Leu Gly Met Arg Met Leu Ala Gly Ser Val Thr
115 120 125
Gly Gly Thr Lys Lys Ile Thr Gln Gln Met Leu Asp Phe Cys Ala Ala His

130 135 140
Lys Ile Tyr Pro Asn Ile Glu Val Ile Pro Ile Gln Lys Ile Asn Glu
145 150 155 160
Ala Leu Glu Arg Val Val Lys Lys Asp Ile Lys Tyr Arg Phe Val Ile
165 170 175
Asp Ile Lys Asn Ser Leu Lys
180

(2) INFORMATION FOR SEQ ID NO:1602:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 182 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..182
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570481

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1602:

Met Arg His Asn Met Asn Gln Pro Gly Lys Ser Leu Gly Val Ile Gly
1 5 10 15
Leu Gly Gly Leu Gly His Met Ala Val Lys Phe Gly Lys Ala Phe Gly
20 25 30
Leu Ser Val Thr Val Phe Ser Thr Ser Ile Ser Lys Lys Glu Glu Ala
35 40 45
Leu Asn Leu Leu Gly Ala Glu Asn Phe Val Ile Ser Ser Asp His Asp
50 55 60
Gln Met Lys Ala Leu Glu Lys Ser Leu Asp Phe Leu Val Asp Thr Ala
65 70 75 80
Ser Gly Asp His Ala Phe Asp Pro Tyr Met Ser Leu Leu Lys Ile Ala
85 90 95
Gly Thr Tyr Val Leu Val Gly Phe Pro Ser Glu Ile Lys Ile Ser Pro
100 105 110
Ala Asn Leu Asn Leu Gly Met Arg Met Leu Ala Gly Ser Val Thr Gly
115 120 125
Gly Thr Lys Ile Thr Gln Gln Met Leu Asp Phe Cys Ala Ala His Lys
130 135 140
Ile Tyr Pro Asn Ile Glu Val Ile Pro Ile Gln Lys Ile Asn Glu Ala
145 150 155 160
Leu Glu Arg Val Val Lys Lys Asp Ile Lys Tyr Arg Phe Val Ile Asp
165 170 175
Ile Lys Asn Ser Leu Lys
180

(2) INFORMATION FOR SEQ ID NO:1603:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 990 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..990
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570485

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1603:

agagctcttta	accggcgaaa	gaaaccaccc	tctgactgtt	aagaaaattc	tcacgcggct	60
ttagatcaga	aacttgggaa	tcggagaagc	tcactgagaa	caatggatat	gagacgtgct	120
tcgatgtgta	tgatgttaat	ttgcgtctcc	ttggtctccc	tttcgggttt	tgccagttt	180
gtgatcttca	gtgaagaaaa	aggaacgtac	aacgacaacg	tCgtaaatg	gaagcttggt	240
ggatttagcg	attccaagaa	cgattggaac	ggtggaanaa	agatcgatga	tattgcactc	300
ttcgctgttc	aagagcacaa	cagacgagag	aatgctgttc	ttgacgttgc	tagatattgt	360

aaggcaacag	agcagggtgt	tgctggcaag	ctataccgct	ttactcttga	agttattgaa	420
gctggtgaga	aaaagattta	tgaagctaaa	gtttgggtga	agCaatggat	gaactttaag	480
cagcttcaag	agttcaagaa	tattatcccc	tccttcaact	tctctgacct	tggtttcaaa	540
ccagatggca	atggatttga	ctggagatca	gtatcaacaa	ataaccctga	agccaagaa	600
gcagcgaagc	acggcatgaa	atcacttcaa	cagaaatcaa	actcactgtt	ccctataaaa	660
ctcatagata	taattcctagc	caggggcaag	gtggttgaag	agcgtgtgaa	attcgaacctg	720
ctgctgaagc	tagagagggg	caacaaactg	gagaagtcca	tggtagaagt	gatgaagatg	780
caaacccgca	agtatgagta	gaagttgcag	atagcttttg	gggtgtgtgc	catgtgtgaa	840
tggatccctt	atagtatata	gtataactaa	tactgctatg	tagtgaaaaa	aaacatggtg	900
attgtttggc	tttaaacaag	gtttcttgta	aataaatata	tgacttcaca	tatgtaaaaa	960
ttacaaatat	gatatgatta	tgctgtgttg				

(2) INFORMATION FOR SEQ ID NO:1604:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 232 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..232

(D) OTHER INFORMATION: / Ceres Seq. ID 1570486

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1604:

Met	Asp	Met	Arg	Arg	Ala	Ser	Met	Cys	Met	Met	Leu	Ile	Cys	Val	Ser
1			5					10					15		
Leu	Val	Leu	Leu	Ser	Gly	Phe	Gly	Gln	Phe	Val	Ile	Cys	Ser	Glu	Glu
			20					25				30			
Lys	Gly	Thr	Tyr	Asn	Asp	Asn	Val	Val	Lys	Met	Lys	Leu	Gly	Gly	Phe
			35				40					45			
Ser	Asp	Ser	Lys	Asn	Asp	Trp	Asn	Gly	Gly	Lys	Glu	Ile	Asp	Asp	Ile
			50				55				60				
Ala	Leu	Phe	Ala	Val	Gln	Glu	His	Asn	Arg	Arg	Glu	Asn	Ala	Val	Leu
			65				70				75			80	
Glu	Leu	Ala	Arg	Val	Leu	Lys	Ala	Thr	Glu	Gln	Val	Val	Ala	Gly	Lys
			85					90						95	
Leu	Tyr	Arg	Leu	Thr	Leu	Glu	Val	Ile	Glu	Ala	Gly	Glu	Lys	Lys	Ile
			100					105					110		
Tyr	Glu	Ala	Lys	Val	Trp	Val	Lys	Pro	Trp	Met	Asn	Phe	Lys	Gln	Leu
			115				120						125		
Gln	Glu	Phe	Lys	Asn	Ile	Ile	Pro	Ser	Phe	Thr	Ile	Ser	Asp	Leu	Gly
			130				135						140		
Phe	Lys	Pro	Asp	Gly	Asn	Gly	Phe	Asp	Trp	Arg	Ser	Val	Ser	Thr	Asn
			145				150				155			160	
Asn	Pro	Glu	Val	Gln	Glu	Ala	Ala	Lys	His	Ala	Met	Lys	Ser	Leu	Gln
			165					170						175	
Gln	Lys	Ser	Asn	Ser	Leu	Phe	Pro	Tyr	Lys	Leu	Ile	Asp	Ile	Ile	Leu
			180					185						190	
Ala	Arg	Ala	Lys	Val	Val	Glu	Glu	Arg	Val	Lys	Phe	Glu	Leu	Leu	Leu
			195				200						205		
Lys	Leu	Glu	Arg	Gly	Asn	Lys	Leu	Glu	Lys	Phe	Met	Val	Glu	Val	Met
			210				215				220				
Lys	Asp	Gln	Thr	Gly	Lys	Tyr	Glu								
			225				230								

(2) INFORMATION FOR SEQ ID NO:1605:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 230 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..230

(D) OTHER INFORMATION: / Ceres Seq. ID 1570487

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1605:

Met Arg Arg Ala Ser Met Cys Met Met Leu Ile Cys Val Ser Leu Val
1 5 10 15
Leu Leu Ser Gly Phe Gly Gln Phe Val Ile Cys Ser Glu Glu Lys Gly
20 25 30
Thr Tyr Asn Asp Asn Val Val Lys Met Lys Leu Gly Gly Phe Ser Asp
35 40 45
Ser Lys Asn Asp Trp Asn Gly Gly Lys Glu Ile Asp Asp Ile Ala Leu
50 55 60
Phe Ala Val Gln Glu His Asn Arg Arg Glu Asn Ala Val Leu Glu Leu
65 70 75 80
Ala Arg Val Leu Lys Ala Thr Glu Gln Val Val Ala Gly Lys Leu Tyr
85 90 95
Arg Leu Thr Leu Glu Val Ile Glu Ala Gly Glu Lys Lys Ile Tyr Glu
100 105 110
Ala Lys Val Trp Val Lys Pro Trp Met Asn Phe Lys Gln Leu Gln Glu
115 120 125
Phe Lys Asn Ile Ile Pro Ser Phe Thr Ile Ser Asp Leu Gly Phe Lys
130 135 140
Pro Asp Gly Asn Gly Phe Asp Trp Arg Ser Val Ser Thr Asn Asn Pro
145 150 155 160
Glu Val Gln Glu Ala Ala Lys His Ala Met Lys Ser Leu Gln Gln Lys
165 170 175
Ser Asn Ser Leu Phe Pro Tyr Lys Leu Ile Asp Ile Ile Leu Ala Arg
180 185 190
Ala Lys Val Val Glu Glu Arg Val Lys Phe Glu Leu Leu Lys Leu
195 200 205
Glu Arg Gly Asn Lys Leu Glu Lys Phe Met Val Glu Val Met Lys Asp
210 215 220
Gln Thr Gly Lys Tyr Glu
225 230

(2) INFORMATION FOR SEQ ID NO:1606:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 225 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..225

(D) OTHER INFORMATION: / Ceres Seq. ID 1570488

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1606:

Met Cys Met Met Leu Ile Cys Val Ser Leu Val Leu Leu Ser Gly Phe
1 5 10 15
Gly Gln Phe Val Ile Cys Ser Glu Glu Lys Gly Thr Tyr Asn Asp Asn
20 25 30
Val Val Lys Met Lys Leu Gly Gly Phe Ser Asp Ser Lys Asn Asp Trp
35 40 45
Asn Gly Gly Lys Glu Ile Asp Asp Ile Ala Leu Phe Ala Val Gln Glu
50 55 60
His Asn Arg Arg Glu Asn Ala Val Leu Glu Leu Ala Arg Val Leu Lys
65 70 75 80
Ala Thr Glu Gln Val Val Ala Gly Lys Leu Tyr Arg Leu Thr Leu Glu
85 90 95
Val Ile Glu Ala Gly Glu Lys Lys Ile Tyr Glu Ala Lys Val Trp Val
100 105 110
Lys Pro Trp Met Asn Phe Lys Gln Leu Gln Glu Phe Lys Asn Ile Ile

115	120	125
Pro Ser Phe Thr Ile Ser Asp Leu Gly Phe Lys	Pro Asp Gly Asn Gly	
130	135	140
Phe Asp Trp Arg Ser Val Ser Thr Asn Asn Pro	Glu Val Gln Glu Ala	
145	150	155
Ala Lys His Ala Met Lys Ser Leu Gln Gln Lys	Ser Asn Ser Leu Phe	
165	170	175
Pro Tyr Lys Leu Ile Asp Ile Ile Leu Ala Arg	Ala Lys Val Val Glu	
180	185	190
Glu Arg Val Lys Phe Glu Leu Leu Leu Lys Leu	Glu Arg Gly Asn Lys	
195	200	205
Leu Glu Lys Phe Met Val Glu Val Met Lys Asp	Gln Thr Gly Lys Tyr	
210	215	220

Glu
225

(2) INFORMATION FOR SEQ ID NO:1607:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 799 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..799
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570489

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1607:

aagcatcaact	atgctcgaaa	atctctcttt	gttcgctttg	tggggaacga	actatggccg	60
agagatggag	gaacacggct	ctactcgta	tcgacatgca	gaacgatttc	atagaggaa	120
gtgctgtgac	gcaagtga	ggaggaaa	ctatagtctc	taatgttacc	agagtcgtcg	180
aactcgcgag	gcagcgtggt	attctcgtaa	tttggtgtgt	tcgagaacat	gatcgtcaag	240
gaagagatgt	tgaattattc	aggcgccata	actacagttc	tgagaaaagtc	gggcagtgta	300
ttaaaggcac	cgtagGagca	gaattggttg	atggattgat	gatcaacgaa	gaagatgat	360
ataagattgt	gaaaactcgt	ttcagtgctt	tctttagtac	taattctcat	tccttctgtc	420
aaacttcagg	ggttaccagg	ttagtgattg	ctgggtgtgca	aacgcgcgaac	tgtatccggc	480
aaacggtgtt	tgtatgcagt	gcgctggatt	atccCaatgt	gactgttatt	acagatgcc	540
cagctgtctg	aacaccagag	atccatactg	cgaatattct	tgacatgaag	aattatggag	600
tcaaaactcc	tacattacac	gagtggtccg	aagaacttgc	ttgacaaa	ccatcctaaa	660
gcccttcgtt	tatctttttc	cttggttgta	catgtaataa	agaaaatggt	aattctgtgt	720
ttgtaagtta	caaaatctcc	accatttggt	gtatactttt	cttgtaattcc	cgtccaaaaa	780
aataaaatgt	attacgtttt					

(2) INFORMATION FOR SEQ ID NO:1608:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 213 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..213
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570490

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1608:

Ala Ser Leu Cys Ser Lys Ile Ser Leu Cys Ser Leu Cys Gly Glu Arg	
1	10
Thr Met Ala Glu Arg Trp Arg Asn Thr Ala Leu Leu Val Ile Asp Met	
20	30
Gln Asn Asp Phe Ile Glu Glu Gly Ala Val Thr Gln Val Lys Gly Gly	
35	45
Lys Ser Ile Val Pro Asn Val Ile Arg Val Val Glu Leu Ala Arg Gln	
50	60

Arg Gly Ile Leu Val Ile Trp Val Val Arg Glu His Asp Arg Gln Gly
65 70 75 80
Arg Asp Val Glu Leu Phe Arg Arg His Asn Tyr Ser Ser Glu Lys Val
85 90 95
Gly Pro Val Ile Lys Gly Thr Val Gly Ala Glu Leu Val Asp Gly Leu
100 105 110
Met Ile Asn Glu Glu Asp Asp Tyr Lys Ile Val Lys Thr Arg Phe Ser
115 120 125
Ala Phe Phe Ser Thr Asn Leu His Ser Phe Leu Gln Thr Ser Gly Val
130 135 140
Thr Lys Leu Val Ile Ala Gly Val Gln Thr Pro Asn Cys Ile Arg Gln
145 150 155 160
Thr Val Phe Asp Ala Val Ala Leu Asp Tyr Pro Asn Val Thr Val Ile
165 170 175
Thr Asp Ala Thr Ala Ala Thr Pro Glu Ile His Thr Ala Asn Ile
180 185 190
Leu Asp Met Lys Asn Ile Gly Val Lys Thr Pro Thr Leu His Glu Trp
195 200 205
Ser Glu Glu Leu Ala
210

(2) INFORMATION FOR SEQ ID NO:1609:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 196 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..196

(D) OTHER INFORMATION: / Ceres Seq. ID 1570491

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1609:

Met Ala Glu Arg Trp Arg Asn Thr Ala Leu Leu Val Ile Asp Met Gln
1 5 10
Asn Asp Phe Ile Glu Glu Gly Ala Val Thr Gln Val Lys Gly Gly Lys
20 25 30
Ser Ile Val Pro Asn Val Ile Arg Val Val Glu Leu Ala Arg Gln Arg
35 40 45
Gly Ile Leu Val Ile Trp Val Val Arg Glu His Asp Arg Gln Gly Arg
50 55 60
Asp Val Glu Leu Phe Arg Arg His Asn Tyr Ser Ser Glu Lys Val Gly
65 70 75 80
Pro Val Ile Lys Gly Thr Val Gly Ala Glu Leu Val Asp Gly Leu Met
85 90 95
Ile Asn Glu Glu Asp Asp Tyr Lys Ile Val Lys Thr Arg Phe Ser Ala
100 105 110
Phe Phe Ser Thr Asn Leu His Ser Phe Leu Gln Thr Ser Gly Val Thr
115 120 125
Lys Leu Val Ile Ala Gly Val Gln Thr Pro Asn Cys Ile Arg Gln Thr
130 135 140
Val Phe Asp Ala Val Ala Leu Asp Tyr Pro Asn Val Thr Val Ile Thr
145 150 155 160
Asp Ala Thr Ala Ala Ala Thr Pro Glu Ile His Thr Ala Asn Ile Leu
165 170 175
Asp Met Lys Asn Ile Gly Val Lys Thr Pro Thr Leu His Glu Trp Ser
180 185 190
Glu Glu Leu Ala
195

(2) INFORMATION FOR SEQ ID NO:1610:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 182 amino acids

(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..182
 (D) OTHER INFORMATION: / Ceres Seq. ID 1570492
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1610:
Met Gln Asn Asp Phe Ile Glu Glu Gly Ala Val Thr Gln Val Lys Gly
1 5 10 15
Gly Lys Ser Ile Val Pro Asn Val Ile Arg Val Val Glu Leu Ala Arg
 20 25 30
Gln Arg Gly Ile Leu Val Ile Trp Val Val Arg Glu His Asp Arg Gln
 35 40 45
Gly Arg Asp Val Glu Leu Phe Arg Arg His Asn Tyr Ser Ser Glu Lys
 50 55 60
Val Gly Pro Val Ile Lys Gly Thr Val Gly Ala Glu Leu Val Asp Gly
65 70 75 80
Leu Met Ile Asn Glu Glu Asp Asp Tyr Lys Ile Val Lys Thr Arg Phe
 85 90 95
Ser Ala Phe Phe Ser Thr Asn Leu His Ser Phe Leu Gln Thr Ser Gly
 100 105 110
Val Thr Lys Leu Val Ile Ala Gly Val Gln Thr Pro Asn Cys Ile Arg
 115 120 125
Gln Thr Val Phe Asp Ala Val Ala Leu Asp Tyr Pro Asn Val Thr Val
 130 135 140
Ile Thr Asp Ala Thr Ala Ala Ala Thr Pro Glu Ile His Thr Ala Asn
145 150 155 160
Ile Leu Asp Met Lys Asn Ile Gly Val Lys Thr Pro Thr Leu His Glu
 165 170 175
Trp Ser Glu Glu Leu Ala
 180

(2) INFORMATION FOR SEQ ID NO:1611:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 642 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..642
(D) OTHER INFORMATION: / Ceres Seq. ID 1570493

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1611:

atcattcaaca atggcatatg caactattct catgatcttc tcgggtggtgg cactaatgtc 60
cggcgagaga gctcatgcag cagtggactg ctcatggtg atactaaaca tggcgtgatt 120
tttgtctttt gtgactagtg gtagtacagt tgtcaaagcg gaaggaaacat gttgttcagg 180
gcttaagact gtggttagga caggaccaga atgtctatgt gaggctttca agaacagtgg 240
ttctcttggt ttaactcttg atctttctaa agctgottct ctccctttctg ttgtgaaagt 300
tgctgtctct cctctgtctc gtttgtgccc ttctgtctct ggagatcttc ctgctactgc 360
ccctggttta tctcCtaagg ccggagcagg agcaaccgag ttgtccagtg gtgcaaatgc 420
ggcaactcca gtttctgtcc cgaggagttc cgaatcgctc ttgctctctg tatcttttgc 480
atttgtctac ttcattggcac ctattctctc ttctattga gtcttaaaat ttaattgtctw 540
cttgttgagt tatttttgtt tgetatgtag ctgaagagtt tgggtgttact gatcatattt 600
acctttcatg tgtaaatatt aatgagaaat ctcttttag tt

(2) INFORMATION FOR SEQ ID NO:1612:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 172 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:

(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..172
 (D) OTHER INFORMATION: / Ceres Seq. ID 1570494
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1612:
Ser Phe Thr Met Ala Tyr Ala Thr Ile Leu Met Ile Phe Ser Val Val
1 5 10 15
Ala Leu Met Ser Gly Glu Arg Ala His Ala Ala Val Asp Cys Ser Ser
 20 25 30
Leu Ile Leu Asn Met Ala Asp Cys Leu Ser Phe Val Thr Ser Gly Ser
 35 40 45
Thr Val Val Lys Pro Glu Gly Thr Cys Cys Ser Gly Leu Lys Thr Val
 50 55 60
Val Arg Thr Gly Pro Glu Cys Leu Cys Glu Ala Phe Lys Asn Ser Gly
65 70 75 80
Ser Leu Gly Leu Thr Leu Asp Leu Ser Lys Ala Ala Ser Leu Pro Ser
 85 90 95
Val Cys Lys Val Ala Ala Pro Pro Ser Ala Arg Cys Gly Leu Ser Val
 100 105 110
Ser Gly Asp Pro Pro Ala Thr Ala Pro Gly Leu Ser Pro Thr Ala Gly
 115 120 125
Ala Gly Ala Pro Ala Leu Ser Ser Gly Ala Asn Ala Ala Thr Pro Val
 130 135 140
Ser Ser Pro Arg Ser Ser Asp Ala Ser Leu Leu Ser Val Ser Phe Ala
145 150 155 160
Phe Val Ile Phe Met Ala Leu Ile Ser Ser Phe Tyr
 165 170
(2) INFORMATION FOR SEQ ID NO:1613:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 169 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..169
 (D) OTHER INFORMATION: / Ceres Seq. ID 1570495
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1613:
Met Ala Tyr Ala Thr Ile Leu Met Ile Phe Ser Val Val Ala Leu Met
1 5 10 15
Ser Gly Glu Arg Ala His Ala Ala Val Asp Cys Ser Ser Leu Ile Leu
 20 25 30
Asn Met Ala Asp Cys Leu Ser Phe Val Thr Ser Gly Ser Thr Val Val
 35 40 45
Lys Pro Glu Gly Thr Cys Cys Ser Gly Leu Lys Thr Val Val Arg Thr
50 55 60
Gly Pro Glu Cys Leu Cys Glu Ala Phe Lys Asn Ser Gly Ser Leu Gly
65 70 75 80
Leu Thr Leu Asp Leu Ser Lys Ala Ala Ser Leu Pro Ser Val Cys Lys
 85 90 95
Val Ala Ala Pro Pro Ser Ala Arg Cys Gly Leu Ser Val Ser Gly Asp
 100 105 110
Pro Pro Ala Thr Ala Pro Gly Leu Ser Pro Thr Ala Gly Ala Gly Ala
 115 120 125
Pro Ala Leu Ser Ser Gly Ala Asn Ala Ala Thr Pro Val Ser Ser Pro
130 135 140
Arg Ser Ser Asp Ala Ser Leu Leu Ser Val Ser Phe Ala Phe Val Ile
145 150 155 160

Phe Met Ala Leu Ile Ser Ser Phe Tyr
165

(2) INFORMATION FOR SEQ ID NO:1614:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 162 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..162
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570496

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1614:

Met	Ile	Phe	Ser	Val	Val	Ala	Leu	Met	Ser	Gly	Glu	Arg	Ala	His	Ala
1			5					10			15				
Ala	Val	Asp	Cys	Ser	Ser	Leu	Ile	Leu	Asn	Met	Ala	Asp	Cys	Leu	Ser
		20					25				30				
Phe	Val	Thr	Ser	Gly	Ser	Thr	Val	Val	Lys	Pro	Glu	Gly	Thr	Cys	Cys
		35				40					45				
Ser	Gly	Leu	Lys	Thr	Val	Val	Arg	Thr	Gly	Pro	Glu	Cys	Leu	Cys	Glu
	50				55				60						
Ala	Phe	Lys	Asn	Ser	Gly	Ser	Leu	Gly	Leu	Thr	Leu	Asp	Leu	Ser	Lys
	65		70					75						80	
Ala	Ala	Ser	Leu	Pro	Ser	Val	Cys	Lys	Val	Ala	Ala	Pro	Pro	Ser	Ala
			85					90						95	
Arg	Cys	Gly	Leu	Ser	Val	Ser	Gly	Asp	Pro	Pro	Ala	Thr	Ala	Pro	Gly
			100					105						110	
Leu	Ser	Pro	Thr	Ala	Gly	Ala	Gly	Ala	Pro	Ala	Leu	Ser	Ser	Gly	Ala
			115				120							125	
Asn	Ala	Ala	Thr	Pro	Val	Ser	Ser	Pro	Arg	Ser	Ser	Asp	Ala	Ser	Leu
	130					135					140				
Leu	Ser	Val	Ser	Phe	Ala	Phe	Val	Ile	Phe	Met	Ala	Leu	Ile	Ser	Ser
	145				150				155					160	
Phe	Tyr														

(2) INFORMATION FOR SEQ ID NO:1615:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 863 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..863
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570497

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1615:

ttttggctgc	acgatctcag	tttttcagat	caatgtttta	caatactcta	gcagagaaca	60
acagcgacgt	aGtgcacgc	gatttggaa	ctaaggtttt	caaggccttg	ttacacttca	120
tgtataaaga	ttccctccca	ggagatgtg	aaccattaac	ggctcatcca	tttgacctat	180
taaggccgtc	cgaaatagat	gataactga	ttgtaaagct	tctggcagct	gcggaatgt	240
acaactctgag	taggtctcaga	ttattgtgtg	aatctcacat	ctgcaaaaggc	atatctatca	300
gctccgtgtc	caagatctta	gctttatccg	acaaatataa	tgcattccgaa	ctaaaaagcg	360
tttccctaaa	attcactgca	gaaaacctag	cagctgttct	gcagacaaaa	gcataatgaag	420
attctgaagga	tgactgtcca	aacctccagt	ctgagctact	aaaggcggtc	gcgtgttatg	480
acgacacaag	tagcagcgga	ggaggaaagt	ctcagagtgt	ttgggtctcaa	ctctctaacg	540
gtgggtgagac	cagtagccga	agggtcaggc	agcgaaccac	ttagaagagc	ttcttccact	600
gtgtttaaaca	aactactttt	gcttaccact	cgtaaaacaga	ttaacgggtt	tatctagtat	660
gtaccgaatg	aaagggaagc	ggagccagaa	attctgtacc	acaagagaag	agctatgcgg	720
ctgtgcacta	gtgattaacc	ggtgcttcac	ctttcagttc	cttcacgtct	ctgtggatttt	780

ttgtgtgtga gtctttttttt caaattctttt tcccagcttc aaattactag aaacttatga 840

tgatataata gaaagagtta act

(2) INFORMATION FOR SEQ ID NO:1616:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 193 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..193
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570498

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1616:

```
Leu Ala Ala Arg Ser Gln Phe Phe Arg Ser Met Phe Tyr Asn Thr Leu
1      5      10      15
Ala Glu Asn Asn Ser Asp Val Val Ile Ser Asp Leu Glu Pro Lys Val
20      25      30
Phe Lys Ala Leu Leu His Phe Met Tyr Lys Asp Ser Leu Pro Gly Asp
35      40      45
Val Glu Pro Leu Thr Ala His Ser Phe Asp Leu Leu Arg Pro Ser Glu
50      55      60
Ile Asp Asp Thr Leu Ile Val Lys Leu Ala Ala Glu Met Tyr
65      70      75      80
Asn Leu Ser Arg Leu Arg Leu Leu Cys Glu Ser His Ile Cys Lys Gly
85      90      95
Ile Ser Ile Ser Ser Val Ser Lys Ile Leu Ala Leu Ser Asp Lys Tyr
100      105      110
Asn Ala Ser Glu Leu Lys Ser Val Ser Leu Lys Phe Thr Ala Glu Asn
115      120      125
Leu Ala Ala Val Leu Gln Thr Lys Ala Tyr Glu Asp Leu Lys Asp Asp
130      135      140
Cys Pro Asn Leu Gln Ser Glu Leu Leu Lys Ala Val Ala Gly Tyr Asp
145      150      155      160
Asp Thr Ser Ser Ser Gly Gly Gly Lys Ser Gln Ser Val Trp Ala Gln
165      170      175
Leu Ser Asn Gly Gly Glu Thr Ser Ser Arg Arg Val Arg Gln Arg Thr
180      185      190
Thr
```

(2) INFORMATION FOR SEQ ID NO:1617:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 183 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..183
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570499

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1617:

```
Met Phe Tyr Asn Thr Leu Ala Glu Asn Asn Ser Asp Val Val Ile Ser
1      5      10      15
Asp Leu Glu Pro Lys Val Phe Lys Ala Leu Leu His Phe Met Tyr Lys
20      25      30
Asp Ser Leu Pro Gly Asp Val Glu Pro Leu Thr Ala His Ser Phe Asp
35      40      45
Leu Leu Arg Pro Ser Glu Ile Asp Asp Thr Leu Ile Val Lys Leu Leu
50      55      60
Ala Ala Ala Glu Met Tyr Asn Leu Ser Arg Leu Arg Leu Leu Cys Glu
```

65				70				75				80
Ser	His	Ile	Cys	Lys	Gly	Ile	Ser	Ile	Ser	Val	Ser	Lys
				85					90			95
Ala	Leu	Ser	Asp	Lys	Tyr	Asn	Ala	Ser	Glu	Leu	Lys	Ser
				100					105			110
Lys	Phe	Thr	Ala	Glu	Asn	Leu	Ala	Val	Leu	Gln	Thr	Lys
				115					120			125
Glu	Asp	Leu	Lys	Asp	Asp	Cys	Pro	Asn	Leu	Gln	Ser	Glu
				130					135			140
Ala	Val	Ala	Gly	Tyr	Asp	Asp	Thr	Ser	Ser	Ser	Gly	Gly
				145					150			155
Gln	Ser	Val	Trp	Ala	Gln	Leu	Ser	Asn	Gly	Gly	Glu	Thr
				160					165			170
Arg	Val	Arg	Gln	Arg	Thr	Thr						175
				180								

(2) INFORMATION FOR SEQ ID NO:1618:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 154 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..154

(D) OTHER INFORMATION: / Ceres Seq. ID 1570500

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1618:

Met	Tyr	Lys	Asp	Ser	Leu	Pro	Gly	Asp	Val	Glu	Pro	Leu	Thr	Ala	His
1															
Ser	Phe	Asp	Leu	Leu	Arg	Pro	Ser	Glu	Ile	Asp	Asp	Thr	Leu	Ile	Val
Lys	Leu	Leu	Ala	Ala	Ala	Glu	Met	Tyr	Asn	Leu	Ser	Arg	Leu	Arg	Leu
Leu	Cys	Glu	Ser	His	Ile	Cys	Lys	Gly	Ile	Ser	Ile	Ser	Ser	Val	Ser
Lys	Ile	Leu	Ala	Leu	Ser	Asp	Lys	Tyr	Asn	Ala	Ser	Glu	Leu	Lys	Ser
Val	Ser	Leu	Lys	Phe	Thr	Ala	Glu	Asn	Leu	Ala	Ala	Val	Leu	Gln	Thr
Lys	Ala	Tyr	Glu	Asp	Leu	Lys	Asp	Asp	Cys	Pro	Asn	Leu	Gln	Ser	Glu
Leu	Leu	Lys	Ala	Val	Ala	Gly	Tyr	Asp	Asp	Thr	Ser	Ser	Ser	Gly	Gly
Gly	Lys	Ser	Gln	Ser	Val	Trp	Ala	Gln	Leu	Ser	Asn	Gly	Gly	Glu	Thr
Ser	Ser	Arg	Arg	Val	Arg	Gln	Arg	Thr	Thr						

(2) INFORMATION FOR SEQ ID NO:1619:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1002 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1002
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570501

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1619:

attcaatttt	tgttggtctt	ttcaaaagt	gaaatacaac	aaaacaatgt	cgggacttag	60
aagattggat	ggcaagatcg	caattataac	aggcggagct	agtgggattg	gagctgaagc	120

ggttaggttg	ttcacggacc	atggagctaa	agtggctcatc	gtggacatac	aagaagagct	180
tgcccaaaac	ctcgccgttt	cgatagggct	agacaaaagca	agttttttacc	gttgtaagt	240
aaccgacgag	acggatgtcg	agaacgcgct	taagtctcacc	gttgaaaaac	acggaagct	300
tgacgttctg	tttagtaaac	cgggggtctt	ggaagcggtt	ggaagcggttc	ttgatttgga	360
tcttgaggcg	tttgatcgaa	cgatggcggt	taacgtctcg	gggtgcggctg	cgttatacaa	420
acacgcggca	cgttcgatgg	tggctagtgg	tactcgtggc	tccattgtat	gtacgacgag	480
tattcgggca	gagataggtg	gtccggggacc	tcatagttac	acgGcttcta	agcagcgctg	540
tctcgggctg	atccgatcac	cggtgtgctg	actggggcag	tacggtatta	gagtcacagg	600
gtgttcacgc	tatgggggtg	ccactgggat	gactagcgcc	tacaatgagg	aagcgggtgaa	660
gatgcttgaa	gaatattggt	aagccctagg	gaatctcaaa	gggtgtgggtg	ttaaagctcg	720
ccacatcgca	gaagcagctt	tggtttttgc	ttctgatgat	tcggtttata	ttagcgggtca	780
gaatctgggt	gttgatgggt	gttttagcgt	cgtaaagctc	atgagcacgt	gagaaacaac	840
taaaaaatga	gggcatagac	tctcttgaca	ctttcatttt	attctctgaa	taaaaattga	900
atttataagt	actttcgatc	attgtgttgt	atgttaggct	cttgagttta	tataaacctt	960
gagtttaata	attttacttt	tcttttagtt	tctcaattct	at		

(2) INFORMATION FOR SEQ ID NO:1620:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 276 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..276

(D) OTHER INFORMATION: / Ceres Seq. ID 1570502

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1620:

Phe	Asn	Phe	Trp	Trp	Ser	Phe	Gln	Lys	Trp	Lys	Tyr	Asn	Lys	Thr	Met
1			5						10					15	
Ser	Gly	Leu	Arg	Arg	Leu	Asp	Gly	Lys	Ile	Ala	Ile	Ile	Thr	Gly	Gly
			20					25					30		
Ala	Ser	Gly	Ile	Gly	Ala	Glu	Ala	Val	Arg	Leu	Phe	Thr	Asp	His	Gly
			35					40					45		
Ala	Lys	Val	Val	Ile	Val	Asp	Ile	Gln	Glu	Glu	Leu	Gly	Gln	Asn	Leu
			50					55					60		
Ala	Val	Ser	Ile	Gly	Leu	Asp	Lys	Ala	Ser	Phe	Tyr	Arg	Cys	Asn	Val
			65					70					75		
Thr	Asp	Glu	Thr	Asp	Val	Glu	Asn	Ala	Val	Lys	Phe	Thr	Val	Glu	Lys
			85					90					95		
His	Gly	Lys	Leu	Asp	Val	Leu	Phe	Ser	Asn	Ala	Gly	Val	Leu	Glu	Ala
			100					105					110		
Phe	Gly	Ser	Val	Leu	Asp	Leu	Asp	Leu	Glu	Ala	Phe	Asp	Arg	Thr	Met
			115					120					125		
Ala	Val	Asn	Val	Arg	Gly	Ala	Ala	Ala	Phe	Ile	Lys	His	Ala	Ala	Arg
			130					135					140		
Ser	Met	Val	Ala	Ser	Gly	Thr	Arg	Gly	Ser	Ile	Val	Cys	Thr	Thr	Ser
			145					150					155		
Ile	Ala	Ala	Glu	Ile	Gly	Gly	Pro	Gly	Pro	His	Ser	Tyr	Thr	Ala	Ser
			165					170					175		
Lys	His	Ala	Leu	Leu	Gly	Leu	Ile	Arg	Ser	Ala	Cys	Ala	Gly	Leu	Gly
			180					185					190		
Gln	Tyr	Gly	Ile	Arg	Val	Asn	Gly	Val	Ala	Pro	Tyr	Gly	Val	Ala	Thr
			195					200					205		
Gly	Met	Thr	Ser	Ala	Tyr	Asn	Glu	Glu	Ala	Val	Lys	Met	Leu	Glu	Glu
			210					215					220		
Tyr	Gly	Glu	Ala	Leu	Gly	Asn	Leu	Lys	Gly	Val	Val	Leu	Lys	Ala	Arg
			225					230					235		
His	Ile	Ala	Glu	Ala	Ala	Leu	Phe	Leu	Ala	Ser	Asp	Asp	Ser	Val	Tyr
			245					250					255		
Ile	Ser	Gly	Gln	Asn	Leu	Val	Val	Asp	Gly	Gly	Phe	Ser	Val	Val	Lys
			260					265					270		

Leu Met Ser Thr
275

(2) INFORMATION FOR SEQ ID NO:1621:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 261 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..261
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570503

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1621:

Met	Ser	Gly	Leu	Arg	Arg	Leu	Asp	Gly	Lys	Ile	Ala	Ile	Ile	Thr	Gly
1			5					10						15	
Gly	Ala	Ser	Gly	Ile	Gly	Ala	Glu	Ala	Val	Arg	Leu	Phe	Thr	Asp	His
			20				25						30		
Gly	Ala	Lys	Val	Val	Ile	Val	Asp	Ile	Gln	Glu	Glu	Leu	Gly	Gln	Asn
			35				40						45		
Leu	Ala	Val	Ser	Ile	Gly	Leu	Asp	Lys	Ala	Ser	Phe	Tyr	Arg	Cys	Asn
			50				55					60			
Val	Thr	Asp	Glu	Thr	Asp	Val	Glu	Asn	Ala	Val	Lys	Phe	Thr	Val	Glu
			65				70					75			80
Lys	His	Gly	Lys	Leu	Asp	Val	Leu	Phe	Ser	Asn	Ala	Gly	Val	Leu	Glu
			85					90					95		
Ala	Phe	Gly	Ser	Val	Leu	Asp	Leu	Asp	Leu	Glu	Ala	Phe	Asp	Arg	Thr
			100					105					110		
Met	Ala	Val	Asn	Val	Arg	Gly	Ala	Ala	Ala	Phe	Ile	Lys	His	Ala	Ala
			115				120					125			
Arg	Ser	Met	Val	Ala	Ser	Gly	Thr	Arg	Gly	Ser	Ile	Val	Cys	Thr	Thr
			130				135					140			
Ser	Ile	Ala	Ala	Glu	Ile	Gly	Gly	Pro	Gly	Pro	His	Ser	Tyr	Thr	Ala
			145				150					155			160
Ser	Lys	His	Ala	Leu	Leu	Gly	Leu	Ile	Arg	Ser	Ala	Cys	Ala	Gly	Leu
			165					170					175		
Gly	Gln	Tyr	Gly	Ile	Arg	Val	Asn	Gly	Val	Ala	Pro	Tyr	Gly	Val	Ala
			180					185					190		
Thr	Gly	Met	Thr	Ser	Ala	Tyr	Asn	Glu	Glu	Ala	Val	Lys	Met	Leu	Glu
			195				200					205			
Glu	Tyr	Gly	Glu	Ala	Leu	Gly	Asn	Leu	Lys	Gly	Val	Val	Leu	Lys	Ala
			210				215					220			
Arg	His	Ile	Ala	Glu	Ala	Ala	Leu	Phe	Leu	Ala	Ser	Asp	Asp	Ser	Val
			225				230					235			240
Tyr	Ile	Ser	Gly	Gln	Asn	Leu	Val	Val	Asp	Gly	Gly	Phe	Ser	Val	Val
			245					250					255		
Lys	Leu	Met	Ser	Thr											
			260												

(2) INFORMATION FOR SEQ ID NO:1622:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 149 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..149
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570504

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1622:

Met Ala Val Asn Val Arg Gly Ala Ala Ala Phe Ile Lys His Ala Ala

1	5	10	15
Arg Ser Met Val Ala Ser Gly Thr Arg Gly Ser Ile Val Cys Thr Thr			
	20	25	30
Ser Ile Ala Ala Glu Ile Gly Gly Pro Gly Pro His Ser Tyr Thr Ala			
	35	40	45
Ser Lys His Ala Leu Leu Gly Leu Ile Arg Ser Ala Cys Ala Gly Leu			
	50	55	60
Gly Gln Tyr Gly Ile Arg Val Asn Gly Val Ala Pro Tyr Gly Val Ala			
	65	70	75
Thr Gly Met Thr Ser Ala Tyr Asn Glu Glu Ala Val Lys Met Leu Glu			
	85	90	95
Glu Tyr Gly Glu Ala Leu Gly Asn Leu Lys Gly Val Val Leu Lys Ala			
	100	105	110
Arg His Ile Ala Glu Ala Ala Leu Phe Leu Ala Ser Asp Asp Ser Val			
	115	120	125
Tyr Ile Ser Gly Gln Asn Leu Val Val Asp Gly Gly Phe Ser Val Val			
	130	135	140
Lys Leu Met Ser Thr			
145			

(2) INFORMATION FOR SEQ ID NO:1623:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 812 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..812

(D) OTHER INFORMATION: / Ceres Seq. ID 1570505

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1623:

aacaaaaaag	cctataaacg	agagagggcg	agaggagagag	gaagacggcg	tgaagcaatg	60
gtgtgcgtga	agctccagaa	gcggctcgcc	gcacccgtaa	tgaatgcgg	gaaaggaaaa	120
gtttggctcg	accccaatga	atcggggcgat	atctctatgg	ccaattccag	gcagaacatt	180
aggaagcttg	tgaaggatgg	tttcattatc	aggaagccta	ctaagatcca	ctcacgttct	240
cgggctaggg	ctttgaaagg	ccaagcgaaa	gggtcgctac	tctggatagc	gtaagagaaa	300
gggtacaaga	gaggcaaggc	taccaaccaa	gattctttgg	atgaggagaa	tgagggtggt	360
gaggcgcttc	ttgagcaagt	accgtgagtc	aaagaagatt	gataggcaca	tgtaccatga	420
catgtacatg	aaagtgaagg	gtaattgttt	caagaacaag	cgtgtgctta	tggagagcat	480
ccacaagaat	aaggctgaga	aggctagaga	gaagaccctc	gctgaccagt	ttgaggccaa	540
gcgtattaag	aacaaggcta	gcaggagagag	aaagtttgcc	agaagagagg	agagattagc	600
tcaggagacct	ggagggtggag	agacaacgac	tcctgCtgcc	gcacctcaac	aaccagaggt	660
aaccagaaga	aagtccaaga	agtgtatttg	tgttgaactt	ttttgcaatt	gaatctttga	720
gtttacctgt	agaagaagcg	tttttttttt	atcttttata	tgattttgtc	ggagattctt	780
ttcttcaaaa	atattttcta	tgttatggat	cc			

(2) INFORMATION FOR SEQ ID NO:1624:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 97 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..97

(D) OTHER INFORMATION: / Ceres Seq. ID 1570506

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1624:

Asn Lys Lys Ala Leu Asn Gly Glu Arg Arg Arg Gly Glu Gly Arg Arg			
1	5	10	15
Arg Glu Ala Met Val Ser Leu Lys Leu Gln Lys Arg Leu Ala Ala Ser			
	20	25	30

Val Met Lys Cys Gly Lys Gly Lys Val Trp Leu Asp Pro Asn Glu Ser
35 40 45
Gly Asp Ile Ser Met Ala Asn Ser Arg Gln Asn Ile Arg Lys Leu Val
50 55 60
Lys Asp Gly Phe Ile Ile Arg Lys Pro Thr Lys Ile His Ser Arg Ser
65 70 75 80
Arg Ala Arg Ala Leu Lys Gly Gln Ala Lys Gly Ser Ser Leu Trp Ile
85 90 95
Arg

(2) INFORMATION FOR SEQ ID NO:1625:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 114 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..114

(D) OTHER INFORMATION: / Ceres Seq. ID 1570507

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1625:

Met Arg Arg Met Arg Val Leu Arg Arg Phe Leu Ser Lys Tyr Arg Glu
1 5 10 15
Ser Lys Lys Ile Asp Arg His Met Tyr His Asp Met Tyr Met Lys Val
20 25 30
Lys Gly Asn Val Phe Lys Asn Lys Arg Val Leu Met Glu Ser Ile His
35 40 45
Lys Met Lys Ala Glu Lys Ala Arg Glu Lys Thr Leu Ala Asp Gln Phe
50 55 60
Glu Ala Lys Arg Ile Lys Asn Lys Ala Ser Arg Glu Arg Lys Phe Ala
65 70 75 80
Arg Arg Glu Glu Arg Leu Ala Gln Gly Pro Gly Gly Gly Glu Thr Thr
85 90 95
Thr Pro Ala Gly Ala Pro Gln Gln Pro Glu Val Thr Lys Lys Lys Ser
100 105 110
Lys Lys

(2) INFORMATION FOR SEQ ID NO:1626:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 111 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..111

(D) OTHER INFORMATION: / Ceres Seq. ID 1570508

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1626:

Met Arg Val Leu Arg Arg Phe Leu Ser Lys Tyr Arg Glu Ser Lys Lys
1 5 10 15
Ile Asp Arg His Met Tyr His Asp Met Tyr Met Lys Val Lys Gly Asn
20 25 30
Val Phe Lys Asn Lys Arg Val Leu Met Glu Ser Ile His Lys Met Lys
35 40 45
Ala Glu Lys Ala Arg Glu Lys Thr Leu Ala Asp Gln Phe Glu Ala Lys
50 55 60
Arg Ile Lys Asn Lys Ala Ser Arg Glu Arg Lys Phe Ala Arg Arg Glu
65 70 75 80
Glu Arg Leu Ala Gln Gly Pro Gly Gly Glu Thr Thr Thr Pro Ala

85 90 95
Gly Ala Pro Gln Gln Pro Glu Val Thr Lys Lys Lys Ser Lys Lys
100 105 110

(2) INFORMATION FOR SEQ ID NO:1627:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 875 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..875

(D) OTHER INFORMATION: / Ceres Seq. ID 1570515

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1627:

```
aaaatgatgc ctgcgacagc gagtgtgtga cgttaaaccc taaatctggt gtctttgtgc      60
aatcgcaaga ttcatctcact cgacactaaa gatcgaaact tttgaattgc agaaattgcg      120
acacttttag ttccaagctc tccaaaggac gttcattgct tggagggtct tgcaatgctt      180
tctctggttt gatgaattcc tcctccaatg gaatgatgaa tgggaagcatc ctctctcagc      240
aacaacatag gacattcatt caaatgggga cgattctcaa atgcgtggat aactcgtgtg      300
ctaaaggagt gatgtgcatt caatccctga gaggtaagaa aggagcaaga cttggcgata      360
tcattgttgg ttacgtgaaa gaagctaacc caattgttca aaaaaaagta aagaaagacg      420
ctgtcccaaa aggtaaaagt aagaaaaggga tggtcgtgta cggtgtggtt gtgcgtgctg      480
cgatgcctaa aggacgtgct gatggaagcc aagtcaagtt tgatgacaat gccattgtag      540
ttgttggcat taaggaaaag aaagggcgaga ataattcaca tggttccaag aggaaaattg      600
agtaacaaca accgactggt acccgagtggt ttggtcctgt tggcgacag atgcgcctca      660
ggaaacagct caagatcctt tctttggctc agcacattgt ttgagacaat acaccacact      720
aaaaacatag ttatgatctc ctttatgtga ctctctttga tccattcatc acttgggttt      780
ctgtgtatcc ttaaacatct caactcatta tttttgttaa ttctaatgaa ttatgaaaac      840
```

(2) INFORMATION FOR SEQ ID NO:1628:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..170

(D) OTHER INFORMATION: / Ceres Seq. ID 1570516

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1628:

```
Met Asn Ser Ser Ser Asn Gly Met Met Asn Gly Ser Ile Leu Ser Gln
1 5 10 15
Gln Gln His Arg Thr Phe Ile Gln Met Gly Thr Ile Leu Lys Cys Val
20 25 30
Asp Asn Ser Cys Ala Lys Glu Val Met Cys Ile Gln Ser Leu Arg Gly
35 40 45
Lys Lys Gly Ala Arg Leu Gly Asp Ile Ile Val Gly Ser Val Lys Glu
50 55 60
Ala Asn Pro Ile Val Gln Lys Lys Val Lys Lys Asp Ala Val Pro Lys
65 70 75 80
Gly Lys Val Lys Lys Gly Met Val Val Tyr Gly Val Val Val Arg Ala
85 90 95
Ala Met Pro Lys Gly Arg Ala Asp Gly Ser Gln Val Lys Phe Asp Asp
100 105 110
Asn Ala Ile Val Val Val Gly Ile Lys Glu Lys Lys Gly Gln Asn Asn
115 120 125
Ser His Gly Ser Lys Arg Lys Met Glu Tyr Asn Gln Pro Thr Gly Thr
130 135 140
Arg Val Phe Gly Pro Val Pro His Glu Met Arg Leu Arg Lys Gln Leu
```

(2) INFORMATION FOR SEO ID NO:1629:

(A) LENGTH: 163 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: lin

MOLECULE TYPE: peptide

(1x) FEATURE:

(1X) FEATURE:
(1X) NAME:

(A) NAME/KEY: peptide
(B) LOCATION: 1 163

(B) LOCATION: 1..163

(D) OTHER INFORMATION: / Ceres Seq. ID 1570517
SEQUENCE DESCRIPTION: STC ID NO: 1628;

```
(x1) SEQUENCE DESCRIPTION: SEQ ID NO:1629:
```

(2) INFORMATION FOR SEQ ID NO:1630:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 162 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

```
(ix) FEATURE:
```

(A) NAME/KEY: peptide

(B) LOCATION: 1..162

(D) OTHER INFORMATION: / Ceres Seq. ID 1570518

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1630:

Met	Asn	Gly	Ser	Ile	Leu	Ser	Gln	Gln	Gln	His	Arg	Thr	Phe	Ile	Gln
1				5					10					15	
Met	Gly	Thr	Ile	Leu	Lys	Cys	Val	Asp	Asn	Ser	Cys	Ala	Lys	Glu	Val
			20					25					30		
Met	Cys	Ile	Gln	Ser	Leu	Arg	Gly	Lys	Lys	Gly	Ala	Arg	Leu	Gly	Asp
			35				40					45			
Ile	Ile	Val	Gly	Ser	Val	Lys	Glu	Ala	Asn	Pro	Ile	Val	Gln	Lys	Lys
	50					55					60				
Val	Lys	Lys	Asp	Ala	Val	Pro	Lys	Gly	Lys	Val	Lys	Lys	Gly	Met	Val
65				70						75				80	
Val	Tyr	Gly	Val	Val	Val	Arg	Ala	Ala	Met	Pro	Lys	Gly	Arg	Ala	Asp
				85					90					95	

Gly Ser Gln Val Lys Phe Asp Asp Asn Ala Ile Val Val Val Gly Ile
100 105 110
Lys Glu Lys Lys Gly Gln Asn Asn Ser His Gly Ser Lys Arg Lys Met
115 120 125
Glu Tyr Asn Gln Pro Thr Gly Thr Arg Val Phe Gly Pro Val Pro His
130 135 140
Glu Met Arg Leu Arg Lys Gln Leu Lys Ile Leu Ser Leu Ala Gln His
145 150 155 160
Ile Val

(2) INFORMATION FOR SEQ ID NO:1631:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1027 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1027

(D) OTHER INFORMATION: / Ceres Seq. ID 1570534

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1631:

attcgctcttc	tccaattttc	tcgcgaagaa	aactttccta	ctttgtttca	atccaaacga	60
gtcaaaatgc	tatatcaagc	tgtttcttca	tcttcttctt	cagctctctc	gctgggtgaat	120
ttccatggcg	tgaagaagga	tgtgtctctc	ttgttacott	ccatttcate	gaactctcga	180
gtttctctcg	gaaaatctgg	aaaattaact	ttctctgttc	gcgcatactaa	aagctcaacc	240
accgacgcgc	taagcggcgt	tgtcttcgag	ccgttttaag	aagtaaaaaa	ggagctcgat	300
ctcgctcccta	ccagctctca	ttctctcactc	gctcgacaaa	agtactcaga	cgagtgcgaa	360
gccgccattc	acgacgagat	caatgtggva	tacaatgtct	cgtatgtgta	tcacgctatg	420
tatgcttact	ttgatcgga	taacatcgcg	ctcaaggctc	ttgcgaagtt	ctttaaggaa	480
tcaagtctcg	aagaagaaga	gcattgctag	aagttaattg	agtatcagaa	caaacctggt	540
gggagggtta	agttacagtc	cattgtaatg	ctcttttcag	agtttgaaca	tggtgacaaa	600
ggagatgctc	tttatggcat	ggagcttgct	ctgtcactgg	agaaactagt	taatgagaag	660
ctcttaaac	ttoacagtgt	tgtcttcagg	aacaatgatg	tccacttggc	agatttttatt	720
gagagcaggt	ttctgacaga	gcaggtggaa	gcaatcaagt	tgatctcaga	atatgtggct	780
caactgcgac	gagttggcaa	aggacacgga	acatggcatt	tcaatcagat	gcttctggaa	840
gggtaagcag	cttcgaggga	ctcttggtgc	tactgtgttt	ctatatgaag	ctctcttagt	900
gatattgatg	gaactacttt	atgtttatgt	ctttagcttt	taagattttg	tgaggtagta	960
gaactctttt	tctgtaagac	acaaaagaca	tgatcacata	actttatatt	ctgtgtataag	1020
gttcacc						

(2) INFORMATION FOR SEQ ID NO:1632:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 281 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..281

(D) OTHER INFORMATION: / Ceres Seq. ID 1570535

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1632:

Ile	Arg	Leu	Leu	Gln	Phe	Ser	Arg	Glu	Glu	Asn	Phe	Pro	Thr	Leu	Phe
1															
			5					10						15	
Gln	Ser	Lys	Arg	Val	Lys	Met	Leu	Ile	Lys	Thr	Val	Ser	Ser	Ser	Ser
			20					25						30	
Ser	Ser	Ala	Leu	Ser	Leu	Val	Asn	Phe	His	Gly	Val	Lys	Lys	Asp	Val
			35				40					45			
Ser	Pro	Leu	Leu	Pro	Ser	Ile	Ser	Ser	Asn	Leu	Arg	Val	Ser	Ser	Gly
			50			55				60					
Lys	Ser	Gly	Lys	Leu	Thr	Phe	Ser	Val	Arg	Ala	Ser	Lys	Ser	Ser	Thr

Met	Leu	Ile	Lys	Thr	Val	Ser	Ser	Ser	Ser	Ser	Ser	Ala	Leu	Ser	Leu
1			5							10			15		
Val	Asn	Phe	His	Gly	Val	Lys	Lys	Asp	Val	Ser	Pro	Leu	Leu	Pro	Ser
		20						25				30			
Ile	Ser	Ser	Asn	Leu	Arg	Val	Ser	Ser	Gly	Lys	Ser	Gly	Lys	Leu	Thr
		35					40					45			
Phe	Ser	Val	Arg	Ala	Ser	Lys	Ser	Ser	Thr	Thr	Asp	Ala	Leu	Ser	Gly
		50				55					60				
Val	Val	Phe	Glu	Pro	Phe	Lys	Glu	Val	Lys	Lys	Glu	Leu	Asp	Leu	Val
65					70					75				80	
Pro	Thr	Ser	Ser	His	Leu	Ser	Leu	Ala	Arg	Gln	Lys	Tyr	Ser	Asp	Glu
				85					90					95	
Cys	Glu	Ala	Ala	Ile	Asn	Glu	Gln	Ile	Asn	Val	Xaa	Tyr	Asn	Val	Ser
		100						105					110		
Tyr	Val	Tyr	His	Ala	Met	Tyr	Ala	Tyr	Phe	Asp	Arg	Asp	Asn	Ile	Ala
		115					120					125			
Leu	Lys	Gly	Leu	Ala	Lys	Phe	Phe	Lys	Glu	Ser	Ser	Leu	Glu	Glu	Arg
		130				135						140			
Glu	His	Ala	Glu	Lys	Leu	Met	Glu	Tyr	Gln	Asn	Lys	Arg	Gly	Gly	Arg
145					150					155				160	
Val	Lys	Leu	Gln	Ser	Ile	Val	Met	Pro	Leu	Ser	Glu	Phe	Glu	His	Val
				165					170				175		

Asp Lys Gly Asp Ala Leu Tyr Gly Met Glu Leu Ala Leu Ser Leu Glu
180 185 190
Lys Leu Val Asn Glu Lys Leu Leu Asn Leu His Ser Val Ala Ser Arg
195 200 205
Asn Asn Asp Val His Leu Ala Asp Phe Ile Glu Ser Glu Phe Leu Thr
210 215 220
Glu Gln Val Glu Ala Ile Lys Leu Ile Ser Glu Tyr Val Ala Gln Leu
225 230 235 240
Arg Arg Val Gly Lys Gly His Gly Thr Trp His Phe Asn Gln Met Leu
245 250 255
Leu Glu Gly

(2) INFORMATION FOR SEQ ID NO:1634:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 142 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..142
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570537

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1634:

Met Tyr Ala Tyr Phe Asp Arg Asp Asn Ile Ala Leu Lys Gly Leu Ala
1 5 10 15
Lys Phe Phe Lys Glu Ser Ser Leu Glu Glu Arg Glu His Ala Glu Lys
20 25 30
Leu Met Glu Tyr Gln Asn Lys Arg Gly Gly Arg Val Lys Leu Gln Ser
35 40 45
Ile Val Met Pro Leu Ser Glu Phe Glu His Val Asp Lys Gly Asp Ala
50 55 60
Leu Tyr Gly Met Glu Leu Ala Leu Ser Leu Glu Lys Leu Val Asn Glu
65 70 75 80
Lys Leu Leu Asn Leu His Ser Val Ala Ser Arg Asn Asn Asp Val His
85 90 95
Leu Ala Asp Phe Ile Glu Ser Glu Phe Leu Thr Glu Gln Val Glu Ala
100 105 110
Ile Lys Leu Ile Ser Glu Tyr Val Ala Gln Leu Arg Arg Val Gly Lys
115 120 125
Gly His Gly Thr Trp His Phe Asn Gln Met Leu Leu Glu Gly
130 135 140

(2) INFORMATION FOR SEQ ID NO:1635:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 976 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..976
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570538

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1635:

agatttcaaaa	tctttgttta	caatctcttc	tctggctatc	ttagagggat	ttttgattga	60
gattttaaaa	ttttctTgag	ttggattagt	tggttggttaa	agagatggat	ccggataccg	120
tgaagtcgac	ctctctgaat	ctggcattcg	ggaatgtatt	ggcggcagct	gctagagatt	180
ataaaaaagg	agttcttgca	aatgaaaaagg	cacaaggatc	aagacctgtGt	caacgaggaa	240
gttgatcttg	acgaattgat	gagatgatcca	gagctagaaa	agttgcacgc	agataggatt	300
gcagcactca	ggagagaagt	ggaaaaagaga	gaagcattca	aaagacaagg	acatggtgaa	360
taccgagaag	ttagcgaagg	cgacttcttg	ggagaagtca	caaggagtga	aaaagtata	420

tgctacttct	accacaagga	gttctatcgc	tgcaagataa	tggaacaagca	tttgaagacc	480
cttctctcca	gacatgtgga	cacaaagtcc	attaagatgg	acgctgagaa	cgctcccttc	540
ttcgtcacca	agcttgcaat	caagactttg	ccgtgtgtta	tcctttttag	caagggaatc	600
gcgatggata	ggcttgtcgg	gtttcaagat	ctaggtgccca	aggacgattt	ctccacgaac	660
aagctggaga	atcttctcgt	caagaaagga	atgcttagtg	aaaagagaaa	agaggaagat	720
gaggaagatt	acgagtatca	agaaagcata	cgctcggtccg	ttaggtcttc	agcgaatgtc	780
gactctgatt	cagattgatc	tcgaagcttt	tctcatagta	gacctccgag	ccctttttgt	840
ttttgttttc	accgctgctc	tggttgaatt	gtttgtgtct	tgaattctat	gcttctataa	900
gtctttatag	tgggaaattt	cggtccacaa	tggttttgtt	tatttgaaaa	ctgcaaaaata	960
tggtgtctaa	ccatat					

(2) INFORMATION FOR SEQ ID NO:1636:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 214 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..214

(D) OTHER INFORMATION: / Ceres Seq. ID 1570539

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1636:

Met	Tyr	Trp	Arg	Gln	Leu	Leu	Glu	Ile	Lys	Arg	Lys	Phe	Leu	Gln
1				5				10				15		
Met	Lys	Arg	His	Lys	Asp	Gln	Asp	Leu	Val	Asn	Glu	Glu	Val	Asp
				20				25				30		
Asp	Glu	Leu	Met	Asp	Asp	Pro	Glu	Leu	Glu	Lys	Leu	His	Ala	Asp
				35				40				45		
Ile	Ala	Ala	Leu	Arg	Arg	Glu	Val	Glu	Lys	Arg	Glu	Ala	Phe	Lys
				50				55				60		
Gln	Gly	His	Gly	Glu	Tyr	Arg	Glu	Val	Ser	Glu	Gly	Asp	Phe	Leu
				65				70				75		
Glu	Val	Thr	Arg	Ser	Glu	Lys	Val	Ile	Cys	His	Phe	Tyr	His	Glu
				85				90				95		
Phe	Tyr	Arg	Cys	Lys	Ile	Met	Asp	Lys	His	Leu	Lys	Thr	Leu	Ala
				100				105				110		
Arg	His	Val	Asp	Thr	Lys	Phe	Ile	Lys	Met	Asp	Ala	Glu	Asn	Ala
				115				120				125		
Phe	Phe	Val	Thr	Lys	Leu	Ala	Ile	Lys	Thr	Leu	Pro	Cys	Val	Ile
				130				135				140		
Phe	Ser	Lys	Gly	Ile	Ala	Met	Asp	Arg	Leu	Val	Gly	Phe	Gln	Asp
				145				150				155		
Gly	Ala	Lys	Asp	Asp	Phe	Ser	Thr	Thr	Lys	Leu	Glu	Asn	Leu	Val
				165				170				175		
Lys	Lys	Gly	Met	Leu	Ser	Glu	Lys	Arg	Lys	Glu	Glu	Asp	Glu	Asp
				180				185				190		
Tyr	Glu	Tyr	Gln	Glu	Ser	Ile	Arg	Arg	Ser	Val	Arg	Ser	Ser	Ala
				195				200				205		
Val	Asp	Ser	Asp	Ser	Asp									
				210										

(2) INFORMATION FOR SEQ ID NO:1637:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 198 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..198

(D) OTHER INFORMATION: / Ceres Seq. ID 1570540

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1637:

Met Lys Arg His Lys Asp Gln Asp Leu Val Asn Glu Glu Val Asp Leu
1 5 10 15
Asp Glu Leu Met Asp Asp Pro Glu Leu Glu Lys Leu His Ala Asp Arg
20 25 30
Ile Ala Ala Leu Arg Arg Glu Val Glu Lys Arg Glu Ala Phe Lys Arg
35 40 45
Gln Gly His Gly Glu Tyr Arg Glu Val Ser Glu Gly Asp Phe Leu Gly
50 55 60
Glu Val Thr Arg Ser Glu Lys Val Ile Cys His Phe Tyr His Lys Glu
65 70 75 80
Phe Tyr Arg Cys Lys Ile Met Asp Lys His Leu Lys Thr Leu Ala Pro
85 90 95
Arg His Val Asp Thr Lys Phe Ile Lys Met Asp Ala Glu Asn Ala Pro
100 105 110
Phe Phe Val Thr Lys Leu Ala Ile Lys Thr Leu Pro Cys Val Ile Leu
115 120 125
Phe Ser Lys Gly Ile Ala Met Asp Arg Leu Val Gly Phe Gln Asp Leu
130 135 140
Gly Ala Lys Asp Asp Phe Ser Thr Thr Lys Leu Glu Asn Leu Leu Val
145 150 155 160
Lys Lys Gly Met Leu Ser Glu Lys Arg Lys Glu Glu Asp Glu Glu Asp
165 170 175
Tyr Glu Tyr Gln Glu Ser Ile Arg Arg Ser Val Arg Ser Ser Ala Asn
180 185 190
Val Asp Ser Asp Ser Asp
195

(2) INFORMATION FOR SEQ ID NO:1638:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 179 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..179

(D) OTHER INFORMATION: / Ceres Seq. ID 1570541

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1638:

Met Asp Asp Pro Glu Leu Glu Lys Leu His Ala Asp Arg Ile Ala Ala
1 5 10 15
Leu Arg Arg Glu Val Glu Lys Arg Glu Ala Phe Lys Arg Gln Gly His
20 25 30
Gly Glu Tyr Arg Glu Val Ser Glu Gly Asp Phe Leu Gly Glu Val Thr
35 40 45
Arg Ser Glu Lys Val Ile Cys His Phe Tyr His Lys Glu Phe Tyr Arg
50 55 60
Cys Lys Ile Met Asp Lys His Leu Lys Thr Leu Ala Pro Arg His Val
65 70 75 80
Asp Thr Lys Phe Ile Lys Met Asp Ala Glu Asn Ala Pro Phe Phe Val
85 90 95
Thr Lys Leu Ala Ile Lys Thr Leu Pro Cys Val Ile Leu Phe Ser Lys
100 105 110
Gly Ile Ala Met Asp Arg Leu Val Gly Phe Gln Asp Leu Gly Ala Lys
115 120 125
Asp Asp Phe Ser Thr Thr Lys Leu Glu Asn Leu Leu Val Lys Lys Gly
130 135 140
Met Leu Ser Glu Lys Arg Lys Glu Glu Asp Glu Glu Asp Tyr Glu Tyr
145 150 155 160
Gln Glu Ser Ile Arg Arg Ser Val Arg Ser Ser Ala Asn Val Asp Ser
165 170 175

Asp Ser Asp

(2) INFORMATION FOR SEQ ID NO:1639:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1089 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1089
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570561

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1639:

acagagacaa	caaactaaag	ttggtggtga	tagagtgaga	gagaaacatg	gaaggcaaa	60
aagaagacgt	caatgttgga	gccacaagt	tcccagagag	acagccgac	ggtacggcg	120
ctcagacgga	gagcaaggac	tataaggaa	caccaccggc	gccgtttttc	gaaccggcg	180
agctcaaatc	ttggtctttc	tacagagcag	ggatagctga	gttcatagcc	actttccttt	240
tcctctacgt	caccgttttg	acagtcacgg	gtgttaagag	agctcccaat	atgtgtgcct	300
ctgttggagt	ccaaggcatc	gcttgggctt	ttggtggcat	gatcttttgt	cttgtttact	360
gtactgtcgg	aatctcagga	ggacatat	atccggcggt	gaacttttgt	ttgttcttgg	420
cgaggaagct	atctttaacc	agagctctgt	tctacatagt	aatgcagtc	cttggagcta	480
tatgttggtg	tggtgtgggt	aaagggtttc	aaccagggct	gtaccagacg	aatgcccgtg	540
gagctaagt	ggtggctcat	ggttacacaa	agggttcagg	tcttggtgca	gagattgttg	600
gaacttttgt	tctggtttac	actgttttct	cagctactga	tgctaagaga	aglgccagag	660
actctcaagt	cgttatctgt	gctccgcttc	caattggggt	tgctgtcttc	ttggtgcaact	720
tggtaccatc	cccaattact	ggaactggca	ttaaccggcg	caggagcttc	ggagctgcc	780
tcatctacaa	caaggaatc	gcttgggatg	accattggat	cttctgggtc	gggtcattca	840
ttggtGctgc	gcttgctgct	ctgtaccatc	agatagtcat	cagagctatt	cttttcaagt	900
ccaagacata	aagtttctca	catattctct	gatcatcatc	aagctaagaa	tatatcaatc	960
tttaattcta	tatgctttct	tctgtttctc	tatgtcatgt	gtgatgatct	ctatatgtac	1020
cactagagct	ttgatcttgt	aacagtgtaa	atgtgttaatc	tattatgtat	caatggcatt	1080
gtatcttgt						

(2) INFORMATION FOR SEQ ID NO:1640:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 287 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..287
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570562

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1640:

Met	Glu	Gly	Lys	Glu	Glu	Asp	Val	Asn	Val	Gly	Ala	Asn	Lys	Phe	Pro
1				5					10					15	
Glu	Arg	Gln	Pro	Ile	Gly	Thr	Ala	Ala	Gln	Thr	Glu	Ser	Lys	Asp	Tyr
			20					25					30		
Lys	Glu	Pro	Pro	Pro	Ala	Pro	Phe	Phe	Glu	Pro	Gly	Glu	Leu	Lys	Ser
			35				40					45			
Trp	Ser	Phe	Tyr	Arg	Ala	Gly	Ile	Ala	Glu	Phe	Ile	Ala	Thr	Phe	Leu
			50				55				60				
Phe	Leu	Tyr	Val	Thr	Val	Leu	Thr	Val	Met	Gly	Val	Lys	Arg	Ala	Pro
			65			70				75				80	
Asn	Met	Cys	Ala	Ser	Val	Gly	Ile	Gln	Gly	Ile	Ala	Trp	Ala	Phe	Gly
				85					90					95	
Gly	Met	Ile	Phe	Ala	Leu	Val	Tyr	Cys	Thr	Ala	Gly	Ile	Ser	Gly	Gly
			100					105					110		
His	Ile	Asn	Pro	Ala	Val	Thr	Phe	Gly	Leu	Phe	Leu	Ala	Arg	Lys	Leu
			115					120					125		

Ser Leu Thr Arg Ala Leu Phe Tyr Ile Val Met Gln Ser Leu Gly Ala
130 135 140
Ile Cys Gly Ala Gly Val Val Lys Gly Phe Gln Pro Gly Leu Tyr Gln
145 150 155 160
Thr Asn Gly Gly Gly Ala Asn Val Val Ala His Gly Tyr Thr Lys Gly
165 170 175
Ser Gly Leu Gly Ala Glu Ile Val Gly Thr Phe Val Leu Val Tyr Thr
180 185 190
Val Phe Ser Ala Thr Asp Ala Lys Arg Ser Ala Arg Asp Ser His Val
195 200 205
Arg Ile Leu Ala Pro Leu Pro Ile Gly Phe Ala Val Phe Leu Val His
210 215 220
Leu Ala Thr Ile Pro Ile Thr Gly Thr Gly Ile Asn Pro Ala Arg Ser
225 230 235 240
Leu Gly Ala Ala Ile Ile Tyr Asn Lys Asp His Ala Trp Asp Asp His
245 250 255
Trp Ile Phe Trp Val Gly Pro Phe Ile Gly Ala Ala Leu Ala Ala Leu
260 265 270
Tyr His Gln Ile Val Ile Arg Ala Ile Pro Phe Lys Ser Lys Thr
275 280 285

(2) INFORMATION FOR SEQ ID NO:1641:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 214 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..214

(D) OTHER INFORMATION: / Ceres Seq. ID 1570563

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1641:

Met Gly Val Lys Arg Ala Pro Asn Met Cys Ala Ser Val Gly Ile Gln
1 5 10
Gly Ile Ala Trp Ala Phe Gly Gly Met Ile Phe Ala Leu Val Tyr Cys
20 25 30
Thr Ala Gly Ile Ser Gly Gly His Ile Asn Pro Ala Val Thr Phe Gly
35 40 45
Leu Phe Leu Ala Arg Lys Leu Ser Leu Thr Arg Ala Leu Phe Tyr Ile
50 55 60
Val Met Gln Ser Leu Gly Ala Ile Cys Gly Ala Gly Val Val Lys Gly
65 70 75 80
Phe Gln Pro Gly Leu Tyr Gln Thr Asn Gly Gly Ala Asn Val Val
85 90 95
Ala His Gly Tyr Thr Lys Gly Ser Gly Leu Gly Ala Glu Ile Val Gly
100 105 110
Thr Phe Val Leu Val Tyr Thr Val Phe Ser Ala Thr Asp Ala Lys Arg
115 120 125
Ser Ala Arg Asp Ser His Val Arg Ile Leu Ala Pro Leu Pro Ile Gly
130 135 140
Phe Ala Val Phe Leu Val His Leu Ala Thr Ile Pro Ile Thr Gly Thr
145 150 155 160
Gly Ile Asn Pro Ala Arg Ser Leu Gly Ala Ala Ile Ile Tyr Asn Lys
165 170 175
Asp His Ala Trp Asp Asp His Trp Ile Phe Trp Val Gly Pro Phe Ile
180 185 190
Gly Ala Ala Leu Ala Ala Leu Tyr His Gln Ile Val Ile Arg Ala Ile
195 200 205
Pro Phe Lys Ser Lys Thr
210

(2) INFORMATION FOR SEQ ID NO:1642:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 206 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..206
 (D) OTHER INFORMATION: / Ceres Seq. ID 1570564
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1642:

Met	Cys	Ala	Ser	Val	Gly	Ile	Gln	Gly	Ile	Ala	Trp	Ala	Phe	Gly	Gly
1			5					10						15	
Met	Ile	Phe	Ala	Leu	Val	Tyr	Cys	Thr	Ala	Gly	Ile	Ser	Gly	Gly	His
			20				25					30			
Ile	Asn	Pro	Ala	Val	Thr	Phe	Gly	Leu	Phe	Leu	Ala	Arg	Lys	Leu	Ser
			35				40					45			
Leu	Thr	Arg	Ala	Leu	Phe	Tyr	Ile	Val	Met	Gln	Ser	Leu	Gly	Ala	Ile
			50			55				60					
Cys	Gly	Ala	Gly	Val	Val	Lys	Gly	Phe	Gln	Pro	Gly	Leu	Tyr	Gln	Thr
65				70				75						80	
Asn	Gly	Gly	Gly	Ala	Asn	Val	Val	Ala	His	Gly	Tyr	Thr	Lys	Gly	Ser
				85				90					95		
Gly	Leu	Gly	Ala	Glu	Ile	Val	Gly	Thr	Phe	Val	Leu	Val	Tyr	Thr	Val
			100				105						110		
Phe	Ser	Ala	Thr	Asp	Ala	Lys	Arg	Ser	Ala	Arg	Asp	Ser	His	Val	Arg
			115				120					125			
Ile	Leu	Ala	Pro	Leu	Pro	Ile	Gly	Phe	Ala	Val	Phe	Leu	Val	His	Leu
			130			135					140				
Ala	Thr	Ile	Pro	Ile	Thr	Gly	Thr	Gly	Ile	Asn	Pro	Ala	Arg	Ser	Leu
145				150				155						160	
Gly	Ala	Ala	Ile	Ile	Tyr	Asn	Lys	Asp	His	Ala	Trp	Asp	Asp	His	Trp
			165					170						175	
Ile	Phe	Trp	Val	Gly	Pro	Phe	Ile	Gly	Ala	Ala	Leu	Ala	Ala	Leu	Tyr
			180				185							190	
His	Gln	Ile	Val	Ile	Arg	Ala	Ile	Pro	Phe	Lys	Ser	Lys	Thr		
			195			200						205			

(2) INFORMATION FOR SEQ ID NO:1643:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1122 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
 (B) LOCATION: 1..1122

(D) OTHER INFORMATION: / Ceres Seq. ID 1570565

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1643:

aaaaatcctg	atttAytgag	ctttaaaCcc	haRaccctc	tcttctctct	tctccacgcc	60
atttcacgaa	ttttcaggtg	ttcgtgaaaa	gatgaatttt	aagaatgtca	aagttcccaa	120
aggtcctggt	gggtgtgtta	tagctgcggt	ggttattggg	gggtcagtc	tttacgggtgc	180
taagcaact	ctctacaatg	tcatgagagg	tcactcgacc	attgtcttta	accgcttgt	240
tggtatcaaa	gacaaggctc	accctgaggg	taactacact	atgattccat	gggtcgaaa	300
gccaatcatc	tatgacgttc	gtgcaaaagg	ttatctagtt	gagagcacat	ctgggagccg	360
tgatctccag	atgggttaaga	tggggcttcg	gggtctccac	cgctcctatg	ctgaccaatt	420
accagagcta	taccgggtccc	ttggtgagaa	taccgcggag	agagtctctg	ctctctatcat	480
ccacagagacc	tgtgaaagctg	tgggtgtctca	gtacaaacga	agccaaacta	ttactcagag	540
agagtcggtg	agttagagaaa	tcaggaaaaat	cctaactcta	agagccgcaa	acttccacat	600
tgactcggtg	gatgtgtcca	tcacaggcct	gacattcgga	aaggagtcca	cggcagccat	660
agaaggaaa	cagggtcgtg	ctcaagaggc	cgaacgggct	aagttcattg	tcgagaaaagc	720

tgaacaggac	aagagaagt	ctgttatccg	cgccgaggga	gaagccaaga	gtgctcagct	780
catttggtcaa	gcaatcgcaa	acaaccaagc	gttcttaaca	ctgaggaaga	tcgaagcagc	840
tagagagatc	gcacagacca	tctctaggtc	ggcgaacaag	gtttacttga	gctctaacga	900
tctgttgctt	aactacacag	ctatggacct	tgaatggaag	cogaagaagt	agagaatgat	960
atgattaaac	cacaccagag	ctctctttcc	ataatcgtat	tttcaattca	cggattcttta	1020
gaccaaagc	tatgagttct	atcttgtgaa	tttcagacac	tatcgtgcgt	ttgtagtctt	1080
tcttttgtga	gatcaagaag	aaaagaaaag	atttatgttt	tt		

(2) INFORMATION FOR SEQ ID NO:1644:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 286 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..286

(D) OTHER INFORMATION: / Ceres Seq. ID 1570566

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1644:

Met	Asn	Phe	Lys	Asn	Val	Lys	Val	Pro	Lys	Gly	Pro	Gly	Gly	Gly	Val
1			5						10					15	
Ile	Ala	Ala	Val	Val	Ile	Gly	Gly	Leu	Ser	Leu	Tyr	Gly	Ala	Thr	His
			20					25					30		
Thr	Leu	Tyr	Asn	Val	Asp	Gly	Gly	His	Arg	Ala	Ile	Val	Phe	Asn	Arg
			35				40					45			
Leu	Val	Gly	Ile	Lys	Asp	Lys	Val	Tyr	Pro	Glu	Gly	Thr	His	Leu	Met
			50			55					60				
Ile	Pro	Trp	Phe	Glu	Arg	Pro	Ile	Ile	Tyr	Asp	Val	Arg	Ala	Lys	Pro
			65		70				75					80	
Tyr	Leu	Val	Glu	Ser	Thr	Ser	Gly	Ser	Arg	Asp	Leu	Gln	Met	Val	Lys
			85					90				95			
Ile	Gly	Leu	Arg	Val	Leu	Thr	Arg	Pro	Met	Ala	Asp	Gln	Leu	Pro	Glu
			100				105					110			
Val	Tyr	Arg	Ser	Leu	Gly	Glu	Asn	Tyr	Arg	Glu	Arg	Val	Leu	Pro	Ser
			115			120					125				
Ile	Ile	His	Glu	Thr	Leu	Lys	Ala	Val	Val	Ala	Gln	Tyr	Asn	Ala	Ser
			130			135					140				
Gln	Leu	Ile	Thr	Gln	Arg	Glu	Ser	Val	Ser	Arg	Glu	Ile	Arg	Lys	Ile
			145		150				155					160	
Leu	Thr	Leu	Arg	Ala	Ala	Asn	Phe	His	Ile	Ala	Leu	Asp	Asp	Val	Ser
			165						170				175		
Ile	Thr	Gly	Leu	Thr	Phe	Gly	Lys	Glu	Phe	Thr	Ala	Ala	Ile	Glu	Gly
			180				185						190		
Lys	Gln	Val	Ala	Ala	Gln	Glu	Ala	Glu	Arg	Ala	Lys	Phe	Ile	Val	Glu
			195				200					205			
Lys	Ala	Glu	Gln	Asp	Lys	Arg	Ser	Ala	Val	Ile	Arg	Ala	Glu	Gly	Glu
			210			215					220				
Ala	Lys	Ser	Ala	Gln	Leu	Ile	Gly	Gln	Ala	Ile	Ala	Asn	Asn	Gln	Ala
			225			230				235				240	
Phe	Leu	Thr	Leu	Arg	Lys	Ile	Glu	Ala	Ala	Arg	Glu	Ile	Ala	Gln	Thr
			245					250					255		
Ile	Ser	Arg	Ser	Ala	Asn	Lys	Val	Tyr	Leu	Ser	Ser	Asn	Asp	Leu	Leu
			260				265					270			
Leu	Asn	Leu	Gln	Ala	Met	Asp	Leu	Asp	Val	Lys	Pro	Lys	Lys		
			275				280					285			

(2) INFORMATION FOR SEQ ID NO:1645:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 223 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide
(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..223

(D) OTHER INFORMATION: / Ceres Seq. ID 1570567

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1645:

```
Met Ile Pro Trp Phe Glu Arg Pro Ile Ile Tyr Asp Val Arg Ala Lys
1      5      10      15
Pro Tyr Leu Val Glu Ser Thr Ser Gly Ser Arg Asp Leu Gln Met Val
      20      25      30
Lys Ile Gly Leu Arg Val Leu Thr Arg Pro Met Ala Asp Gln Leu Pro
      35      40      45
Glu Val Tyr Arg Ser Leu Gly Glu Asn Tyr Arg Glu Arg Val Leu Pro
      50      55      60
Ser Ile Ile His Glu Thr Leu Lys Ala Val Val Ala Gln Tyr Asn Ala
      65      70      75      80
Ser Gln Leu Ile Thr Gln Arg Glu Ser Val Ser Arg Glu Ile Arg Lys
      85      90      95
Ile Leu Thr Leu Arg Ala Ala Asn Phe His Ile Ala Leu Asp Asp Val
      100      105      110
Ser Ile Thr Gly Leu Thr Phe Gly Lys Glu Phe Thr Ala Ala Ile Glu
      115      120      125
Gly Lys Gln Val Ala Ala Gln Glu Ala Glu Arg Ala Lys Phe Ile Val
      130      135      140
Glu Lys Ala Glu Gln Asp Lys Arg Ser Ala Val Ile Arg Ala Glu Gly
      145      150      155      160
Glu Ala Lys Ser Ala Gln Leu Ile Gly Gln Ala Ile Ala Asn Asn Gln
      165      170      175
Ala Phe Leu Thr Leu Arg Lys Ile Glu Ala Ala Arg Glu Ile Ala Gln
      180      185      190
Thr Ile Ser Arg Ser Ala Asn Lys Val Tyr Leu Ser Ser Asn Asp Leu
      195      200      205
Leu Leu Asn Leu Gln Ala Met Asp Leu Asp Val Lys Pro Lys Lys
      210      215      220
```

(2) INFORMATION FOR SEQ ID NO:1646:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 193 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..193

(D) OTHER INFORMATION: / Ceres Seq. ID 1570568

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1646:

```
Met Val Lys Ile Gly Leu Arg Val Leu Thr Arg Pro Met Ala Asp Gln
1      5      10      15
Leu Pro Glu Val Tyr Arg Ser Leu Gly Glu Asn Tyr Arg Glu Arg Val
      20      25      30
Leu Pro Ser Ile Ile His Glu Thr Leu Lys Ala Val Val Ala Gln Tyr
      35      40      45
Asn Ala Ser Gln Leu Ile Thr Gln Arg Glu Ser Val Ser Arg Glu Ile
      50      55      60
Arg Lys Ile Leu Thr Leu Arg Ala Ala Asn Phe His Ile Ala Leu Asp
      65      70      75      80
Asp Val Ser Ile Thr Gly Leu Thr Phe Gly Lys Glu Phe Thr Ala Ala
      85      90      95
Ile Glu Gly Lys Gln Val Ala Ala Gln Glu Ala Glu Arg Ala Lys Phe
      100      105      110
Ile Val Glu Lys Ala Glu Gln Asp Lys Arg Ser Ala Val Ile Arg Ala
```

[illegible]

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 903 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..903
(D) OTHER INFORMATION: / Ceres Seq. ID 1570569

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1647:

ctctcaactc	gcgcgaGcta	aacttttatg	gagaaaccct	aatcggcgac	aatgggtatt	60
ctctcgtgact	ctatcccaaa	gaggcgtgcc	actgaggcca	agcgaatcca	atggaggaa	120
aagcgaaga	atgagatggg	gcgcagcgcca	gccaaaccca	agctctcaag	caacgaacgc	180
ctcagaagaa	taagagttcg	tgtgtgaaat	gttaagtggc	gtgcgctgag	ctgcgtacat	240
ggtaactact	ctgtgggga	tgaagcaact	accgcgaaga	ccagagtcct	tgatgtgttc	300
tacaattgct	ccaaacaatg	cgttgctacgt	actaagacac	tgtctcaagag	tgctatttgt	360
cagggttgc	ctgtctcttt	gcagcagttg	tacctctcgc	ttgagtggtg	tgagcttggg	420
cgcgaaga	agagtgttc	ttccaccaa	aaggacggag	aggaaggtgc	agagcgacgt	480
gttgcgactg	ctgaggagg	caagaagaag	accaccctcc	tgagaagaat	tgagagccgt	540
caagagggtc	gcagttggt	ttcacacatt	gaggaccaat	ttgcagtggg	acgtttgttg	600
gctgtgtact	cttcaaggcc	tgggcagtcg	gggcgtgctg	atggatacat	cttgggaagt	660
aagtgatgg	tgtttacat	gagaagaatc	gaggaaga	ctgaagaagg	ctctgcgaag	720
agtcctcttc	tatctgcctt	gagcttttgt	cttgcagact	gtttttgagt	ttcagtttca	780
attgtctgaa	tcaaatgttt	tttgtatgat	ctttgtggtat	tttcttataa	ctccatcaag	840
ttattatggt	acaattgttt	tgtcttgat	ttctttata	atttttaact	ataatttca	900
tcc						

(2) INFORMATION FOR SEQ ID NO:1648:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 222 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..222
(D) OTHER INFORMATION: / Ceres Seq. ID 1570570

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1648:

Met	Gly	Ile	Ser	Arg	Asp	Ser	Ile	His	Lys	Arg	Arg	Ala	Thr	Gly	Gly
1			5					10					15		
Lys	Gln	Lys	Gln	Trp	Arg	Lys	Lys	Arg	Lys	Tyr	Glu	Met	Gly	Arg	Gln
		20					25					30			
Pro	Ala	Asn	Thr	Lys	Leu	Ser	Ser	Asn	Lys	Thr	Val	Arg	Arg	Ile	Arg
		35				40						45			
Val	Arg	Gly	Gly	Asn	Val	Lys	Trp	Arg	Ala	Leu	Arg	Leu	Asp	Thr	Gly
	50					55				60					
Asn	Tyr	Ser	Trp	Gly	Ser	Glu	Ala	Thr	Thr	Arg	Lys	Thr	Arg	Val	Leu
65				70						75				80	

Asp	Val	Val	Tyr	Asn	Ala	Ser	Asn	Asn	Glu	Leu	Val	Arg	Thr	Lys	Thr	
			85						90					95		
Leu	Val	Lys	Ser	Ala	Ile	Val	Gln	Val	Asp	Ala	Ala	Pro	Phe	Lys	Gln	
			100					105					110			
Trp	Tyr	Leu	Ser	His	Tyr	Gly	Val	Glu	Leu	Gly	Arg	Lys	Lys	Lys	Ser	
		115				120					125					
Ala	Ser	Ser	Thr	Lys	Lys	Asp	Gly	Glu	Glu	Gly	Glu	Glu	Ala	Ala	Val	
		130				135					140					
Ala	Ala	Pro	Glu	Glu	Val	Lys	Lys	Ser	Asn	His	Leu	Leu	Arg	Lys	Ile	
		145				150				155					160	
Ala	Ser	Arg	Gln	Glu	Gly	Arg	Ser	Leu	Asp	Ser	His	Ile	Glu	Asp	Gln	
			165						170					175		
Phe	Ala	Ser	Gly	Arg	Leu	Leu	Ala	Cys	Ile	Ser	Ser	Arg	Pro	Gly	Gln	
		180						185					190			
Cys	Gly	Arg	Ala	Asp	Gly	Tyr	Ile	Leu	Glu	Gly	Lys	Glu	Leu	Glu	Phe	
		195				200						205				
Tyr	Met	Lys	Lys	Ile	Gln	Lys	Lys	Lys	Gly	Lys	Gly	Ala	Ala			
	210					215					220					

(2) INFORMATION FOR SEQ ID NO:1649:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 194 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..194

(D) OTHER INFORMATION: / Ceres Seq. ID 1570571

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1649:

Met	Gly	Arg	Gln	Pro	Ala	Asn	Thr	Lys	Leu	Ser	Ser	Asn	Lys	Thr	Val	
1			5						10				15			
Arg	Arg	Ile	Arg	Val	Arg	Gly	Gly	Asn	Val	Lys	Trp	Arg	Ala	Leu	Arg	
		20					25						30			
Leu	Asp	Thr	Gly	Asn	Tyr	Ser	Trp	Gly	Ser	Glu	Ala	Thr	Thr	Arg	Lys	
		35					40					45				
Thr	Arg	Val	Leu	Asp	Val	Val	Tyr	Asn	Ala	Ser	Asn	Asn	Glu	Leu	Val	
		50				55					60					
Arg	Thr	Lys	Thr	Leu	Val	Lys	Ser	Ala	Ile	Val	Gln	Val	Asp	Ala	Ala	
		65			70				75					80		
Pro	Phe	Lys	Gln	Trp	Tyr	Leu	Ser	His	Tyr	Gly	Val	Glu	Leu	Gly	Arg	
			85					90					95			
Lys	Lys	Lys	Ser	Ala	Ser	Ser	Thr	Lys	Lys	Asp	Gly	Glu	Glu	Gly	Glu	
		100					105					110				
Glu	Ala	Ala	Val	Ala	Ala	Pro	Glu	Glu	Val	Lys	Lys	Ser	Asn	His	Leu	
		115				120						125				
Leu	Arg	Lys	Ile	Ala	Ser	Arg	Gln	Glu	Gly	Arg	Ser	Leu	Asp	Ser	His	
		130				135					140					
Ile	Glu	Asp	Gln	Phe	Ala	Ser	Gly	Arg	Leu	Leu	Ala	Cys	Ile	Ser	Ser	
		145			150				155						160	
Arg	Pro	Gly	Gln	Cys	Gly	Arg	Ala	Asp	Gly	Tyr	Ile	Leu	Glu	Gly	Lys	
			165						170					175		
Glu	Leu	Glu	Phe	Tyr	Met	Lys	Lys	Ile	Gln	Lys	Lys	Lys	Gly	Lys	Gly	
			180					185					190			

(2) INFORMATION FOR SEQ ID NO:1650:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 830 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..830
(D) OTHER INFORMATION: / Ceres Seq. ID 1570576
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1650:
attctctctt agtctctcta cggaacctgt cttctgtct tgtccaaaaa cggatttttta 60
agagtacaag tgaagtttatt ttggggggccg aaatctgtcc tggaggatcac agaagcaaga 120
tgaagtttaat agatcgatag aatgaggtta acggagctgc tcttacgggtg ctcacatcagt 180
gtcttcgctc tctctcgccgt tattctagtt gtgacagaca ctgagggtcaa gcttatcttc 240
aatatcaaga agacgggcaa gtacacggac atgaaggcgg ttgtgtctct ggtggtgctct 300
aatgggtagat ctgcggtttta ttctttgttg caatcagttc gttgcgtggt gggtagcagt 360
aaaggaagag ttttgtttas taagcctctt gcttgggctt tttctcbgg gtagcaggcg 420
atggcgctact tgaatgtggc agccattgca gcaacagcag agtctgggtKT gWRattgtcta 480
gggaaggaga ggaagatttt caatggatga gagtgtgtac tatgtatgga aagttcttca 540
accaaatgag tataggagtc tctagcgctt tgttagcctc cattgctatg gttttcgctct 600
cctgcatttc tgcttttagt ctcttcgcgt gtacaggtgc caccaaaagac cgcagaacca 660
cgccgtgggt aagtgaatgc ggcctttgtc ttagtgtgtg tgaataatgt Ygtgtgttaa 720
aaaacatata gtaaaaaaag tgtaggcctc tgttggttct tcttcttctt cttcttgatg 780
atgttatatg tgacaaacaa tatgtataaac tagactattg atgttctgtg
(2) INFORMATION FOR SEQ ID NO:1651:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 122 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..122
(D) OTHER INFORMATION: / Ceres Seq. ID 1570577
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1651:
Met Arg Leu Thr Glu Leu Leu Leu Arg Cys Ser Ile Ser Val Phe Ala
1 5 10 15
Leu Leu Ala Leu Ile Leu Val Val Thr Asp Thr Glu Val Lys Leu Ile
20 25 30
Phe Thr Ile Lys Lys Thr Ala Lys Tyr Thr Asp Met Lys Ala Val Val
35 40 45
Phe Leu Val Val Ala Asn Gly Ile Ala Ala Val Tyr Ser Leu Leu Gln
50 55 60
Ser Val Arg Cys Val Val Gly Thr Met Lys Gly Lys Val Leu Phe Xaa
65 70 75 80
Lys Pro Leu Ala Trp Ala Phe Phe Xaa Gly Asp Gln Ala Met Ala Tyr
85 90 95
Leu Asn Val Ala Ala Ile Ala Ala Thr Ala Glu Ser Gly Xaa Xaa Leu
100 105 110
Leu Gly Lys Glu Arg Lys Ile Cys Asn Gly
115 120
(2) INFORMATION FOR SEQ ID NO:1652:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 79 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..79
(D) OTHER INFORMATION: / Ceres Seq. ID 1570578
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1652:

```

Met Lys Ala Val Val Phe Leu Val Val Ala Asn Gly Ile Ala Ala Val
1           5           10          15
Tyr Ser Leu Leu Gln Ser Val Arg Cys Val Val Gly Thr Met Lys Gly
          20          25          30
Lys Val Leu Phe Xaa Lys Pro Leu Ala Trp Ala Phe Phe Xaa Gly Asp
          35          40          45
Gln Ala Met Ala Tyr Leu Asn Val Ala Ala Ile Ala Ala Thr Ala Glu
          50          55          60
Ser Gly Xaa Xaa Leu Leu Gly Lys Glu Arg Lys Ile Cys Asn Gly
65          70          75

```

(2) INFORMATION FOR SEQ ID NO:1653:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 736 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..736

(D) OTHER INFORMATION: / Ceres Seq. ID 1570583

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1653:

```

ctgaaccctt cgattttcga ttctctctcg agccttctct ccttctctcG tttMetctctc 60
aagaggattt tgattgtctc cttactctct ccatgtcaag ttctggtgct ccttcacgca 120
agactctgag taagatgcgc actaatcgtc ttcagaaaga gcttgtggaa tggcagatga 180
atccacctac tgggtttcaaa cacaaagtca ctgataatct ccaaagatgg ataattgaag 240
ttattggagc tccaggaaact ctatatgcc aacgatactta tcagcttcaa gttgattttc 300
cagaacatta tccataggaa tcgcacaaag tgatttttct tcactccagct cctctgcatc 360
ctcacattta cagcaatggg catatttgtc tagatatttt gtatgattgg tggctctccag 420
ccatgacggt gacttctatc tgcattagca tctcttccat gctctcaagc tcgactgaaa 480
agcaacgacc aaccgataat gaccgatgtg tgaagaattg taagaacgga agatctccaa 540
aggagaccgg atgggtggtc cagcagcata aagtataaac ctcgatcaac caaaaaaat 600
gtaaaatagt ccaaaacagt ctttgagggt tggttgtctat ttttaattta attgggttta 660
agctgtccca aaccctattc caaaatccgt gatgtataaa aacaacacaa taaatttgac 720
taattttgaa tcttcc

```

(2) INFORMATION FOR SEQ ID NO:1654:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 191 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..191

(D) OTHER INFORMATION: / Ceres Seq. ID 1570584

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1654:

```

Glu Pro Phe Asp Phe Arg Phe Phe Leu Glu Pro Ser Phe Leu Pro Ser
1           5           10          15
Xaa Leu Leu Gln Glu Asp Phe Asp Cys Leu Leu Thr Leu Ser Met Ser
          20          25          30
Ser Ser Gly Ala Pro Ser Arg Lys Thr Leu Ser Lys Ile Ala Thr Asn
          35          40          45
Arg Leu Gln Lys Glu Leu Val Glu Trp Gln Met Asn Pro Pro Thr Gly
          50          55          60
Phe Lys His Lys Val Thr Asp Asn Leu Gln Arg Trp Ile Ile Glu Val
65          70          75          80
Ile Gly Ala Pro Gly Thr Leu Tyr Ala Asn Asp Thr Tyr Gln Leu Gln
          85          90          95
Val Asp Phe Pro Glu His Tyr Pro Met Glu Ser Pro Gln Val Ile Phe
          100          105          110

```

Leu His Pro Ala Pro Leu His Pro His Ile Tyr Ser Asn Gly His Ile
115 120 125
Cys Leu Asp Ile Leu Tyr Asp Ser Trp Ser Pro Ala Met Thr Val Ser
130 135 140
Ser Ile Cys Ile Ser Ile Leu Ser Met Leu Ser Ser Thr Glu Lys
145 150 155 160
Gln Arg Pro Thr Asp Asn Asp Arg Tyr Val Lys Asn Cys Lys Asn Gly
165 170 175
Arg Ser Pro Lys Glu Thr Arg Trp Trp Phe His Asp Asp Lys Val
180 185 190

(2) INFORMATION FOR SEQ ID NO:1655:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 161 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..161

(D) OTHER INFORMATION: / Ceres Seq. ID 1570585

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1655:

Met Ser Ser Ser Gly Ala Pro Ser Arg Lys Thr Leu Ser Lys Ile Ala
1 5 10 15
Thr Asn Arg Leu Gln Lys Glu Leu Val Glu Trp Gln Met Asn Pro Pro
20 25 30
Thr Gly Phe Lys His Lys Val Thr Asp Asn Leu Gln Arg Trp Ile Ile
35 40 45
Glu Val Ile Gly Ala Pro Gly Thr Leu Tyr Ala Asn Asp Thr Tyr Gln
50 55 60
Leu Gln Val Asp Phe Pro Glu His Tyr Pro Met Glu Ser Pro Gln Val
65 70 75 80
Ile Phe Leu His Pro Ala Pro Leu His Pro His Ile Tyr Ser Asn Gly
85 90 95
His Ile Cys Leu Asp Ile Leu Tyr Asp Ser Trp Ser Pro Ala Met Thr
100 105 110
Val Ser Ser Ile Cys Ile Ser Ile Leu Ser Met Leu Ser Ser Ser Thr
115 120 125
Glu Lys Gln Arg Pro Thr Asp Asn Asp Arg Tyr Val Lys Asn Cys Lys
130 135 140
Asn Gly Arg Ser Pro Lys Glu Thr Arg Trp Trp Phe His Asp Asp Lys
145 150 155 160
Val

(2) INFORMATION FOR SEQ ID NO:1656:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 133 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..133

(D) OTHER INFORMATION: / Ceres Seq. ID 1570586

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1656:

Met Asn Pro Pro Thr Gly Phe Lys His Lys Val Thr Asp Asn Leu Gln
1 5 10 15
Arg Trp Ile Ile Glu Val Ile Gly Ala Pro Gly Thr Leu Tyr Ala Asn
20 25 30
Asp Thr Tyr Gln Leu Gln Val Asp Phe Pro Glu His Tyr Pro Met Glu

	35		40		45	
Ser	Pro	Gln	Val	Ile	Phe	Leu
50					55	His
Tyr	Ser	Asn	Gly	His	Ile	Cys
65					70	Leu
Pro	Ala	Met	Thr	Val	Ser	Ser
					85	Ile
Ser	Ser	Ser	Thr	Glu	Lys	Gln
					100	Arg
Lys	Asn	Cys	Lys	Asn	Gly	Arg
					115	Ser
His	Asp	Asp	Lys	Val		
					130	

(2) INFORMATION FOR SEQ ID NO:1657:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 936 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..936
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570603

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1657:

ctagacgtcg	aagatgaaGt	tcaacgTbga	gaatccaact	actggatgcc	agaagaagct	60
cgagatcgac	gatgaccaga	aactacgtgc	gttttacgac	aagagaatct	ctcaagaagt	120
cagtgagat	gctttggcg	aggagtcca	aggatacggt	tcaagatca	agggtggtg	180
cgataagcaa	ggtttcccaa	tgaagcagg	agttttgact	ccaggccgtg	ttcgcccttt	240
gcttcacoga	ggaaactcct	gcttcagagg	acatggaagg	akaactgggtg	agaggagaag	300
aaagtctgtt	cgtggttgca	ttgtgagccc	tgactctctc	gttctgaacc	ttgtcattgt	360
gaagaagggt	gagaacgata	ttcctgggct	taccgatact	gagaagccaa	gaatgagagg	420
accaaagaga	gcctccaaga	tcctgtaact	gtttaacctc	aagaaggaag	atgatgtcag	480
gacctatgtc	aacacttacc	gccgcaagtt	cacaaacaag	aagggcaagg	aagttagcaa	540
agcccctaag	atccagaggg	ttgtgacccc	attgactctt	cagaggaaga	gagctagaat	600
tgctgacaag	aagaagaaaa	ttgctaaggc	taattctgat	gctgctgatt	accagaagct	660
tctgcctcgt	aggttgaagg	aacagcgtga	caggaggagt	gagagtgttg	caagaagag	720
gtcgagactc	tctctcgtgt	ctgccaagcc	ctctgtcaca	gcttaaaaaa	gcttgagaat	780
caaatcaaa	atgtcAcSSc	ttctctgttt	tgctctcttt	tcttctccgg	ctattaaaaa	840
gttagttcga	gttcatattc	agctgttttt	gttccaagac	atgggttacac	aatcgctttg	900

(2) INFORMATION FOR SEQ ID NO:1658:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 250 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..250
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570604

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1658:

Met	Lys	Phe	Asn	Xaa	Glu	Asn	Pro	Thr	Thr	Gly	Cys	Gln	Lys	Lys	Leu
1				5					10				15		
Glu	Ile	Asp	Asp	Asp	Gln	Lys	Leu	Arg	Ala	Phe	Tyr	Asp	Lys	Arg	Ile
				20				25					30		
Ser	Gln	Glu	Val	Ser	Gly	Asp	Ala	Leu	Gly	Glu	Glu	Phe	Lys	Gly	Tyr
				35				40					45		
Val	Phe	Lys	Ile	Lys	Gly	Gly	Cys	Asp	Lys	Gln	Gly	Phe	Pro	Met	Lys
				50				55					60		

Gln Gly Val Leu Thr Pro Gly Arg Val Arg Leu Leu Leu His Arg Gly
65 70 75 80
Thr Pro Cys Phe Arg Gly His Gly Arg Xaa Thr Gly Glu Arg Arg Arg
85 90 95
Lys Ser Val Arg Gly Cys Ile Val Ser Pro Asp Leu Ser Val Leu Asn
100 105 110
Leu Val Ile Val Lys Lys Gly Glu Asn Asp Leu Pro Gly Leu Thr Asp
115 120 125
Thr Glu Lys Pro Arg Met Arg Gly Pro Lys Arg Ala Ser Lys Ile Arg
130 135 140
Lys Leu Phe Asn Leu Lys Lys Glu Asp Asp Val Arg Thr Tyr Val Asn
145 150 155 160
Thr Tyr Arg Arg Lys Phe Thr Asn Lys Lys Gly Lys Glu Val Ser Lys
165 170 175
Ala Pro Lys Ile Gln Arg Leu Val Thr Pro Leu Thr Leu Gln Arg Lys
180 185 190
Arg Ala Arg Ile Ala Asp Lys Lys Lys Lys Ile Ala Lys Ala Asn Ser
195 200 205
Asp Ala Ala Asp Tyr Gln Lys Leu Leu Ala Ser Arg Leu Lys Glu Gln
210 215 220
Arg Asp Arg Arg Ser Glu Ser Leu Ala Lys Lys Arg Ser Arg Leu Ser
225 230 235 240
Ser Ala Ala Ala Lys Pro Ser Val Thr Ala
245 250

(2) INFORMATION FOR SEQ ID NO:1659:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 188 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..188

(D) OTHER INFORMATION: / Ceres Seq. ID 1570605

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1659:

Met Lys Gln Gly Val Leu Thr Pro Gly Arg Val Arg Leu Leu Leu His
1 5 10 15
Arg Gly Thr Pro Cys Phe Arg Gly His Gly Arg Xaa Thr Gly Glu Arg
20 25 30
Arg Arg Lys Ser Val Arg Gly Cys Ile Val Ser Pro Asp Leu Ser Val
35 40 45
Leu Asn Leu Val Ile Val Lys Lys Gly Glu Asn Asp Leu Pro Gly Leu
50 55 60
Thr Asp Thr Glu Lys Pro Arg Met Arg Gly Pro Lys Arg Ala Ser Lys
65 70 75 80
Ile Arg Lys Leu Phe Asn Leu Lys Lys Glu Asp Asp Val Arg Thr Tyr
85 90 95
Val Asn Thr Tyr Arg Arg Lys Phe Thr Asn Lys Lys Gly Lys Glu Val
100 105 110
Ser Lys Ala Pro Lys Ile Gln Arg Leu Val Thr Pro Leu Thr Leu Gln
115 120 125
Arg Lys Arg Ala Arg Ile Ala Asp Lys Lys Lys Lys Ile Ala Lys Ala
130 135 140
Asn Ser Ser Asp Ala Ala Asp Tyr Gln Lys Leu Leu Ala Ser Arg Leu Lys
145 150 155 160
Glu Gln Arg Asp Arg Arg Ser Glu Ser Leu Ala Lys Lys Arg Ser Arg
165 170 175
Leu Ser Ser Ala Ala Lys Pro Ser Val Thr Ala
180 185

(2) INFORMATION FOR SEQ ID NO:1660:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 833 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..833
(D) OTHER INFORMATION: / Ceres Seq. ID 1570606
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1660:
agacgtcgaa gatgaagttc aacgttgccg agttcaaaagg atacgttttc aagatcaagg 60
gtgggtgcga taagcaagggt ttcccaatga agcagggagt ttgactcca gcccggtgtc 120
gccttttgct tcaccgagga actcctttgct tcagaggaca tgggaaggaga actggttgaga 180
ggagaagaaa gtctgttcgt ggttgcaattg tgagccctga tctctctgt ctgaaccttg 240
tcatttgtaa gaaggggtgag aacgatcttc ctgggcttac cgatactgag aagccaagaa 300
tgagaggacc aaagagagacc tccaagatcc tgaacctgtt taacctcaag aaggaagatg 360
atgtcaggac ctatgtcaac acttaccgcc gcaagttcac aaacaagaag ggcaaggaa 420
ttagcaaaag ccctaaagatc cagaggcttg tgacccatt gactcttcag aggaagagag 480
ctagaattgc tgacaagaag aagaaaattg ctaaggctaa ttctgatgct gctgattacc 540
agaagcttct cgctcgaag ttgaaggaa acgctgacag gaggagtga agTttggcAa 600
agaagaggtc gagactctct tctgctgctg ccaagccctc tgtcacagct taaaaaagct 660
tgagaatcaa atcaaaagatg tcacctttct agtCtttggt ctcttttctt ctccggctat 720
taaaaaagtta gttcgagttc atattcagct gtttttgttc caagacatgg gtacacaatc 780
gctttgggct tgtttcatga tttatgcttt tagttgaaga ccaattttaa ctc
(2) INFORMATION FOR SEQ ID NO:1661:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 216 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..216
(D) OTHER INFORMATION: / Ceres Seq. ID 1570607
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1661:
Thr Ser Lys Met Lys Phe Asn Val Ala Glu Phe Lys Gly Tyr Val Phe
1 5 10 15
Lys Ile Lys Gly Gly Cys Asp Lys Gln Gly Phe Pro Met Lys Gln Gly
20 25 30
Val Leu Thr Pro Gly Arg Val Arg Leu Leu Leu His Arg Gly Thr Pro
35 40 45
Cys Phe Arg Gly His Gly Arg Arg Thr Gly Glu Arg Arg Arg Lys Ser
50 55 60
Val Arg Gly Cys Ile Val Ser Pro Asp Leu Ser Val Leu Asn Leu Val
65 70 75 80
Ile Val Lys Lys Gly Glu Asn Asp Leu Pro Gly Leu Thr Asp Thr Glu
85 90 95
Lys Pro Arg Met Arg Gly Pro Lys Arg Ala Ser Lys Ile Arg Lys Leu
100 105 110
Phe Asn Leu Lys Lys Glu Asp Asp Val Arg Thr Tyr Val Asn Thr Tyr
115 120 125
Arg Arg Lys Phe Thr Asn Lys Lys Gly Lys Glu Val Ser Lys Ala Pro
130 135 140
Lys Ile Gln Arg Leu Val Thr Pro Leu Thr Lys Gln Arg Lys Arg Ala
145 150 155 160
Arg Ile Ala Asp Lys Lys Lys Ile Ala Lys Ala Asn Ser Asp Ala
165 170 175
Ala Asp Tyr Gln Lys Leu Leu Ala Ser Arg Leu Lys Glu Gln Arg Asp
180 185 190

Arg Arg Ser Glu Ser Leu Ala Lys Lys Arg Ser Arg Leu Ser Ser Ala
195 200 205
Ala Ala Lys Pro Ser Val Thr Ala
210 215

(2) INFORMATION FOR SEQ ID NO:1662:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 213 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..213
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570608

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1662:

Met Lys Phe Asn Val Ala Glu Phe Lys Gly Tyr Val Phe Lys Ile Lys
1 5 10 15
Gly Gly Cys Asp Lys Lys Gln Gly Phe Pro Met Lys Gln Gly Val Leu Thr
20 25 30
Pro Gly Arg Val Arg Leu Leu Leu His Arg Gly Thr Pro Cys Phe Arg
35 40 45
Gly His Gly Arg Arg Thr Gly Glu Arg Arg Arg Lys Ser Val Arg Gly
50 55 60
Cys Ile Val Ser Pro Asp Leu Ser Val Leu Asn Leu Val Ile Val Lys
65 70 75 80
Lys Gly Glu Asn Asp Leu Pro Gly Leu Thr Asp Thr Glu Lys Pro Arg
85 90 95
Met Arg Gly Pro Lys Arg Ala Ser Lys Ile Arg Lys Leu Phe Asn Leu
100 105 110
Lys Lys Glu Asp Asp Val Arg Thr Tyr Val Asn Thr Tyr Arg Arg Lys
115 120 125
Phe Thr Asn Lys Lys Gly Lys Glu Val Ser Lys Ala Pro Lys Ile Gln
130 135 140
Arg Leu Val Thr Pro Leu Thr Leu Gln Arg Lys Arg Ala Arg Ile Ala
145 150 155 160
Asp Lys Lys Lys Lys Ile Ala Lys Ala Asn Ser Asp Ala Ala Asp Tyr
165 170 175
Gln Lys Leu Leu Ala Ser Arg Leu Lys Glu Gln Arg Asp Arg Arg Ser
180 185 190
Glu Ser Leu Ala Lys Lys Arg Ser Arg Leu Ser Ser Ala Ala Ala Lys
195 200 205
Pro Ser Val Thr Ala
210

(2) INFORMATION FOR SEQ ID NO:1663:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 188 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..188
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570609

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1663:

Met Lys Gln Gly Val Leu Thr Pro Gly Arg Val Arg Leu Leu Leu His
1 5 10 15
Arg Gly Thr Pro Cys Phe Arg Gly His Gly Arg Arg Thr Gly Glu Arg
20 25 30
Arg Arg Lys Ser Val Arg Gly Cys Ile Val Ser Pro Asp Leu Ser Val

35	40	45
Leu Asn Leu Val Ile Val Lys Lys Gly Glu Asn Asp Leu Pro Gly Leu		
50	55	60
Thr Asp Thr Glu Lys Pro Arg Met Arg Gly Pro Lys Arg Ala Ser Lys		
65	70	75
Ile Arg Lys Leu Phe Asn Leu Lys Lys Glu Asp Val Arg Thr Tyr		
85	90	95
Val Asn Thr Tyr Arg Arg Lys Phe Thr Asn Lys Lys Gly Lys Glu Val		
100	105	110
Ser Lys Ala Pro Lys Ile Gln Arg Leu Val Thr Pro Leu Thr Leu Gln		
115	120	125
Arg Lys Arg Ala Arg Ile Ala Asp Lys Lys Lys Ile Ala Lys Ala		
130	135	140
Asn Ser Asp Ala Ala Asp Tyr Gln Lys Leu Leu Ala Ser Arg Leu Lys		
145	150	155
Glu Gln Arg Asp Arg Arg Ser Glu Ser Leu Ala Lys Lys Arg Ser Arg		
165	170	175
Leu Ser Ser Ala Ala Lys Pro Ser Val Thr Ala		
180	185	

(2) INFORMATION FOR SEQ ID NO:1664:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 721 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..721
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570610

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1664:

agtttagatt	ctttatccga	ctactttgtt	catcggtttt	gtttttcttt	ttgtcttcgcg	60
gaagcggaat	tacatgtcgg	aagcagcaca	gctcagaaga	ggctctaaagc	ctaaagggaa	120
gacttatggg	ttgaccaatc	agaagagacg	agagatcaga	ggatctcttg	atcttttcga	180
catagacggg	tcaggtagca	tcgatgctag	cgagctcaac	gtgtctatga	ggctctcttg	240
atttgagatg	aataatcagc	aaataaacga	attgatggca	gaagtagata	aaaaccaaag	300
tggagccata	gatttcgacg	aatttgtgca	tatgatgaca	accaaatcgc	gagaacgaga	360
ctccatagac	gaattgtcta	agggcgttta	gatcattgac	cacgacaata	gtgggaagat	420
ttcacctcgt	gatataaaga	tgatttgctaa	agaattggga	gaaaatttca	cagataatga	480
tatagaagaa	atgatcgaa	aagcagaccg	tgacaagaat	ggagaagtta	acttgaggga	540
gttcataaas	gatgatgaag	agaacctctt	tcggctaagt	ataaatcaat	tagtaattgg	600
tgtgaataat	atttgttaat	caccttgatt	tataataata	aagaagtgtg	atttgtggct	660
tggtogaata	aaaatgtatt	gttgtataaa	ataataaatg	taattcacat	ccattatttt	720

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(2) INFORMATION FOR SEQ ID NO:1665:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 181 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..181
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570611

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1665:

Met Ser Glu Ala Ala Gln Leu Arg Arg Gly Leu Lys Pro Lys Gly Lys	
1	10
Thr Tyr Gly Leu Thr Asn Gln Lys Arg Arg Glu Ile Arg Glu Ile Phe	
20	30
Asp Leu Phe Asp Ile Asp Gly Ser Gly Ser Ile Asp Ala Ser Glu Leu	

(2) INFORMATION FOR SEO ID NO:1666:

(A) LENGTH: 130 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: lin

MOLECULE TYPE: peptid

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..130

(D) OTHER INFORMATION: / Ceres Seq. ID 1570612

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1666:

(2) INFORMATION FOR SEQ ID NO:1667:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 123 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..123

(D) OTHER INFORMATION: / Ceres Seq. ID 1570613

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1667:

Met Asn Asn Gln Gln Ile Asn Glu Leu Met Ala Glu Val Asp Lys Asn
1 5 10 15
Gln Ser Gly Ala Ile Asp Phe Asp Glu Phe Val His Met Met Thr Thr
20 25 30
Lys Phe Gly Glu Arg Asp Ser Ile Asp Glu Leu Ser Lys Ala Phe Lys
35 40 45
Ile Ile Asp His Asp Asn Ser Gly Lys Ile Ser Pro Arg Asp Ile Lys
50 55 60
Met Ile Ala Lys Glu Leu Gly Glu Asn Phe Thr Asp Asn Asp Ile Glu
65 70 75 80
Glu Met Ile Glu Glu Ala Asp Arg Asp Lys Asp Gly Glu Val Asn Leu
85 90 95
Glu Glu Phe Met Xaa Asp Asp Glu Glu Asn Leu Phe Arg Leu Ser Ile
100 105 110
Asn Gln Leu Val Met Val Val Asn Asn Ile Cys
115 120

(2) INFORMATION FOR SEQ ID NO:1668:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 922 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..922
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570618

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1668:

actcagagac	ttgttgtgaa	gttgaaactc	tctgaccgta	gctttcttat	ctttcattca	60
ggttcaactac	tatgtacagt	ctcacattca	aatgaatgag	taccgggacg	gtgtgtgtatt	120
gccatctgct	tcaagaagac	agggacgacc	aatttgcact	tgtttgaaaa	tttttgatat	180
gtctgtgttta	aagctttcag	ctttaagtca	aattaaagtta	atgactgcta	taacacaacat	240
agatgatttg	aactatccag	agaagacaga	gacatactat	gttgtcaatg	tcctgtacat	300
attctctgct	tggttgaaaa	ccataaagcc	tctgttgcaa	gagagaacaa	agaagaagat	360
tcaagtctctg	aaaggttgcg	ggaaagatga	gttgctaaag	ataatggact	atgagtctct	420
cccacatttc	tgtagaagag	aagggtctgg	atctggtagg	catatctcaa	atggaaacagt	480
agacaattgt	ttctctctgg	atcactcttt	ccaccaagac	ctttatgatt	atgtcaagca	540
gcaggctctg	gttaaaagat	caggtgcacc	gatcagacat	ggttcagtc	acgttaagtt	600
ccctgagcca	gacaccgaag	gcaacaagat	cttcgatacc	ttagaaaaatg	agttccagaa	660
gcttggaaat	gaccagaaga	tctgagtgat	ctacaaccct	tataaacaga	attgcccata	720
agaaaaccga	atttgtctct	ggttgatgag	cagtatattaa	gataagaatc	aatcaccttt	780
acttgtatta	ctagttttcgc	ttgcatcagc	tMcgatgcag	gttttgytta	aaaagaagat	840
ggaacacaat	ttcctcggaa	ttgatctttt	gatctagtac	cattatatat	atagaactca	900
ttcttattta	tgctcttttg	cc				

(2) INFORMATION FOR SEQ ID NO:1669:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 197 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..197
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570619

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1669:

Met Asn Glu Tyr Arg Asp Arg Val Val Leu Pro Ser Ala Ser Lys Lys
1 5 10 15
Gln Gly Arg Pro Ile Cys Thr Cys Leu Lys Ile Leu Asp Met Ser Gly
20 25 30
Leu Lys Leu Ser Ala Leu Ser Gln Ile Lys Leu Met Thr Ala Ile Thr

(2) INFORMATION FOR SEO ID NO:1670:

(A) LENGTH: 168 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

MOLECULE TYPE: peptid

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..168

(D) OTHER INFORMATION: / Ceres Seq. ID 1570620

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1670:
```

(2) INFORMATION FOR SEQ ID NO:1671:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 154 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..154
 (D) OTHER INFORMATION: / Ceres Seq. ID 1570621
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1671:

Met	Thr	Ala	Ile	Thr	Thr	Ile	Asp	Asp	Leu	Asn	Tyr	Pro	Glu	Lys	Thr
1			5						10				15		
Glu	Thr	Tyr	Tyr	Val	Val	Asn	Val	Pro	Tyr	Ile	Phe	Ser	Ala	Cys	Trp
			20				25					30			
Lys	Thr	Ile	Lys	Pro	Leu	Leu	Gln	Glu	Arg	Thr	Lys	Lys	Lys	Ile	Gln
		35					40				45				
Val	Leu	Lys	Gly	Cys	Gly	Lys	Asp	Glu	Leu	Leu	Lys	Ile	Met	Asp	Tyr
		50				55					60				
Glu	Ser	Leu	Pro	His	Phe	Cys	Arg	Arg	Glu	Gly	Ser	Gly	Ser	Gly	Arg
		65			70				75				80		
His	Ile	Ser	Asn	Gly	Thr	Val	Asp	Asn	Cys	Phe	Ser	Leu	Asp	His	Ser
			85					90					95		
Phe	His	Gln	Asp	Leu	Tyr	Asp	Tyr	Val	Lys	Gln	Gln	Ala	Leu	Val	Lys
		100						105					110		
Gly	Ser	Gly	Ala	Pro	Ile	Arg	His	Gly	Ser	Val	His	Val	Lys	Phe	Pro
		115				120						125			
Glu	Pro	Asp	Thr	Glu	Gly	Asn	Lys	Ile	Phe	Asp	Thr	Leu	Glu	Asn	Glu
		130				135					140				
Phe	Gln	Lys	Leu	Gly	Asn	Asp	Gln	Lys	Ile						
		145				150									

(2) INFORMATION FOR SEQ ID NO:1672:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1082 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..1082
(D) OTHER INFORMATION: / Ceres Seq. ID 1570622

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1672:

gtttgtccct	ccttctacgc	cgcacactat	cttttctctct	cactcagact	tcctcttccat	60
ctcaagagaa	atggctgaat	ccaaggtagt	ggttccagag	tctgtgctaa	agaagatcaa	120
gagggcaagag	gaatgggcat	tggccaagaa	agatgaagct	gtagctgcta	agaagaagag	180
gtttgaggcc	cgcaagctta	tottcaagag	agctgagcag	tatgccaaa	aatacgcgtg	240
gaaggataac	gagttgatcc	gattgaagcg	ggaggctaag	ttgaaaggag	gtttctacgt	300
tgacctgag	gctaagtgtc	tctttatcat	tcgtatccgt	ggatccaatg	ccattgaccc	360
aaaaaccaag	aagattctgc	agctctcg	tttgagacag	gtagggttca	cagtttgtta	420
ttttcatcca	gctatatattag	octaacatat	gattattgat	taatatgtgt	tatatgttca	480
aactaatatg	tgatagttgc	ctgttcatca	tttttaaaag	agagtagaag	actattgcgt	540
tgccaagaag	tttacttttcg	tatacatattg	tgcatgctct	caatgggtgtg	tttcttaagg	600
tgaacaaggc	aacagtaaac	atGctgcgcc	gagttgaacc	atacgtgact	tacggataacc	660
caaaacttgaa	gagcgttaag	gaactgatct	acaaaagagg	ttatggaaa	ctgaaccacc	720
agaggatagc	acttactgac	aactccattg	tggatcaggc	tctcggaaa	catgggatca	780
tctgcgttga	ggatctcatc	cagagatca	tgactgttgg	acctcacttc	aaggaagcca	840
acaaacttct	gtggccattc	caattgaagg	caccactcgg	tggccttaag	aagaagagaa	900
accactacgt	cgaaggtgtg	gatgctggaa	acaggggaaa	tttcatcaac	gagcttgctca	960
ggagaatgaa	ttgatgaag	cttctctctt	tatctttgca	aatttcaag	attttgggac	1020
cgagtttttt	tttttttttt	ttcaagttat	cagagacttg	tgatctttta	tcagagatag	1080

gc

(2) INFORMATION FOR SEQ ID NO:1673:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 147 amino acids
(B) TYPE: amino acid

(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..147
 (D) OTHER INFORMATION: / Ceres Seq. ID 1570623
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1673:
Phe Cys Pro Pro Ser Thr Pro His Thr Ile Phe Ser Ser His Ser Asp
1 5 10 15
Phe Leu Phe Ile Ser Arg Glu Met Ala Glu Ser Lys Val Val Val Pro
 20 25 30
Glu Ser Val Leu Lys Lys Ile Lys Arg Gln Glu Glu Trp Ala Leu Ala
35 40 45
Lys Lys Asp Glu Ala Val Ala Ala Lys Lys Lys Ser Val Glu Ala Arg
50 55 60
Lys Leu Ile Phe Lys Arg Ala Glu Gln Tyr Ala Lys Glu Tyr Ala Glu
65 70 75 80
Lys Asp Asn Glu Leu Ile Arg Leu Lys Arg Glu Ala Lys Leu Lys Gly
 85 90 95
Gly Phe Tyr Val Asp Pro Glu Ala Lys Leu Leu Phe Ile Ile Arg Ile
 100 105 110
Arg Gly Ile Asn Ala Ile Asp Pro Lys Thr Lys Lys Ile Leu Gln Leu
115 120 125
Leu Arg Leu Arg Gln Val Gly Phe Thr Val Cys Tyr Phe His Pro Ala
130 135 140
Ile Leu Ala
145
(2) INFORMATION FOR SEQ ID NO:1674:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 124 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..124
 (D) OTHER INFORMATION: / Ceres Seq. ID 1570624
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1674:
Met Ala Glu Ser Lys Val Val Val Pro Glu Ser Val Leu Lys Lys Ile
1 5 10 15
Lys Arg Gln Glu Trp Ala Leu Ala Lys Lys Asp Glu Ala Val Ala
20 25 30
Ala Lys Lys Lys Ser Val Glu Ala Arg Lys Leu Ile Phe Lys Arg Ala
35 40 45
Glu Gln Tyr Ala Lys Glu Tyr Ala Glu Lys Asp Asn Glu Leu Ile Arg
50 55 60
Leu Lys Arg Glu Ala Lys Leu Lys Gly Gly Phe Tyr Val Asp Pro Glu
65 70 75 80
Ala Lys Leu Leu Phe Ile Ile Arg Ile Arg Gly Ile Asn Ala Ile Asp
 85 90 95
Pro Lys Thr Lys Lys Ile Leu Gln Leu Leu Arg Leu Arg Gln Val Gly
100 105 110
Phe Thr Val Cys Tyr Phe His Pro Ala Ile Leu Ala
115 120
(2) INFORMATION FOR SEQ ID NO:1675:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 117 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:

(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..117
 (D) OTHER INFORMATION: / Ceres Seq. ID 1570625
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1675:
Met Leu Arg Arg Val Glu Pro Tyr Val Thr Tyr Gly Tyr Pro Asn Leu
1 5 10 15
Lys Ser Val Lys Glu Leu Ile Tyr Lys Arg Gly Tyr Gly Lys Leu Asn
 20 25 30
His Gln Arg Ile Ala Leu Thr Asp Asn Ser Ile Val Asp Gln Ala Leu
 35 40 45
Gly Lys His Gly Ile Ile Cys Val Glu Asp Leu Ile His Glu Ile Met
 50 55 60
Thr Val Gly Pro His Phe Lys Glu Ala Asn Asn Phe Leu Trp Pro Phe
65 70 75 80
Gln Leu Lys Ala Pro Leu Gly Gly Leu Lys Lys Arg Asn His Tyr
 85 90 95
Val Glu Gly Gly Asp Ala Gly Asn Arg Glu Asn Phe Ile Asn Glu Leu
 100 105 110
Val Arg Arg Met Asn
 115

(2) INFORMATION FOR SEQ ID NO:1676:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 784 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:

- (A) NAME/KEY: -
 (B) LOCATION: 1..784
 (D) OTHER INFORMATION: / Ceres Seq. ID 1570636
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1676:

aatccaatca	aaacacacag	agagaagaaa	aactcagaag	aaaagccaaa	gagtgaaca	60
aaaatggcgt	cgacgactct	ctcaatcgca	acaacaatcc	gttcctcatc	ttatcctact	120
ctcgcttcca	tcaatcaact	cccttcccga	accaccacca	tcgaattccc	ctctcgcttc	180
gggtggtggt	catcatccac	attgaccac	cgtgcaaccc	atctccgtcc	aatcgccgcc	240
gtcgaagctc	cgagaaaaat	cgagaagatc	ggatccgaaa	tctcatccct	aacctcgaa	300
gaagctcgta	tctctgctga	ctatctccaa	gacaaaattc	gtgtctcccc	acctctctta	360
gCccccgcag	cagcggcggt	tgctgtccca	gccagcgggt	gcgcggcgcc	tgtagtgga	420
gagcaaacag	agttcgatgt	ggttatcaat	gaagttccca	gcagttcccc	tattcgagt	480
ttaaaagctg	ttagggcttt	aactagcttg	gcggtgaagg	aagctaagga	gctaatacga	540
ggattaccaa	agaagtttaa	agaaggtatc	actaaagatg	aagctgaaga	aactaagaag	600
actcttgaag	aagctggctg	taaaagtctc	attgcttaag	gtttttatta	aaaaaaaaaa	660
agaagtgtgt	atctttttct	gaatttgatt	ggtcttttgt	gttgtttagt	atagtttgcg	720
tctggaattg	ttgagaattt	gttgtaattt	gaatcacatt	tggtttccca	ttagctgatt	780

tctgc

(2) INFORMATION FOR SEQ ID NO:1677:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 212 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:

- (A) NAME/KEY: peptide
 (B) LOCATION: 1..212
 (D) OTHER INFORMATION: / Ceres Seq. ID 1570637
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1677:

```

Asn Pro Ile Lys Thr His Arg Glu Lys Lys Asn Ser Glu Glu Lys Pro
1      5      10      15
Lys Ser Glu Thr Lys Met Ala Ser Thr Thr Leu Ser Ile Ala Thr Thr
20      25      30
Ile Arg Ser Ser Ser Tyr Pro Thr Leu Ala Ser Ile Asn His Phe Pro
35      40      45
Ser Arg Thr Thr Thr Ile Glu Phe Pro Ser Arg Phe Gly Gly Gly Ser
50      55      60
Ser Ser Thr Leu Thr His Arg Ala Thr His Leu Arg Pro Ile Ala Ala
65      70      75      80
Val Glu Ala Pro Glu Lys Ile Glu Lys Ile Gly Ser Glu Ile Ser Ser
85      90      95
Leu Thr Leu Glu Glu Ala Arg Ile Leu Val Asp Tyr Leu Gln Asp Lys
100     105     110
Phe Gly Val Ser Pro Leu Ser Leu Ala Pro Ala Ala Ala Val Ala
115     120     125
Ala Pro Ala Asp Gly Gly Ala Ala Ala Val Val Glu Glu Gln Thr Glu
130     135     140
Phe Asp Val Val Ile Asn Glu Val Pro Ser Ser Arg Ile Ala Val
145     150     155     160
Ile Lys Ala Val Arg Ala Leu Thr Ser Leu Ala Leu Lys Glu Ala Lys
165     170     175
Glu Leu Ile Glu Gly Leu Pro Lys Lys Phe Lys Glu Gly Ile Thr Lys
180     185     190
Asp Glu Ala Glu Glu Thr Lys Lys Thr Leu Glu Glu Ala Gly Ala Lys
195     200     205
Val Ser Ile Ala
210

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(2) INFORMATION FOR SEQ ID NO:1678:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 191 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..191

(D) OTHER INFORMATION: / Ceres Seq. ID 1570638

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1678:

```

Met Ala Ser Thr Thr Leu Ser Ile Ala Thr Thr Ile Arg Ser Ser Ser
1      5      10      15
Tyr Pro Thr Leu Ala Ser Ile Asn His Phe Pro Ser Arg Thr Thr Thr
20      25      30
Ile Glu Phe Pro Ser Arg Phe Gly Gly Gly Ser Ser Ser Thr Leu Thr
35      40      45
His Arg Ala Thr His Leu Arg Pro Ile Ala Ala Val Glu Ala Pro Glu
50      55      60
Lys Ile Glu Lys Ile Gly Ser Glu Ile Ser Ser Leu Thr Leu Glu Glu
65      70      75      80
Ala Arg Ile Leu Val Asp Tyr Leu Gln Asp Lys Phe Gly Val Ser Pro
85      90      95
Leu Ser Leu Ala Pro Ala Ala Ala Ala Val Ala Ala Pro Ala Asp Gly
100     105     110
Gly Ala Ala Ala Val Val Glu Glu Gln Thr Glu Phe Asp Val Val Ile
115     120     125
Asn Glu Val Pro Ser Ser Ser Arg Ile Ala Val Ile Lys Ala Val Arg
130     135     140
Ala Leu Thr Ser Leu Ala Leu Lys Glu Ala Lys Glu Leu Ile Glu Gly
145     150     155     160
Leu Pro Lys Lys Phe Lys Glu Gly Ile Thr Lys Asp Glu Ala Glu Glu

```


165 170 175
Thr Lys Lys Thr Leu Glu Glu Ala Gly Ala Lys Val Ser Ile Ala
180 185 190

(2) INFORMATION FOR SEQ ID NO:1679:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1039 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1039
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570655

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1679:

atattacc	ttgtagaa	aaaga	aaagaa	agcaaga	ac	acttgac	gtt	ttctaga	tag	60
agatgga	agg	gaaaga	agag	gatgttc	gag	tgggag	ctaa	caagtcc	ccg	120
cgataggt	ac	tcggctc	ag	acggaca	aaag	actaca	agga	gccacca	cc	180
tcgagcc	agg	cgagctg	agt	tcgtgtc	ctc	tctacag	agc	cggaatc	gcc	240
ccaccttc	ct	gtttcata	c	ataacgat	t	gcacagt	gat	gggagt	gaag	300
acatgtgt	gc	ctctgttg	ga	atccaagg	ca	ttgcttg	ggc	tttcggt	ggc	360
cccttgct	c	ctgtactgt	c	ggaatct	ctg	gtgggcac	at	aaaccca	gcg	420
gtctgttc	t	ggctcgt	aag	ctgtca	attga	cgagagc	gtg	cttttaca	tc	480
gtctcgg	gagc	catctgc	ggcg	gc	gggag	gtg	t	caaagG	Gctt	540
ctctcgg	gagc	aggagcca	ac	agtcgc	tc	acggctac	ac	taagggg	ctc	600
ctgagata	aat	cggaacct	tc	gtctgtg	ctc	acacgg	cttc	ctccgcc	aat	660
gaagcgct	gc	tgactccc	ac	gttcgat	tt	tggcacc	act	cccaatc	ggg	720
tcttggtt	ca	cttgcgca	gcg	attcca	atca	cgggaac	agg	aattaacca	gc	780
ttggagct	gc	aatcatct	ac	aacaagg	acc	acgcttg	ggga	cgacctgt	at	840
tcggacc	att	cattggag	ca	gtcttgc	ggg	ctctttac	ca	caactgt	tc	900
ttccattc	aa	gtccagat	cc	tgattgt	att	tctttctt	ta	aaacttc	aa	960
ttgtttgt	a	attgagct	gt	aaaatatt	g	agagatct	gg	atcatgt	gtt	1020
aatggact	gt	tc	tttttc	t						

(2) INFORMATION FOR SEQ ID NO:1680:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 286 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..286
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570656

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1680:

Met Glu Gly Lys Glu Glu Asp Val Arg Val Gly Ala Asn Lys Phe Pro	1	5	10	15
Glu Arg Gln Pro Ile Gly Thr Ser Ala Glu Thr Asp Lys Asp Tyr Lys	20	25	30	
Glu Pro Pro Pro Ala Pro Phe Phe Glu Pro Gly Glu Leu Ser Ser Trp	35	40	45	
Ser Phe Tyr Arg Ala Gly Ile Ala Glu Phe Ile Ala Thr Phe Leu Phe	50	55	60	
Leu Tyr Ile Thr Val Leu Thr Val Met Gly Val Lys Arg Ala Pro Asn	65	70	75	80
Met Cys Ala Ser Val Gly Ile Gln Gly Ile Ala Trp Ala Phe Gly Gly	85	90	95	
Met Ile Phe Ala Leu Val Tyr Cys Thr Ala Gly Ile Ser Gly Gly His	100	105	110	
Ile Asn Pro Ala Val Thr Phe Gly Leu Phe Leu Ala Arg Lys Leu Ser	115	120	125	

Leu Thr Arg Ala Val Phe Tyr Ile Val Met Gln Cys Leu Gly Ala Ile
130 135 140
Cys Gly Ala Gly Val Val Lys Gly Phe Gln Pro Asn Pro Tyr Gln Thr
145 150 155 160
Leu Gly Gly Gly Ala Asn Thr Val Ala His Gly Tyr Thr Lys Gly Ser
165 170 175
Gly Leu Gly Ala Glu Ile Ile Gly Thr Phe Val Leu Val Tyr Thr Val
180 185 190
Phe Ser Ala Thr Asp Ala Lys Arg Ser Ala Arg Asp Ser His Val Pro
195 200 205
Ile Leu Ala Pro Leu Pro Ile Gly Phe Ala Val Phe Leu Val His Leu
210 215 220
Ala Thr Ile Pro Ile Thr Gly Thr Gly Ile Asn Pro Ala Arg Ser Leu
225 230 235 240
Gly Ala Ala Ile Ile Tyr Asn Lys Asp His Ala Trp Asp Asp His Trp
245 250 255
Ile Phe Trp Val Gly Pro Phe Ile Gly Ala Ala Leu Ala Ala Leu Tyr
260 265 270
His Gln Leu Val Ile Arg Ala Ile Pro Phe Lys Ser Arg Ser
275 280 285

(2) INFORMATION FOR SEQ ID NO:1681:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 214 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..214

(D) OTHER INFORMATION: / Ceres Seq. ID 1570657

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1681:

Met Gly Val Lys Arg Ala Pro Asn Met Cys Ala Ser Val Gly Ile Gln
1 5 10 15
Gly Ile Ala Trp Ala Phe Gly Gly Met Ile Phe Ala Leu Val Tyr Cys
20 25 30
Thr Ala Gly Ile Ser Gly Gly His Ile Asn Pro Ala Val Thr Phe Gly
35 40 45
Leu Phe Leu Ala Arg Lys Leu Ser Leu Thr Arg Ala Val Phe Tyr Ile
50 55 60
Val Met Gln Cys Leu Gly Ala Ile Cys Gly Ala Gly Val Val Lys Gly
65 70 75 80
Phe Gln Pro Asn Pro Tyr Gln Thr Leu Gly Gly Ala Asn Thr Val
85 90 95
Ala His Gly Tyr Thr Lys Gly Ser Gly Leu Gly Ala Glu Ile Ile Gly
100 105 110
Thr Phe Val Leu Val Tyr Thr Val Phe Ser Ala Thr Asp Ala Lys Arg
115 120 125
Ser Ala Arg Asp Ser His Val Pro Ile Leu Ala Pro Leu Pro Ile Gly
130 135 140
Phe Ala Val Phe Leu Val His Leu Ala Thr Ile Pro Ile Thr Gly Thr
145 150 155 160
Gly Ile Asn Pro Ala Arg Ser Leu Gly Ala Ala Ile Ile Tyr Asn Lys
165 170 175
Asp His Ala Trp Asp Asp His Trp Ile Phe Trp Val Gly Pro Phe Ile
180 185 190
Gly Ala Ala Leu Ala Ala Leu Tyr His Gln Leu Val Ile Arg Ala Ile
195 200 205
Pro Phe Lys Ser Arg Ser
210

(2) INFORMATION FOR SEQ ID NO:1682:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 206 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..206
(D) OTHER INFORMATION: / Ceres Seq. ID 1570658
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1682:

Met	Cys	Ala	Ser	Val	Gly	Ile	Gln	Gly	Ile	Ala	Trp	Ala	Phe	Gly	Gly
1			5					10					15		
Met	Ile	Phe	Ala	Leu	Val	Tyr	Cys	Thr	Ala	Gly	Ile	Ser	Gly	Gly	His
			20				25					30			
Ile	Asn	Pro	Ala	Val	Thr	Phe	Gly	Leu	Phe	Leu	Ala	Arg	Lys	Leu	Ser
			35				40					45			
Leu	Thr	Arg	Ala	Val	Phe	Tyr	Ile	Val	Met	Gln	Cys	Leu	Gly	Ala	Ile
			50			55					60				
Cys	Gly	Ala	Gly	Val	Val	Lys	Gly	Phe	Gln	Pro	Asn	Pro	Tyr	Gln	Thr
65				70				75						80	
Leu	Gly	Gly	Gly	Ala	Asn	Thr	Val	Ala	His	Gly	Tyr	Thr	Lys	Gly	Ser
				85				90					95		
Gly	Leu	Gly	Ala	Glu	Ile	Ile	Gly	Thr	Phe	Val	Leu	Val	Tyr	Thr	Val
			100				105						110		
Phe	Ser	Ala	Thr	Asp	Ala	Lys	Arg	Ser	Ala	Arg	Asp	Ser	His	Val	Pro
			115				120					125			
Ile	Leu	Ala	Pro	Leu	Pro	Ile	Gly	Phe	Ala	Val	Phe	Leu	Val	His	Leu
			130			135					140				
Ala	Thr	Ile	Pro	Ile	Thr	Gly	Thr	Gly	Ile	Asn	Pro	Ala	Arg	Ser	Leu
145				150				155						160	
Gly	Ala	Ala	Ile	Ile	Tyr	Asn	Lys	Asp	His	Ala	Trp	Asp	Asp	His	Trp
			165				170						175		
Ile	Phe	Trp	Val	Gly	Pro	Phe	Ile	Gly	Ala	Ala	Leu	Ala	Ala	Leu	Tyr
			180				185						190		
His	Gln	Leu	Val	Ile	Arg	Ala	Ile	Pro	Phe	Lys	Ser	Arg	Ser		
			195			200						205			

(2) INFORMATION FOR SEQ ID NO:1683:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1142 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..1142
(D) OTHER INFORMATION: / Ceres Seq. ID 1570669
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1683:

aagcacttca	ctctctaatt	tcttctcttc	tatctctcac	catattcgcg	attaaaaact	60
ctcaactttt	ctctcaaat	tctgatcctt	taatccaaca	gttagaagaa	gattcatctg	120
atcatggccc	tcgaagcgat	gaacaactcca	acttcttctt	tcaccagaa	cgaaacgaaa	180
gaagatttga	tgaacgacgc	cgttttcatt	gagcgtggcg	ttaaacgcga	acgcgtccaaa	240
cgtcagcggt	ctcacagccc	tcttctgtct	tcttctctac	cgctcgatc	tcgaccacaaa	300
tcccagaaac	aagatcttac	ggaagaagag	tatctcgctc	tttgtctcct	catgtcgtct	360
aaagatcaac	cgctcgcaaac	cgcatctcat	caacagtcgc	aatcggttaac	gcgcgcgcga	420
gaatcaaaaga	accttccgta	caagtgtaac	gtctgtgaaa	aagcgttttc	ttcatatcag	480
gctttaggcg	gtccacaagc	aagtcaccga	atcaaacacc	caaccgtaat	ctcaacaaact	540
gcgatgatt	caacagctcc	accatctccc	atcgctcgccg	gagaaaaaaa	ctcgattgct	600
gcctccggaa	agatCcaaga	gtgttcaatc	tgctcataaa	tgtttccgac	gggtcaagct	660
ttaggcggtc	acaaacggtg	tcactacgaa	ggcaacctcg	gcgcgcgagg	aggaggaggga	720

agcaaatcaa	tcagtcacag	tggaagcgtg	tcgagcacgg	tatcggaaga	aaggagccac	780
cgtggattca	tcgatctaaa	cctaccggcg	ttacctgaac	tcagccttca	tcacaatcca	840
atcgtcgacg	aagagatctt	gagtcggttg	accggtaaaa	aaccgctttt	gttgaccgat	900
cacgaccaag	tcatacaaga	agaagattta	tctttaaaaa	tctaatactc	gactattaat	960
tcttggtttt	tcattttcat	ttttttagtt	acaaattttt	aattgttctg	atttgggattg	1020
aatattggta	tattgttagg	gattgataca	aaaatttgat	gattgattaa	gtcagaatttt	1080
cttttaatt	atgtaacta	atctcttgat	cagtcaccctc	tgtataaata	ttgcgtggca	1140
tt						

(2) INFORMATION FOR SEQ ID NO:1684:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 273 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..273

(D) OTHER INFORMATION: / Ceres Seq. ID 1570670

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1684:

Met	Ala	Leu	Glu	Ala	Met	Asn	Thr	Pro	Thr	Ser	Ser	Phe	Thr	Arg	Ile
1			5						10					15	
Glu	Thr	Lys	Glu	Asp	Leu	Met	Asn	Asp	Ala	Val	Phe	Ile	Glu	Pro	Trp
			20					25					30		
Leu	Lys	Arg	Lys	Arg	Ser	Lys	Arg	Gln	Arg	Ser	His	Ser	Pro	Ser	Ser
			35				40					45			
Ser	Ser	Ser	Ser	Pro	Pro	Arg	Ser	Arg	Pro	Lys	Ser	Gln	Asn	Gln	Asp
			50				55				60				
Leu	Thr	Glu	Glu	Glu	Tyr	Leu	Ala	Leu	Cys	Leu	Leu	Met	Leu	Ala	Lys
			65			70				75				80	
Asp	Gln	Pro	Ser	Gln	Thr	Arg	Phe	His	Gln	Gln	Ser	Gln	Ser	Leu	Thr
				85					90					95	
Pro	Pro	Pro	Glu	Ser	Lys	Asn	Leu	Pro	Tyr	Lys	Cys	Asn	Val	Cys	Glu
			100					105						110	
Lys	Ala	Phe	Pro	Ser	Tyr	Gln	Ala	Leu	Gly	Gly	His	Lys	Ala	Ser	His
			115				120					125			
Arg	Ile	Lys	Pro	Pro	Thr	Val	Ile	Ser	Thr	Thr	Ala	Asp	Asp	Ser	Thr
			130			135					140				
Ala	Pro	Thr	Ile	Ser	Ile	Val	Ala	Gly	Glu	Lys	His	Pro	Ile	Ala	Ala
			145			150				155				160	
Ser	Gly	Lys	Ile	His	Glu	Cys	Ser	Ile	Cys	His	Lys	Val	Phe	Pro	Thr
			165					170						175	
Gly	Gln	Ala	Leu	Gly	Gly	His	Lys	Arg	Cys	His	Tyr	Glu	Gly	Asn	Leu
			180				185						190		
Gly	Gly	Gly	Gly	Gly	Gly	Gly	Ser	Lys	Ser	Ile	Ser	His	Ser	Gly	Ser
			195				200					205			
Val	Ser	Ser	Thr	Val	Ser	Glu	Glu	Arg	Ser	His	Arg	Gly	Phe	Ile	Asp
			210			215					220				
Leu	Asn	Leu	Pro	Ala	Leu	Pro	Glu	Leu	Ser	Leu	His	His	Asn	Pro	Ile
			225			230				235				240	
Val	Asp	Glu	Glu	Ile	Leu	Ser	Pro	Leu	Thr	Gly	Lys	Lys	Pro	Leu	Leu
			245					250						255	
Leu	Thr	Asp	His	Asp	Gln	Val	Ile	Lys	Lys	Glu	Asp	Leu	Ser	Leu	Lys
			260					265					270		
Ile															

(2) INFORMATION FOR SEQ ID NO:1685:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 268 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

- (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..268
(D) OTHER INFORMATION: / Ceres Seq. ID 1570671

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1686:

Met	Asn	Thr	Pro	Thr	Ser	Ser	Phe	Thr	Arg	Ile	Glu	Thr	Lys	Glu	Asp
1				5						10				15	
Leu	Met	Asn	Asp	Ala	Val	Phe	Ile	Glu	Pro	Trp	Leu	Lys	Arg	Lys	Arg
			20					25					30		
Ser	Lys	Arg	Gln	Arg	Ser	His	Ser	Pro	Ser	Ser	Ser	Ser	Ser	Ser	Pro
			35				40						45		
Pro	Arg	Ser	Arg	Pro	Lys	Ser	Gln	Asn	Gln	Asp	Leu	Thr	Glu	Glu	Glu
			50			55					60				
Tyr	Leu	Ala	Leu	Cys	Leu	Leu	Met	Leu	Ala	Lys	Asp	Gln	Pro	Ser	Gln
65				70					75					80	
Thr	Arg	Phe	His	Gln	Gln	Ser	Gln	Ser	Leu	Thr	Pro	Pro	Pro	Glu	Ser
			85						90					95	
Lys	Asn	Leu	Pro	Tyr	Lys	Cys	Asn	Val	Cys	Glu	Lys	Ala	Phe	Pro	Ser
			100					105					110		
Tyr	Gln	Ala	Leu	Gly	Gly	His	Lys	Ala	Ser	His	Arg	Ile	Lys	Pro	Pro
			115				120						125		
Thr	Val	Ile	Ser	Thr	Thr	Ala	Asp	Asp	Ser	Thr	Ala	Pro	Thr	Ile	Ser
			130			135					140				
Ile	Val	Ala	Gly	Glu	Lys	His	Pro	Ile	Ala	Ala	Ser	Gly	Lys	Ile	His
			145		150				155					160	
Glu	Cys	Ser	Ile	Cys	His	Lys	Val	Phe	Pro	Thr	Gly	Gln	Ala	Leu	Gly
			165					170					175		
Gly	His	Lys	Arg	Cys	His	Tyr	Glu	Gly	Asn	Leu	Gly	Gly	Gly	Gly	Gly
			180				185						190		
Gly	Gly	Ser	Lys	Ser	Ile	Ser	His	Ser	Gly	Ser	Val	Ser	Ser	Thr	Val
			195				200					205			
Ser	Glu	Glu	Arg	Ser	His	Arg	Gly	Phe	Ile	Asp	Leu	Asn	Leu	Pro	Ala
			210			215					220				
Leu	Pro	Glu	Leu	Ser	Leu	His	His	Asn	Pro	Ile	Val	Asp	Glu	Glu	Ile
			225		230				235					240	
Leu	Ser	Pro	Leu	Thr	Gly	Lys	Lys	Pro	Leu	Leu	Leu	Thr	Asp	His	Asp
			245					250					255		
Gln	Val	Ile	Lys	Lys	Glu	Asp	Leu	Ser	Leu	Lys	Ile				
			260				265								

(2) INFORMATION FOR SEQ ID NO:1686:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 251 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..251
(D) OTHER INFORMATION: / Ceres Seq. ID 1570672

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1686:

Met	Asn	Asp	Ala	Val	Phe	Ile	Glu	Pro	Trp	Leu	Lys	Arg	Lys	Arg	Ser
1				5					10					15	
Lys	Arg	Gln	Arg	Ser	His	Ser	Pro	Ser	Ser	Ser	Ser	Ser	Ser	Pro	Pro
			20				25						30		
Arg	Ser	Arg	Pro	Lys	Ser	Gln	Asn	Gln	Asp	Leu	Thr	Glu	Glu	Glu	Tyr
			35				40					45			
Leu	Ala	Leu	Cys	Leu	Leu	Met	Leu	Ala	Lys	Asp	Gln	Pro	Ser	Gln	Thr
			50			55				60					

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Arg Phe His Gln Gln Ser Gln Ser Leu Thr Pro Pro Pro Glu Ser Lys
65              70              75              80
Asn Leu Pro Tyr Lys Cys Asn Val Cys Glu Lys Ala Phe Pro Ser Tyr
      85              90              95
Gln Ala Leu Gly Gly His Lys Ala Ser His Arg Ile Lys Pro Thr
      100              105              110
Val Ile Ser Thr Thr Ala Asp Asp Ser Thr Ala Pro Thr Ile Ser Ile
      115              120              125
Val Ala Gly Glu Lys His Pro Ile Ala Ala Ser Gly Lys Ile His Glu
      130              135              140
Cys Ser Ile Cys His Lys Val Phe Pro Thr Gly Gln Ala Leu Gly Gly
145              150              155              160
His Lys Arg Cys His Tyr Glu Gly Asn Leu Gly Gly Gly Gly Gly Gly
      165              170              175
Gly Ser Lys Ser Ile Ser His Ser Gly Ser Val Ser Ser Thr Val Ser
      180              185              190
Glu Glu Arg Ser His Arg Gly Phe Ile Asp Leu Asn Leu Pro Ala Leu
      195              200              205
Pro Glu Leu Ser Leu His His Asn Pro Ile Val Asp Glu Glu Ile Leu
      210              215              220
Ser Pro Leu Thr Gly Lys Lys Pro Leu Leu Leu Thr Asp His Asp Gln
225              230              235              240
Val Ile Lys Lys Glu Asp Leu Ser Leu Lys Ile
      245              250

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(2) INFORMATION FOR SEQ ID NO:1687:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1083 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1083
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570681

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1687:

```

ttttttacga tctggtgctg gataagcctt ttgcttcatt ctcaactctc tctctatcca 60
aaaaagctcc tccatttcaa tggcgacaGc atcagctctc tcatcactct ctctactctc 120
actccacacc cgaacctctt ctctcatctc ctctctctcc acaaaatcca tcgtctcttt 180
ctctctcttc ctcaaccgcc gcttctcatc tctcactctc gtcaaaagct catcgaccga 240
taccgaaacc atcttcttcg aagacgaaac accagaaata accgcaaatg tcgtcttcga 300
cccaccaatt gctccccgaq attcgtctct cctccgtatt tcgacgaagg aagcgacgag 360
acagaggaag agatcgctac cgcttttgaa gagctctatg gacctgcgta tagtggtgag 420
agtatgcttg ggaaagatat ttatgtgatg gactcaaagc ataagaagag ttcagggtatt 480
ggtgggaagc caaagaaga gataagtaga gatgggtttg aagagagagt tgtgcaagtt 540
aggagagtga ctaagggttg taaaggaggg aagcaattga agtttagagc tatcgttgtt 600
gttggtgata aacaaggaaa tgttggtgtt ggttggtgcta aggtctaaaga agttgttgtg 660
gctgttcaga aatctgctat tgatgctagg agaaacattg ttcaagttcc tatgactaag 720
tattctactt tccctcacag atcagagggg gattatggag cagccaagggt gatgcttaga 780
cctgcttcac caggtactgg tgtgattgct ggaggagcgg ttaggattgt gctagagatg 840
cgaggagtgc agaatgcatt ggggaaacag cttggaagca acaatgctct caacaatgcg 900
agagccactc ttgcagcagt acaacagatg agacagttcc gcgatgttgc acaagagcgt 960
ggaatcccca tggaagaact ctggaagtga aaactcatct tcgctttaac attttcatcc 1020
tcttttgttg agatttcttg taatgatgta attcatgaga aaatatgttt attttgaatt 1080
agc

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(2) INFORMATION FOR SEQ ID NO:1688:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 329 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1.329

(D) OTHER INFORMATION: / Ceres Seq. ID 1570682

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1688:

Phe Phe Thr Ile Trp Cys Trp Ile Ser Leu Leu His Ser His Phe
1 5 10 15
Leu Pro His Pro Lys Lys Leu Leu His Phe Asn Gly Asp Ser Ile Ser
20 25 30
Ser Leu Ile Thr Leu Phe Thr Leu Thr Pro His Pro Asn Leu Phe Ser
35 40 45
His Leu Leu Phe Leu His Lys Ile His Arg Leu Phe Leu Leu Pro
50 55 60
Gln Pro Pro Leu Leu Ile Ser His Ser Arg Gln Ser Leu Ile Asp Arg
65 70 75 80
Tyr Arg Asn His Leu Leu Arg Arg Arg Asn Thr Arg Asn Asn Arg Lys
85 90 95
Cys Arg Leu Arg Pro Thr Asn Cys Ser Arg Arg Phe Val Ser Pro Pro
100 105 110
Tyr Phe Asp Glu Gly Ser Asp Glu Thr Glu Glu Ile Ala Thr Ala
115 120 125
Phe Glu Glu Leu Tyr Gly Pro Ala Tyr Ser Gly Glu Ser Met Leu Gly
130 135 140
Lys Asp Ile Tyr Val Met Asp Ser Lys His Lys Lys Ser Ser Gly Ile
145 150 155 160
Gly Gly Lys Pro Lys Lys Asp Lys Ile Arg Asp Gly Phe Glu Glu Arg
165 170 175
Val Val Gln Val Arg Arg Val Thr Lys Val Val Lys Gly Gly Lys Gln
180 185 190
Leu Lys Phe Arg Ala Ile Val Val Val Gly Asp Lys Gln Gly Asn Val
195 200 205
Gly Val Gly Cys Ala Lys Ala Lys Glu Val Val Ala Val Gln Lys
210 215 220
Ser Ala Ile Asp Ala Arg Arg Asn Ile Val Gln Val Pro Met Thr Lys
225 230 235 240
Tyr Ser Thr Phe Pro His Arg Ser Glu Gly Asp Tyr Gly Ala Ala Lys
245 250 255
Val Met Leu Arg Pro Ala Ser Pro Gly Thr Gly Val Ile Ala Gly Gly
260 265 270
Ala Val Arg Ile Val Leu Glu Met Ala Gly Val Glu Asn Ala Leu Gly
275 280 285
Lys Gln Leu Gly Ser Asn Asn Ala Leu Asn Asn Ala Arg Ala Thr Leu
290 295 300
Ala Ala Val Gln Gln Met Arg Gln Phe Arg Asp Val Ala Gln Glu Arg
305 310 315 320
Gly Ile Pro Met Glu Glu Leu Trp Lys
325

(2) INFORMATION FOR SEQ ID NO:1689:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 188 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..188

(D) OTHER INFORMATION: / Ceres Seq. ID 1570683

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1689:

Met Leu Gly Lys Asp Ile Tyr Val Met Asp Ser Lys His Lys Lys Ser

1	5	10	15
Ser Gly Ile Gly Gly Lys Pro Lys Lys Asp Lys Ile Arg Asp Gly Phe	20	25	30
Glu Glu Arg Val Val Gln Val Arg Arg Val Thr Lys Val Val Lys Gly	35	40	45
Gly Lys Gln Leu Lys Phe Arg Ala Ile Val Val Val Gly Asp Lys Gln	50	55	60
Gly Asn Val Gly Val Gly Cys Ala Lys Ala Lys Glu Val Val Ala Ala	65	70	75
Val Gln Lys Ser Ala Ile Asp Ala Arg Arg Asn Ile Val Gln Val Pro	85	90	95
Met Thr Lys Tyr Ser Thr Phe Pro His Arg Ser Glu Gly Asp Tyr Gly	100	105	110
Ala Ala Lys Val Met Leu Arg Pro Ala Ser Pro Gly Thr Gly Val Ile	115	120	125
Ala Gly Gly Ala Val Arg Ile Val Leu Glu Met Ala Gly Val Glu Asn	130	135	140
Ala Leu Gly Lys Gln Leu Gly Ser Asn Asn Ala Leu Asn Asn Ala Arg	145	150	155
Ala Thr Leu Ala Ala Val Gln Gln Met Arg Gln Phe Arg Asp Val Ala	165	170	175
Gln Glu Arg Gly Ile Pro Met Glu Glu Leu Trp Lys	180	185	

(2) INFORMATION FOR SEQ ID NO:1690:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 180 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..180
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570684

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1690:

Met Asp Ser Lys His Lys Lys Ser Ser Gly Ile Gly Gly Lys Pro Lys	1	5	10	15
Lys Asp Lys Ile Arg Asp Gly Phe Glu Glu Arg Val Val Gln Val Arg	20	25	30	
Arg Val Thr Lys Val Val Lys Gly Gly Lys Gln Leu Lys Phe Arg Ala	35	40	45	
Ile Val Val Val Gly Asp Lys Gln Gly Asn Val Gly Val Gly Cys Ala	50	55	60	
Lys Ala Lys Glu Val Val Ala Ala Val Gln Lys Ser Ala Ile Asp Ala	65	70	75	80
Arg Arg Asn Ile Val Gln Val Pro Met Thr Lys Tyr Ser Thr Phe Pro	85	90	95	
His Arg Ser Glu Gly Asp Tyr Gly Ala Ala Lys Val Met Leu Arg Pro	100	105	110	
Ala Ser Pro Gly Thr Gly Val Ile Ala Gly Gly Ala Val Arg Ile Val	115	120	125	
Leu Glu Met Ala Gly Val Glu Asn Ala Leu Gly Lys Gln Leu Gly Ser	130	135	140	
Asn Asn Ala Leu Asn Asn Ala Arg Ala Thr Leu Ala Ala Val Gln Gln	145	150	155	160
Met Arg Gln Phe Arg Asp Val Ala Gln Glu Arg Gly Ile Pro Met Glu	165	170	175	
Glu Leu Trp Lys	180			

(2) INFORMATION FOR SEQ ID NO:1691:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1547 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..1547
(D) OTHER INFORMATION: / Ceres Seq. ID 1570692

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1691:

actctctttc	ttttctatgt	tcttttcgga	cagaacaaaa	ctccctaatic	caaagtgtcaa	60
ttctctttgt	ctactctctga	ataatcatct	ctcttcaaac	ctatttcaat	tttaactatc	120
gatcttcggc	taagtcttcca	atggcgccgg	cggtttgcctc	tcttcccaca	tttagtgtcg	180
tcaatttcctc	caagatttccc	agaagaagaa	tccgtttttc	ttgtctccaaa	aagccctctcg	240
aagttctgtt	ttcttccggc	aatactcgtt	acactaagca	gagaggggca	tttaccatcat	300
tgaagaagat	tgcgatttca	ttagctttat	cggttggttt	aatggtttca	gtaccttcga	360
ttgcttttgc	tcaccaatgt	cacgcaGtGg	cgaatccagt	gattccagat	gtttcagttg	420
tgatctccgg	tctctccgatt	aaagatccgg	aagctttact	aagatatgca	ttgcctattg	480
acaacaaagc	catcagggaa	gtgcagaagc	ctcttgaggga	tatcactgat	agcctcaaga	540
ttgctggcgt	taaggctcta	gattctgttg	aacggaaatg	gaggcaggca	agtagaacat	600
tgacgaaggg	gaaaaagtata	attgtggcag	gttttgctga	atcgaaagag	gatcatggta	660
atgaaatgat	tgaaaagtgt	gaagctggga	tgcaagatat	gcttaagata	gtggaagatc	720
gaaaaagaga	cgcagtttgt	ccaaaacaga	aagaaattct	caaatatggt	ggcggaatag	780
aagaggtat	ggttgatggc	tttccatatg	aagtgccgga	agagtatcgg	aacatgcctc	840
tctcgaaggg	aagagctagt	gtggacatga	aggtcaagat	caaggacaat	cccaacatcg	900
aggactgtgt	gttcccgatt	gttcttgatg	gttataaacg	ccctgttacc	gccggaaaact	960
ttgtggactt	ggtagagagg	catttctacg	atggcatgga	gatccagaga	tctgatggat	1020
ttgtgtgtaca	aacgggagat	ccagagggtc	ctcggaagg	atttatcgat	ccaagcacag	1080
agaaaaacgag	gacggttctc	ctagagatta	ttgtgactgg	agagaaaacg	cttttttacg	1140
gctcaactct	tgaagaactt	ggcttttaca	aggtccaggt	ttgtgatctt	tcaaacagct	1200
ttgggacaa	ggcaatggca	agagaagagt	ttgagaatga	ctcaggatca	agccaagtgt	1260
tttggctgct	aaaagagagt	gagctgacac	caagcaattc	caacatcttg	gatggtcggt	1320
acgctgtctt	tggttacgtt	actgataaac	aagattttct	agctgatctt	aaagtgtggt	1380
atgttatcga	atccattcaa	gttgctctcg	gtttagagaa	cctcgctaac	ccgagttaca	1440
aaatcgccgg	ttaaactctc	ttatcttttt	ctttttctg	gttcgtaatt	aatactctgt	1500
ttattttaat	tttgtgagag	tatatataag	gtgcagtgtc	ttttccc		

(2) INFORMATION FOR SEQ ID NO:1692:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 437 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..437
(D) OTHER INFORMATION: / Ceres Seq. ID 1570693

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1692:

Met	Ala	Ala	Ala	Phe	Ala	Ser	Leu	Pro	Thr	Phe	Ser	Val	Val	Asn	Ser
1			5					10			15				
Ser	Arg	Phe	Pro	Arg	Arg	Arg	Ile	Gly	Phe	Ser	Cys	Ser	Lys	Lys	Pro
			20					25			30				
Leu	Glu	Val	Arg	Cys	Ser	Ser	Gly	Asn	Thr	Arg	Tyr	Thr	Lys	Gln	Arg
			35					40			45				
Gly	Ala	Phe	Thr	Ser	Leu	Lys	Glu	Cys	Ala	Ile	Ser	Leu	Ala	Leu	Ser
			50					55			60				
Val	Gly	Leu	Met	Val	Ser	Val	Pro	Ser	Ile	Ala	Leu	Pro	Pro	Asn	Ala
			65					70			75				80
His	Ala	Val	Ala	Asn	Pro	Val	Ile	Pro	Asp	Val	Ser	Val	Leu	Ile	Ser
			85					90			95				
Gly	Pro	Pro	Ile	Lys	Asp	Pro	Glu	Ala	Leu	Leu	Arg	Tyr	Ala	Leu	Pro

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100      105      110
Ile Asp Asn Lys Ala Ile Arg Glu Val Gln Lys Pro Leu Glu Asp Ile
115      120      125
Thr Asp Ser Leu Lys Ile Ala Gly Val Lys Ala Leu Asp Ser Val Glu
130      135      140
Arg Asn Val Arg Gln Ala Ser Arg Thr Leu Gln Gln Gly Lys Ser Ile
145      150      155
Ile Val Ala Gly Phe Ala Glu Ser Lys Lys Asp His Gly Asn Glu Met
165      170      175
Ile Glu Lys Leu Glu Ala Gly Met Gln Asp Met Leu Lys Ile Val Glu
180      185      190
Asp Arg Lys Arg Asp Ala Val Ala Pro Lys Gln Lys Glu Ile Leu Lys
195      200      205
Tyr Val Gly Gly Ile Glu Glu Asp Met Val Asp Gly Phe Pro Tyr Glu
210      215      220
Val Pro Glu Glu Tyr Arg Asn Met Pro Leu Leu Lys Gly Arg Ala Ser
225      230      235
Val Asp Met Lys Val Lys Ile Lys Asp Asn Pro Asn Ile Glu Asp Cys
245      250      255
Val Phe Arg Ile Val Leu Asp Gly Tyr Asn Ala Pro Val Thr Ala Gly
260      265      270
Asn Phe Val Asp Leu Val Glu Arg His Phe Tyr Asp Gly Met Glu Ile
275      280      285
Gln Arg Ser Asp Gly Phe Val Val Gln Thr Gly Asp Pro Glu Gly Pro
290      295      300
Ala Glu Gly Phe Ile Asp Pro Ser Thr Glu Lys Thr Arg Thr Val Pro
305      310      315
Leu Glu Ile Met Val Thr Gly Glu Lys Thr Pro Phe Tyr Gly Ser Thr
325      330      335
Leu Glu Glu Leu Gly Leu Tyr Lys Ala Gln Val Val Ile Pro Phe Asn
340      345      350
Ala Phe Gly Thr Met Ala Met Ala Arg Glu Glu Phe Glu Asn Asp Ser
355      360      365
Gly Ser Ser Gln Val Phe Trp Leu Leu Lys Glu Ser Glu Leu Thr Pro
370      375      380
Ser Asn Ser Asn Ile Leu Asp Gly Arg Tyr Ala Val Phe Gly Tyr Val
385      390      395
Thr Asp Asn Glu Asp Phe Leu Ala Asp Leu Lys Val Gly Asp Val Ile
405      410      415
Glu Ser Ile Gln Val Val Ser Gly Leu Glu Asn Leu Ala Asn Pro Ser
420      425      430
Tyr Lys Ile Ala Gly
435

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(2) INFORMATION FOR SEQ ID NO:1693:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 370 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..370

(D) OTHER INFORMATION: / Ceres Seq. ID 1570694

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1693:

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Met Val Ser Val Pro Ser Ile Ala Leu Pro Pro Asn Ala His Ala Val
1      5      10      15
Ala Asn Pro Val Ile Pro Asp Val Ser Val Leu Ile Ser Gly Pro Pro
20      25      30
Ile Lys Asp Pro Glu Ala Leu Leu Arg Tyr Ala Leu Pro Ile Asp Asn
35      40      45

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Lys Ala Ile Arg Glu Val Gln Lys Pro Leu Glu Asp Ile Thr Asp Ser
50 55 60
Leu Lys Ile Ala Gly Val Lys Ala Leu Asp Ser Val Glu Arg Asn Val
65 70 75 80
Arg Gln Ala Ser Arg Thr Leu Gln Gln Gly Lys Ser Ile Ile Val Ala
85 90 95
Gly Phe Ala Glu Ser Lys Lys Asp His Gly Asn Glu Met Ile Glu Lys
100 105 110
Leu Glu Ala Gly Met Gln Asp Met Leu Lys Ile Val Glu Asp Arg Lys
115 120 125
Arg Asp Ala Val Ala Pro Lys Gln Lys Glu Ile Leu Lys Tyr Val Gly
130 135 140
Gly Ile Glu Glu Asp Met Val Asp Gly Phe Pro Tyr Glu Val Pro Glu
145 150 155 160
Glu Tyr Arg Asn Met Pro Leu Leu Lys Gly Arg Ala Ser Val Asp Met
165 170 175
Lys Val Lys Ile Lys Asp Asn Pro Asn Ile Glu Asp Cys Val Phe Arg
180 185 190
Ile Val Leu Asp Gly Tyr Asn Ala Pro Val Thr Ala Gly Asn Phe Val
195 200 205
Asp Leu Val Glu Arg His Phe Tyr Asp Gly Met Glu Ile Gln Arg Ser
210 215 220
Asp Gly Phe Val Val Gln Thr Gly Asp Pro Glu Gly Pro Ala Glu Gly
225 230 235 240
Phe Ile Asp Pro Ser Thr Glu Lys Thr Arg Thr Val Pro Leu Glu Ile
245 250 255
Met Val Thr Gly Glu Lys Thr Pro Phe Tyr Gly Ser Thr Leu Glu Glu
260 265 270
Leu Gly Leu Tyr Lys Ala Gln Val Val Ile Pro Phe Asn Ala Phe Gly
275 280 285
Thr Met Ala Met Ala Arg Glu Glu Phe Glu Asn Asp Ser Gly Ser Ser
290 295 300
Gln Val Phe Trp Leu Leu Lys Glu Ser Glu Leu Thr Pro Ser Asn Ser
305 310 315 320
Asn Ile Leu Asp Gly Arg Tyr Ala Val Phe Gly Tyr Val Thr Asp Asn
325 330 335
Glu Asp Phe Leu Ala Asp Leu Lys Val Gly Asp Val Ile Glu Ser Ile
340 345 350
Gln Val Val Ser Gly Leu Glu Asn Leu Ala Asn Pro Ser Tyr Lys Ile
355 360 365
Ala Gly
370

(2) INFORMATION FOR SEQ ID NO:1694:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 262 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..262
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570695

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1694:

Met Ile Glu Lys Leu Glu Ala Gly Met Gln Asp Met Leu Lys Ile Val
1 5 10 15
Glu Asp Arg Lys Arg Asp Ala Val Ala Pro Lys Gln Lys Glu Ile Leu
20 25 30
Lys Tyr Val Gly Gly Ile Glu Glu Asp Met Val Asp Gly Phe Pro Tyr
35 40 45
Glu Val Pro Glu Glu Tyr Arg Asn Met Pro Leu Leu Lys Gly Arg Ala

50	55	60
Ser Val Asp Met Lys	Val Lys Ile Lys Asp	Asn Pro Asn Ile Glu Asp
65	70	75
Cys Val Phe Arg Ile	Val Leu Asp Gly Tyr	Asn Ala Pro Val Thr Ala
85	90	95
Gly Asn Phe Val Asp	Leu Val Glu Arg His Phe Tyr Asp Gly Met Glu	
100	105	110
Ile Gln Arg Ser Asp	Gly Phe Val Val Gln Thr Gly Asp Pro Glu Gly	
115	120	125
Pro Ala Glu Gly Phe	Ile Asp Pro Ser Thr Glu Lys Thr Arg Thr Val	
130	135	140
Pro Leu Glu Ile Met	Val Thr Gly Glu Lys Thr Pro Phe Tyr Gly Ser	
145	150	155
Thr Leu Glu Glu Leu	Gly Leu Tyr Lys Ala Gln Val Val Ile Pro Phe	
165	170	175
Asn Ala Phe Gly Thr	Met Ala Met Ala Arg Glu Glu Phe Glu Asn Asp	
180	185	190
Ser Gly Ser Ser Gln	Val Phe Trp Leu Leu Lys Glu Ser Glu Leu Thr	
195	200	205
Pro Ser Asn Ser Asn	Ile Leu Asp Gly Arg Tyr Ala Val Phe Gly Tyr	
210	215	220
Val Thr Asp Asn Glu	Asp Phe Leu Ala Asp Leu Lys Val Gly Asp Val	
225	230	235
Ile Glu Ser Ile Gln	Val Val Ser Gly Leu Glu Asn Leu Ala Asn Pro	
245	250	255
Ser Tyr Lys Ile Ala	Gly	
260		

(2) INFORMATION FOR SEQ ID NO:1695:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1393 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1393
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570696

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1695:

atcgattagg	gtttaggaac	cttgtcatcg	gaaatcattt	cttgtctttg	tttgtttattc	60
gaagctttctc	ctgctttattt	gatacatatt	ctctctttcca	gttactctac	atggaacctac	120
ctggtgtgttaa	ggagaaacatc	ctgcatcccg	cttctctgcc	gatgaagaag	cgacggatcg	180
atocacactga	gtcagctgat	ggttctgcga	ttaacgcttc	taactctagt	agcactcggtg	240
gtaacgatac	ggtgatgaac	atggcgggagt	ttggtaacga	caactccaac	aatcaggagt	300
ctcaacaagt	ttgcactttt	ttcaagaagc	caacgaaaag	taaaaaacata	aggaagaagaa	360
ccattgacgc	tgatgaagaa	gacggagatt	cgaaaagcga	aaagctctatt	ttacaaaaatc	420
taaaagaaat	tgcaaaaccc	gatagcaact	tgtacttttc	ttctggacca	ctactagaaa	480
cgagtggagc	tccttgagaga	cccgtttttc	actacgattc	atccaaaggaa	atccaggtttc	540
gaagacgacg	tgagcaacaa	gcgacccttg	aaactgaaac	cgacttcaat	caagacgctc	600
gagctatccg	tgaaaagagt	cttaaaaaag	cagaccatgc	attgaagggg	aataagaaaaa	660
agggcttcaga	tgagaagctg	tacaaaaggaa	ttcatggata	tacagatcac	aaagctgggt	720
ttagaagaga	acaaaacaatc	ctgagcgaga	aaagctggag	ctcaacggg	cttttaagag	780
cttctgctca	catcagagta	ctggcttagat	tcgattacca	gccagacatt	tgcaaggatt	840
acaagaagaa	cggatactgt	gatatggag	attcgtgtaa	gttcttgcgt	gacgctgggg	900
attacaagacc	gggatggcag	atagagaaga	agtgggaaga	ggcagagaaa	gttaggaaga	960
gaataaagac	tatgggaggt	gaggatgacg	atgatgaggg	tgacaaggat	agcgacgaag	1020
acgaaaattgc	attgcccttt	gcttgccttca	tttgacaggga	gccttttctt	gatccagttg	1080
tcaccaaatg	caagcattac	ttctgtgagc	attgtgcttt	aaagcatcac	acgaagaaca	1140
agaaatgctt	tgtgtgttaac	caaccaacaa	tggggatttt	caatgcagca	catgagatca	1200
agaagaggat	ggctgaagaa	cggagtaaac	ctgaacaagg	attgtgaagt	cctttcttcca	1260
caggacaaaa	agggcaaaaac	tatacatttg	attattttgct	tgaggaaagc	ttttttgttt	1320

(2) INFORMATION FOR SEQ ID NO:1696:

(A) LENGTH: 414 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..414

(D) OTHER INFORMATION: / Ceres Seq. ID 1570697

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1696:

Arg	Leu	Gly	Phe	5	Arg	Asn	Leu	Val	Ile	Gly	Asn	His	Phe	Leu	Ser	Leu
1										10					15	
Phe	Val	Ile	Arg	20	Ser	Phe	Ser	Cys	Leu	Phe	Asp	Thr	Tyr	Ser	Leu	Phe
									25	Val	Val	Lys	Glu	Asn	Ile	Val
Gln	Leu	Leu	Tyr	Met	Glu	Pro	Phe	Val	Val	Val	Lys	Glu	Asn	Ile	Val	Ala
									40				45			
Ser	Ala	Ser	Ser	Pro	Met	Lys	Lys	Arg	Arg	Ile	Asp	His	Thr	Glu	Ser	
												60				
Ala	Asp	Gly	Ser	Ala	Ile	Asn	Ala	Ser	Asn	Ser	Ser	Ser	Ile	Gly	Gly	
65						70				75					80	
Asn	Asp	Thr	Val	Met	Asn	Met	Ala	Glu	Phe	Gly	Asn	Asp	Asn	Ser	Asn	
						85			90					95		
Asn	Gln	Glu	Ser	Gln	Gln	Val	Cys	Thr	Phe	Phe	Lys	Lys	Pro	Thr	Lys	
									105				110			
Ser	Ser	Asn	Ile	Arg	Lys	Arg	Thr	Ile	Asp	Ala	Asp	Glu	Glu	Asp	Gly	
												125				
Asp	Ser	Ser	Ser	Glu	Ser	Ser	Ile	Leu	Gln	Asn	Leu	Lys	Lys	Val	Ala	
											140					
Lys	Pro	Asp	Ser	Asn	Leu	Tyr	Phe	Ser	Ser	Gly	Pro	Ser	Thr	Arg	Thr	
145						150				155					160	
Ser	Gly	Ala	Pro	Glu	Arg	Pro	Val	Phe	His	Tyr	Asp	Ser	Ser	Lys	Glu	
						165			170					175		
Ile	Gln	Val	Gln	Asn	Asp	Ser	Gly	Ala	Thr	Ala	Thr	Leu	Glu	Thr	Glu	
									185				190			
Thr	Asp	Phe	Asn	Gln	Asp	Ala	Arg	Ala	Ile	Arg	Glu	Arg	Val	Leu	Lys	
								200				205				
Lys	Ala	Asp	His	Ala	Leu	Lys	Gly	Asn	Lys	Lys	Lys	Ala	Ser	Asp	Glu	
											220					
Lys	Leu	Tyr	Lys	Gly	Ile	His	Gly	Tyr	Thr	Asp	His	Lys	Ala	Gly	Phe	
225						230				235					240	
Arg	Arg	Glu	Gln	Thr	Ile	Ser	Ser	Glu	Lys	Ala	Gly	Gly	Ser	His	Gly	
						245			250					255		
Pro	Leu	Arg	Ala	Ser	Ala	His	Ile	Arg	Val	Ser	Ala	Arg	Phe	Asp	Tyr	
									265				270			
Gln	Pro	Asp	Ile	Cys	Lys	Asp	Tyr	Lys	Glu	Thr	Gly	Tyr	Cys	Gly	Tyr	
									280				285			
Gly	Asp	Ser	Cys	Lys	Phe	Leu	His	Asp	Arg	Gly	Asp	Tyr	Lys	Pro	Gly	
											300					
Trp	Gln	Ile	Glu	Lys	Glu	Trp	Glu	Glu	Ala	Glu	Lys	Val	Arg	Lys	Arg	
305						310				315					320	
Asn	Lys	Ala	Met	Gly	Val	Glu	Asp	Asp	Asp	Asp	Glu	Ala	Asp	Lys	Asp	
										330				335		
Ser	Asp	Glu	Asp	Glu	Asn	Ala	Leu	Pro	Phe	Ala	Cys	Phe	Ile	Cys	Arg	

370	375	380
Cys Asn Gln Pro Thr Met Gly Ile Phe Asn Ala Ala His Glu Ile Lys		
385	390	395
Lys Arg Met Ala Glu Glu Arg Ser Lys Ala Glu Gln Gly Leu		400
	405	410

(2) INFORMATION FOR SEQ ID NO:1697:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 378 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..378

(D) OTHER INFORMATION: / Ceres Seq. ID 1570698

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1697:

Met	Glu	Pro	Phe	Val	Val	Lys	Glu	Asn	Ile	Val	Ala	Ser	Ala	Ser	Ser
1			5						10					15	
Pro	Met	Lys	Lys	Arg	Arg	Ile	Asp	His	Thr	Glu	Ser	Ala	Asp	Gly	Ser
			20					25					30		
Ala	Ile	Asn	Ala	Ser	Asn	Ser	Ser	Ser	Ile	Gly	Gly	Asn	Asp	Thr	Val
		35					40						45		
Met	Asn	Met	Ala	Glu	Phe	Gly	Asn	Asp	Asn	Ser	Asn	Asn	Gln	Glu	Ser
	50					55					60				
Gln	Gln	Val	Cys	Thr	Phe	Phe	Lys	Lys	Pro	Thr	Lys	Ser	Lys	Asn	Ile
	65				70					75				80	
Arg	Lys	Arg	Thr	Ile	Asp	Ala	Asp	Glu	Glu	Asp	Gly	Asp	Ser	Lys	Ser
			85					90					95		
Glu	Ser	Ser	Ile	Leu	Gln	Asn	Leu	Lys	Lys	Val	Ala	Lys	Pro	Asp	Ser
			100					105					110		
Asn	Leu	Tyr	Phe	Ser	Ser	Gly	Pro	Ser	Thr	Arg	Thr	Ser	Gly	Ala	Pro
	115						120					125			
Glu	Arg	Pro	Val	Phe	His	Tyr	Asp	Ser	Ser	Lys	Glu	Ile	Gln	Val	Gln
		130				135					140				
Asn	Asp	Ser	Gly	Ala	Thr	Ala	Thr	Leu	Glu	Thr	Glu	Thr	Asp	Phe	Asn
	145				150				155					160	
Gln	Asp	Ala	Arg	Ala	Ile	Arg	Glu	Arg	Val	Leu	Lys	Lys	Ala	Asp	His
			165						170					175	
Ala	Leu	Lys	Gly	Asn	Lys	Lys	Lys	Ala	Ser	Asp	Glu	Lys	Leu	Tyr	Lys
			180					185					190		
Gly	Ile	His	Gly	Tyr	Thr	Asp	His	Lys	Ala	Gly	Phe	Arg	Arg	Glu	Gln
		195					200					205			
Thr	Ile	Ser	Ser	Glu	Lys	Ala	Gly	Gly	Ser	His	Gly	Pro	Leu	Arg	Ala
			210			215					220				
Ser	Ala	His	Ile	Arg	Val	Ser	Ala	Arg	Phe	Asp	Tyr	Gln	Pro	Asp	Ile
			225			230				235				240	
Cys	Lys	Asp	Tyr	Lys	Glu	Thr	Gly	Tyr	Cys	Gly	Tyr	Gly	Asp	Ser	Cys
			245						250					255	
Lys	Phe	Leu	His	Asp	Arg	Gly	Asp	Tyr	Lys	Pro	Gly	Trp	Gln	Ile	Glu
			260				265					270			
Lys	Glu	Trp	Glu	Glu	Ala	Glu	Lys	Val	Arg	Lys	Arg	Asn	Lys	Ala	Met
		275				280						285			
Gly	Val	Glu	Asp	Asp	Asp	Asp	Glu	Ala	Asp	Lys	Asp	Ser	Asp	Glu	Asp
			290			295					300				
Glu	Asn	Ala	Leu	Pro	Phe	Ala	Cys	Phe	Ile	Cys	Arg	Glu	Pro	Phe	Leu
			305			310				315				320	
Asp	Pro	Val	Val	Thr	Lys	Cys	Lys	His	Tyr	Phe	Cys	Glu	His	Cys	Ala
			325						330					335	
Leu	Lys	His	His	Thr	Lys	Asn	Lys	Lys	Cys	Phe	Val	Cys	Asn	Gln	Pro
			340					345						350	

Thr Met Gly Ile Phe Asn Ala Ala His Glu Ile Lys Lys Arg Met Ala
355 360 365
Glu Glu Arg Ser Lys Ala Glu Gln Gly Leu
370 375

(2) INFORMATION FOR SEQ ID NO:1698:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 361 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..361

(D) OTHER INFORMATION: / Ceres Seq. ID 1570699

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1698:

Met	Lys	Lys	Arg	Arg	Ile	Asp	His	Thr	Glu	Ser	Ala	Asp	Gly	Ser	Ala
1				5					10				15		
Ile	Asn	Ala	Ser	Asn	Ser	Ser	Ser	Ile	Gly	Gly	Asn	Asp	Thr	Val	Met
			20					25					30		
Asn	Met	Ala	Glu	Phe	Gly	Asn	Asp	Asn	Ser	Asn	Gln	Glu	Ser	Gln	
		35					40				45				
Gln	Val	Cys	Thr	Phe	Phe	Lys	Lys	Pro	Thr	Lys	Ser	Lys	Asn	Ile	Arg
		50				55				60					
Lys	Arg	Thr	Ile	Asp	Ala	Asp	Glu	Glu	Asp	Gly	Asp	Ser	Lys	Ser	Glu
		65			70				75					80	
Ser	Ser	Ile	Leu	Gln	Asn	Leu	Lys	Lys	Val	Ala	Lys	Pro	Asp	Ser	Asn
			85					90						95	
Leu	Tyr	Phe	Ser	Ser	Gly	Pro	Ser	Thr	Arg	Thr	Ser	Gly	Ala	Pro	Glu
			100					105					110		
Arg	Pro	Val	Phe	His	Tyr	Asp	Ser	Ser	Lys	Glu	Ile	Gln	Val	Gln	Asn
		115					120					125			
Asp	Ser	Gly	Ala	Thr	Ala	Thr	Leu	Glu	Thr	Glu	Thr	Asp	Phe	Asn	Gln
		130				135					140				
Asp	Ala	Arg	Ala	Ile	Arg	Glu	Arg	Val	Leu	Lys	Lys	Ala	Asp	His	Ala
		145			150					155				160	
Leu	Lys	Gly	Asn	Lys	Lys	Lys	Ala	Ser	Asp	Glu	Lys	Leu	Tyr	Lys	Gly
			165					170						175	
Ile	His	Gly	Tyr	Thr	Asp	His	Lys	Ala	Gly	Phe	Arg	Arg	Glu	Gln	Thr
			180					185					190		
Ile	Ser	Ser	Glu	Lys	Ala	Gly	Gly	Ser	His	Gly	Pro	Leu	Arg	Ala	Ser
		195					200					205			
Ala	His	Ile	Arg	Val	Ser	Ala	Arg	Phe	Asp	Tyr	Gln	Pro	Asp	Ile	Cys
		210					215					220			
Lys	Asp	Tyr	Lys	Glu	Thr	Gly	Tyr	Cys	Gly	Tyr	Gly	Asp	Ser	Cys	Lys
		225				230				235				240	
Phe	Leu	His	Asp	Arg	Gly	Asp	Tyr	Lys	Pro	Gly	Trp	Gln	Ile	Glu	Lys
			245						250					255	
Glu	Trp	Glu	Glu	Ala	Glu	Lys	Val	Arg	Lys	Arg	Asn	Lys	Ala	Met	Gly
		260					265						270		
Val	Glu	Asp	Asp	Asp	Asp	Glu	Ala	Asp	Lys	Asp	Ser	Asp	Glu	Asp	Glu
		275					280					285			
Asn	Ala	Leu	Pro	Phe	Ala	Cys	Phe	Ile	Cys	Arg	Glu	Pro	Phe	Leu	Asp
		290				295						300			
Pro	Val	Val	Thr	Lys	Cys	Lys	His	Tyr	Phe	Cys	Glu	His	Cys	Ala	Leu
		305				310				315				320	
Lys	His	His	Thr	Lys	Asn	Lys	Lys	Cys	Phe	Val	Cys	Asn	Gln	Pro	Thr
			325						330					335	
Met	Gly	Ile	Phe	Asn	Ala	Ala	His	Glu	Ile	Lys	Lys	Arg	Met	Ala	Glu
			340					345					350		
Glu	Arg	Ser	Lys	Ala	Glu	Gln	Gly	Leu							

355 360

(2) INFORMATION FOR SEQ ID NO:1699:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 609 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..609

(D) OTHER INFORMATION: / Ceres Seq. ID 1570716

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1699:

gaaaaatggt	gaaaaaagcg	tattagcaga	Gggacaaaag	cttttaggg	ttttagattt	60
cctctgagag	agaattttcg	aaagcttcag	agagatttcc	aactacgtta	gccatggcga	120
gcaccaagt	tcaaaaggatt	atgacccaac	ctatcaactt	gatttttagg	tttctcaaaa	180
gtaaaagctg	gatccagatt	tggctatttg	agcagaaaga	tttgaggatt	gaaggaagaa	240
tcactggttt	tgacgaatac	atgaatctag	ttttggatga	ggctgaagaa	gtgagcatca	300
agaagaacac	caggaaaacca	cttggaaaga	ttttactcaa	aggagacaa	ataactctga	360
tgatgaacac	gggaaaagtga	tgtctgtctc	aaacaactct	cttcgatgac	cttcaagctg	420
atgttaata	tctgtttgagt	tcttcctcag	cttaattggg	acttgacgat	accctctttt	480
cttcaatgtc	gtataaatata	ttgcaatgta	gtgagtga	aaggagcttg	atcgaatcta	540
gtggattgg	tggttaaaac	ttcaaaaaag	agatttgggc	ccttttggtt	aaatctagtg	600
taattggc						

(2) INFORMATION FOR SEQ ID NO:1700:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 88 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..88

(D) OTHER INFORMATION: / Ceres Seq. ID 1570717

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1700:

Met	Ala	Ser	Thr	Lys	Val	Gln	Arg	Ile	Met	Thr	Gln	Pro	Ile	Asn	Leu	
1				5					10					15		
Ile	Phe	Arg	Phe	Leu	Gln	Ser	Lys	Ala	Arg	Ile	Gln	Ile	Trp	Leu	Phe	
				20				25					30			
Glu	Gln	Lys	Asp	Leu	Arg	Ile	Glu	Gly	Arg	Ile	Thr	Gly	Phe	Asp	Glu	
				35				40					45			
Tyr	Met	Asn	Leu	Val	Leu	Asp	Glu	Ala	Glu	Glu	Val	Ser	Ile	Lys	Lys	
				50				55					60			
Asn	Thr	Arg	Lys	Pro	Leu	Gly	Arg	Ile	Leu	Leu	Lys	Gly	Asp	Asn	Ile	
				65				70					75		80	
Thr	Leu	Met	Met	Asn	Thr	Gly	Lys									

(2) INFORMATION FOR SEQ ID NO:1701:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 79 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..79

(D) OTHER INFORMATION: / Ceres Seq. ID 1570718

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1701:

Met	Thr	Gln	Pro	Ile	Asn	Leu	Ile	Phe	Arg	Phe	Leu	Gln	Ser	Lys	Ala	
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	--

1	5	10	15
Arg Ile Gln Ile Trp Leu Phe Glu Gln Lys Asp Leu Arg Ile Glu Gly			
	20	25	30
Arg Ile Thr Gly Phe Asp Glu Tyr Met Asn Leu Val Leu Asp Glu Ala			
	35	40	45
Glu Glu Val Ser Ile Lys Lys Asn Thr Arg Lys Pro Leu Gly Arg Ile			
	50	55	60
Leu Leu Lys Gly Asp Asn Ile Thr Leu Met Met Asn Thr Gly Lys			
	65	70	75

(2) INFORMATION FOR SEQ ID NO:1702:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 533 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..533

(D) OTHER INFORMATION: / Ceres Seq. ID 1570719

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1702:

atcacacaaac	tcacaattac	aaaagctaaa	cagttctcta	aaatcaaatc	aagttttttt	60
cgaagagaag	attagaaat	gtctaacWaa	cagtcagagc	atgagcttca	acgcaggcca	120
agctaaaggc	caaactcagg	agaaggcaag	caacttgatg	gacaaggcct	ccaatgtgac	180
ccaatctgtc	aaggaatcta	tccaagaggg	tggaagcagc	ctgaagcaga	aggcaacaag	240
tgccagtgag	accattaaag	aaaagaccgg	catcagcaaa	tgagaagcac	gttctaataa	300
taatttatgt	tttctgtttt	cgtttttatt	ctaccagaaa	taataattag	atagatatgt	360
ctatctaaat	ccaagactat	ggatttcgat	cgaagccatt	taggcgatta	cttttgcttt	420
tctatgtttt	ttttatatat	ctatatatct	aagagttttt	gactcttgtc	tattgataat	480
ttgtagccat	gcagttattt	ctataatatt	taataaaatg	acatgwttac	atg	

(2) INFORMATION FOR SEQ ID NO:1703:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 93 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..93

(D) OTHER INFORMATION: / Ceres Seq. ID 1570720

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1703:

Ser His Asn Ser Gln Leu Gln Lys Leu Asn Ser Ser Leu Lys Ser Asn			
	5	10	15
Gln Val Phe Phe Glu Glu Lys Ile Arg Lys Cys Leu Xaa Asn Ser Gln			
	20	25	30
Ser Met Ser Phe Asn Ala Gly Gln Ala Lys Gly Gln Thr Gln Glu Lys			
	35	40	45
Ala Ser Asn Leu Met Asp Lys Ala Ser Asn Ala Ala Gln Ser Ala Lys			
	50	55	60
Glu Ser Ile Gln Glu Gly Gly Gln Gln Leu Lys Gln Lys Ala Gln Gly			
	65	70	75
Ala Ser Glu Thr Ile Lys Glu Lys Thr Gly Ile Ser Lys			
	85	90	

(2) INFORMATION FOR SEQ ID NO:1704:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 60 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..60

(D) OTHER INFORMATION: / Ceres Seq. ID 1570721

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1704:

```
Met Ser Phe Asn Ala Gly Gln Ala Lys Gly Gln Thr Gln Glu Lys Ala
1           5           10           15
Ser Asn Leu Met Asp Lys Ala Ser Asn Ala Ala Gln Ser Ala Lys Glu
20           25           30
Ser Ile Gln Glu Gly Gly Gln Gln Leu Lys Gln Lys Ala Gln Gly Ala
35           40           45
Ser Glu Thr Ile Lys Glu Lys Thr Gly Ile Ser Lys
50           55           60
```

(2) INFORMATION FOR SEQ ID NO:1705:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1062 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1062

(D) OTHER INFORMATION: / Ceres Seq. ID 1570735

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1705:

```
aatgatctga tctgatctcc caaaaattcc caaatccaaa tctacgaatc tccgtctcct      60
ccgtgcattt ttcgcaggta gagagagaga tcaaacccaa gagacacaga gagagtatcc      120
accgatggaa tccgcagcaa cggctgttgt acctccggca gccgcgcgca ccaccgccaac      180
cgccaccgat gataatctcc aatcaagcga ctcatcatct cccgcgcgac cggttaaacg      240
attgatccac gctcttttgc agcgacaaca acatcttctc gacaaaaacgg ttccctcacg      300
tctctatoga tggatogcat gtctctgtgt tgtattgac tacatogttc gtgtttactt      360
tgttgaaggc ttctaatca tcaactacgc catcggcatc taccttttga atctcatcat      420
tgcttttcta tctctcaag aagatccgca agcttctctc acttcgggtg gttctcttcc      480
tactcggaga tccgatgagt atcgtctctt cgttccgctg ctccctgagt tcaaaattctg      540
gttatcgatc ataagggcct tcatcatcgg atttatgatg acgtttctcg aggtgtttga      600
tgtacctgta ttctggccaa tacttctctt ctactgggtg atgttgtttt tctctacgat      660
gaggaacacg atacagcata tgatcaaata cagatatgtc cctttctctt ttggggaaaaa      720
gcagtatgga aagaaacccg ctccaacaga gacgagtgaa tgatcaatca aaactgttca      780
ggtaacgaat ttacagctct tttagagaga gtacgatttg aaaaggtcgg tcttttgttc      840
tctttttgat gccatatact ttgttaggga tgaagtagag atagacatat ttgtgctctt      900
tatcatctcg actatttttac tggtttcacc tgaactcaat gtacaactctt atttttttac      960
atcctttttt cagtggagaa ataattgtGt cataactgac ccttttgtaa tcatcatggt      1020
ggaaaactaa agactaatca gtaatcactg tccggttcta tc
```

(2) INFORMATION FOR SEQ ID NO:1706:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 212 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..212

(D) OTHER INFORMATION: / Ceres Seq. ID 1570736

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1706:

```
Met Glu Ser Ala Ala Thr Ala Val Val Pro Pro Ala Ala Ala Thr
1           5           10           15
Thr Ala Thr Ala Thr Asp Asp Asn Leu Gln Ser Ser Asp Ser Ser Ser
20           25           30
Pro Ala Asp Ala Val Asn Arg Leu Ile His Ala Phe Ser Gln Arg Gln
35           40           45
```

```

Gln His Leu Leu Asp Lys Thr Val Pro His Val Leu Tyr Arg Trp Ile
  50                      55                      60
Ala Cys Leu Cys Val Val Leu Ile Tyr Ile Val Arg Val Tyr Phe Val
  65                      70                      75                      80
Glu Gly Phe Tyr Ile Ile Thr Tyr Ala Ile Gly Ile Tyr Leu Leu Asn
                      85                      90                      95
Leu Ile Ile Ala Phe Leu Ser Pro Gln Glu Asp Pro Glu Ala Ser Leu
                      100                    105                    110
Thr Ser Gly Gly Ser Leu Pro Thr Arg Arg Ser Asp Glu Tyr Arg Pro
                      115                    120                    125
Phe Val Arg Arg Leu Pro Glu Phe Lys Phe Trp Leu Ser Ile Ile Arg
                      130                    135                    140
Ala Phe Ile Ile Gly Phe Met Met Thr Phe Phe Glu Val Phe Asp Val
  145                    150                    155                    160
Pro Val Phe Trp Pro Ile Leu Leu Phe Tyr Trp Val Met Leu Phe Phe
                      165                    170                    175
Leu Thr Met Arg Lys Gln Ile Gln His Met Ile Lys Tyr Arg Tyr Val
                      180                    185                    190
Pro Phe Ser Phe Gly Lys Lys Gln Tyr Gly Lys Lys Pro Ala Pro Thr
                      195                    200                    205
Glu Ser Ser Glu
210

```

(2) INFORMATION FOR SEQ ID NO:1707:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 562 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..562
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570737

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1707:

```

atttcatttt cgttttcact ttctccgaac atccaaaagc ttgtagcttg ctctctcaaat      60
cttccttgaaa aatgaaggtt gccgctgctt tctctctcgc cgttttgggc ggaaacgccta      120
atccttcagc cgagaatatc aaagatatca tcggagctgt tgggtcgat gttgatggag      180
agagcattga gcttcattg aaagaagtga gtggttaagg cattgtcgag ctgattgctt      240
ctggtaggga gaaatttagc tctgtgccat ctggtggtgg tgtggctgtt tcagctgcctc      300
catcaagcgg tgggtggtgt gctgctgctg ctgcccCtgc ggagaagaaa gaagccaaga      360
aggaagagaa agaagagtct gatgatgaca tgggattcac tctcttcgag taaggttttt      420
gtccccacgg aaaggagtcg agatttgatt tttgtgtctc ttagtgttgc tggbytttgc      480
tcctctttgt agttcgtgtt tattaaagat tcttgatta cgaattttac tcgttagata      540
atgaagcaag aagagttttt tc

```

(2) INFORMATION FOR SEQ ID NO:1708:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..113
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570738

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1708:

```

Met Lys Val Ala Ala Ala Phe Leu Leu Ala Val Leu Gly Gly Asn Ala
  1                      5                      10                      15
Asn Pro Ser Ala Glu Asn Ile Lys Asp Ile Ile Gly Ala Val Gly Ala
                      20                      25                      30
Asp Val Asp Gly Glu Ser Ile Glu Leu Leu Lys Glu Val Ser Gly

```

(2) INFORMATION FOR SEQ ID NO:1709:

(A) LENGTH: 526 base pairs

(C) STRANDEDNESS: sing

(D) TOPOLOGY: linear

MOLECULE TYPE: DNA (g

(ix) FEATURE:

(18) FEATURE: (B) NAME:

```
(A) NAME/KEY: -
(B) LOCATION: 1
```

(B) LOCATION: 1.526

(D) OTHER INFORMATION: / Ceres Seq. ID 1570751
SEQUENCE DESCRIPTION: SEQ. ID NO. 1700:

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:1709:

agagatgata	tgaatcaag	gagacacaaa	cttaagaaaa	aaaacacaaa	aaaaaaagag	150
agaggtgaaa	tgtattttc	gtctgcgcga	cttatttcga	tttcttcata	gctttctcgg	160
tgtttctcga	ccggcgatac	catgacagcc	tcaaaaagac	tagcagacga	gaagatgagg	170
aaattctcga	aaaaactatt	aaagagaaga	tttgtttcgt	gagaccacac	caagatgagg	180
agagatatac	acgttggtgc	gaatctctgc	ttctctctgc	ttctctctgc	ttctctctgc	190
ctgaagctga	aaagacgatt	gagctcaact	acggcgagca	tggcattcac	caaaacacag	200
ctcctctctc	tgtagaagtt	gtcaaatctt	agaaattctt	ttctgtcttc	ttttttttct	210
tgaacttttt	ataactcaag	tatccacacc	ttaagtatac	atcagtaaat	gaagattatt	220
				tdttctc		480

(2) INFORMATION FOR SEQ ID NO:1710:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 36 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(11) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..36

(D) OTHER INFORMATION: / Ceres Seq. ID 1570752

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1710:

Arg Asp Ile Leu Lys Ser Arg Arg Gln Lys Leu Lys Lys Lys Asn Pro
1 5 10 15
Lys Lys Lys Glu Arg Gly Glu Ile Asp Phe Leu Leu Ala Ile Val Ile
20 25 30
Ser Ile Ser Asn
35

(2) INFORMATION FOR SEQ ID NO:1711:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 68 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

```
(ix) FEATURE:
```

(A) NAME/KEY: peptide

(B) LOCATION: 1..68

(D) OTHER INFORMATION: / Ceres Seq. ID 1570753

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1711:

Met Thr Thr Ser Lys Arg Leu Ala Asp Arg Lys Ile Glu Lys Phe Asp
1 5 10 15
Lys Asn Ile Leu Lys Arg Gly Phe Val Pro Glu Thr Thr Thr Lys Lys
20 25 30
Gly Lys Asp Tyr Pro Val Gly Pro Ile Leu Leu Gly Phe Phe Val Phe
35 40 45
Val Val Ile Gly Ser Ser Leu Phe Gln Ile Ile Arg Thr Ala Thr Ser
50 55 60
Gly Gly Met Ala
65

(2) INFORMATION FOR SEQ ID NO:1712:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 664 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..664
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570759

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1712:

tcacctatct ctgcagcgga gcttcttctt ctcttagggc ttccacgcga ctacgcctgc 60
caaaatcatt ctacaggaag catgaagcca gtcttctgtg ggaactttga gtatgatgcy 120
cgcggaaggtg acctggaacg actattcagg aaatacggca aggttgagag ggttgatatg 180
aaagctgggtg ttgcttttgt atacatggaa gatgaaaggg atgcggaaga tgccatccga 240
gcacttgacc gctttgaatt tgggcgtaag ggacgcagac ttcgtgttga atggacaaaag 300
agtgaacgtg gaggtgataa aagatctggt ggtggttcaa ggagatcctc atccagcatg 360
agaccttcca agactctctt tgtgattaac ttgatgcggg ataatactag gaccocgggat 420
ctagagaaac actttgagcc gtatggaaaac atcgtaaaac ttaggatcag gaggaatttt 480
gcatttatcc agtacgaggc acaagaggat gccaccagag cattggatgc ttcaaaataac 540
agtaagctga tggataaggt gatctcggtg gagtatgctg tgAaggatga tgatgctaga 600
atcatataaa cctcaactta taattataga cacttttata tttaaatcag ctacgttttg 660
tggc

(2) INFORMATION FOR SEQ ID NO:1713:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 202 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..202
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570760

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1713:

Ser Pro Ile Ser Arg Arg Glu Leu Leu Leu Leu Gly Leu Pro Arg
1 5 10 15
Asp Tyr Ala Cys Gln Asn His Ser Thr Gly Ser Met Lys Pro Val Phe
20 25 30
Cys Gly Asn Phe Glu Tyr Asp Ala Arg Glu Gly Asp Leu Glu Arg Leu
35 40 45
Phe Arg Lys Tyr Gly Lys Val Glu Arg Val Asp Met Lys Ala Gly Phe
50 55 60
Ala Phe Val Tyr Met Glu Asp Glu Arg Asp Ala Glu Asp Ala Ile Arg
65 70 75 80
Ala Leu Asp Arg Phe Glu Phe Gly Arg Lys Gly Arg Arg Leu Arg Val
85 90 95
Glu Trp Thr Lys Ser Glu Arg Gly Gly Asp Lys Arg Ser Gly Gly Gly
100 105 110

Ser Arg Arg Ser Ser Ser Ser Met Arg Pro Ser Lys Thr Leu Phe Val
115 120 125
Ile Asn Phe Asp Ala Asp Asn Thr Arg Thr Arg Asp Leu Glu Lys His
130 135 140
Phe Glu Pro Tyr Gly Lys Ile Val Asn Val Arg Ile Arg Arg Asn Phe
145 150 155 160
Ala Phe Ile Gln Tyr Glu Ala Gln Glu Asp Ala Thr Arg Ala Leu Asp
165 170 175
Ala Ser Asn Asn Ser Lys Leu Met Asp Lys Val Ile Ser Val Glu Tyr
180 185 190
Ala Val Lys Asp Asp Asp Ala Arg Ile Ile
195 200

(2) INFORMATION FOR SEQ ID NO:1714:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 175 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..175
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570761

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1714:

Met Lys Pro Val Phe Cys Gly Asn Phe Glu Tyr Asp Ala Arg Glu Gly
1 5 10 15
Asp Leu Glu Arg Leu Phe Arg Lys Tyr Gly Lys Val Glu Arg Val Asp
20 25 30
Met Lys Ala Gly Phe Ala Phe Val Tyr Met Glu Asp Glu Arg Asp Ala
35 40 45
Glu Asp Ala Ile Arg Ala Leu Asp Arg Phe Glu Phe Gly Arg Lys Gly
50 55 60
Arg Arg Leu Arg Val Glu Trp Thr Lys Ser Glu Arg Gly Gly Asp Lys
65 70 75 80
Arg Ser Gly Gly Gly Ser Arg Arg Ser Ser Ser Ser Met Arg Pro Ser
85 90 95
Lys Thr Leu Phe Val Ile Asn Phe Asp Ala Asp Asn Thr Arg Thr Arg
100 105 110
Asp Leu Glu Lys His Phe Glu Pro Tyr Gly Lys Ile Val Asn Val Arg
115 120 125
Ile Arg Arg Asn Phe Ala Phe Ile Gln Tyr Glu Ala Gln Glu Asp Ala
130 135 140
Thr Arg Ala Leu Asp Ala Ser Asn Asn Ser Lys Leu Met Asp Lys Val
145 150 155 160
Ile Ser Val Glu Tyr Ala Val Lys Asp Asp Asp Ala Arg Ile Ile
165 170 175

(2) INFORMATION FOR SEQ ID NO:1715:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 143 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..143
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570762

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1715:

Met Lys Ala Gly Phe Ala Phe Val Tyr Met Glu Asp Glu Arg Asp Ala
1 5 10 15
Glu Asp Ala Ile Arg Ala Leu Asp Arg Phe Glu Phe Gly Arg Lys Gly

(2) INFORMATION FOR SEO ID NO:1716:

(A) LENGTH: 537 base pairs

- (A) LENGTH: 537 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..537
(D) OTHER INFORMATION: / Ceres Seq. ID 1570775

atgctacata	actcaaaagta	acaaacatac	acatatataaca	tatagaagaag	tcgRaAMaca	60
aaagatcggg	ttgcgaatgg	ctccaaacatg	ctcaactacta	cttgctttat	tccttgtgac	120
caaatatttc	atctgacaacc	tcattaccct	gagttgcgca	gcaataactt	gcccaagagt	180
cggttcacaa	ctttgcagact	gcctgaagtgt	tcctaacctc	atcaaatctg	agctcggggc	240
acacgactgt	aggcctgtgt	gctctattct	ctttgtgtct	attgatctcg	attgtgcggt	300
ttgcctttgc	acccgcgtcca	agctcagcct	ctttggcatc	accatcgaca	ctctattcca	360
ctctaaattg	gctctttaaag	ctcgttgtaag	taacctctct	gattggattc	gttgcccaac	420
atagctacaa	tatatatcata	ttttctattc	atgtgtcttga	attggttttg	tcataacatc	480
aaattccaac	ctttattcat	ctataagcaa	ataaccagta	aaattaaagc	ttttatgc	

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 140 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..140
(D) OTHER INFORMATION: / Ceres Seq. ID 1570776

1	Cys	Tyr	Ile	Thr	Gln	Ser	Asn	Lys	His	Thr	His	Ile	Thr	Tyr	Arg	Lys
				5						10				15		
1	Ile	Xaa	Xaa	Gln	Lys	Ile	Gly	Met	Ser	Met	Ala	Pro	Lys	Thr	Ser	Thr
				20					25				30			
Thr	Leu	Ala	Leu	Phe	Leu	Val	Thr	Asn	Ile	Leu	Phe	Leu	Asn	Leu	Ile	
				35			40					45				
Thr	Leu	Ser	Cys	Ala	Asp	Asn	Thr	Cys	Pro	Arg	Asp	Val	Leu	Lys	Leu	
	50					55					60					
Ser	Thr	Cys	Ser	Asn	Val	Leu	Asn	Leu	Ile	Asn	Leu	Lys	Leu	Gly	Ala	
65					70					75				80		
Pro	Ala	Met	Arg	Pro	Cys	Cys	Ser	Ile	Leu	Phe	Gly	Leu	Ile	Asp	Leu	
				85					90				95			
Asp	Val	Ala	Val	Cys	Leu	Cys	Thr	Ala	Leu	Lys	Leu	Ser	Leu	Leu	Gly	

(2) INFORMATION FOR SEQ ID NO:1718:

(A) LENGTH: 117 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: lin

MOLECULE TYPE: peptide

(1X) FEATURE:
(B) NAME:

(A) NAME/KEY: peptide
(B) LOCATION: 1 113

(B) LOCATION: 1..117

(D) OTHER INFORMATION: / Ceres Seq. ID 1570777

115

(1) SEQUENCE CHARACTERISTICS:

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

MOLECULE TYPE: peptid

{A} NAN

(B) LOCATION: 1..115

(D) OTHER INFORMATION

SEQUENCE DESCRIPTION: SEQ ID NO:1719:

	100	105	110
Cys Pro Thr			

115

(2) INFORMATION FOR SEQ ID NO:1720:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 644 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..644
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570779

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1720:

atcgaaaagt	ctacgaattt	aggGtttaat	ttgtgttaat	gagccaccgt	gtttcgattc	60
tatcatctca	ttttccacot	gcctccgcgc	tcattggcttc	cgagaaagaa	gctgctctcg	120
cgcgcacotc	ttccgattct	cccaccatat	ttgacaagat	catcagcaaa	gagattccat	180
ccaccgtggt	ttttgaggat	gacaaggctc	tagcttttag	ggacataaac	ccccagggtc	240
ctgttcacat	cctccttatt	ccaaaagtga	gggatggcct	aactggcctc	tctaaggctg	300
aggaaggcca	catcgacatc	ttgggcgcgc	ttctctacac	tgccaaagctt	gtagcaaaac	360
aagaaggcct	agcagagggt	ttcagaattg	ttatcaatga	tggtcctcaa	ggctgtcaat	420
cggtgtatca	cattcatggt	catctcattg	gaggacgccca	aatgaactgg	cctcctgggt	480
aaagatcatc	ttgaagtggg	ttgttttcc	gatgataaga	gggacgctta	gagtttgctc	540
tctgtacta	atgtctctat	aaataaaaaa	acgtggggaca	tgacttttat	gattgttatg	600
caaaacotta	ttttatgtta	tgaaaaggat	atttcactgt	tttc		

(2) INFORMATION FOR SEQ ID NO:1721:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 147 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..147
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570780

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1721:

Met	Ser	His	Arg	Val	Ser	Ile	Leu	Ser	Ser	His	Phe	Ser	Pro	Ala	Ser	
1				5					10					15		
Ala	Val	Met	Ala	Ser	Glu	Lys	Glu	Ala	Ala	Leu	Ala	Ala	Thr	Pro	Ser	
				20				25					30			
Asp	Ser	Pro	Thr	Ile	Phe	Asp	Lys	Ile	Ile	Ser	Lys	Glu	Ile	Pro	Ser	
				35				40				45				
Thr	Val	Val	Phe	Glu	Asp	Asp	Lys	Val	Leu	Ala	Phe	Arg	Asp	Ile	Thr	
				50				55				60				
Pro	Gln	Gly	Pro	Val	His	Ile	Leu	Leu	Ile	Pro	Lys	Val	Arg	Asp	Gly	
				65				70				75			80	
Leu	Thr	Gly	Leu	Ser	Lys	Ala	Glu	Glu	Arg	His	Ile	Asp	Ile	Leu	Gly	
				85				90					95			
Arg	Leu	Leu	Tyr	Thr	Ala	Lys	Leu	Val	Ala	Lys	Gln	Glu	Gly	Leu	Ala	
				100				105					110			
Glu	Gly	Phe	Arg	Ile	Val	Ile	Asn	Asp	Gly	Pro	Gln	Gly	Cys	Gln	Ser	
				115				120					125			
Val	Tyr	His	Ile	His	Val	His	Leu	Ile	Gly	Gly	Arg	Gln	Met	Asn	Trp	
				130			135					140				
Pro	Pro	Gly														
145																

(2) INFORMATION FOR SEQ ID NO:1722:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..129
 (D) OTHER INFORMATION: / Ceres Seq. ID 1570781
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1722:
Met Ala Ser Glu Lys Glu Ala Ala Leu Ala Ala Thr Pro Ser Asp Ser
1 5 10 15
Pro Thr Ile Phe Asp Lys Ile Ile Ser Lys Glu Ile Pro Ser Thr Val
 20 25 30
Val Phe Glu Asp Asp Lys Val Leu Ala Phe Arg Asp Ile Thr Pro Gln
 35 40 45
Gly Pro Val His Ile Leu Leu Ile Pro Lys Val Arg Asp Gly Leu Thr
 50 55 60
Gly Leu Ser Lys Ala Glu Glu Arg His Ile Asp Ile Leu Gly Arg Leu
65 70 75 80
Leu Tyr Thr Ala Lys Leu Val Ala Lys Gln Glu Gly Leu Ala Glu Gly
 85 90 95
Phe Arg Ile Val Ile Asn Asp Gly Pro Gln Gly Cys Gln Ser Val Tyr
 100 105 110
His Ile His Val His Leu Ile Gly Gly Arg Gln Met Asn Trp Pro Pro
 115 120 125
Gly

(2) INFORMATION FOR SEQ ID NO:1723:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 521 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
 (A) NAME/KEY: -
 (B) LOCATION: 1..521
 (D) OTHER INFORMATION: / Ceres Seq. ID 1570782
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1723:
acttaaacgc aacagatttg tcacgaagah gaaatcagtg tagcaaacac catccatccc 60
tgagcaaaaga tagaagaaaa gctatgactg atttgcaaat ggaggtagag gtatatacca 120
attcttcttt gcaggagtct ctcccgaagc cgcaagtcac gtacagatgt aagaaatgta 180
gaaggatagt tgctattgag gaaaacatag tcccgcacatg accaggaaaag ggtgaagaat 240
gctttgcttg gaaaaagaga agtggaaact ctgaacaagt gcaatgctct tccatctttg 300
tcgagcctat gaaatggatg cagacaatac atgatggagt ggtggaagag aagcttctat 360
gttttgatg taacgggaga ttagggttatt tcaactgggc tgggatgcaa tgtagctgtg 420
gtgcatgggt taatccggct tttcagctta ataaaagccg aatagacgag tgtaaatccg 480
agcccaaaacc gaacctgaat atggaaactt gatgaaaaAg g

(2) INFORMATION FOR SEQ ID NO:1724:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 169 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..169
 (D) OTHER INFORMATION: / Ceres Seq. ID 1570783
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1724:
Leu Asn Arg Thr Asp Leu Ser Arg Arg Xaa Asn Gln Cys Ser Lys His
1 5 10 15
His Pro Ser Leu Ser Lys Asp Arg Arg Lys Ala Met Thr Asp Leu Gln
 20 25 30

Met Glu Val Glu Val Asp Thr Asn Ser Ser Leu Gln Glu Ser Leu Pro
35 40 45
Lys Pro Gln Val Met Tyr Arg Cys Lys Lys Cys Arg Arg Ile Val Ala
50 55 60
Ile Glu Glu Asn Ile Val Pro His Glu Pro Gly Lys Gly Glu Glu Cys
65 70 75 80
Phe Ala Trp Lys Lys Arg Ser Gly Asn Ser Glu Gln Val Gln Cys Ser
85 90 95
Ser Ile Phe Val Glu Pro Met Lys Trp Met Gln Thr Ile His Asp Gly
100 105 110
Val Val Glu Glu Lys Leu Leu Cys Phe Gly Cys Asn Gly Arg Leu Gly
115 120 125
Tyr Phe Asn Trp Ala Gly Met Gln Cys Ser Cys Gly Ala Trp Val Asn
130 135 140
Pro Ala Phe Gln Leu Asn Lys Ser Arg Ile Asp Glu Cys Lys Ser Glu
145 150 155 160
Pro Asn Pro Asn Leu Asn Met Glu Thr
165

(2) INFORMATION FOR SEQ ID NO:1725:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 142 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..142

(D) OTHER INFORMATION: / Ceres Seq. ID 1570784

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1725:

Met Thr Asp Leu Gln Met Glu Val Glu Val Asp Thr Asn Ser Ser Leu
1 5 10 15
Gln Glu Ser Leu Pro Lys Pro Gln Val Met Tyr Arg Cys Lys Lys Cys
20 25 30
Arg Arg Ile Val Ala Ile Glu Glu Asn Ile Val Pro His Glu Pro Gly
35 40 45
Lys Gly Glu Glu Cys Phe Ala Trp Lys Lys Arg Ser Gly Asn Ser Glu
50 55 60
Gln Val Gln Cys Ser Ser Ile Phe Val Glu Pro Met Lys Trp Met Gln
65 70 75 80
Thr Ile His Asp Gly Val Val Glu Glu Lys Leu Cys Phe Gly Cys
85 90 95
Asn Gly Arg Leu Gly Tyr Phe Asn Trp Ala Gly Met Gln Cys Ser Cys
100 105 110
Gly Ala Trp Val Asn Pro Ala Phe Gln Leu Asn Lys Ser Arg Ile Asp
115 120 125
Glu Cys Lys Ser Glu Pro Asn Pro Asn Leu Asn Met Glu Thr
130 135 140

(2) INFORMATION FOR SEQ ID NO:1726:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 137 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..137

(D) OTHER INFORMATION: / Ceres Seq. ID 1570785

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1726:

Met Glu Val Glu Val Asp Thr Asn Ser Ser Leu Gln Glu Ser Leu Pro

1	5	10	15
Lys Pro Gln Val Met Tyr Arg Cys Lys Lys Cys Arg Arg Ile Val Ala	20	25	30
Ile Glu Glu Asn Ile Val Pro His Glu Pro Gly Lys Gly Glu Glu Cys	35	40	45
Phe Ala Trp Lys Lys Arg Ser Gly Asn Ser Glu Gln Val Gln Cys Ser	50	55	60
Ser Ile Phe Val Glu Pro Met Lys Trp Met Gln Thr Ile His Asp Gly	65	70	75
Val Val Glu Glu Lys Leu Leu Cys Phe Gly Cys Asn Gly Arg Leu Gly	85	90	95
Tyr Phe Asn Trp Ala Gly Met Gln Cys Ser Cys Gly Ala Trp Val Asn	100	105	110
Pro Ala Phe Gln Leu Asn Lys Ser Arg Ile Asp Glu Cys Lys Ser Glu	115	120	125
Pro Asn Pro Asn Leu Asn Met Glu Thr	130	135	

(2) INFORMATION FOR SEQ ID NO:1727:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 744 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..744
- (D) OTHER INFORMATION: / Ceres Seq. ID 1507086

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1727:

ttcaactcac	aaagcatcac	ataacactca	cacacacact	ttctcttctc	ttattttctc	60
agttctttta	actctttttc	ctacctatat	tcaaatggcc	accgtcgagg	ttgaacaagt	120
gactccagta	gcagctgaga	acatcgaggt	gccaccacca	aaggctgtgg	agtcggagga	180
agtcaccacc	gtctccgagt	ctcttccagc	tccggttaaca	gaatctcaag	cgcctgtcga	240
agtaacaact	aaagatttgg	tcgtggaaga	gacagagaaa	ccaatcgag	aaacagagga	300
agctcaagtt	gaaactccgg	aggttgtgga	gatcaagaaa	gatgaagaag	ctccggttga	360
aactccgggt	gttgtggagg	atgagagcaa	aacagaggaa	gttgtagagg	cgaagaagaa	420
ggaagaagta	gaagaaaaga	agacagagga	agctccagtg	gttggtggag	aagagaagaa	480
gccagaggca	gaggaggaga	aAcccgccgt	ggaagcctcc	gtgacagctc	cagtggagaa	540
ggctgatgag	taaatgtgaa	gaaaaaaact	gtcttttgaa	agacaaaaga	agaagaaaat	600
gttagcaagt	aatttatttg	ctactttaag	tactttgtgt	cttgttatgt	ttttgagtct	660
atgactcttc	ttgtcttttg	tttttaactc	ttcttaagta	ctattttcaa	tggttatcat	720
ttttaataag	atatacatta	tttt				

(2) INFORMATION FOR SEQ ID NO:1728:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 183 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..183
- (D) OTHER INFORMATION: / Ceres Seq. ID 1507087

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1728:

Ser Leu Thr Lys Ala Ser His Asn Thr His Thr His Thr Phe Ser Ser	1	5	10	15
Leu Ile Phe Ser Val Leu Leu Thr Leu Phe Ser Thr Tyr Ile Gln Met	20	25	30	
Ala Thr Val Glu Val Glu Gln Val Thr Pro Val Ala Ala Glu Asn Ile	35	40	45	
Glu Val Pro Pro Pro Lys Ala Val Glu Ser Glu Glu Val Thr Thr Val				

50	55	60
Ser Glu Ser Leu Pro Ala Pro Val Thr Glu Ser Gln Ala Pro Val Glu		
65	70	75
Val Thr Thr Lys Asp Leu Val Val Glu Glu Thr Glu Lys Pro Ile Glu		80
	85	90
Glu Thr Glu Glu Ala Gln Val Glu Thr Pro Glu Val Val Glu Ile Lys		95
	100	105
Lys Asp Glu Glu Ala Pro Val Glu Thr Pro Val Val Val Glu Asp Glu		110
	115	120
Ser Lys Thr Glu Glu Val Val Glu Ala Lys Lys Glu Glu Glu Val Glu		125
	130	135
Glu Lys Lys Thr Glu Glu Ala Pro Val Val Val Glu Glu Glu Lys Lys		140
145	150	155
Pro Glu Ala Glu Glu Lys Pro Ala Val Glu Ala Ser Val Thr Ala		160
	165	170
Pro Val Glu Lys Ala Asp Glu		175
	180	

(2) INFORMATION FOR SEQ ID NO:1729:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 152 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..152

(D) OTHER INFORMATION: / Ceres Seq. ID 1570788

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1729:

Met Ala Thr Val Glu Val Glu Gln Val Thr Pro Val Ala Ala Glu Asn	
1	5
Ile Glu Val Pro Pro Lys Ala Val Glu Ser Glu Glu Val Thr Thr	10
	20
Val Ser Glu Ser Leu Pro Ala Pro Val Thr Glu Ser Gln Ala Pro Val	25
	30
Glu Val Thr Thr Lys Asp Leu Val Val Glu Glu Thr Glu Lys Pro Ile	35
	40
Glu Glu Thr Glu Glu Ala Gln Val Glu Thr Pro Glu Val Val Glu Ile	45
65	50
Lys Lys Asp Glu Glu Ala Pro Val Glu Thr Pro Val Val Val Glu Asp	55
	60
Glu Ser Lys Thr Glu Glu Val Val Glu Ala Lys Lys Glu Glu Glu Val	65
	70
Glu Glu Lys Lys Thr Glu Glu Ala Pro Val Val Val Glu Glu Glu Lys	75
	80
Lys Pro Glu Ala Glu Glu Glu Lys Pro Ala Val Glu Ala Ser Val Thr	85
	90
Ala Pro Val Glu Lys Ala Asp Glu	95
145	100
	105
	110
	115
	120
	125
	130
	135
	140

(2) INFORMATION FOR SEQ ID NO:1730:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 458 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..458

(D) OTHER INFORMATION: / Ceres Seq. ID 1570793

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1730:

cattttcgac cgctacaacg attcctatct cagacgaatc ggatccaatg ttttctctta 60
cgtgaacatg gtctgtgctg gcCtgcggaa ttcaatcccc aagtcacatg tatactgcc 120
agtcogagaa gogaagcgCa Ngtctcctcg accatttctt tgcggagCtc ggtaccatgg 180
atatgaagag gctctcgtcg ctattgaacg aagatccacg aatcatggag agacgcagtg 240
ccatctcaaa goggctagaa ttgtatcgag cagcccaatc cgagatcgat gctgttgctt 300
ggccaagtgt ataccggcat gtcatgtcca ctgttttgct cggttctggt cggtgtggct 360
cagactcgga gcagagattt agggctctga atttgtataa gatgatcttc ccgataccat 420
gcagtatcgt ttatataaac atccacattg ttgtcccc

(2) INFORMATION FOR SEQ ID NO:1731:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 126 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..126

(D) OTHER INFORMATION: / Ceres Seq. ID 1570794

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1731:

1 Phe Asp Arg Tyr Asn Asp Ser Tyr Leu Arg Arg Ile Gly Ser Asn
5 10 15
Val Leu Ser Tyr Val Asn Met Val Cys Ala Gly Leu Arg Asn Ser Ile
20 25 30
Pro Lys Ser Ile Val Tyr Cys Gln Val Arg Glu Ala Lys Arg Xaa Ser
35 40 45
Pro Arg Pro Phe Leu Cys Gly Ala Arg Tyr His Gly Tyr Glu Glu Ala
50 55 60
Leu Val Ala Ile Glu Arg Arg Ser Ser Asn His Gly Glu Thr Gln Cys
65 70 75 80
His Leu Lys Ala Ala Arg Ile Val Ser Ser Ser Pro Ile Arg Asp Arg
85 90 95
Cys Cys Cys Leu Val Gln Val Ile Pro Ala Cys His Val His Cys Phe
100 105 110
Ala Arg Phe Trp Ser Val Trp Leu Arg Leu Gly Ala Glu Ile
115 120 125

(2) INFORMATION FOR SEQ ID NO:1732:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 104 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..104

(D) OTHER INFORMATION: / Ceres Seq. ID 1570795

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1732:

1 Met Val Cys Ala Gly Leu Arg Asn Ser Ile Pro Lys Ser Ile Val Tyr
5 10 15
Cys Gln Val Arg Glu Ala Lys Arg Xaa Ser Pro Arg Pro Phe Leu Cys
20 25 30
Gly Ala Arg Tyr His Gly Tyr Glu Glu Ala Leu Val Ala Ile Glu Arg
35 40 45
Arg Ser Ser Asn His Gly Glu Thr Gln Cys His Leu Lys Ala Ala Arg
50 55 60
Ile Val Ser Ser Ser Pro Ile Arg Asp Arg Cys Cys Cys Leu Val Gln
65 70 75 80
Val Ile Pro Ala Cys His Val His Cys Phe Ala Arg Phe Trp Ser Val
85 90 95
Trp Leu Arg Leu Gly Ala Glu Ile

100

(2) INFORMATION FOR SEQ ID NO:1733:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 527 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..527

(D) OTHER INFORMATION: / Ceres Seq. ID 1507096

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1733:

aattttgctt	tgagacgacg	aaacgaagdg	agaaagagac	aagccctaaa	aatcgctttg	60
agacgataaa	tcttataaat	cttcgattcg	tccacgatga	tctccctgtg	tgtgtgtttt	120
actttgtgaa	aggtgattgg	gaacaaatgg	gacacatata	ttgaactctt	ccaggctgat	180
tacgctgaag	gggatgctct	tgacgcgctt	ggatttagtc	gttactgctg	caggcgatg	240
cttatgactc	atgtcgatct	aatcgaaaag	cttctaact	acaacactat	ggagaaatcc	300
gaccccaatt	aaagaaagat	gctataatga	atacaaatc	atcaagagct	aaagtgtagg	360
agtgagggcat	ctcattcatg	tgaaagtctt	aataaaaacca	caatgtttca	gaaattttgt	420
tgaattttaga	aactaggaat	gttgataatt	caatgttttc	tgatgttctt	gttcggtttt	480
agaagacaac	ttttcgagct	acaaataaag	ctcaagcttg	tagagcc		

(2) INFORMATION FOR SEQ ID NO:1734:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 71 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..71

(D) OTHER INFORMATION: / Ceres Seq. ID 1507097

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1734:

Met	Ile	Val	Pro	Val	Arg	Cys	Phe	Thr	Cys	Gly	Lys	Val	Ile	Gly	Asn	
1				5						10				15		
Lys	Trp	Asp	Thr	Tyr	Leu	Glu	Leu	Leu	Gln	Ala	Asp	Tyr	Ala	Glu	Gly	
				20				25					30			
Asp	Ala	Leu	Asp	Ala	Leu	Gly	Leu	Val	Arg	Tyr	Cys	Cys	Arg	Arg	Met	
		35				40						45				
Leu	Met	Thr	His	Val	Asp	Leu	Ile	Glu	Lys	Leu	Leu	Asn	Tyr	Asn	Thr	
		50				55						60				
Met	Glu	Lys	Ser	Asp	Pro	Asn										
65						70										

(2) INFORMATION FOR SEQ ID NO:1735:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 605 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..605

(D) OTHER INFORMATION: / Ceres Seq. ID 1507098

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1735:

aaaaataaaaa	cctttactta	tcttctttct	tctcacttct	cagacctcaa	tttccaagca	60
gagatgacgg	tgaagataag	gCtcgcgcgt	cttggttgta	aacaccgacc	cttctatcgt	120
gtagtgtgct	ccgatgaaaa	atcgcgacag	gacggtaaac	aaatcgaggt	gttaggcttt	180
tatgatccac	tccaaggcaa	agaagatgcg	gatagagtga	gcctcaaat	cgacagaatc	240
aagtactggt	tatctgttgg	agctcaacca	acagacacag	tggaaagcat	gcttttcagg	300

gccggtttga taccacacaa gcctatggta gtggtcggtt caaaaaatgg gcagaagtct 360
acgagccaac atgtttcacc cattacaggt gaaatcttga actaagagtg ttgatgcggt 420
gagcaagaaa gagccttttg tgtctgtgtg aaaggagttt atgtaatggt gttaaagact 480
tttctgttta tgtgaaagga gttaatgtaa tgttgtttaa gacttttgct ttctatgtga 540
aagcagcttta atgttatgtt ggtaaagact tttctgcaac agagtttggt gaatttttaw 600
tcytt

(2) INFORMATION FOR SEQ ID NO:1736:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 134 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..134

(D) OTHER INFORMATION: / Ceres Seq. ID 1570799

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1736:

Lys Ile Lys Thr Phe Thr Tyr Leu Leu Ser Ser His Phe Ser Asp Leu
1 5 10 15
Asn Phe Gln Ala Glu Met Thr Val Lys Ile Arg Leu Ala Arg Leu Gly
20 25 30
Cys Lys His Arg Pro Phe Tyr Arg Val Val Val Ala Asp Glu Lys Ser
35 40 45
Arg Arg Asp Gly Lys Gln Ile Glu Val Leu Gly Phe Tyr Asp Pro Leu
50 55 60
Gln Gly Lys Glu Asp Ala Asp Arg Val Ser Leu Lys Phe Asp Arg Ile
65 70 75 80
Lys Tyr Trp Leu Ser Val Gly Ala Gln Pro Thr Asp Thr Val Glu Ser
85 90 95
Met Leu Phe Arg Ala Gly Leu Ile Pro Pro Lys Pro Met Val Val Val
100 105 110
Gly Ser Lys Asn Gly Gln Lys Ser Thr Ser Gln His Val Ser Pro Ile
115 120 125
Thr Gly Glu Ile Leu Asn
130

(2) INFORMATION FOR SEQ ID NO:1737:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 113 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..113

(D) OTHER INFORMATION: / Ceres Seq. ID 1570800

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1737:

Met Thr Val Lys Ile Arg Leu Ala Arg Leu Gly Cys Lys His Arg Pro
1 5 10 15
Phe Tyr Arg Val Val Val Ala Asp Glu Lys Ser Arg Arg Asp Gly Lys
20 25 30
Gln Ile Glu Val Leu Gly Phe Tyr Asp Pro Leu Gln Gly Lys Glu Asp
35 40 45
Ala Asp Arg Val Ser Leu Lys Phe Asp Arg Ile Lys Tyr Trp Leu Ser
50 55 60
Val Gly Ala Gln Pro Thr Asp Thr Val Glu Ser Met Leu Phe Arg Ala
65 70 75 80
Gly Leu Ile Pro Pro Lys Pro Met Val Val Val Gly Ser Lys Asn Gly
85 90 95
Gln Lys Ser Thr Ser Gln His Val Ser Pro Ile Thr Gly Glu Ile Leu

Asn 100 105 110

(2) INFORMATION FOR SEQ ID NO:1738:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 511 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..511

(D) OTHER INFORMATION: / Ceres Seq. ID 1570805

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1738:

atttgaacga	gattgtatta	agaagtaac	tatatggaNa	cgCgcaacgc	gCttattttgt	60
gtccaagggtc	ctggatatata	aactgctcga	gacattattt	taccgcccctc	tgtggaaatc	120
attgataata	cacagcatat	agctacctta	acagaaccaa	tagattttgtg	tattgaatta	180
aaaattgaga	ggaatcgcg	atatagtcta	aaaatgtcaa	ataaactttga	agacagaagt	240
tatcctatcg	atgctgtatt	catgcctgtt	gaaaaatgcca	atcatagtat	tcattcttat	300
gggaatggga	atgaaaaaca	agagattctt	ttctagaaa	tatggacaaa	tggagttta	360
actcctaag	aagcacttca	tcaagcctcc	cggaatttga	ttattttatt	tattcctttt	420
ctacatatag	aagaagaaac	gttctattta	gagaacaatc	aacatcaagt	tactttacc	480
ttttttcctt	ttcataatcg	attagttaac	c			

(2) INFORMATION FOR SEQ ID NO:1739:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 159 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..159

(D) OTHER INFORMATION: / Ceres Seq. ID 1570806

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1739:

Met	Xaa	Thr	Arg	Asn	Ala	Leu	Ile	Cys	Val	Gln	Gly	Pro	Gly	Tyr	Ile
1				5					10					15	
Thr	Ala	Arg	Asp	Ile	Ile	Leu	Pro	Pro	Ser	Val	Glu	Ile	Ile	Asp	Asn
			20				25				30				
Thr	Gln	His	Ile	Ala	Thr	Leu	Thr	Glu	Pro	Ile	Asp	Leu	Cys	Ile	Glu
		35				40					45				
Leu	Lys	Ile	Glu	Arg	Asn	Arg	Gly	Tyr	Ser	Leu	Lys	Met	Ser	Asn	Asn
		50			55					60					
Phe	Glu	Asp	Arg	Ser	Tyr	Pro	Ile	Asp	Ala	Val	Phe	Met	Pro	Val	Glu
		65			70				75					80	
Asn	Ala	Asn	His	Ser	Ile	His	Ser	Tyr	Gly	Asn	Gly	Asn	Glu	Lys	Gln
			85						90					95	
Glu	Ile	Leu	Phe	Leu	Glu	Ile	Trp	Thr	Asn	Gly	Ser	Leu	Thr	Pro	Lys
			100				105						110		
Glu	Ala	Leu	His	Gln	Ala	Ser	Arg	Asn	Leu	Ile	Asn	Leu	Phe	Ile	Pro
			115				120					125			
Phe	Leu	His	Val	Glu	Glu	Glu	Thr	Phe	Tyr	Leu	Glu	Asn	Asn	Gln	His
			130				135					140			
Gln	Val	Thr	Leu	Pro	Phe	Phe	Pro	Phe	His	Asn	Arg	Leu	Val	Asn	
			145				150					155			

(2) INFORMATION FOR SEQ ID NO:1740:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 99 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..99
(D) OTHER INFORMATION: / Ceres Seq. ID 1570807
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1740:
Met Ser Asn Asn Phe Glu Asp Arg Ser Tyr Pro Ile Asp Ala Val Phe
1 5 10 15
Met Pro Val Glu Asn Ala Asn His Ser Ile His Ser Tyr Gly Asn Gly
20 25 30
Asn Glu Lys Gln Glu Ile Leu Phe Leu Glu Ile Trp Thr Asn Gly Ser
35 40 45
Leu Thr Pro Lys Glu Ala Leu His Gln Ala Ser Arg Asn Leu Ile Asn
50 55 60
Leu Phe Ile Pro Phe Leu His Val Glu Glu Thr Phe Tyr Leu Glu
65 70 75 80
Asn Asn Gln His Gln Val Thr Leu Pro Phe Phe Pro Phe His Asn Arg
85 90 95
Leu Val Asn

(2) INFORMATION FOR SEQ ID NO:1741:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 83 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..83
(D) OTHER INFORMATION: / Ceres Seq. ID 1570808
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1741:
Met Pro Val Glu Asn Ala Asn His Ser Ile His Ser Tyr Gly Asn Gly
1 5 10 15
Asn Glu Lys Gln Glu Ile Leu Phe Leu Glu Ile Trp Thr Asn Gly Ser
20 25 30
Leu Thr Pro Lys Glu Ala Leu His Gln Ala Ser Arg Asn Leu Ile Asn
35 40 45
Leu Phe Ile Pro Phe Leu His Val Glu Glu Thr Phe Tyr Leu Glu
50 55 60
Asn Asn Gln His Gln Val Thr Leu Pro Phe Phe Pro Phe His Asn Arg
65 70 75 80
Leu Val Asn

(2) INFORMATION FOR SEQ ID NO:1742:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 475 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..475
(D) OTHER INFORMATION: / Ceres Seq. ID 1570816
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1742:
gttgatcgga aaggaaaagt aaaaaagaga gatctgagaa atgggaaatg agacgaagac 60
caacgggtgt cctgcaagta tggccggagg Cggaggattc agagctaaaa tggaaacatta 120
cgtttacagt ggtgaaaaga agcacgtctt ggtcgggattc ggaatcgtca ccatcatctt 180
cggagttcct tggattttga tgactcaagg gtcaaagcat caatctcacc aagattacat 240

ggacaaggcc gataaagctc gaaaagcagc cctctcatcg tcttcatcag ctaacaagta 300
gtctgtctga aggattgagtg catttgcaca ctgttatctc atactcattt tccacacaaa 360
gttaaaactt agtcaaaaatc tgagcttttt ttgtgattta gattcaaaat catttcatc 420
ttcatgcacc atgttttggtt atocgttttt taataaaaag atcaaagatt ctatc

(2) INFORMATION FOR SEQ ID NO:1743:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 86 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..86

(D) OTHER INFORMATION: / Ceres Seq. ID 1570817

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1743:

Met	Gly	Asn	Glu	Thr	Lys	Thr	Asn	Gly	Gly	Pro	Ala	Ser	Met	Ala	Gly	
1					5				10					15		
Gly	Gly	Gly	Phe	Arg	Ala	Lys	Met	Glu	His	Tyr	Val	Tyr	Ser	Gly	Glu	
			20					25					30			
Lys	Lys	His	Val	Leu	Val	Gly	Ile	Gly	Ile	Val	Thr	Ile	Ile	Phe	Gly	
		35					40					45				
Val	Pro	Trp	Tyr	Leu	Met	Thr	Gln	Gly	Ser	Lys	His	Gln	Ser	His	Gln	
	50					55					60					
Asp	Tyr	Met	Asp	Lys	Ala	Asp	Lys	Ala	Arg	Lys	Ala	Arg	Leu	Ser	Ser	
65				70					75					80		
Ser	Ser	Ser	Ala	Asn	Lys											
				85												

(2) INFORMATION FOR SEQ ID NO:1744:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 73 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..73

(D) OTHER INFORMATION: / Ceres Seq. ID 1570818

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1744:

Met	Ala	Gly	Gly	Gly	Phe	Arg	Ala	Lys	Met	Glu	His	Tyr	Val	Tyr	
1				5				10					15		
Ser	Gly	Glu	Lys	Lys	His	Val	Leu	Val	Gly	Ile	Gly	Ile	Val	Thr	Ile
		20						25					30		
Ile	Phe	Gly	Val	Pro	Trp	Tyr	Leu	Met	Thr	Gln	Gly	Ser	Lys	His	Gln
		35					40					45			
Ser	His	Gln	Asp	Tyr	Met	Asp	Lys	Ala	Asp	Lys	Ala	Arg	Lys	Ala	Arg
	50				55						60				
Leu	Ser	Ser	Ser	Ser	Ser	Ala	Asn	Lys							
65					70										

(2) INFORMATION FOR SEQ ID NO:1745:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 63 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..63

(D) OTHER INFORMATION: / Ceres Seq. ID 1570819

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1745:

Met Glu His Tyr Val Tyr Ser Gly Glu Lys Lys His Val Leu Val Gly
1 5 10 15
Ile Gly Ile Val Thr Ile Ile Phe Gly Val Pro Trp Tyr Leu Met Thr
20 25 30
Gln Gly Ser Lys His Gln Ser His Gln Asp Tyr Met Asp Lys Ala Asp
35 40 45
Lys Ala Arg Lys Ala Arg Leu Ser Ser Ser Ser Ala Asn Lys
50 55 60

(2) INFORMATION FOR SEQ ID NO:1746:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 805 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..805
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570823

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1746:

aaagtaaccc caaaagaaaa aaagcaaaaa gagaggaaaa gaaaaaaaat gacgaagacg 60
atgatgatct tcgcggcgac gatgacggcg atggctttgc ttacagttcc tgcgattgaa 120
gcacaaaactg agtgcgtgag Caagctagtc ccttgcttca acgacctgaa cagcaacaa 180
acgcgggtga aagaatgttg cgactcgata aaagaagcgg tggagaagga acttacatgt 240
ctctgtacaa tctacaccag tccaggtttg ctgcgtcagt tcaacgtcac cactgagaaa 300
gctctcgggtc ttacgcgtgc ttgcaacgtc accactgac tcctccgcttg taccgctaaa 360
ggagctcccat cgccaaaaagc ttctttacct cctccagctc cagcagggaa taccaaaaaa 420
gacgcggagc ctgggaacaa gctcgcgggt tatggagtca ccacgctgat cttgtctttt 480
atctcatoca tcttctctcg aattccttta cccggtttta ttattattag ctcaataaat 540
tctsgagagt tgyttgcttt ttggtctaac ttatttaata tttaagaaa aacaaaGaaG 600
tattttttgt tcaatgttta tgtattatca ttgattcatc attgagtc cc atgttagtat 660
atttaccgggt ttcaatcgga cctatcatct tgcatactgt ttttgagtgt ggatgtgtgt 720
tggttttatgt aactctctac tctatgggac ttaattattc tactgtgtga ctggatttaa 780
ttgatgtaaa aactgtCgtt ggttt

(2) INFORMATION FOR SEQ ID NO:1747:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 166 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..166
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570824

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1747:

Lys Val Thr Pro Lys Glu Lys Lys Gln Arg Glu Arg Lys Arg Lys Lys
1 5 10 15
Met Thr Lys Thr Met Met Ile Phe Ala Ala Thr Met Thr Ala Met Ala
20 25 30
Leu Leu Ser Val Pro Ala Ile Glu Ala Gln Thr Glu Cys Val Ser Lys
35 40 45
Leu Val Pro Cys Phe Asn Asp Leu Asn Thr Thr Thr Thr Pro Val Lys
50 55 60
Glu Cys Cys Asp Ser Ile Lys Glu Ala Val Glu Lys Glu Leu Thr Cys
65 70 75 80
Leu Cys Thr Ile Tyr Thr Ser Pro Gly Leu Leu Ala Gln Phe Asn Val
85 90 95
Thr Thr Glu Lys Ala Leu Gly Leu Ser Arg Arg Cys Asn Val Thr Thr
100 105 110

Asp Leu Ser Ala Cys Thr Ala Lys Gly Ala Pro Ser Pro Lys Ala Ser
115 120 125
Leu Pro Pro Pro Ala Pro Ala Gly Asn Thr Lys Lys Asp Ala Gly Ala
130 135 140
Gly Asn Lys Leu Ala Gly Tyr Gly Val Thr Thr Val Ile Leu Ser Leu
145 150 155 160
Ile Ser Ser Ile Phe Phe
165

(2) INFORMATION FOR SEQ ID NO:1748:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 150 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..150

(D) OTHER INFORMATION: / Ceres Seq. ID 1570825

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1748:

Met Thr Lys Thr Met Met Ile Phe Ala Ala Thr Met Thr Ala Met Ala
1 5 10 15
Leu Leu Ser Val Pro Ala Ile Glu Ala Gln Thr Glu Cys Val Ser Lys
20 25 30
Leu Val Pro Cys Phe Asn Asp Leu Asn Thr Thr Thr Thr Pro Val Lys
35 40 45
Glu Cys Cys Asp Ser Ile Lys Glu Ala Val Glu Lys Glu Leu Thr Cys
50 55 60
Leu Cys Thr Ile Tyr Thr Ser Pro Gly Leu Leu Ala Gln Phe Asn Val
65 70 75 80
Thr Thr Glu Lys Ala Leu Gly Leu Ser Arg Arg Cys Asn Val Thr Thr
85 90 95
Asp Leu Ser Ala Cys Thr Ala Lys Gly Ala Pro Ser Pro Lys Ala Ser
100 105 110
Leu Pro Pro Pro Ala Pro Ala Gly Asn Thr Lys Lys Asp Ala Gly Ala
115 120 125
Gly Asn Lys Leu Ala Gly Tyr Gly Val Thr Thr Val Ile Leu Ser Leu
130 135 140
Ile Ser Ser Ile Phe Phe
145 150

(2) INFORMATION FOR SEQ ID NO:1749:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 146 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..146

(D) OTHER INFORMATION: / Ceres Seq. ID 1570826

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1749:

Met Met Ile Phe Ala Ala Thr Met Thr Ala Met Ala Leu Leu Ser Val
1 5 10 15
Pro Ala Ile Glu Ala Gln Thr Glu Cys Val Ser Lys Leu Val Pro Cys
20 25 30
Phe Asn Asp Leu Asn Thr Thr Thr Thr Pro Val Lys Glu Cys Cys Asp
35 40 45
Ser Ile Lys Glu Ala Val Glu Lys Glu Leu Thr Cys Leu Cys Thr Ile
50 55 60
Tyr Thr Ser Pro Gly Leu Leu Ala Gln Phe Asn Val Thr Thr Glu Lys

(2) INFORMATION FOR SEQ ID NO:1750:

(A) LENGTH: 659 base pairs

- (B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(1x) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..659
(D) OTHER INFORMATION: / Ceres Seq. ID 1570827

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1750:

aaaaaacac	gcgcgtagagt	ttcttaagaa	caacagctgac	gaaaaggttt	ttagggtttc	60
ataatctcc	agaatctccg	caagatgaac	attcttcgaat	gaaagacag	ccaggttcaa	120
ttatcttcgc	aactgtaac	tggcggcaac	tactggactt	gagacccctc	tcgatcagat	180
ttattcttggt	attacaaagt	agcagacga	ctgtctggga	gtctctaaag	gtttgagcca	240
ggctacaaat	atgaactctg	atgaatctca	tgaactgtgt	ttttccaca	agaaagagt	300
acaaacaacat	gtgtctgggt	tgtacatcat	cagagggagc	aacatgagtg	ttatcgggga	360
ctgtcgagag	gactgtgatg	ctagctctga	tttttccgaag	ctgagagccc	atcogtga	420
accctgagt	cattgattga	atataagttg	ggtgagaaa	tcatattctc	tcattcaaa	480
ctataaaac	aagagaagat	tigtattgt	acaattctgg	tagttttctg	tatgtctgtg	540
agtttctcta	tttgtgtcat	ctagagacaa	aaagctatga	atatatttat	tttcaaacgt	600
tttgtctgta	aaCCTtaaat	catGCCaat	CcttttgatA	caqAacctag	gtttctCct	

(2) INFORMATION FOR SEQ ID NO:1751:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 98 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..98
(D) OTHER INFORMATION: / Ceres Seq. ID 1570828

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1751:

[illegible]

(2) INFORMATION FOR SEQ ID NO:1752:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 543 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:

(A) NAME/KEY: -
(B) LOCATION: 1..543
(D) OTHER INFORMATION: / Ceres Seq. ID 1570829

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1752:

ataaaatcga	ttttctctca	caaatcttat	tctctttcga	cttcagtgcc	ggcgcatcca	60
gagattcaaa	ctcagagaaa	atggtggcga	caggcttatt	cgtggggcta	aacaaaggac	120
acgttggtac	caaacgcgag	caacctctcc	gccttaacaa	cagaaaagg	aaaacaagca	180
aaaggactat	ttttatcagg	aattctcatca	aggaagttgc	gggtcaagct	ccctatgaga	240
agaggatcac	tgagcttttg	aaggttggtta	aagacaagag	agctctttaa	gttgccaagc	300
gaaagtgtgg	aactcacaca	agagctaaac	gaaagagaga	ggagatgtct	agtgttctcc	360
gcaagatgag	gtctggtggt	gctggtgcac	ccgagaagaa	gaagtgatgc	gctgactctg	420
gttcagcgct	ctgtttcttc	taaaccagtt	ttctgttttt	tgaatttttt	gGcagtacct	480
tgtgtttcct	ttggatatatt	tgtagcagag	ataattaaat	gttaaaaaca	aaccattatg	540

acg

- (2) INFORMATION FOR SEQ ID NO:1753:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 134 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1..134
(D) OTHER INFORMATION: / Ceres Seq. ID 1570830

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1753:

Lys	Ile	Asp	Phe	Leu	Ser	Gln	Ile	Leu	Phe	Ser	Phe	Asp	Phe	Ser	Gly
1				5				10					15		
Gly	Ala	Phe	Arg	Asp	Ser	Asn	Ser	Glu	Lys	Met	Val	Ala	Thr	Gly	Leu
				20				25					30		
Phe	Val	Gly	Leu	Asn	Lys	Gly	His	Val	Val	Thr	Lys	Arg	Glu	Gln	Pro
				35				40				45			
Pro	Arg	Pro	Asn	Asn	Arg	Lys	Gly	Lys	Thr	Ser	Lys	Arg	Thr	Ile	Phe
				50				55				60			
Ile	Arg	Asn	Leu	Ile	Lys	Glu	Val	Ala	Gly	Gln	Ala	Pro	Tyr	Glu	Lys
				65				70				75		80	
Arg	Ile	Thr	Glu	Leu	Leu	Lys	Val	Gly	Lys	Asp	Lys	Arg	Ala	Leu	Lys
				85				90				95			
Val	Ala	Lys	Arg	Lys	Leu	Gly	Thr	His	Lys	Arg	Ala	Lys	Arg	Lys	Arg
				100				105				110			
Glu	Glu	Met	Ser	Ser	Val	Leu	Arg	Lys	Met	Arg	Ser	Gly	Gly	Ala	Gly
				115				120				125			
Ala	Ser	Glu	Lys	Lys	Lys										
				130											

- (2) INFORMATION FOR SEQ ID NO:1754:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 108 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1..108

(D) OTHER INFORMATION: / Ceres Seq. ID 1570831

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1754:

```
Met Val Ala Thr Gly Leu Phe Val Gly Leu Asn Lys Gly His Val Val
1      5      10      15
Thr Lys Arg Glu Gln Pro Pro Arg Pro Asn Asn Arg Lys Gly Lys Thr
      20      25      30
Ser Lys Arg Thr Ile Phe Ile Arg Asn Leu Ile Lys Glu Val Ala Gly
      35      40      45
Gln Ala Pro Tyr Glu Lys Arg Ile Thr Glu Leu Leu Lys Val Gly Lys
      50      55      60
Asp Lys Arg Ala Leu Lys Val Ala Lys Arg Lys Leu Gly Thr His Lys
65      70      75      80
Arg Ala Lys Arg Lys Arg Glu Glu Met Ser Ser Val Leu Arg Lys Met
      85      90      95
Arg Ser Gly Gly Ala Gly Ala Ser Glu Lys Lys
      100     105
```

(2) INFORMATION FOR SEQ ID NO:1755:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 552 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..552
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570836

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1755:

```
agatcagtgga ttgttcgatg aacgaagagg agccagacaa agaacacgtg gcggattota      60
ctatgtcggc ggcgcgcatt gatgtgtg cggtctgag atcggtgttt cagcgggttaa      120
accaggcggc ggagaaagcg ggtcgtgggt cggatcagat acgggtcgta gcggtgagta      180
agacgaaacc agtttctctg attgcgcaag tatacgacgc ttgtcagagg tcttttgag      240
agaattatgt gcaagagatc attgagaagg cacctcagct tccagaagat atagagtggc      300
atttcatttg gaatttgcag agcaacaaag tgaagccttt gctatgtaaa ttgactttgc      360
tatttcaaag tcttcatctt tagttttttt gatttgagtt actaaattgg gtgtaaaact      420
ccacacttga gttctattct taattctttg gtttgatcag ctggtgttcc taacctgttg      480
accgtggaag gtgttgatga tgaaaaggta aaagtctctc tttgttatat ttaaagagRa      540
aattggtttg tt
```

(2) INFORMATION FOR SEQ ID NO:1756:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 126 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..126
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570837

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1756:

```
Ile Ser Asp Cys Ser Met Asn Glu Glu Glu Pro Asp Lys Glu His Val
1      5      10      15
Ala Asp Ser Thr Met Ser Ala Ala Ala Ile Asp Gly Val Ala Ala Leu
      20      25      30
Arg Ser Val Phe Gln Arg Val Asn Gln Ala Ala Glu Lys Ala Gly Arg
      35      40      45
Gly Ser Asp Gln Ile Arg Val Val Ala Val Ser Lys Thr Lys Pro Val
      50      55      60
Ser Leu Ile Arg Gln Val Tyr Asp Ala Gly Gln Arg Ser Phe Gly Glu
65      70      75      80
Asn Tyr Val Gln Glu Ile Ile Glu Lys Ala Pro Gln Leu Pro Glu Asp
```


(2) INFORMATION FOR SEO ID NO:1757:

(i) SEQUENCE CHARACTERISTICS:

(i) SEQUENCE CHARACTERISTICS:

- (ii) MOLECULE TYPE: peptide

(A) NAME/KEY: peptide

- (B) LOCATION: 1..121

- (D) OTHER INFORMATION

- SEQUENCE DESCRIPTION: SEO ID NO:1757:

Asp Glu Glu Glu Pro Asp Lys Glu His Val Al

(2) INFORMATION FOR SEQ ID NO:1758:

(A) LENGTH: 106 amino ac

- (A) LENGTH: 106 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

```
(ix) FEATURE:
```

- (A) NAME/KEY: peptide

- (B) LOCATION: 1..106

- (D) OTHER INFORMATION: / Ceres Seq. ID 1570839

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1758:

(2) INFORMATION FOR SEQ ID NO:1759:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 676 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..676
(D) OTHER INFORMATION: / Ceres Seq. ID 1570852

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1759:

```
aacaatccct acaacggcta catctacact tcttttcaag agagagcaac ttttatctcc 60
cacgccaaaca cggcgaaGct agccacgaca tacggcgaca caactctcgc caaatctgt 120
ggaacaatcg cggcgatga gaagcggcac gagatggcgt atacggcgat cgtcgagaag 180
ctattcgaga ttgatccga tggatccgta caagctctag cgagtatgat gaggaagcga 240
atcacgatgc cggctcagct gatgcacgac ggtcgcgatg acaatctgtt cgateattac 300
gctgctgtgg cgcagagaat cggagtgtat accgcgacgg attacgcagg gattttggag 360
tttttgttgc ggcggtggga ggtggagaag ttagggatgg gtttgtccgg tgaagggaagg 420
agagcacagg attatctgtg taccttgccg cagaggatca ggaggtttaga ggaaagagct 480
gacgatagag tcaaacgtgc gtcaaatgtc aaacctctg ttctgttcag ctggatttac 540
gggagagaag ttgaactata aacgacaatg gttgttgcgt ttcactgtat tagactctta 600
aacgttatgg gccctactaa tgtaatatgg gaagtaaatg taataaagaa acgctaaaa 660
atcttgcggt ttagtgc
```

(2) INFORMATION FOR SEQ ID NO:1760:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 186 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..186
(D) OTHER INFORMATION: / Ceres Seq. ID 1570853

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1760:

```
Asn Asn Pro Tyr Asn Gly Tyr Ile Tyr Thr Ser Phe Gln Glu Arg Ala
1 5 10 15
Thr Phe Ile Ser His Ala Asn Thr Ala Lys Leu Ala Thr Thr Tyr Gly
20 25 30
Asp Thr Thr Leu Ala Lys Ile Cys Gly Thr Ile Ala Ala Asp Glu Lys
35 40 45
Arg His Glu Met Ala Tyr Thr Arg Ile Val Glu Lys Leu Phe Glu Ile
50 55 60
Asp Pro Asp Gly Thr Val Gln Ala Leu Ala Ser Met Met Arg Lys Arg
65 70 75 80
Ile Thr Met Pro Ala Gln Leu Met His Asp Gly Arg Asp Asp Asn Leu
85 90 95
Phe Asp His Tyr Ala Ala Val Ala Gln Arg Ile Gly Val Tyr Thr Ala
100 105 110
Thr Asp Tyr Ala Gly Ile Leu Glu Phe Leu Leu Arg Arg Trp Glu Val
115 120 125
Glu Lys Leu Gly Met Gly Leu Ser Gly Glu Gly Arg Arg Ala Gln Asp
130 135 140
Tyr Leu Cys Thr Leu Pro Gln Arg Ile Arg Arg Leu Glu Glu Arg Ala
145 150 155 160
Asp Asp Arg Val Lys Arg Ala Ser Lys Ser Lys Pro Ser Val Ser Phe
165 170 175
Ser Trp Ile Tyr Gly Arg Glu Val Glu Leu
180 185
```

(2) INFORMATION FOR SEQ ID NO:1761:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 135 amino acids

- (B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..135
 (D) OTHER INFORMATION: / Ceres Seq. ID 1570854
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1761:

Met	Ala	Tyr	Thr	Arg	Ile	Val	Glu	Lys	Leu	Phe	Glu	Ile	Asp	Pro	Asp	
1				5				10					15			
Gly	Thr	Val	Gln	Ala	Leu	Ala	Ser	Met	Met	Arg	Lys	Arg	Ile	Thr	Met	
			20					25					30			
Pro	Ala	Gln	Leu	Met	His	Asp	Gly	Arg	Asp	Asp	Asn	Leu	Phe	Asp	His	
			35					40					45			
Tyr	Ala	Ala	Val	Ala	Gln	Arg	Ile	Gly	Val	Tyr	Thr	Ala	Thr	Asp	Tyr	
			50				55					60				
Ala	Gly	Ile	Leu	Glu	Phe	Leu	Leu	Arg	Arg	Trp	Glu	Val	Glu	Lys	Leu	
65				70				75						80		
Gly	Met	Gly	Leu	Ser	Gly	Glu	Gly	Arg	Arg	Ala	Gln	Asp	Tyr	Leu	Cys	
			85					90						95		
Thr	Leu	Pro	Gln	Arg	Ile	Arg	Arg	Leu	Glu	Glu	Arg	Ala	Asp	Asp	Arg	
			100					105						110		
Val	Lys	Arg	Ala	Ser	Lys	Ser	Lys	Pro	Ser	Val	Ser	Phe	Ser	Trp	Ile	
			115					120						125		
Tyr	Gly	Arg	Glu	Val	Glu	Leu										
			130			135										

(2) INFORMATION FOR SEQ ID NO:1762:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 111 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
 (B) LOCATION: 1..111
 (D) OTHER INFORMATION: / Ceres Seq. ID 1570855

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1762:

Met	Met	Arg	Lys	Arg	Ile	Thr	Met	Pro	Ala	Gln	Leu	Met	His	Asp	Gly	
1			5					10					15			
Arg	Asp	Asp	Asn	Leu	Phe	Asp	His	Tyr	Ala	Ala	Val	Ala	Gln	Arg	Ile	
			20					25					30			
Gly	Val	Tyr	Thr	Ala	Thr	Asp	Tyr	Ala	Gly	Ile	Leu	Glu	Phe	Leu	Leu	
			35					40					45			
Arg	Arg	Trp	Glu	Val	Glu	Lys	Leu	Gly	Met	Gly	Leu	Ser	Gly	Glu	Gly	
			50					55					60			
Arg	Arg	Ala	Gln	Asp	Tyr	Leu	Cys	Thr	Leu	Pro	Gln	Arg	Ile	Arg	Arg	
65				70				75						80		
Leu	Glu	Glu	Arg	Ala	Asp	Asp	Arg	Val	Lys	Arg	Ala	Ser	Lys	Ser	Lys	
			85					90						95		
Pro	Ser	Val	Ser	Phe	Ser	Trp	Ile	Tyr	Gly	Arg	Glu	Val	Glu	Leu		
			100					105						110		

(2) INFORMATION FOR SEQ ID NO:1763:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 646 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..646
(D) OTHER INFORMATION: / Ceres Seq. ID 1570862

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1763:

tctcgagtac	acctcatcat	tcttcttcgt	gtgagagaga	tctttttgga	aaacgaaaac	60
Gggatttagc	gtatagcagc	ttccaccgtt	tcgccaatt	tcactgagct	tcaagtgaac	120
atgagtaaac	caatggaaga	ggataccaac	cagggaaaaga	ctgaggagga	ggagttcaac	180
actggaccac	tctctgtttt	gatgatgagt	gttaagaata	acactcaggt	gttgatcaat	240
tgccgtaaca	acaggaacct	ccttggccga	gttagggcct	ttgacaggca	ctgcaacatg	300
gttctttgaa	atgtcagaga	aatgtggact	gaggttccga	aaaccggaaa	aggaagaaga	360
aaagctcttc	ctgttaacag	agatcgattc	atcagcaaga	tgttctgcg	tggagactca	420
gtcattatcg	tcttcaggaa	ccccaagtga	gagaagctct	tcttatgata	attctcgctt	480
cttctgttca	aatcctaatt	gttgcatcaa	cagtgagaac	atgttttgat	tatgagcttt	540
aaatctacta	gtgttgCctt	gtatttttca	cttctcttct	atctttgact	tgaacgcag	600
ccagtgaaact	ttgtaatact	aaaagagaag	ttctttwttt	cttttt		

(2) INFORMATION FOR SEQ ID NO:1764:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 109 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..109

(D) OTHER INFORMATION: / Ceres Seq. ID 1570863

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1764:

Met	Ser	Lys	Pro	Met	Glu	Glu	Asp	Thr	Asn	Gln	Gly	Lys	Thr	Glu	Glu
1					5				10					15	
Glu	Glu	Phe	Asn	Thr	Gly	Pro	Leu	Ser	Val	Leu	Met	Met	Ser	Val	Lys
			20					25					30		
Asn	Asn	Thr	Gln	Val	Leu	Ile	Asn	Cys	Arg	Asn	Asn	Arg	Lys	Leu	Leu
			35				40					45			
Gly	Arg	Val	Arg	Ala	Phe	Asp	Arg	His	Cys	Asn	Met	Val	Leu	Glu	Asn
			50			55				60					
Val	Arg	Glu	Met	Trp	Thr	Glu	Val	Pro	Lys	Thr	Gly	Lys	Gly	Lys	Lys
			65		70				75					80	
Lys	Ala	Leu	Pro	Val	Asn	Arg	Asp	Arg	Phe	Ile	Ser	Lys	Met	Phe	Leu
			85				90						95		
Arg	Gly	Asp	Ser	Val	Ile	Ile	Val	Leu	Arg	Asn	Pro	Lys			
			100				105								

(2) INFORMATION FOR SEQ ID NO:1765:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..105

(D) OTHER INFORMATION: / Ceres Seq. ID 1570864

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1765:

Met	Glu	Glu	Asp	Thr	Asn	Gln	Gly	Lys	Thr	Glu	Glu	Glu	Phe	Asn
1					5				10				15	
Thr	Gly	Pro	Leu	Ser	Val	Leu	Met	Met	Ser	Val	Lys	Asn	Asn	Thr
			20				25					30		
Val	Leu	Ile	Asn	Cys	Arg	Asn	Asn	Arg	Lys	Leu	Leu	Gly	Arg	Val
			35			40					45			
Ala	Phe	Asp	Arg	His	Cys	Asn	Met	Val	Leu	Glu	Asn	Val	Arg	Glu
			50			55					60			

Trp Thr Glu Val Pro Lys Thr Gly Lys Gly Lys Lys Lys Ala Leu Pro
65 70 75 80
Val Asn Arg Asp Arg Phe Ile Ser Lys Met Phe Leu Arg Gly Asp Ser
65 90 95
Val Ile Ile Val Leu Arg Asn Pro Lys
100 105

(2) INFORMATION FOR SEQ ID NO:1766:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 82 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..82

(D) OTHER INFORMATION: / Ceres Seq. ID 1570865

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1766:

Met Met Ser Val Lys Asn Asn Thr Gln Val Leu Ile Asn Cys Arg Asn
1 5 10 15
Asn Arg Lys Leu Leu Gly Arg Val Arg Ala Phe Asp Arg His Cys Asn
20 25 30
Met Val Leu Glu Asn Val Arg Glu Met Trp Thr Glu Val Pro Lys Thr
35 40 45
Gly Lys Gly Lys Lys Lys Ala Leu Pro Val Asn Arg Asp Arg Phe Ile
50 55 60
Ser Lys Met Phe Leu Arg Gly Asp Ser Val Ile Val Leu Arg Asn
65 70 75 80
Pro Lys

(2) INFORMATION FOR SEQ ID NO:1767:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 502 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..502

(D) OTHER INFORMATION: / Ceres Seq. ID 1570869

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1767:

atcagaaaaac acaaatcttta aaactttctg gaaaaacaaa aatgttcagga agaggaaaaag 60
gaggaaaaag gttaggcaaa ggaggagcaa agagacacag aaaggttcta agagacaaca 120
ttcaaggaat cacaaagcca gcgattcgct gtcttgctcg tagaggaggt gtgaagagaa 180
tcagtgatt gatctatgaa gaaacgagag gtgtgttgaa gatctttctg gagaatgtga 240
ttagagatgc tgttaacttac actgagcatg cgaggaggaa gacggtgact gctatggatg 300
ttgtttatgc cttgaagaga caaggaagaa ctctatatgg atttggtggt tgatcaattt 360
gagatctggg tttctgtggt aatgatgata atttaagtct tgcgatcaag aaattccaga 420
aattgggttg aattttaggg tttcgttttg tgttgtaatt agggcagcat tgtaattggat 480
taatgataag tacCatttgc cc

(2) INFORMATION FOR SEQ ID NO:1768:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 116 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..116

(D) OTHER INFORMATION: / Ceres Seq. ID 1570870

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1768:

Gln	Lys	Thr	Gln	Ile	Leu	Lys	Leu	Ser	Gly	Lys	Thr	Lys	Met	Ser	Gly		
1			5						10					15			
Arg	Gly	Lys	Gly	Gly	Lys	Gly	Leu	Gly	Lys	Gly	Gly	Ala	Lys	Arg	His		
			20					25					30				
Arg	Lys	Val	Leu	Arg	Asp	Asn	Ile	Gln	Gly	Ile	Thr	Lys	Pro	Ala	Ile		
		35				40					45						
Arg	Arg	Leu	Ala	Arg	Arg	Gly	Gly	Val	Lys	Arg	Ile	Ser	Gly	Leu	Ile		
	50				55					60							
Tyr	Glu	Glu	Thr	Arg	Gly	Val	Leu	Lys	Ile	Phe	Leu	Glu	Asn	Val	Ile		
65				70					75				80				
Arg	Asp	Ala	Val	Thr	Tyr	Thr	Glu	His	Ala	Arg	Arg	Lys	Thr	Val	Thr		
			85					90					95				
Ala	Met	Asp	Val	Val	Tyr	Ala	Leu	Lys	Arg	Gln	Gly	Arg	Thr	Leu	Tyr		
		100					105					110					
Gly	Phe	Gly	Gly														
		115															

(2) INFORMATION FOR SEQ ID NO:1769:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 103 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..103

(D) OTHER INFORMATION: / Ceres Seq. ID 1570871

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1769:

Met	Ser	Gly	Arg	Gly	Lys	Gly	Gly	Lys	Gly	Leu	Gly	Lys	Gly	Gly	Ala		
1			5					10					15				
Lys	Arg	His	Arg	Lys	Val	Leu	Arg	Asp	Asn	Ile	Gln	Gly	Ile	Thr	Lys		
			20					25					30				
Pro	Ala	Ile	Arg	Arg	Leu	Ala	Arg	Arg	Gly	Gly	Val	Lys	Arg	Ile	Ser		
		35				40					45						
Gly	Leu	Ile	Tyr	Glu	Glu	Thr	Arg	Gly	Val	Leu	Lys	Ile	Phe	Leu	Glu		
	50				55				60								
Asn	Val	Ile	Arg	Asp	Ala	Val	Thr	Tyr	Thr	Glu	His	Ala	Arg	Arg	Lys		
65				70				75				80					
Thr	Val	Thr	Ala	Met	Asp	Val	Val	Tyr	Ala	Leu	Lys	Arg	Gln	Gly	Arg		
			85					90				95					
Thr	Leu	Tyr	Gly	Phe	Gly	Gly											
		100															

(2) INFORMATION FOR SEQ ID NO:1770:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 634 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..634

(D) OTHER INFORMATION: / Ceres Seq. ID 1570895

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1770:

atttgcaga	ttgggttggga	tggtcttcgt	atgcttgatc	caagtactag	ccgaactttg	60
agaatatatc	ctcttgagaa	catcacaaga	tgcgaaaaac	tagattcgtc	tattctggct	120
ttctggctca	agactccggt	agacattgaa	gctaaacgta	tcagattgca	atcaaatagt	180
tacaccacca	acacccctct	ggacactgtg	acggctgcac	tgtttcagcg	caaggagatc	240
gggggaagta	gcaggcctcc	cacctctgga	aaactggttg	aacaaactcg	tgagaagaaa	300

aaaggattgg gtgattggat gaacattata aagcctgtta atgaggagaa agatcattgg	360
gtacctgatg aagctgttcc taagtgcaca tcatgtggtt cagatttcgg tgcatttata	420
cgaaggcacc actgcaggaa ttgttggtgaa gtcttctgtg acaagtgtac tcaaggcagg	480
attgctctca ctgctgagga taatgtctct caagtccgtg tttgtgaccg gtgcatggca	540
gaagtgtcac aaaggttgag taatgCcaag gaaaccactg gcaggaaatg gagCctgcag	600
agccatgaag accttgctag aaagttwcag gagg	

(2) INFORMATION FOR SEQ ID NO:1771:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 211 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..211

(D) OTHER INFORMATION: / Ceres Seq. ID 1570896

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1771:

Ile Cys Gln Ile Gly Leu Asp Gly Leu Arg Met Leu Asp Pro Ser Thr	
1 5 10 15	
Ser Arg Thr Leu Arg Ile Tyr Pro Leu Glu Asn Ile Thr Arg Cys Glu	
20 25 30	
Lys Leu Asp Ser Ser Ile Leu Ala Phe Trp Ser Lys Thr Pro Val Asp	
35 40 45	
Ile Glu Ala Lys Arg Ile Arg Leu Gln Ser Asn Ser Tyr Thr Thr Asn	
50 55 60	
Thr Leu Leu Asp Thr Val Thr Ala Ala Met Phe Gln Ala Lys Glu Ile	
65 70 75 80	
Gly Gly Ser Ser Arg Pro Pro Thr Ser Gly Lys Leu Val Glu Gln Thr	
85 90 95	
Ala Glu Lys Lys Lys Gly Leu Gly Asp Trp Met Asn Ile Ile Lys Pro	
100 105 110	
Val Asn Glu Glu Lys Asp His Trp Val Pro Asp Glu Ala Val Ser Lys	
115 120 125	
Cys Thr Ser Cys Gly Ser Asp Phe Gly Ala Phe Ile Arg Arg His His	
130 135 140	
Cys Arg Asn Cys Gly Glu Val Phe Cys Asp Lys Cys Thr Gln Gly Arg	
145 150 155 160	
Ile Ala Leu Thr Ala Glu Asp Asn Ala Pro Gln Val Arg Val Cys Asp	
165 170 175	
Arg Cys Met Ala Glu Val Ser Gln Arg Leu Ser Asn Ala Lys Glu Thr	
180 185 190	
Thr Gly Arg Asn Val Ser Leu Gln Ser His Glu Asp Leu Ala Arg Lys	
195 200 205	
Xaa Gln Glu	
210	

(2) INFORMATION FOR SEQ ID NO:1772:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 201 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..201

(D) OTHER INFORMATION: / Ceres Seq. ID 1570897

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1772:

Met Leu Asp Pro Ser Thr Ser Arg Thr Leu Arg Ile Tyr Pro Leu Glu	
1 5 10 15	
Asn Ile Thr Arg Cys Glu Lys Leu Asp Ser Ser Ile Leu Ala Phe Trp	

```

                20                25                30
Ser Lys Thr Pro Val Asp Ile Glu Ala Lys Arg Ile Arg Leu Gln Ser
   35                40                45
Asn Ser Tyr Thr Thr Asn Thr Leu Leu Asp Thr Val Thr Ala Ala Met
   50                55                60
Phe Gln Ala Lys Glu Ile Gly Gly Ser Ser Arg Pro Pro Thr Ser Gly
   65                70                75
Lys Leu Val Glu Gln Thr Ala Glu Lys Lys Lys Gly Leu Gly Asp Trp
   85                90                95
Met Asn Ile Ile Lys Pro Val Asn Glu Glu Lys Asp His Trp Val Pro
   100                105                110
Asp Glu Ala Val Ser Lys Cys Thr Ser Cys Gly Ser Asp Phe Gly Ala
   115                120                125
Phe Ile Arg Arg His His Cys Arg Asn Cys Gly Glu Val Phe Cys Asp
   130                135                140
Lys Cys Thr Gln Gly Arg Ile Ala Leu Thr Ala Glu Asp Asn Ala Pro
   145                150                155
Gln Val Arg Val Cys Asp Arg Cys Met Ala Glu Val Ser Gln Arg Leu
   165                170                175
Ser Asn Ala Lys Glu Thr Thr Gly Arg Asn Val Ser Leu Gln Ser His
   180                185                190
Glu Asp Leu Ala Arg Lys Xaa Gln Glu
   195                200

```

(2) INFORMATION FOR SEQ ID NO:1773:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 138 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..138
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570898

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1773:

```

Met Phe Gln Ala Lys Glu Ile Gly Gly Ser Ser Arg Pro Pro Thr Ser
  1                5                10                15
Gly Lys Leu Val Glu Gln Thr Ala Glu Lys Lys Lys Gly Leu Gly Asp
   20                25                30
Trp Met Asn Ile Ile Lys Pro Val Asn Glu Glu Lys Asp His Trp Val
   35                40                45
Pro Asp Glu Ala Val Ser Lys Cys Thr Ser Cys Gly Ser Asp Phe Gly
   50                55                60
Ala Phe Ile Arg Arg His His Cys Arg Asn Cys Gly Glu Val Phe Cys
   65                70                75
Asp Lys Cys Thr Gln Gly Arg Ile Ala Leu Thr Ala Glu Asp Asn Ala
   85                90                95
Pro Gln Val Arg Val Cys Asp Arg Cys Met Ala Glu Val Ser Gln Arg
   100                105                110
Leu Ser Asn Ala Lys Glu Thr Thr Gly Arg Asn Val Ser Leu Gln Ser
   115                120                125
His Glu Asp Leu Ala Arg Lys Xaa Gln Glu
   130                135

```

(2) INFORMATION FOR SEQ ID NO:1774:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 525 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..525

(D) OTHER INFORMATION: / Ceres Seq. ID 1570913

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1774:

aagatggcca	agtaacaaga	gattgcgaag	aagaagagag	aggctaaagc	cgatagaaaa	60
cgagccattc	acggcgatcc	tctaccaaat	aaattgaaga	ccagaactcc	ggtccctccc	120
gtctccggca	aacgtcagag	aaagctcctt	cgcaaattgc	gcagagagca	gaaagatatg	180
gtggagaagg	gtcttgttac	tatggaagat	gtggagatgg	cttctgctca	agctgcatca	240
gaagactcca	agaaatcccc	cagaaaaattt	agcgttaaga	agagcttgaa	gttgaacaaa	300
ctaaataata	aaggcaaaaa	gaagaaaaaac	cagaaaagcca	gtggtgaaaa	atctgctgat	360
tgtatgctag	aatgagtgct	gtgtatacct	gtaaacccat	tctctctaac	ggatgataga	420
ggtttctcaa	tgtctgggtta	gattctttcca	aaaatgtgaa	acgtgtgttt	ttgcatccgg	480
aggatGcgNa	aGcagaggaa	tggagggttt	gatatgattt	tattt		

(2) INFORMATION FOR SEQ ID NO:1775:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 124 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..124

(D) OTHER INFORMATION: / Ceres Seq. ID 1570914

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1775:

Lys	Met	Ala	Lys	Tyr	Asn	Glu	Ile	Ala	Lys	Lys	Lys	Arg	Glu	Ala	Lys
1				5					10					15	
Ala	Asp	Arg	Lys	Arg	Ala	Ile	His	Gly	Asp	Pro	Leu	Thr	Asn	Lys	Leu
			20					25					30		
Lys	Thr	Arg	Thr	Pro	Val	Pro	Ser	Val	Ser	Gly	Lys	Arg	Gln	Arg	Lys
			35				40					45			
Leu	Leu	Arg	Lys	Trp	Arg	Arg	Glu	Gln	Lys	Asp	Met	Val	Glu	Lys	Gly
			50				55				60				
Leu	Val	Thr	Met	Glu	Asp	Val	Glu	Met	Ala	Ser	Ala	Gln	Ala	Ala	Ser
			65				70				75			80	
Glu	Asp	Ser	Lys	Lys	Ser	Pro	Arg	Lys	Phe	Ser	Val	Lys	Lys	Ser	Leu
			85						90					95	
Lys	Leu	Asn	Lys	Leu	Asn	Asn	Lys	Gly	Lys	Lys	Lys	Lys	Asn	Gln	Lys
			100					105						110	
Ala	Ser	Gly	Gly	Lys	Ser	Ala	Asp	Cys	Met	Leu	Glu				
			115					120							

(2) INFORMATION FOR SEQ ID NO:1776:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 123 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..123

(D) OTHER INFORMATION: / Ceres Seq. ID 1570915

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1776:

Met	Ala	Lys	Tyr	Asn	Glu	Ile	Ala	Lys	Lys	Arg	Glu	Ala	Lys	Ala
1				5					10					15
Asp	Arg	Lys	Arg	Ala	Ile	His	Gly	Asp	Pro	Leu	Thr	Asn	Lys	Leu
			20					25					30	
Thr	Arg	Thr	Pro	Val	Pro	Ser	Val	Ser	Gly	Lys	Arg	Gln	Arg	Lys
			35				40					45		
Leu	Arg	Lys	Trp	Arg	Arg	Glu	Gln	Lys	Asp	Met	Val	Glu	Lys	Gly
			50				55				60			

Val Thr Met Glu Asp Val Glu Met Ala Ser Ala Gln Ala Ala Ser Glu
65 70 75 80
Asp Ser Lys Lys Ser Pro Arg Lys Phe Ser Val Lys Lys Ser Leu Lys
85 90 95
Leu Asn Lys Leu Asn Asn Lys Gly Lys Lys Lys Asn Gln Lys Ala
100 105 110
Ser Gly Glu Lys Ser Ala Asp Cys Met Leu Glu
115 120

(2) INFORMATION FOR SEQ ID NO:1777:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 65 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..65

(D) OTHER INFORMATION: / Ceres Seq. ID 1570916

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1777:

Met Val Glu Lys Gly Leu Val Thr Met Glu Asp Val Glu Met Ala Ser
1 5 10 15
Ala Gln Ala Ala Ser Glu Asp Ser Lys Lys Ser Pro Arg Lys Phe Ser
20 25 30
Val Lys Lys Ser Leu Lys Leu Asn Lys Leu Asn Asn Lys Gly Lys Lys
35 40 45
Lys Lys Asn Gln Lys Ala Ser Gly Glu Lys Ser Ala Asp Cys Met Leu
50 55 60

Glu

65

(2) INFORMATION FOR SEQ ID NO:1778:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 475 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..475

(D) OTHER INFORMATION: / Ceres Seq. ID 1570931

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1778:

aattttcaaaa aaaagcagat taaaacagag attagcgagt gagagagaga gacaaagata 60
tagagcttct cgtgaagcaa cagtgaagaa aaggaaagt aatcgccat gatgatcgcc 120
ttcgcttaag ccgcagaatc cgctttcttc ttcttgcttg gctccgctgt tctcgctccg 180
gaagaataga gtttatcaga cgatttggat acaaggaaaat aatcaaaagca acagaaggtt 240
tccgtaaagt tatttacacc aactatcacg ggtctgcata cagagctaaa ttcaaaggtg 300
gtgaggttgc ttgtgtcaaa gaactcacgt ctcttgatct tggacgagaa aggtttgatg 360
aggaagttca gcttttgggt cgcttacgtc accgtcatct ccttacActt cgtgggtttt 420
gcatttttagt cttgaacaat catctcagtc tgtattttga atttggttca ctctct

(2) INFORMATION FOR SEQ ID NO:1779:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 122 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..122

(D) OTHER INFORMATION: / Ceres Seq. ID 1570932

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1779:

Met Asp Asp Arg Leu Arg Leu Ser Arg Arg Ile Arg Phe Leu Leu Leu
1 5 10 15
Ala Trp Leu Arg Arg Ser Arg Ser Gly Arg Ile Glu Phe Ile Arg Arg
20 25 30
Phe Gly Tyr Lys Glu Ile Ile Lys Ala Thr Glu Gly Phe Arg Lys Val
35 40 45
Ile Tyr Thr Asn Tyr His Gly Ser Ala Tyr Arg Ala Lys Phe Lys Gly
50 55 60
Gly Glu Val Ala Leu Val Lys Glu Leu Thr Ala Leu Asp Leu Gly Arg
65 70 75 80
Glu Arg Phe Asp Glu Glu Val Gln Leu Leu Gly Arg Leu Arg His Arg
85 90 95
His Leu Leu Thr Leu Arg Gly Phe Cys Ile Leu Val Leu Asn His
100 105 110
Leu Ser Leu Tyr Phe Glu Phe Gly Ser Leu
115 120

(2) INFORMATION FOR SEQ ID NO:1780:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 850 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..850
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570936

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1780:

acacacacac acatgttctt cgttgctgct tcgttgggtt aaaaactttt ttAtttgttt 60
cttgcttttt gtaaagtcac agataacaaa taaataagaa aaatggagaa tctaccacct 120
ggttatcgct ccaatgttgg tgtttgtcta atcaactcgg ataattogtt atttttagct 180
tctagattga atgttccagg agcatggcag atgccacagg gaggcattga agatggggag 240
gatccaaagt cagcagccat gagagaatta caagaagaaa ctggtgttgt ttacgctgaa 300
atcgctcagc aggtcccaaa ttggttgaca tatgattttc caccagcagt aaaagcaaaa 360
gttaaccgct ttggggcggt tgaatggcat ggtcaagctc agaaaatggta tttagtgaga 420
ctgaggaacg atgaggacga gaaagagatc aatctagcga acaacgaagc ggattcagag 480
tttgcggagt ggaatggggt gaagccagaa gaagtggtag agcaagcagt ggattacaaa 540
aggccaacct atgaagaagt catcaagact ttggttcgtt tcttaaacga cacaggaaga 600
gctgctaaat gtaaatcagc caagtgggtga tataagatac caagaaccaa tgtttgtctt 660
tttatttttt ttgttaactg ttgtttttct ttttttgggc gttctctttt agtagaaccc 720
ttttggaatg caaaagcttt ctctaggggt tttttacttt catttttgta aattgtttat 780
tggtacgtag aaagtttttt gggttttatt taacgtgggg gtcattgtaa taaagtctgt 840
gtctggattc

(2) INFORMATION FOR SEQ ID NO:1781:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 175 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..175
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570937

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1781:

Met Glu Asn Leu Pro Pro Gly Tyr Arg Pro Asn Val Gly Val Cys Leu
1 5 10 15
Ile Asn Ser Asp Asn Cys Val Phe Val Ala Ser Arg Leu Asn Val Pro
20 25 30
Gly Ala Trp Gln Met Pro Gln Gly Gly Ile Glu Asp Gly Gly Asp Pro

(2) INFORMATION FOR SEQ ID NO:1782:

(A) LENGTH: 139 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(A) NAME/KEY: peptide

(B) LOCATION: 1..139

(D) OTHER INFORMATION

SEQUENCE DESCRIPTION: SEQ ID NO:1782:

Pro Gln Gly Gly Ile Glu Asp Gly Glu Asp Pr

(2) INFORMATION FOR SEQ ID NO:1783:

(A) LENGTH: 123 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: lin

MOLECULE TYPE: peptid

(ix) FEATURE:

(IX) FEATURE.
(A) NAME

(B) LOCATION: 1..123

(D) OTHER INFORMATION

SEQUENCE DESCRIPTION: SEQ ID NO:1783:

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:1783:
Arg Glu Leu Gln Gln Gln Thr Gly Val Val Ser

Met Arg Glu Leu Gln Glu Glu Thr Gly Val Val Ser Ala Glu Ile Val
1 5 10 15

Ser Glu Val Pro Asn Trp Leu Thr Tyr Asp Phe Pro Pro Ala Val Lys
20 25 30
Ala Lys Val Asn Arg Leu Trp Gly Gly Glu Trp His Gly Gln Ala Gln
35 40 45
Lys Trp Tyr Leu Val Arg Leu Arg Asn Asp Glu Asp Glu Lys Glu Ile
50 55 60
Asn Leu Ala Asn Asn Glu Ala Asp Ser Glu Phe Ala Glu Trp Lys Trp
65 70 75 80
Ala Lys Pro Glu Glu Val Val Glu Gln Ala Val Asp Tyr Lys Arg Pro
85 90 95
Thr Tyr Glu Glu Val Ile Lys Thr Phe Gly Ser Phe Leu Asn Asp Thr
100 105 110
Gly Arg Ala Ala Lys Cys Lys Ser Ala Lys Trp
115 120

(2) INFORMATION FOR SEQ ID NO:1784:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 651 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..651

(D) OTHER INFORMATION: / Ceres Seq. ID 1570951

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1784:

```

cttttttgc gaccattttt gtttctgagt tgttcttctt gattagcttt gtccgcttg 60
aaccacaacat ggcgagtcctt ggccatatag ccagagaatc atcagacatc acacgcctcg 120
cccagtttta caaagaggtg tttgggttcg aggagatcga aagtccctgat tttggagacc 180
taaaagtggt gtggctaaac ttaccaggtg cttttgcaat gcacattatc cagagaaacc 240
cttcaacaaa tcttcagaa ggtccttaca gtgtacctc agcggttaag gatcctagcc 300
atctcccaat gggtcatcat atctgtttct ctgtcccaaa ttctgactct ttctctcatt 360
ctctcaagga gaaagggata gaaacttttc agaagtctct gcctgatgga aaagtcaagc 420
aagttttctt ctttgatcct gatggaaacg gattagaggt agcaagtgcg tcatgagcct 480
tgaacctgaa atatgtggta tcactactta tagaatgaaa taaagtatt gtataataa 540
tcagtttgtt gaaataaaaat ctatatgtat aggtttgatg ttaactttgt acaGcttacg 600
cctcaaaagt cgtgtcatgt gctttgaatg ktggatgtaw cgrattttatg c

```

(2) INFORMATION FOR SEQ ID NO:1785:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 157 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..157

(D) OTHER INFORMATION: / Ceres Seq. ID 1570952

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1785:

Phe Leu Ser Thr Ile Phe Val Ser Glu Leu Phe Phe Leu Ile Ser Phe
1 5 10 15
Val Arg Leu Glu Pro Asn Met Ala Ser Leu Gly His Ile Ala Arg Glu
20 25 30
Ser Ser Asp Ile Thr Arg Leu Ala Gln Phe Tyr Lys Glu Val Phe Gly
35 40 45
Phe Glu Glu Ile Glu Ser Pro Asp Phe Gly Asp Leu Lys Val Val Trp
50 55 60
Leu Asn Leu Pro Gly Ala Phe Ala Met His Ile Gln Arg Asn Pro
65 70 75 80
Ser Thr Asn Leu Pro Glu Gly Pro Tyr Ser Ala Thr Ser Ala Val Lys
85 90 95

Asp Pro Ser His Leu Pro Met Gly His His Ile Cys Phe Ser Val Pro
100 105 110
Asn Phe Asp Ser Phe Leu His Ser Leu Lys Glu Lys Gly Ile Glu Thr
115 120 125
Phe Gln Lys Ser Leu Pro Asp Gly Lys Val Lys Gln Val Phe Phe Phe
130 135 140
Asp Pro Asp Gly Asn Gly Leu Glu Val Ala Ser Arg Ser
145 150 155

(2) INFORMATION FOR SEQ ID NO:1786:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 135 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..135

(D) OTHER INFORMATION: / Ceres Seq. ID 1570953

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1786:

Met Ala Ser Leu Gly His Ile Ala Arg Glu Ser Ser Asp Ile Thr Arg
1 5 10 15
Leu Ala Gln Phe Tyr Lys Glu Val Phe Gly Phe Glu Glu Ile Glu Ser
20 25 30
Pro Asp Phe Gly Asp Leu Lys Val Val Trp Leu Asn Leu Pro Gly Ala
35 40 45
Phe Ala Met His Ile Ile Gln Arg Asn Pro Ser Thr Asn Leu Pro Glu
50 55 60
Gly Pro Tyr Ser Ala Thr Ser Ala Val Lys Asp Pro Ser His Leu Pro
65 70 75 80
Met Gly His His Ile Cys Phe Ser Val Pro Asn Phe Asp Ser Phe Leu
85 90 95
His Ser Leu Lys Glu Lys Gly Ile Glu Thr Phe Gln Lys Ser Leu Pro
100 105 110
Asp Gly Lys Val Lys Gln Val Phe Phe Phe Asp Pro Asp Gly Asn Gly
115 120 125
Leu Glu Val Ala Ser Arg Ser
130 135

(2) INFORMATION FOR SEQ ID NO:1787:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 85 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..85

(D) OTHER INFORMATION: / Ceres Seq. ID 1570954

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1787:

Met His Ile Ile Gln Arg Asn Pro Ser Thr Asn Leu Pro Glu Gly Pro
1 5 10 15
Tyr Ser Ala Thr Ser Ala Val Lys Asp Pro Ser His Leu Pro Met Gly
20 25 30
His His Ile Cys Phe Ser Val Pro Asn Phe Asp Ser Phe Leu His Ser
35 40 45
Leu Lys Glu Lys Gly Ile Glu Thr Phe Gln Lys Ser Leu Pro Asp Gly
50 55 60
Lys Val Lys Gln Val Phe Phe Phe Asp Pro Asp Gly Asn Gly Leu Glu
65 70 75 80
Val Ala Ser Arg Ser

85

(2) INFORMATION FOR SEQ ID NO:1788:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1092 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1092
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570974

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1788:

```
aacttttggc gagaaaaatca gagacagaag aagaagaaaaa gcaaaaaaaa gcaaaacatg    60
aaggcgacga cgaagactcc gatccacgtg gtgtgggtcat gggttaggag acaacctccg    120
aaggtgaagg cttttctcgc cgtgggtcact ggcattggcg ctttggttct tctcagattc    180
attgttaacg atcacgacaa tctcttcgtt gccgctgagg ctgttcattc catcgggatc    240
tgtgtgtcta tctacaaact catgaaggag aagacctgtg ccggattgtc actgaaatct    300
caggagctta cggcgatat tttagctgtt aggcgtgtatt gtacgattgt aatggaatat    360
gatatacata ccaattcttga cttggctact ttgggaacaa ctctctgggt tatatttatg    420
attcgttttca agttaagagc tagttacatg gaggacaaaag acaactttcc tctctattat    480
gtgcttggcg cctgtgttgc attagctgtg ttcattccat catcgacctc tcataacata    540
ataaacagaa ttctcatgggc tttatgtgta taacctgaag ctgtttcagt actacctcag    600
ctacgagtga tgcagaacac aaagattgtt gaacctgtca cggctcatta tgtttttgca    660
cttgagatag caaggttccct cagctgtgcc cactgggttt tacaggttgt ggacacgcgg    720
ggacgggttc ttgtagcatt gggttatgga ttgtggccat caatggttct gatctcagaa    780
attgttcaaa ctttcatctt gccagatttc tgttactact acgtcaaaa gcttttcgga    840
ggccagctgt tcttcgcgct accgtctgga gtagNtataa gttcaaaaaga tagaaatact    900
ccaacagatg cctgcgatga gcttgacgga aattctaatt gggaaagata gctcaatttt    960
tctttacctc tgatttcatc gtttatgtgt cttgaggttt ccccaagtg ctcggttaac    1020
aattaatttt acagtgttgt atatittgcc tatcaaggga tttaacgtct ttcaggtcga    1080
taagttatct tt
```

(2) INFORMATION FOR SEQ ID NO:1789:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 316 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..316
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570975

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1789:

```
Asn Phe Cys Arg Glu Asn Gln Arg Gln Lys Lys Lys Ser Glu Lys
1      5      10      15
Lys Gln Asn Met Lys Ala Thr Thr Lys Thr Pro Ile His Val Val Trp
      20      25      30
Ser Trp Val Arg Arg Gln Pro Lys Val Lys Ala Phe Leu Ala Val
      35      40      45
Val Thr Gly Met Ala Ala Leu Val Leu Leu Arg Phe Ile Val His Asp
      50      55      60
His Asp Asn Leu Phe Val Ala Ala Glu Ala Val His Ser Ile Gly Ile
      65      70      75      80
Cys Val Leu Ile Tyr Lys Leu Met Lys Glu Lys Thr Cys Ala Gly Leu
      85      90      95
Ser Leu Lys Ser Gln Glu Leu Thr Ala Ile Phe Leu Ala Val Arg Leu
      100      105      110
Tyr Cys Ser Ile Val Met Glu Tyr Asp Ile His Thr Ile Leu Asp Leu
      115      120      125
Ala Thr Leu Gly Thr Thr Leu Trp Val Ile Phe Met Ile Arg Phe Lys
```

130	135	140
Leu Arg Ala Ser Tyr Met Glu Asp Lys Asp Asn Phe Pro Leu Tyr Tyr		
145	150	155
Val Leu Ala Pro Cys Val Ala Leu Ala Val Phe Ile His Pro Ser Thr		160
	165	170
Ser His Asn Ile Ile Asn Arg Ile Ser Trp Ala Leu Cys Val Tyr Leu		175
	180	185
Glu Ala Val Ser Val Leu Pro Gln Leu Arg Val Met Gln Asn Thr Lys		190
	195	200
Ile Val Glu Pro Phe Thr Ala His Tyr Val Phe Ala Leu Gly Val Ala		205
	210	215
Arg Phe Leu Ser Cys Ala His Trp Val Leu Gln Val Val Asp Thr Arg		220
225	230	235
Gly Arg Leu Leu Val Ala Leu Gly Tyr Gly Leu Trp Pro Ser Met Val		240
	245	250
Leu Ile Ser Glu Ile Val Gln Thr Phe Ile Leu Ala Asp Phe Cys Tyr		255
	260	265
Tyr Tyr Val Lys Ser Val Phe Gly Gly Gln Leu Val Leu Arg Leu Pro		270
	275	280
Ser Gly Val Xaa Ile Ser Ser Lys Asp Arg Asn Thr Pro Thr Met Ser		285
	290	295
Cys Asp Glu Leu Asp Gly Asn Ser Asn Trp Glu Arg		300
305	310	315

(2) INFORMATION FOR SEQ ID NO:1790:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 297 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..297

(D) OTHER INFORMATION: / Ceres Seq. ID 1570976

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1790:

Met Lys Ala Thr Thr Lys Thr Pro Ile His Val Val Trp Ser Trp Val	
1	5
Arg Arg Gln Pro Pro Lys Val Lys Ala Phe Leu Ala Val Val Thr Gly	
	20
Met Ala Ala Leu Val Leu Leu Arg Phe Ile Val His Asp His Asp Asn	
	35
Leu Phe Val Ala Ala Glu Ala Val His Ser Ile Gly Ile Cys Val Leu	
50	55
Ile Tyr Lys Leu Met Lys Glu Lys Thr Cys Ala Gly Leu Ser Leu Lys	
65	70
Ser Gln Glu Leu Thr Ala Ile Phe Leu Ala Val Arg Leu Tyr Cys Ser	
	85
Ile Val Met Glu Tyr Asp Ile His Thr Ile Leu Asp Leu Ala Thr Leu	
	100
Gly Thr Thr Leu Trp Val Ile Phe Met Ile Arg Phe Lys Leu Arg Ala	
	115
Ser Tyr Met Glu Asp Lys Asp Asn Phe Pro Leu Tyr Trp Val Leu Ala	
	130
Pro Cys Val Ala Leu Ala Val Phe Ile His Pro Ser Thr Ser His Asn	
145	150
Ile Ile Asn Arg Ile Ser Trp Ala Leu Cys Val Tyr Leu Glu Ala Val	
	165
Ser Val Leu Pro Gln Leu Arg Val Met Gln Asn Thr Lys Ile Val Glu	
	180
Pro Phe Thr Ala His Tyr Val Phe Ala Leu Gly Val Ala Arg Phe Leu	
	195
	200
	205

Ser Cys Ala His Trp Val Leu Gln Val Val Asp Thr Arg Gly Arg Leu
210 215 220
Leu Val Ala Leu Gly Tyr Gly Leu Trp Pro Ser Met Val Leu Ile Ser
225 230 235 240
Glu Ile Val Gln Thr Phe Ile Leu Ala Asp Phe Cys Tyr Tyr Tyr Val
245 250 255
Lys Ser Val Phe Gly Gly Gln Leu Val Leu Arg Leu Pro Ser Gly Val
260 265 270
Xaa Ile Ser Ser Lys Asp Arg Asn Thr Pro Thr Met Ser Cys Asp Glu
275 280 285
Leu Asp Gly Asn Ser Asn Trp Glu Arg
290 295

(2) INFORMATION FOR SEQ ID NO:1791:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 265 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..265

(D) OTHER INFORMATION: / Ceres Seq. ID 1570977

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1791:

Met Ala Ala Leu Val Leu Leu Arg Phe Ile Val His Asp His Asp Asn
1 5 10 15
Leu Phe Val Ala Ala Glu Ala Val His Ser Ile Gly Ile Cys Val Leu
20 25 30
Ile Tyr Lys Leu Met Lys Glu Lys Thr Cys Ala Gly Leu Ser Leu Lys
35 40 45
Ser Gln Glu Leu Thr Ala Ile Phe Leu Ala Val Arg Leu Tyr Cys Ser
50 55 60
Ile Val Met Glu Tyr Asp Ile His Thr Ile Leu Asp Leu Ala Thr Leu
65 70 75 80
Gly Thr Thr Leu Trp Val Ile Phe Met Ile Arg Phe Lys Leu Arg Ala
85 90 95
Ser Tyr Met Glu Asp Lys Asp Asn Phe Pro Leu Tyr Tyr Val Leu Ala
100 105 110
Pro Cys Val Ala Leu Ala Val Phe Ile His Pro Ser Thr Ser His Asn
115 120 125
Ile Ile Asn Arg Ile Ser Trp Ala Leu Cys Val Tyr Leu Glu Ala Val
130 135 140
Ser Val Leu Pro Gln Leu Arg Val Met Gln Asn Thr Lys Ile Val Glu
145 150 155 160
Pro Phe Thr Ala His Tyr Val Phe Ala Leu Gly Val Ala Arg Phe Leu
165 170 175
Ser Cys Ala His Trp Val Leu Gln Val Val Asp Thr Arg Gly Arg Leu
180 185 190
Leu Val Ala Leu Gly Tyr Gly Leu Trp Pro Ser Met Val Leu Ile Ser
195 200 205
Glu Ile Val Gln Thr Phe Ile Leu Ala Asp Phe Cys Tyr Tyr Tyr Val
210 215 220
Lys Ser Val Phe Gly Gly Gln Leu Val Leu Arg Leu Pro Ser Gly Val
225 230 235 240
Xaa Ile Ser Ser Lys Asp Arg Asn Thr Pro Thr Met Ser Cys Asp Glu
245 250 255
Leu Asp Gly Asn Ser Asn Trp Glu Arg
260 265

(2) INFORMATION FOR SEQ ID NO:1792:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1710 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -
(B) LOCATION: 1..1710
(D) OTHER INFORMATION: / Ceres Seq. ID 1570998

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1792:

tatcaagaat	ttggacgagt	coatcgacca	caaagcactg	catgatactt	tttcatcggt	60
ttggaacatt	gtgtcgtgca	aggtagctgt	cgattcttca	ggccagctcaa	aaggctatgg	120
gtttgtgcga	tacgccaatt	agaatctgc	ccagaaagct	atagagaaac	tgaacggcatc	180
gttgctcaat	gacaagcaag	tgtatgtggg	tcctttcctg	aggagacaag	aaagagactc	240
cactgctaac	aaaacgaat	tcaccaatgt	gtatgtgaag	aatctcggcg	aaagtaactac	300
cgatgatgac	ttgaagaatg	cttttggcga	gtatggaaag	ataacaagtg	ctgtcgtgat	360
gaaagatgga	gaagggaagt	ccaagggtct	tgggtttgtc	aactttgaaa	atgctgatga	420
tgctcgtagg	gctgtggagt	ctctcaatgg	gcacaaattt	gatgataagg	agtggatagt	480
tggtagagcc	cagaagaagt	cagagaggga	aacakaacta	agggtccggt	atgaacagaa	540
tttgaaggaa	gctgcagaca	agtttaaaag	ttcaaacctg	tatgttaaga	atttggatcc	600
tagcatattca	gagagaagac	ttaaagagat	ctttctctct	tttggtaaccg	ttacatctag	660
caaggtgatg	cgggatccta	atggaacaa	caaaggctca	ggttttgttg	ctttcgcaac	720
tcocgaagaa	gcaactgaag	ctatgtcaca	gttgagcggt	aaaatgatcg	aaagcaagcc	780
actctatgtg	gctattgcac	agcgggaagg	agacagaagg	ctcagactac	aggctcagtt	840
ttcccaagtg	aggccagttg	caatgcagcc	gtctgttggg	ccccgcagtc	cagtttatcc	900
ccccgggtgt	ctcgttatgt	gacaaacaa	gttctatggt	caggcccccct	ctgcaatgat	960
tcctcccgag	cctgggttatg	gataccaaca	gcagcttggg	ctcgggaatga	gaactgggtgg	1020
gggtcctgtga	cccagtttct	tcagtgcctat	gggttcagcca	cagcagcagc	gtcctggagg	1080
aggaagacgt	cctgggggaa	tccaacactc	ccagcagca	aatcccatga	tcagcaaca	1140
gatgcatcca	aggggtcgga	tgttcocgta	tccccaaggg	cgtgggtgta	gtgggtgatgt	1200
gcctccatcat	gatattggca	acaaactgcc	attgactatt	ggagctttgg	cttcaaatct	1260
gtctaagtct	actccagagc	aacagaggac	gatgctgggt	gaggtgctgt	accocgttgg	1320
ggagcagagt	gaggcagagt	ctgcagccaa	agtgaactgg	atgcttttgg	agatggacca	1380
gactgaagtg	ctccatctgt	tggagtcaac	agaagctctc	aaggccaaag	ttgcagaggg	1440
tatggatggt	ctcaggagtg	tcgctgctgg	tgctgcaaac	gagcagctcg	cttccttgaa	1500
ctctctctaa	attgcttttt	atcatttgat	ctttggcttt	tgctctctcc	atacaattgg	1560
agttgtttct	ttgtctattg	ttttctccct	gggaatttgg	attcctccac	ataaCtgctg	1620
ttgtgtttat	ttaaaccttc	gtttttaaa	cacaaaggaa	aaacctatct	gctttgttct	1680

(2) INFORMATION FOR SEQ ID NO:1793:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 502 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1..502
(D) OTHER INFORMATION: / Ceres Seq. ID 1570999

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1793:

Ile	Lys	Asn	Leu	Asp	Glu	Ser	Ile	Asp	His	Lys	Ala	Leu	His	Asp	Thr
1			5					10					15		
Phe	Ser	Ser	Phe	Gly	Asn	Ile	Val	Ser	Cys	Lys	Val	Ala	Val	Asp	Ser
			20					25					30		
Ser	Gly	Gln	Ser	Lys	Gly	Tyr	Gly	Phe	Val	Gln	Tyr	Ala	Asn	Glu	Glu
			35					40					45		
Ser	Ala	Gln	Lys	Ala	Ile	Glu	Lys	Leu	Asn	Gly	Met	Leu	Leu	Asn	Asp
			50				55				60				
Lys	Gln	Val	Tyr	Val	Gly	Pro	Phe	Leu	Arg	Arg	Gln	Glu	Arg	Asp	Ser
			65				70			75			80		
Thr	Ala	Asn	Lys	Thr	Lys	Phe	Thr	Asn	Val	Tyr	Val	Lys	Asn	Leu	Ala

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1.443

(D) OTHER INFORMATION: / Ceres Seq. ID 1571000

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1794:

Met	Leu	Leu	Asn	Asp	Lys	Gln	Val	Tyr	Val	Gly	Pro	Phe	Leu	Arg	Arg
1			5						10					15	
Gln	Glu	Arg	Asp	Ser	Thr	Ala	Asn	Lys	Thr	Lys	Phe	Thr	Asn	Val	Tyr
			20					25					30		
Val	Lys	Asn	Leu	Ala	Glu	Ser	Thr	Asp	Asp	Asp	Leu	Lys	Asn	Ala	
		35					40				45				
Phe	Gly	Glu	Tyr	Gly	Lys	Ile	Thr	Ser	Ala	Val	Val	Met	Lys	Asp	Gly
		50				55					60				
Glu	Gly	Lys	Ser	Lys	Gly	Phe	Gly	Phe	Val	Asn	Phe	Glu	Asn	Ala	Asp
		65			70					75				80	
Asp	Ala	Ala	Arg	Ala	Val	Glu	Ser	Leu	Asn	Gly	His	Lys	Phe	Asp	Asp
			85						90					95	
Lys	Glu	Trp	Tyr	Val	Gly	Arg	Ala	Gln	Lys	Lys	Ser	Glu	Arg	Glu	Thr
			100					105					110		
Xaa	Leu	Arg	Val	Arg	Tyr	Glu	Gln	Asn	Leu	Lys	Glu	Ala	Ala	Asp	Lys
		115					120					125			
Phe	Lys	Ser	Ser	Asn	Leu	Tyr	Val	Lys	Asn	Leu	Asp	Pro	Ser	Ile	Ser
		130					135					140			
Asp	Glu	Lys	Leu	Lys	Glu	Ile	Phe	Ser	Pro	Phe	Gly	Thr	Val	Thr	Ser
		145			150					155				160	
Ser	Lys	Val	Met	Arg	Asp	Pro	Asn	Gly	Thr	Ser	Lys	Gly	Ser	Gly	Phe
			165						170					175	
Val	Ala	Phe	Ala	Thr	Pro	Glu	Glu	Ala	Thr	Glu	Ala	Met	Ser	Gln	Leu
			180					185					190		
Ser	Gly	Lys	Met	Ile	Glu	Ser	Lys	Pro	Leu	Tyr	Val	Ala	Ile	Ala	Gln
		195					200					205			
Arg	Lys	Glu	Asp	Arg	Arg	Val	Arg	Leu	Gln	Ala	Gln	Phe	Ser	Gln	Val
		210				215					220				
Arg	Pro	Val	Ala	Met	Gln	Pro	Ser	Val	Gly	Pro	Arg	Met	Pro	Val	Tyr
		225			230					235				240	
Pro	Pro	Gly	Gly	Pro	Gly	Ile	Gly	Gln	Gln	Met	Phe	Tyr	Gly	Gln	Ala
			245						250					255	
Pro	Pro	Ala	Met	Ile	Pro	Pro	Gln	Pro	Gly	Tyr	Gly	Tyr	Gln	Gln	Gln
		260					265						270		
Leu	Val	Pro	Gly	Met	Arg	Pro	Gly	Gly	Gly	Pro	Val	Pro	Ser	Phe	Phe
		275					280					285			
Met	Pro	Met	Val	Gln	Pro	Gln	Gln	Gln	Arg	Pro	Gly	Gly	Gly	Arg	Arg
		290				295					300				
Pro	Gly	Gly	Ile	Gln	His	Ser	Gln	Gln	Gln	Asn	Pro	Met	Met	Gln	Gln
			310							315				320	
Gln	Met	His	Pro	Arg	Gly	Arg	Met	Phe	Arg	Tyr	Pro	Gln	Gly	Arg	Gly
			325						330					335	
Gly	Ser	Gly	Asp	Val	Pro	Pro	Tyr	Asp	Met	Gly	Asn	Asn	Met	Pro	Leu
			340					345					350		
Thr	Ile	Gly	Ala	Leu	Ala	Ser	Asn	Leu	Ser	Asn	Ala	Thr	Pro	Glu	Gln
		355					360					365			
Gln	Arg	Thr	Met	Leu	Gly	Glu	Val	Leu	Tyr	Pro	Leu	Val	Glu	Gln	Val
		370				375						380			
Glu	Ala	Glu	Ser	Ala	Ala	Lys	Val	Thr	Gly	Met	Leu	Leu	Glu	Met	Asp
		385			390					395				400	
Gln	Thr	Glu	Val	Leu	His	Leu	Leu	Glu	Ser	Pro	Glu	Ala	Leu	Lys	Ala
			405						410				415		
Lys	Val	Ala	Glu	Ala	Met	Asp	Val	Leu	Arg	Ser	Val	Ala	Ala	Gly	Ala
			420					425					430		
Ala	Thr	Glu	Gln	Leu	Ala	Ser	Leu	Asn	Leu	Ser					
		435					440								

(2) INFORMATION FOR SEQ ID NO:1795:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 383 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..383
(D) OTHER INFORMATION: / Ceres Seq. ID 1571001
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1795:

Met Lys Asp Gly Glu Gly Lys Ser Lys Gly Phe Gly Phe Val Asn Phe
1 5 10 15
Glu Asn Ala Asp Asp Ala Ala Arg Ala Val Glu Ser Leu Asn Gly His
20 25 30
Lys Phe Asp Asp Lys Glu Trp Tyr Val Gly Arg Ala Gln Lys Lys Ser
35 40 45
Glu Arg Glu Thr Xaa Leu Arg Val Arg Tyr Glu Gln Asn Leu Lys Glu
50 55 60
Ala Ala Asp Lys Phe Lys Ser Ser Asn Leu Tyr Val Lys Asn Leu Asp
65 70 75 80
Pro Ser Ile Ser Asp Glu Lys Leu Lys Glu Ile Phe Ser Pro Phe Gly
85 90 95
Thr Val Thr Ser Ser Lys Val Met Arg Asp Pro Asn Gly Thr Ser Lys
100 105 110
Gly Ser Gly Phe Val Ala Phe Ala Thr Pro Glu Glu Ala Thr Glu Ala
115 120 125
Met Ser Gln Leu Ser Gly Lys Met Ile Glu Ser Lys Pro Leu Tyr Val
130 135 140
Ala Ile Ala Gln Arg Lys Glu Asp Arg Arg Val Arg Leu Gln Ala Gln
145 150 155 160
Phe Ser Gln Val Arg Pro Val Ala Met Gln Pro Ser Val Gly Pro Arg
165 170 175
Met Pro Val Tyr Pro Pro Gly Gly Pro Gly Ile Gly Gln Gln Met Phe
180 185 190
Tyr Gly Gln Ala Pro Pro Ala Met Ile Pro Pro Gln Pro Gly Tyr Gly
195 200 205
Tyr Gln Gln Gln Leu Val Pro Gly Met Arg Pro Gly Gly Gly Pro Val
210 215 220
Pro Ser Phe Phe Met Pro Met Val Gln Pro Gln Gln Gln Arg Pro Gly
225 230 235 240
Gly Gly Arg Arg Pro Gly Gly Ile Gln His Ser Gln Gln Gln Asn Pro
245 250 255
Met Met Gln Gln Gln Met His Pro Arg Gly Arg Met Phe Arg Tyr Pro
260 265 270
Gln Gly Arg Gly Gly Ser Gly Asp Val Pro Pro Tyr Asp Met Gly Asn
275 280 285
Asn Met Pro Leu Thr Ile Gly Ala Leu Ala Ser Asn Leu Ser Asn Ala
290 295 300
Thr Pro Glu Gln Gln Arg Thr Met Leu Gly Glu Val Leu Tyr Pro Leu
305 310 315 320
Val Glu Gln Val Glu Ala Glu Ser Ala Ala Lys Val Thr Gly Met Leu
325 330 335
Leu Glu Met Asp Gln Thr Glu Val Leu His Leu Leu Glu Ser Pro Glu
340 345 350
Ala Leu Lys Ala Lys Val Ala Glu Ala Met Asp Val Leu Arg Ser Val
355 360 365
Ala Ala Gly Ala Ala Thr Glu Gln Leu Ala Ser Leu Asn Leu Ser
370 375 380

- (2) INFORMATION FOR SEQ ID NO:1796:
(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 862 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..862

(D) OTHER INFORMATION: / Ceres Seq. ID 1571014

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1796:

agtttctctt	tacttccctc	tttctctgag	ctatggagat	tactgtaate	gctttctcct	60
caatcgatga	aggaatttga	agttgggata	tcaaaaccgg	gacagagcag	cttcaattca	120
agccgtgtgc	ttctccggcg	catgggtctc	ccgcgcgtcg	caaaaaattc	tcgcctcttc	180
tcagctctcg	gcgagaaata	cttctggctc	gattttttac	tggtcttgga	ctaagcctca	240
agctgaagt	aagagctacc	cagtggaaac	aataaaggct	cttgacagca	acaatgaagg	300
aacttattta	gttgggtggg	gaatctctgg	agatatctac	ctttggggag	ttgcgactgg	360
gaagttgctt	aagaagtggc	atgggttcaag	gcgcgttcac	agatcttcag	cgacggagga	420
ttggactact	tgggcaaccc	gagcttggtc	cacgcctcaga	gcactctagc	catttgggct	480
actcaagtta	ttctcatggg	agctgttgaa	ggctacagag	tcgcccggaga	tggtccattg	540
ggagaaacag	aggacttgct	ttaccacagg	ggcagcttcg	acccattggg	cctcgctact	600
gaccccagg	ctttcgacga	gttgaagggt	aaggagctca	agaacgggaag	gttggctatg	660
ttctctatgt	ttggattctt	cggtcaagcc	atcgtcaccc	gaaagggacc	tttggagaac	720
ctcgccgacc	atttggccga	cccagtcac	aacaacgctt	gggccttcgc	caccaacttc	780
gtccccggaa	agtgagcgcc	tgcttattat	gtgaatgaga	gcagagaaag	agagtttggt	840
tgtygtctat	tctatgtaaa	ac				

(2) INFORMATION FOR SEQ ID NO:1797:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 72 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..72

(D) OTHER INFORMATION: / Ceres Seq. ID 1571015

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1797:

Met	Glu	Ile	Thr	Val	Ile	Ala	Ser	Ser	Ser	Ile	Asp	Glu	Gly	Ile	Gly
1			5							10				15	
Ser	Trp	Asp	Leu	Lys	Thr	Gly	Thr	Gly	Gln	Leu	Gln	Phe	Lys	Pro	Cys
			20					25					30		
Ala	Ser	Pro	Ala	His	Gly	Leu	Thr	Ala	Val	Gly	Lys	Asn	Phe	Ser	Pro
		35					40					45			
Pro	Leu	Ser	Ser	Arg	Arg	Glu	Ile	Leu	Leu	Ala	Arg	Phe	Phe	Thr	Gly
		50				55					60				
Leu	Gly	Leu	Ser	Leu	Lys	Leu	Lys								
		65				70									

(2) INFORMATION FOR SEQ ID NO:1798:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 55 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..55

(D) OTHER INFORMATION: / Ceres Seq. ID 1571016

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1798:

Met	Lys	Glu	Leu	Glu	Val	Gly	Ile	Ser	Lys	Pro	Gly	Gln	Ser	Ser	Phe
1			5						10					15	

Asn Ser Ser Arg Val Leu Leu Arg Arg Met Val Ser Pro Pro Ser Ala
20 25 30
Lys Ile Ser Arg Leu Leu Ser Ala Leu Gly Glu Lys Tyr Phe Trp Leu
35 40 45
Asp Phe Leu Leu Val Leu Asp
50 55

(2) INFORMATION FOR SEQ ID NO:1799:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 99 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..99

(D) OTHER INFORMATION: / Ceres Seq. ID 1571017

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1799:

Met Gly Ala Val Glu Gly Tyr Arg Val Ala Gly Asp Gly Pro Leu Gly
1 5 10 15
Glu Ala Glu Asp Leu Leu Tyr Pro Gly Gly Ser Phe Asp Pro Leu Gly
20 25 30
Leu Ala Thr Asp Pro Glu Ala Phe Ala Glu Leu Lys Val Lys Glu Leu
35 40 45
Lys Asn Gly Arg Leu Ala Met Phe Ser Met Phe Gly Phe Phe Val Gln
50 55 60
Ala Ile Val Thr Gly Lys Gly Pro Leu Glu Asn Leu Ala Asp His Leu
65 70 75 80
Ala Asp Pro Val Asn Asn Asn Ala Trp Ala Phe Ala Thr Asn Phe Val
85 90 95
Pro Gly Lys

(2) INFORMATION FOR SEQ ID NO:1800:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1244 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1244

(D) OTHER INFORMATION: / Ceres Seq. ID 1571021

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1800:

acaSRcatat acattcacat tactaatctc tcaagatttc acaattttct tgtgattttc 60
tctcagtttc ttatttctgt tcataacatg gatgccatga gtacgctaga cgagagctct 120
acaaactacag attccattcc ggcgagaaag tcactgtctc cggcgagttt actatataga 180
atgggaagcgt gaacaagcgt ggtacttgat tcagagaacg gtgtcgaagt cgaagtgcga 240
gccgaatcaa gaagacttcc ttcttcaaga ttcaaaagtg ttgttctcca accaaatgga 300
agatgggagc ctcagattta cgagaaacat caacgcgtgt ggcttggtag ttccaacgag 360
gaagaacgaag cagctcgtgc ttacgcgctc gcggctcacc gtttccgtgg ccgcgatgcc 420
gttactaatt tcaaaagacac gaaggttcga agagaggttg agttctttaa ttccgatgtg 480
aaatcagaga tcgtagatat gttgagaaaa cacacttaca aagaagagtt agaccaaaagg 540
aaacgttaacc gtgacggttaa cggaaaagag acgacggcgt ttgctttggc ttgatgggtg 600
gttatgacgg ggttttaaac ggccgagttt ctgtttgaga aaacggtaac gccaaagtac 660
gtcgggaaac taaacccgtt agttatacca aaacaccaag cggagaaaaa ttttccgcta 720
ccgttaggta ataataacgt tcccgttaaa ggtatgctgt tgaatttoga agacgttaac 780
gggaaagtgt ggaggtttccg ttactcttat tggaatagta gtcaaatgta tgtgttgacg 840
aaaggttggg gtatgattcgt taaagagaag agactttgtg ctggtgattt gatcagtttt 900
aaaagatcca acgatcaaga tcaaaaattc tttatcgggt ggaaatcgaa atccgggttg 960
gatctagaga cgggtcgggt tatgagattt tttgggggtg atatttcttt aaacgccgtc 1020

gttgtagtga aggaacaac ggaggtgtta atgtcgtcgt taaggtgtaa gaatcaacga 1080
gttttgaat aacaatttaa caacttggga aagaaaaaaa aagctttttg attttaattt 1140
ctcttcaacg ttaattcttg tgagattatt tatgtgttaa gttgtaacaa gtggaaaaaa 1200
ttaattaggt gtcaacaaa tcttgtgtta atattctttg tatg

(2) INFORMATION FOR SEQ ID NO:1801:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 362 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..362

(D) OTHER INFORMATION: / Ceres Seq. ID 1571022

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1801:

Thr	Xaa	Ile	Tyr	Ile	His	Ile	Thr	Asn	Leu	Ser	Arg	Phe	His	Asn	Phe
1				5										10	15
Leu	Val	Ile	Phe	Ser	Gln	Phe	Leu	Ile	Ser	Phe	His	Asn	Met	Asp	Ala
			20					25					30		
Met	Ser	Ser	Val	Asp	Glu	Ser	Ser	Thr	Thr	Asp	Ser	Ile	Pro	Ala	
			35				40				45				
Arg	Lys	Ser	Ser	Ser	Pro	Ala	Ser	Leu	Leu	Tyr	Arg	Met	Gly	Ser	Gly
	50					55					60				
Thr	Ser	Val	Val	Leu	Asp	Ser	Glu	Asn	Gly	Val	Glu	Val	Glu	Val	Glu
65					70				75				80		
Ala	Glu	Ser	Arg	Lys	Leu	Pro	Ser	Ser	Arg	Phe	Lys	Gly	Val	Val	Pro
			85						90				95		
Gln	Pro	Asn	Gly	Arg	Trp	Gly	Ala	Gln	Ile	Tyr	Glu	Lys	His	Gln	Arg
			100				105						110		
Val	Trp	Leu	Gly	Thr	Phe	Asn	Glu	Glu	Asp	Glu	Ala	Ala	Arg	Ala	Tyr
		115				120					125				
Asp	Val	Ala	Ala	His	Arg	Phe	Arg	Gly	Arg	Asp	Ala	Val	Thr	Asn	Phe
	130				135						140				
Lys	Asp	Thr	Thr	Phe	Glu	Glu	Glu	Val	Glu	Phe	Leu	Asn	Ala	His	Ser
	145				150					155				160	
Lys	Ser	Glu	Ile	Val	Asp	Met	Leu	Arg	Lys	His	Thr	Tyr	Lys	Glu	Glu
			165						170					175	
Leu	Asp	Gln	Arg	Lys	Arg	Asn	Arg	Asp	Gly	Asn	Gly	Lys	Glu	Thr	Thr
			180				185						190		
Ala	Phe	Ala	Leu	Ala	Ser	Met	Val	Val	Met	Thr	Gly	Phe	Lys	Thr	Ala
			195			200					205				
Glu	Leu	Leu	Phe	Glu	Lys	Thr	Val	Thr	Pro	Ser	Asp	Val	Gly	Lys	Leu
	210					215					220				
Asn	Arg	Leu	Val	Ile	Pro	Lys	His	Gln	Ala	Glu	Lys	His	Phe	Pro	Leu
225					230				235					240	
Pro	Leu	Gly	Asn	Asn	Asn	Val	Ser	Val	Lys	Gly	Met	Leu	Leu	Asn	Phe
			245						250					255	
Glu	Asp	Val	Asn	Gly	Lys	Val	Trp	Arg	Phe	Arg	Tyr	Ser	Tyr	Trp	Asn
		260					265						270		
Ser	Ser	Gln	Ser	Tyr	Val	Leu	Thr	Lys	Gly	Trp	Ser	Arg	Phe	Val	Lys
		275					280					285			
Glu	Lys	Arg	Leu	Cys	Ala	Gly	Asp	Leu	Ile	Ser	Phe	Lys	Arg	Ser	Asn
	290					295					300				
Asp	Gln	Asp	Gln	Lys	Phe	Phe	Ile	Gly	Trp	Lys	Ser	Lys	Ser	Gly	Leu
	305				310				315					320	
Asp	Leu	Glu	Thr	Gly	Arg	Val	Met	Arg	Leu	Phe	Gly	Val	Asp	Ile	Ser
			325						330					335	
Leu	Asn	Ala	Val	Val	Val	Val	Lys	Glu	Thr	Thr	Glu	Val	Leu	Met	Ser
			340					345					350		
Ser	Leu	Arg	Cys	Lys	Asn	Gln	Arg	Val	Leu						

355 360
(2) INFORMATION FOR SEQ ID NO:1802:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 333 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..333
(D) OTHER INFORMATION: / Ceres Seq. ID 1571023
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1802:
Met Asp Ala Met Ser Ser Val Asp Glu Ser Ser Thr Thr Thr Asp Ser
1 5 10 15
Ile Pro Ala Arg Lys Ser Ser Ser Pro Ala Ser Leu Leu Tyr Arg Met
20 25 30
Gly Ser Gly Thr Ser Val Val Leu Asp Ser Glu Asn Gly Val Glu Val
35 40 45
Glu Val Glu Ala Glu Ser Arg Lys Leu Pro Ser Ser Arg Phe Lys Gly
50 55 60
Val Val Pro Gln Pro Asn Gly Arg Trp Gly Ala Gln Ile Tyr Glu Lys
65 70 75 80
His Gln Arg Val Trp Leu Gly Thr Phe Asn Glu Glu Asp Glu Ala Ala
85 90 95
Arg Ala Tyr Asp Val Ala Ala His Arg Phe Arg Gly Arg Asp Ala Val
100 105 110
Thr Asn Phe Lys Asp Thr Thr Phe Glu Glu Val Glu Phe Leu Asn
115 120 125
Ala His Ser Lys Ser Glu Ile Val Asp Met Leu Arg Lys His Thr Tyr
130 135 140
Lys Glu Glu Leu Asp Gln Arg Lys Arg Asn Asp Gly Asn Gly Lys
145 150 155 160
Glu Thr Thr Ala Phe Ala Leu Ala Ser Met Val Val Met Thr Gly Phe
165 170 175
Lys Thr Ala Glu Leu Leu Phe Glu Lys Thr Val Thr Pro Ser Asp Val
180 185 190
Gly Lys Leu Asn Arg Leu Val Ile Pro Lys His Gln Ala Glu Lys His
195 200 205
Phe Pro Leu Pro Leu Gly Asn Asn Asn Val Ser Val Lys Gly Met Leu
210 215 220
Leu Asn Phe Glu Asp Val Asn Gly Lys Val Trp Arg Phe Arg Tyr Ser
225 230 235 240
Tyr Trp Asn Ser Ser Gln Ser Tyr Val Leu Thr Lys Gly Trp Ser Arg
245 250 255
Phe Val Lys Glu Lys Arg Leu Cys Ala Gly Asp Leu Ile Ser Phe Lys
260 265 270
Arg Ser Asn Asp Gln Asp Gln Lys Phe Phe Ile Gly Trp Lys Ser Lys
275 280 285
Ser Gly Leu Asp Leu Glu Thr Gly Arg Val Met Arg Leu Phe Gly Val
290 295 300
Asp Ile Ser Leu Asn Ala Val Val Val Lys Glu Thr Thr Glu Val
305 310 315 320
Leu Met Ser Ser Leu Arg Cys Lys Asn Gln Arg Val Leu
325 330

(2) INFORMATION FOR SEQ ID NO:1803:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 330 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..330
(D) OTHER INFORMATION: / Ceres Seq. ID 1571024
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1803:

```
Met Ser Ser Val Asp Glu Ser Ser Thr Thr Asp Ser Ile Pro Ala
1      5      10      15
Arg Lys Ser Ser Ser Pro Ala Ser Leu Leu Tyr Arg Met Gly Ser Gly
20      25      30
Thr Ser Val Val Leu Asp Ser Glu Asn Gly Val Glu Val Glu Val Glu
35      40      45
Ala Glu Ser Arg Lys Leu Pro Ser Ser Arg Phe Lys Gly Val Val Pro
50      55      60
Gln Pro Asn Gly Arg Trp Gly Ala Gln Ile Tyr Glu Lys His Gln Arg
65      70      75
Val Trp Leu Gly Thr Phe Asn Glu Glu Asp Glu Ala Ala Arg Ala Tyr
85      90      95
Asp Val Ala Ala His Arg Phe Arg Gly Arg Asp Ala Val Thr Asn Phe
100     105     110
Lys Asp Thr Thr Phe Glu Glu Glu Val Glu Phe Leu Asn Ala His Ser
115     120     125
Lys Ser Glu Ile Val Asp Met Leu Arg Lys His Thr Tyr Lys Glu Glu
130     135     140
Leu Asp Gln Arg Lys Arg Asn Arg Asp Gly Asn Gly Lys Glu Thr Thr
145     150     155
Ala Phe Ala Leu Ala Ser Met Val Val Met Thr Gly Phe Lys Thr Ala
165     170     175
Glu Leu Leu Phe Glu Lys Thr Val Thr Pro Ser Asp Val Gly Lys Leu
180     185     190
Asn Arg Leu Val Ile Pro Lys His Gln Ala Glu Lys His Phe Pro Leu
195     200     205
Pro Leu Gly Asn Asn Asn Val Ser Val Lys Gly Met Leu Leu Asn Phe
210     215     220
Glu Asp Val Asn Gly Lys Val Trp Arg Phe Arg Tyr Ser Tyr Trp Asn
225     230     235
Ser Ser Gln Ser Tyr Val Leu Thr Lys Gly Trp Ser Arg Phe Val Lys
245     250     255
Glu Lys Arg Leu Cys Ala Gly Asp Leu Ile Ser Phe Lys Arg Ser Asn
260     265     270
Asp Gln Asp Gln Lys Phe Phe Ile Gly Trp Lys Ser Lys Ser Gly Leu
275     280     285
Asp Leu Glu Thr Gly Arg Val Met Arg Leu Phe Gly Val Asp Ile Ser
290     295     300
Leu Asn Ala Val Val Val Lys Glu Thr Thr Glu Val Leu Met Ser
305     310     315
Ser Leu Arg Cys Lys Asn Gln Arg Val Leu
325     330
```

(2) INFORMATION FOR SEQ ID NO:1804:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1140 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..1140
(D) OTHER INFORMATION: / Ceres Seq. ID 1571031

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1804:

ctttctcaga ttctctcttt cccgagaaaa ttggaagaaa cagagattca tcattttctc

ttctctcaca	aatcagatc	tgcaaaactc	tcagatcact	catgggttgg	atttcaaac	120
ctaccggttt	gattctcgtc	gccaccatct	tcttctcgtt	ttcttcaatc	tcgggtcagg	180
attctcgtcgt	tgagaacaat	gagagacaag	aatctgaagg	atctggtaaa	gagcttggtc	240
gtcgtggaat	gggttggtact	gaacgaattg	gagttgtatc	tgttgtagac	aatattggtg	300
ctcttggttt	gaactctagac	cttgatgcta	ctgctcctag	tgtatttgat	gccttggttt	360
cgagtttctc	gatgatactt	gtcaccgaga	ttggggatga	aacttttata	atagcgcgat	420
tgatggctat	gcgacatcct	aaagctactg	ttttatctgg	tgcactctca	gccttggtttg	480
tkakgactat	actGttctac	tggacttggt	aggatagtgc	caaaacttgat	atcgaggaga	540
cacaccaata	gtgctgctac	agtgccttat	gcattttttg	gtttgcgact	actctacatt	600
gccttgagggt	ctactgattc	aaagtcaaat	cagaagaaaag	aaatggagga	agttgaagag	660
aagctcgagt	caggtcaagg	gaagacaccc	ttccgtcgtt	tattctcaag	attttgtacc	720
ccaatatttc	tggaagtcctt	catcttaacc	tttctagctg	aatgggggtga	ccgttagccag	780
atcgctacaa	tagctttggc	gactcacaag	aacgccaatg	gagtgcccat	tggggcaagt	840
attggacaca	ctgtgtgtac	ttcactagca	gttggtggag	gaagcatcgt	ggcttcaagg	900
atctcgcaac	gtacgggtcgc	aactgttgga	gccttactct	tcctcggttt	ttcagttctc	960
tcctattttc	atcctccatt	gtagtaaatg	tgcttctttc	gaaaatgggt	gttagagaca	1020
atttctaagt	aaagtttcaa	tttttttttt	gattttaatt	taagtttgat	ttttgtttaa	1080
tatcaatggc	caaaatggcc	aaaccaaaga	atccaacgcc	tatgctttta	caatttactt	1140

(2) INFORMATION FOR SEQ ID NO:1805:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 136 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..136
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571032

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1805:

Met	Gly	Leu	Ile	Ser	Asn	Pro	Thr	Arg	Leu	Ile	Leu	Val	Ala	Thr	Ile
1			5					10						15	
Phe	Phe	Leu	Val	Ser	Ser	Ile	Ser	Gly	Gln	Asp	Ser	Val	Val	Glu	Asn
			20					25						30	
Asn	Glu	Arg	Gln	Glu	Ser	Glu	Gly	Ser	Gly	Lys	Glu	Leu	Gly	Arg	Arg
			35				40					45			
Gly	Met	Val	Gly	Thr	Glu	Arg	Ile	Gly	Val	Asp	Thr	Val	Val	Asp	Asn
			50				55				60				
Ile	Gly	Ala	Leu	Gly	Leu	Asn	Leu	Asp	Leu	Asp	Ala	Thr	Ala	Pro	Ser
65				70					75					80	
Val	Phe	Asp	Ala	Leu	Phe	Ser	Ser	Phe	Ser	Met	Ile	Leu	Val	Thr	Glu
			85						90					95	
Ile	Gly	Asp	Glu	Thr	Phe	Ile	Ile	Ala	Ala	Leu	Met	Ala	Met	Arg	His
			100					105						110	
Pro	Lys	Ala	Thr	Val	Leu	Ser	Gly	Ala	Leu	Ser	Ala	Leu	Phe	Xaa	Xaa
			115				120							125	
Thr	Ile	Leu	Phe	Tyr	Trp	Thr	Trp								
			130				135								

(2) INFORMATION FOR SEQ ID NO:1806:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 87 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..87
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571033

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1806:

Met Val Gly Thr Glu Arg Ile Gly Val Asp Thr Val Val Asp Asn Ile
1 5 10 15
Gly Ala Leu Gly Leu Asn Leu Asp Leu Asp Ala Thr Ala Pro Ser Val
20 25 30
Phe Asp Ala Leu Phe Ser Ser Phe Ser Met Ile Leu Val Thr Glu Ile
35 40 45
Gly Asp Glu Thr Phe Ile Ile Ala Ala Leu Met Ala Met Arg His Pro
50 55 60
Lys Ala Thr Val Leu Ser Gly Ala Leu Ser Ala Leu Phe Xaa Xaa Thr
65 70 75 80
Ile Leu Phe Tyr Trp Thr Trp
85

(2) INFORMATION FOR SEQ ID NO:1807:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..113
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571034

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1807:

Met Glu Glu Val Glu Glu Lys Leu Glu Ser Gly Gln Gly Lys Thr Pro
1 5 10 15
Phe Arg Arg Leu Phe Ser Arg Phe Cys Thr Pro Ile Phe Leu Glu Ser
20 25 30
Phe Ile Leu Thr Phe Leu Ala Glu Trp Gly Asp Arg Ser Gln Ile Ala
35 40 45
Thr Ile Ala Leu Ala Thr His Lys Asn Ala Ile Gly Val Ala Ile Gly
50 55 60
Ala Ser Ile Gly His Thr Val Cys Thr Ser Leu Ala Val Val Gly Gly
65 70 75 80
Ser Met Leu Ala Ser Arg Ile Ser Gln Arg Thr Val Ala Thr Val Gly
85 90 95
Gly Leu Leu Phe Leu Gly Phe Ser Val Ser Ser Tyr Phe Tyr Pro Pro
100 105 110
Leu

(2) INFORMATION FOR SEQ ID NO:1808:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 782 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..782
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571042

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1808:

atcaaccacaa	acaaaacata	aaaaacaagt	ggaagcttta	aaacgagagg	gagagagcaa	60
aaatggcgac	gtcgggaacg	tacgtgacgg	aaagttccgct	aaaaggatcg	gccgagaaat	120
actacaagag	gtggaagaac	gagaaccatg	tcttccctga	tgctatcgcg	caccacatcc	180
aaaatgttac	cgttcacgaa	ggcgaacatg	actctcacgg	Gtctatcagg	agttggaact	240
acacatggga	tggaaaaggag	gaggtgttca	aggagagaag	agagatagac	gatgagacca	300
aaacgttgac	gttaagagga	cttgagggtc	acgtgatgga	gcagctcaaa	gtgtacgacg	360
tcgtctacca	attcatctcc	aaatctgagg	atacctgcac	cggcaaaaac	actttaatat	420
gggagaagcg	caacgatgat	tccccagaac	caagcggcta	catgaaattc	gtcaagagct	480
tggttgctga	catgggaaac	cacgttagca	aaacttaatc	atcattccca	cagtcgctcg	540

catcatcatc atcatcatca tcatcatcat catcatcatc atcatcatca tcatcatcat	600
catcatcatc atcatcatca tctctgattta taagttaaga tgttttcagt ataataaatg	660
gggtcttggt gatcggttcat tctcatgtgt aaaccgtttg gttctgtatg atgcttcgat	720
atattgttat gttcatgac atagtctggg ttcatataa tgattcttaa gattaattta	780

(2) INFORMATION FOR SEQ ID NO:1809:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 151 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..151

(D) OTHER INFORMATION: / Ceres Seq. ID 1571043

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1809:

Met Ala Thr Ser Gly Thr Tyr Val Thr Glu Val Pro Leu Lys Gly Ser	
1 5 10 15	
Ala Glu Lys Tyr Tyr Lys Arg Trp Lys Asn Glu Asn His Val Phe Pro	
20 25 30	
Asp Ala Ile Gly His His Ile Gln Asn Val Thr Val His Glu Gly Glu	
35 40 45	
His Asp Ser His Gly Ser Ile Arg Ser Trp Asn Tyr Thr Trp Asp Gly	
50 55 60	
Lys Glu Glu Val Phe Lys Glu Arg Arg Glu Ile Asp Asp Glu Thr Lys	
65 70 75 80	
Thr Leu Thr Leu Arg Gly Leu Glu Gly His Val Met Glu Gln Leu Lys	
85 90 95	
Val Tyr Asp Val Val Tyr Gln Phe Ile Pro Lys Ser Glu Asp Thr Cys	
100 105 110	
Ile Gly Lys Ile Thr Leu Ile Trp Glu Lys Arg Asn Asp Ser Pro	
115 120 125	
Glu Pro Ser Gly Tyr Met Lys Phe Val Lys Ser Leu Val Ala Asp Met	
130 135 140	
Gly Asn His Val Ser Lys Thr	
145 150	

(2) INFORMATION FOR SEQ ID NO:1810:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 682 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..682

(D) OTHER INFORMATION: / Ceres Seq. ID 1571044

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1810:

agtgaagtga agaagaatca gagaaaatgc cgccgaaatt ggatccatct caaatcgctgc	60
acgtctacgt ccgagtcacc ggaggKgaN gtccggagcag cgtcttcaact cgctccaaag	120
atcggtccac tgggtctggtg accaaagaag atcggagaag acatcgccaa agagacagcg	180
aaagaatgga aaggtctctgc agtcaccgttg aagcttacgg tacagaatcg tcaagctaag	240
gtcacagtgg ttccatccgc agcggtctcta gtcacaaag ccctcaagga gccagagaga	300
gataggaaga aagtgaagaa catcaaacat atgggcaaca tttcgtttga tgatgtgatt	360
gagattgcta agataatgct tctatagatt atcgctaagg aattgagtg aacagtgaag	420
gagattttag gaactttgtt ctctgttggt tgcactgttg atggtaaga cctaaggat	480
cttcaggaag aaattaacag tgggtgacatt gatattctta acgagtata aaggttttta	540
cttttgagtt ctctatcggt ttattttttg tatttgatt tgaggatttg gtattagtaa	600
tactatattt cgggaagtga gaattgttg cttttgccca tttgaatctt tctctgggat	660
taatcaaat gttcaatttt ct	

(2) INFORMATION FOR SEQ ID NO:1811:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 69 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..69
(D) OTHER INFORMATION: / Ceres Seq. ID 1571045

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1811:

```
Val Ser Glu Arg Arg Ile Arg Glu Asn Ala Ala Glu Ile Gly Ser Ile
1          5          10          15
Ser Asn Arg Arg Arg Leu Arg Pro Ser His Arg Arg Xaa Xaa Ser Glu
          20          25          30
Gln Arg Leu His Ser Leu Gln Arg Ser Val His Ser Val Trp His Gln
          35          40          45
Arg Arg Ser Glu Lys Thr Ser Pro Lys Arg Gln Arg Lys Asn Gly Lys
50          55          60
Val Phe Glu Ser Pro
65
```

(2) INFORMATION FOR SEQ ID NO:1812:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 70 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..70
(D) OTHER INFORMATION: / Ceres Seq. ID 1571046

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1812:

```
Met Pro Pro Lys Leu Asp Pro Ser Gln Ile Val Asp Val Tyr Val Arg
1          5          10          15
Val Thr Gly Xaa Glu Xaa Arg Ser Ser Val Phe Thr Arg Ser Lys Asp
          20          25          30
Arg Ser Thr Arg Ser Gly Thr Lys Glu Asp Arg Arg Arg His Arg Gln
          35          40          45
Arg Asp Ser Glu Arg Met Glu Arg Ser Ser Ser His Arg Glu Ala Tyr
50          55          60
Gly Thr Glu Ser Ser Ser
65          70
```

(2) INFORMATION FOR SEQ ID NO:1813:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..50
(D) OTHER INFORMATION: / Ceres Seq. ID 1571047

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1813:

```
Met Arg Pro Arg Ser Ile Ala Lys Glu Leu Ser Gly Thr Val Lys Glu
1          5          10          15
Ile Leu Gly Thr Cys Val Ser Val Gly Cys Thr Val Asp Gly Lys Asp
          20          25          30
Pro Lys Asp Leu Gln Glu Glu Ile Asn Ser Gly Asp Ile Asp Ile Pro
```

35 40 45

Asn Glu
50

(2) INFORMATION FOR SEQ ID NO:1814:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 585 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -
(B) LOCATION: 1..585
(D) OTHER INFORMATION: / Ceres Seq. ID 1571062

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1814:

ataaacacaaa	agaatttgaa	ccaacaaagc	aaaacatgaa	aggcacattc	actaacttgc	60
ttgtgtctct	ctctattgca	cttgtttgtg	ccaatgtcgg	tgctaggaaa	gttatctccg	120
aagataccca	attcaaggat	gaaaaatctt	tcctcggagg	cagtgggcagc	ggtgatggct	180
tagggcttgg	ccttgggtga	ggagctggtc	ttggtgggct	tgggattggg	gctgggatcg	240
gcgcgggagc	cggactaggg	ttaggtggag	gcggttttgg	gggaggagcc	ggtggcgagc	300
tcggtggcct	tccttgaacg	tattgacaag	tgtgcgtgtg	agagctgatt	ctcagcttat	360
tactaattaa	ttaagttact	ttcattctct	taataaaatc	tagaggggtt	gaatttcgga	420
ttcttcagc	tttaatttaa	acttcaatat	ttgaaccaaa	aaaggtotta	gctactagag	480
gtaatgctcg	taatcgtatt	atgtgtAacg	cgggttctga	tattcttatg	tgcaagtgtg	540
gaacgtttct	cttttattca	ctatatagca	ttactttctt	ttttt		

(2) INFORMATION FOR SEQ ID NO:1815:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 104 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1..104
(D) OTHER INFORMATION: / Ceres Seq. ID 1571063

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1815:

Lys	Gln	Lys	Glu	Phe	Glu	Pro	Thr	Lys	Gln	Asn	Met	Lys	Gly	Thr	Phe	
1			5						10					15		
Thr	Asn	Leu	Leu	Val	Leu	Leu	Leu	Ile	Ala	Leu	Val	Cys	Ala	Asn	Val	
			20					25					30			
Gly	Ala	Arg	Lys	Val	Ile	Ser	Glu	Asp	Thr	Gln	Phe	Lys	Asp	Glu	Lys	
		35					40					45				
Ser	Phe	Leu	Gly	Gly	Ser	Gly	Ser	Gly	Asp	Gly	Leu	Gly	Leu	Gly	Leu	
	50					55					60					
Gly	Gly	Gly	Ala	Gly	Leu	Gly	Gly	Leu	Gly	Ile	Gly	Ala	Gly	Ile	Gly	
	65					70				75				80		
Ala	Gly	Ala	Gly	Leu	Gly	Leu	Gly	Gly	Gly	Phe	Gly	Gly	Gly	Ala		
			85					90					95			
Gly	Gly	Gly	Leu	Gly	Gly	Leu	Pro									
			100													

(2) INFORMATION FOR SEQ ID NO:1816:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 93 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1..93

(D) OTHER INFORMATION: / Ceres Seq. ID 1571064

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1816:

Met Lys Gly Thr Phe Thr Asn Leu Leu Val Leu Leu Leu Ile Ala Leu
1 5 10 15
Val Cys Ala Asn Val Gly Ala Arg Lys Val Ile Ser Glu Asp Thr Gln
20 25 30
Phe Lys Asp Glu Lys Ser Phe Leu Gly Gly Ser Gly Ser Gly Asp Gly
35 40 45
Leu Gly Leu Gly Leu Gly Gly Ala Gly Leu Gly Gly Leu Gly Ile
50 55 60
Gly Ala Gly Ile Gly Ala Gly Ala Gly Leu Gly Leu Gly Gly Gly Gly
65 70 75 80
Phe Gly Gly Gly Ala Gly Gly Gly Leu Gly Gly Leu Pro
85 90

(2) INFORMATION FOR SEQ ID NO:1817:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 718 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..718

(D) OTHER INFORMATION: / Ceres Seq. ID 1571079

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1817:

attcaaaagac atacaaaata attgagtttt ttttttttaa ttgaaacaa atgggggttga 60
gtgggtgttct tcaatgtggag gttgaggtta agtctccggc tgaaaaagttc tgggtagccc 120
tcggcgacagg catacaatctc ttcccacaaag ctttccctaa cgactacaaa accatccaag 180
ttctagccgg cgacggcaca gctcctggct ccattcgctt cattacttat ggagaaggat 240
ttccactgggt gaagatatgc gcggagagga tcgaagcagt ggatttggag aacaaaagca 300
tgtcatacag tcattattgc ggcgaatgt tggagtacta caaaacgttc aaaggaacca 360
tcaccgttat tcttaagaac ggtggcagcc ttctgaaatg gtctgggtgag ttgagaaga 420
cggcccatga gattgatgac ccacacgtca tcaaggactt tgotgtcaag aacttcaag 480
agatagatga gtatctcctt aagcaaaacta gtgcctaaca ctagaacctt taaattatat 540
Maagaggggt cgatcgcttc tataagattt ttctaattaa gaagttagt aaagtggaaac 600
ctctttatga atatccaagt ttgtgatttc ggagtttatg cagcctagta ggccataaag 660
tttttacaac agccaattta gtcgaacatt ttgaaaaaat cgaacctttt ggtaaaagc

(2) INFORMATION FOR SEQ ID NO:1818:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 155 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..155

(D) OTHER INFORMATION: / Ceres Seq. ID 1571080

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1818:

Met Gly Leu Ser Gly Val Leu His Val Glu Val Glu Val Lys Ser Pro
1 5 10 15
Ala Glu Lys Phe Trp Val Ala Leu Gly Asp Gly Ile Asn Leu Phe Pro
20 25 30
Lys Ala Phe Pro Asn Asp Tyr Lys Thr Ile Gln Val Leu Ala Gly Asp
35 40 45
Gly Asn Ala Pro Gly Ser Ile Arg Leu Ile Thr Tyr Gly Glu Gly Ser
50 55 60
Pro Leu Val Lys Ile Ser Ala Glu Arg Ile Glu Ala Val Asp Leu Glu
65 70 75 80
Asn Lys Ser Met Ser Tyr Ser Ile Ile Gly Gly Glu Met Leu Glu Tyr

(2) INFORMATION FOR SEQ ID NO:1819:

(2) INFORMATION FOR SEQ ID NO:1821:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 76 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..76
(D) OTHER INFORMATION: / Ceres Seq. ID 1571087
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1821:
Met Gly Leu Asp Lys Asn Thr Lys Thr Pro Cys Gly Phe Cys Phe Val
1 5 10 15
Leu Phe Tyr Ser Arg Glu Asp Thr Glu Asp Ala Val Lys Tyr Ile Ser
20 25 30
Gly Thr Ile Leu Asp Asp Arg Pro Ile Arg Val Asp Phe Asp Trp Gly
35 40 45
Phe Gln Glu Gly Arg Gln Trp Gly Arg Gly Arg Ser Gly Gly Gln Val
50 55 60
Arg Asp Glu Tyr Arg Thr Asp Tyr Asp Pro Gly His
65 70 75

(2) INFORMATION FOR SEQ ID NO:1822:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 756 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:

(A) NAME/KEY: -
(B) LOCATION: 1..756
(D) OTHER INFORMATION: / Ceres Seq. ID 1571092

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1822:

aaacaactac aaacaacatt tctgagattg cgccggagtc aaggagaggg agagagcgat 60
ccaacggttg agatgtttct acgggcaatc ggacggccat tattggctaa agtgaagcag 120
acgacgggga tcgtcggtgt tgacgttgtt cccaacgcga gagcgggtgt gatcgatctc 180
tacagcaaaa ccctaaagga gatccaagct gtgcccggagg atgaagggtta ccgtNaaagc 240
ggtggaatca ttacgcgcgc aacgtctcaa tgtgtgcaa gaagaagaag attggggagat 300
gattgagaag cggcttggtt gtggtcaagt cgaagagctt atcgaagagg ctgcgcatga 360
gctcacacac attgggaaaa tgatcgagtg ggaatccttg ggtgtaccag atgattacga 420
gtgtgaagtg attgagaatg atgcgcgcgat tccaaagcat gttcctcagc accgacctgg 480
tcctcttctt gagcagttct ataaaacgct tgaaggtcta attgcagagt ctaaaacaga 540
gatcccgact gctacaccca gogatccgca gttgaaggag taacttccag tttttacAYa 600
tatbCgtRvt GcTtTgttgt tttttggcta gagttgtttc cgaatcagtg gtaacgcctc 660
tgaaataaatt gcttaataat ttccataacg atacaatatg ctgttcacaa atgtttttatc 720
actcttatta aacaaatgat gttcttctcc ttttgc

(2) INFORMATION FOR SEQ ID NO:1823:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 101 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1..101
(D) OTHER INFORMATION: / Ceres Seq. ID 1571093

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1823:

Lys Gln Leu Gln Thr Thr Phe Leu Arg Leu Arg Arg Ser Gln Gly Glu
1 5 10 15
Gly Glu Ser Asp Pro Thr Val Glu Met Phe Leu Arg Ala Ile Gly Arg

```

                20                25                30
Pro Leu Leu Ala Lys Val Lys Gln Thr Thr Gly Ile Val Gly Leu Asp
   35                40                45
Val Val Pro Asn Ala Arg Ala Val Leu Ile Asp Leu Tyr Ser Lys Thr
   50                55                60
Leu Lys Glu Ile Gln Ala Val Pro Glu Asp Glu Gly Tyr Arg Xaa Ser
   65                70                75                80
Gly Gly Ile Ile His Ala Pro Thr Ser Gln Cys Val Gln Gly Arg Arg
   85                90                95
Arg Leu Gly Asp Asp
   100

```

(2) INFORMATION FOR SEQ ID NO:1824:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..120
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571094

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1824:

```

Met Lys Gly Thr Xaa Lys Ala Val Glu Ser Phe Thr Arg Gln Arg Leu
1      5      10      15
Asn Val Cys Lys Glu Glu Glu Asp Trp Glu Met Ile Glu Lys Arg Leu
   20      25      30
Gly Cys Gly Gln Val Glu Glu Leu Ile Glu Glu Ala Arg Asp Glu Leu
   35      40      45
Thr Leu Ile Gly Lys Met Ile Glu Trp Asp Pro Trp Gly Val Pro Asp
   50      55      60
Asp Tyr Glu Cys Glu Val Ile Glu Asn Asp Ala Pro Ile Pro Lys His
   65      70      75      80
Val Pro Gln His Arg Pro Gly Pro Leu Pro Glu Gln Phe Tyr Lys Thr
   85      90      95
Leu Glu Gly Leu Ile Ala Glu Ser Lys Thr Glu Ile Pro Ala Ala Thr
   100     105     110
Pro Ser Asp Pro Gln Leu Lys Glu
   115     120

```

(2) INFORMATION FOR SEQ ID NO:1825:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 94 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..94
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571095

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1825:

```

Met Ile Glu Lys Arg Leu Gly Cys Gly Gln Val Glu Glu Ile Glu
1      5      10      15
Glu Ala Arg Asp Glu Leu Thr Leu Ile Gly Lys Met Ile Glu Trp Asp
   20      25      30
Pro Trp Gly Val Pro Asp Asp Tyr Glu Cys Glu Val Ile Glu Asn Asp
   35      40      45
Ala Pro Ile Pro Lys His Val Pro Gln His Arg Pro Gly Pro Leu Pro
   50      55      60
Glu Gln Phe Tyr Lys Thr Leu Glu Gly Leu Ile Ala Glu Ser Lys Thr
   65      70      75      80

```

Glu Ile Pro Ala Ala Thr Pro Ser Asp Pro Gln Leu Lys Glu
85 90

(2) INFORMATION FOR SEQ ID NO:1826:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1219 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1219
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571116

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1826:

aaaaaaaaactt	gcaaaaactct	cgctccgagat	atatcgactc	cgcgaccctc	cactactctt	60
ctgctgatct	acacacacac	acacaaaaaa	aaaaaaactc	aatcgccagc	acaactggcg	120
aagctcacac	tctctctctt	cccttctctt	ctcatctctt	cctcatccat	cgctttccaa	180
tcagacgagc	tctctcggtg	cgacgacgaa	tttggcttag	aaggagcaaa	gccccgctcc	240
accgatcttt	acacatcttc	ttcttctctg	ccacagcagc	agcaacagac	tccaactatc	300
cgagagaagat	actcagatcc	taccgatttg	gattcaaaa	tccaatttac	tctcgaacat	360
gccttcgggtg	actctgattt	ctccccgcgc	ggtaactttt	ccgctcgctc	caaaaacctgg	420
agtcattggcg	gaaagacatt	aacgaagctg	cgattctcta	ggaatgattt	ttctgtctaaa	480
gagaaagatg	cattcaagaa	tctgctgaaa	ggagatgact	tttatcggtt	tcggctctca	540
tttaaatgtg	ttagtccacc	agggagagag	ttTgtgattg	catcagtgag	agctagatgt	600
ctaccacggg	atggccttga	tgagcatctt	attatacaca	tgggaaggtg	taacatcttg	660
gcagttagtt	atggttctcc	tggggcggtg	caatatctct	gcccaattgaa	acttcacaga	720
aaatggctgt	ttaactctca	cacaattctg	aaaagcagtg	agcaggcgcc	aagaactcca	780
atattcactg	aggagattct	aggcagtgag	aatgtagagg	gagaagttga	accaccacca	840
gagagatcat	tttggcgcaa	atattggatg	tatttgatac	cgctgggact	cgtagtgatg	900
aatgccttta	cacaagcatc	aaacatggct	gaagaaccgc	cggttggaac	ggcaggaggg	960
gcacaagtgc	aaccagctgc	caggagaaga	tgattccact	tttactcttc	ccaaagcaat	1020
gaaagctgca	gctggttaga	gatgatgatt	caacagatct	tcagttaaac	catcttgcca	1080
tcatttgggt	ttatgtaac	tttaatttta	atcctcgatc	gggtgtgttt	tgtactcaac	1140
aatcgggaaa	tcaaaaatct	tgtcttcatg	acatatcaag	aacaaagaca	tttagcagct	1200
tcctatctct	gttttgatc					

(2) INFORMATION FOR SEQ ID NO:1827:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 330 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..330
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571117

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1827:

Lys	Lys	Thr	Cys	Lys	Thr	Leu	Val	Arg	Asp	Ile	Ser	Thr	Pro	Arg	Pro
1			5					10						15	
Ser	Thr	Thr	Leu	Leu	Ile	Tyr	Thr	His	Thr	His	Lys	Lys	Lys	Lys	
			20				25					30			
Thr	Gln	Ser	Pro	Ala	Thr	Met	Ala	Lys	Leu	Thr	Leu	Leu	Phe	Phe	Leu
			35				40					45			
Ser	Phe	Leu	Ile	Phe	Ser	Ser	Ser	Ile	Ala	Phe	Gln	Ser	Asp	Glu	Leu
			50				55					60			
Leu	Val	Asp	Asp	Asp	Glu	Phe	Gly	Leu	Glu	Gly	Ala	Lys	Pro	Arg	Ser
							70				75			80	
Thr	Asp	Leu	Tyr	Thr	Ser	Ser	Ser	Ser	Ser	Pro	Gln	Gln	Gln	Gln	
							85					90		95	
Thr	Pro	Thr	Ile	Arg	Arg	Arg	Tyr	Ser	Asp	Pro	Thr	Asp	Leu	Asp	Ser
							100					105		110	

Lys Val Gln Phe Thr Leu Glu His Ala Phe Gly Asp Ser Asp Phe Ser
115 120 125
Pro Ala Gly Thr Phe Ser Ala Arg Leu Lys Thr Trp Ser His Gly Gly
130 135 140
Lys Thr Leu Thr Lys Leu Arg Phe Ser Arg Asn Asp Phe Ser Ala Lys
145 150 155 160
Glu Lys Asp Ala Phe Lys Asn Leu Leu Lys Gly Asp Asp Phe Tyr Arg
165 170 175
Ile Arg Leu Pro Ser Asn Val Val Ser Pro Pro Gly Arg Glu Phe Val
180 185 190
Ile Ala Ser Val Arg Ala Arg Cys Leu Pro Arg Asp Gly Leu Asp Glu
195 200 205
His Phe Ile Ile His Met Glu Gly Ala Asn Ile Leu Ala Val Ser Tyr
210 215 220
Gly Ser Pro Gly Ala Cys Gln Tyr Pro Arg Gln Leu Lys Leu Pro Ala
225 230 235 240
Lys Trp Ser Phe Asn Ser His Thr Ile Leu Lys Ser Ser Glu Gln Ala
245 250 255
Pro Arg Thr Pro Ile Phe Thr Glu Glu Ile Leu Gly Ser Glu Asn Val
260 265 270
Glu Gly Glu Val Glu Pro Pro Pro Glu Arg Ser Phe Trp Ala Lys Tyr
275 280 285
Trp Met Tyr Leu Ile Pro Leu Gly Leu Val Val Met Asn Ala Val Thr
290 295 300
Gln Ala Ser Asn Met Ala Glu Glu Pro Ala Gly Gly Gln Ala Gly Gly
305 310 315 320
Ala Gln Val Gln Pro Ala Ala Arg Arg Arg
325 330

(2) INFORMATION FOR SEQ ID NO:1828:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 292 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..292

(D) OTHER INFORMATION: / Ceres Seq. ID 1571118

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1828:

Met Ala Lys Leu Thr Leu Leu Phe Phe Leu Ser Phe Leu Ile Phe Ser
1 5 10 15
Ser Ser Ile Ala Phe Gln Ser Asp Glu Leu Val Asp Asp Asp Glu
20 25 30
Phe Gly Leu Glu Gly Ala Lys Pro Arg Ser Thr Asp Leu Tyr Thr Ser
35 40 45
Ser Ser Ser Ser Pro Gln Gln Gln Gln Thr Pro Thr Ile Arg Arg
50 55 60
Arg Tyr Ser Asp Pro Thr Asp Leu Asp Ser Lys Val Gln Phe Thr Leu
65 70 75 80
Glu His Ala Phe Gly Asp Ser Asp Phe Ser Pro Ala Gly Thr Phe Ser
85 90 95
Ala Arg Leu Lys Thr Trp Ser His Gly Gly Lys Thr Leu Thr Lys Leu
100 105 110
Arg Phe Ser Arg Asn Asp Phe Ser Ala Lys Glu Lys Asp Ala Phe Lys
115 120 125
Asn Leu Leu Lys Gly Asp Asp Phe Tyr Arg Ile Arg Leu Pro Ser Asn
130 135 140
Val Val Ser Pro Pro Gly Arg Glu Phe Val Ile Ala Ser Val Arg Ala
145 150 155 160
Arg Cys Leu Pro Arg Asp Gly Leu Asp Glu His Phe Ile Ile His Met

Ser	Thr	Lys	Thr	Asn	Met	Ala	Leu	Gln	Lys	Phe	Pro	Leu	Leu	Gly	Leu
1				5				10					15		
Phe	Leu	Val	Leu	Thr	Ile	Leu	Val	Ser	Ser	Ala	Thr	Ala	Asp	Gly	His
			20					25					30		
Val	Cys	Pro	Pro	Ser	Thr	Lys	Leu	Ser	Arg	Arg	Cys	Asn	Asn	Asp	Lys
		35				40						45			
Glu	Asn	Val	Val	Val	Ser	Phe	Phe	His	Arg	Tyr	Lys	Val	Ile	Ser	Glu
	50					55					60				
Tyr	Pro	Val	Ser	Ile	Lys	Tyr	Leu	Leu	Met	Phe	Phe	Val	Phe	Val	Phe
65					70					75				80	
Tyr	Phe	Leu	Phe	Val	Asp	Asn	Gln	Glu	Pro	Met	Asp	Tyr	Trp	Ser	Ile
				85					90					95	

Ile Pro Leu Gly Arg Gly Pro Lys Asn Leu Leu Val Phe Ser Ile Leu
100 105 110
Phe Tyr Phe Asn Phe Tyr Ile Leu
115 120

(2) INFORMATION FOR SEQ ID NO:1831:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..115
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571121

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1831:

Met Ala Leu Gln Lys Phe Pro Leu Leu Gly Leu Phe Leu Val Leu Thr
1 5 10 15
Ile Leu Val Ser Ser Ala Thr Ala Asp Gly His Val Cys Pro Pro Ser
20 25 30
Thr Lys Leu Ser Arg Arg Cys Asn Asn Asp Lys Glu Asn Val Val Val
35 40 45
Ser Phe Phe His Arg Tyr Lys Val Ile Ser Glu Tyr Pro Val Ser Ile
50 55 60
Lys Tyr Leu Leu Met Phe Phe Val Phe Val Phe Tyr Phe Leu Phe Val
65 70 75 80
Asp Asn Gln Glu Pro Met Asp Tyr Trp Ser Ile Ile Pro Leu Gly Arg
85 90 95
Gly Pro Lys Asn Leu Leu Val Phe Ser Ile Leu Phe Tyr Phe Asn Phe
100 105 110
Tyr Ile Leu
115

(2) INFORMATION FOR SEQ ID NO:1832:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 515 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..515
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571126

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1832:

aatatttttc gttccaaacg aaaaccctaa aagagaaaaa tgggtgcagcg 60
tcttgtttac cgtctggagc acagCtaacg caccaaatcg aaccagcacc gtatcgtcaa 120
gactccaggga ggtaaaattgg tgtatcaaac cacaaagaag aaagctagtgt gccccaaatg 180
tcctgtttact ggcaagcgta ttcaaggaat ccctcacttg aggcctctgt agtacaagag 240
gtcaagattta tcaagaaaca ggaggactgt aaaccgagca tacggtggag tcttgtctgg 300
ttctgcagtc agggaaaagga tcatttcgggc attccttgtc gaagagcaaa agatgtgtgaa 360
gaaagtgttg aaactccaaa aggcctaagga gaaagtagcc cccaaggctt aagcttttat 420
gttttattct tctctgtttt ggaattatgg ctatgttcaa gtgataggac ttggtgcagt 480
catgtgagga catctatggt actcgcacaa ttttt

(2) INFORMATION FOR SEQ ID NO:1833:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 136 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..136
(D) OTHER INFORMATION: / Ceres Seq. ID 1571127

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1833:

Ile Phe Phe Val Pro Asn Glu Asn Pro Lys Arg Glu Lys Glu Ala Lys
1 5 10 15
Met Val Gln Arg Leu Val Tyr Arg Ser Arg His Ser Tyr Ala Thr Lys
20 25 30
Ser Asn Gln His Arg Ile Val Lys Thr Pro Gly Gly Lys Leu Val Tyr
35 40 45
Gln Thr Thr Lys Lys Lys Ala Ser Gly Pro Lys Cys Pro Val Thr Gly
50 55 60
Lys Arg Ile Gln Gly Ile Pro His Leu Arg Pro Ser Glu Tyr Lys Arg
65 70 75 80
Ser Arg Leu Ser Arg Asn Arg Arg Thr Val Asn Arg Ala Tyr Gly Gly
85 90 95
Val Leu Ser Gly Ser Ala Val Arg Glu Arg Ile Ile Arg Ala Phe Leu
100 105 110
Val Glu Glu Gln Lys Ile Val Lys Lys Val Leu Lys Leu Gln Lys Ala
115 120 125
Lys Glu Lys Val Ala Pro Lys Ala
130 135

(2) INFORMATION FOR SEQ ID NO:1834:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 72 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..72
(D) OTHER INFORMATION: / Ceres Seq. ID 1571128

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1834:

Tyr Ser Ser Phe Gln Thr Lys Thr Leu Lys Glu Lys Arg Arg Arg Lys
1 5 10 15
Trp Cys Ser Val Leu Phe Thr Gly Arg Asp Thr Ala Thr Pro Pro Asn
20 25 30
Arg Thr Ser Thr Val Ser Ser Arg Leu Gln Glu Val Asn Trp Cys Ile
35 40 45
Lys Pro Gln Arg Arg Lys Leu Val Ala Pro Asn Val Leu Leu Leu Ala
50 55 60
Ser Val Phe Lys Glu Ser Leu Thr
65 70

(2) INFORMATION FOR SEQ ID NO:1835:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..120
(D) OTHER INFORMATION: / Ceres Seq. ID 1571129

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1835:

Met Val Gln Arg Leu Val Tyr Arg Ser Arg His Ser Tyr Ala Thr Lys
1 5 10 15
Ser Asn Gln His Arg Ile Val Lys Thr Pro Gly Gly Lys Leu Val Tyr
20 25 30
Gln Thr Thr Lys Lys Lys Ala Ser Gly Pro Lys Cys Pro Val Thr Gly

35 40 45
Lys Arg Ile Gln Gly Ile Pro His Leu Arg Pro Ser Glu Tyr Lys Arg
50 55 60
Ser Arg Leu Ser Arg Asn Arg Arg Thr Val Asn Arg Ala Tyr Gly Gly
65 70 75 80
Val Leu Ser Gly Ser Ala Val Arg Glu Arg Ile Ile Arg Ala Phe Leu
85 90 95
Val Glu Glu Gln Lys Ile Val Lys Lys Val Leu Lys Leu Gln Lys Ala
100 105 110
Lys Glu Lys Val Ala Pro Lys Ala
115 120

(2) INFORMATION FOR SEQ ID NO:1836:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 705 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..705

(D) OTHER INFORMATION: / Ceres Seq. ID 1571134

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1836:

acatctcact gctcactact ctcaactgtaa tcccttagat cttcttttca aatttcaatg 60
gcgtccgggtg atgtttgaagta tccgtgtcttc gttaggagtc tagcatgggc cactgatgac 120
agagctcttg agactgcctt cgctcaatac ggcgacgtta ttgattccaa gatcattaac 180
gatcgctaga ctggaagatc aaggggattc ggattcgtca ccttcaagga tgagaaagcc 240
atgaagatg cgattgaggg aatgaacgga caagatctcg atggcctgag catcactgtt 300
aacgaggtc agtcacgagg aagcgggtgg gcgagaggcc accgtggagg tgggtggcgtt 360
ggataCgcga gcggcgggtg tggaggttac tccggtggag gtggtagcta cggaggtggc 420
ggcggtagac Gcggaggttg aggaggatac agcggcggcg gcggttactc ctcaagaggt 480
ggtggtgagc gaagctacgg tgggtggaaga cgtgaggagg gaggaggata cgggtggtgt 540
gaaggaggag gttacggagg aagcgggtgt ggtggaggat ggtaattcct ttaattaggt 600
ttgggattac caatgaatgt tctctctctc gcttgttatg ctctactctg gttttgtgtg 660
ttctctattt tgttattctt ccgttaatgt aatgaaagag ttgttt

(2) INFORMATION FOR SEQ ID NO:1837:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 175 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..175

(D) OTHER INFORMATION: / Ceres Seq. ID 1571135

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1837:

Met Ala Ser Gly Asp Val Glu Tyr Arg Cys Phe Val Gly Gly Leu Ala
1 5 10 15
Trp Ala Thr Asp Asp Arg Ala Leu Glu Thr Ala Phe Ala Gln Tyr Gly
20 25 30
Asp Val Ile Asp Ser Lys Ile Ile Asn Asp Arg Glu Thr Gly Arg Ser
35 40 45
Arg Gly Phe Gly Phe Val Thr Phe Lys Asp Glu Lys Ala Met Lys Asp
50 55 60
Ala Ile Glu Gly Met Asn Gly Gln Asp Leu Asp Gly Arg Ser Ile Thr
65 70 75 80
Val Asn Glu Ala Gln Ser Arg Gly Ser Gly Gly Gly Gly His Arg
85 90 95
Gly Gly Gly Gly Gly Gly Tyr Arg Ser Gly Gly Gly Gly Gly Tyr Ser
100 105 110

Gly Gly Gly Gly Ser Tyr Gly Gly Gly Gly Gly Arg Arg Glu Gly Gly
115 120 125
Gly Gly Tyr Ser Gly Gly Gly Tyr Ser Ser Arg Gly Gly Gly Gly
130 135 140
Gly Ser Tyr Gly Gly Gly Arg Arg Glu Gly Gly Gly Tyr Gly Gly
145 150 155 160
Gly Glu Gly Gly Gly Tyr Gly Gly Ser Gly Gly Gly Gly Trp
165 170 175

(2) INFORMATION FOR SEQ ID NO:1838:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 114 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..114

(D) OTHER INFORMATION: / Ceres Seq. ID 1571136

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1838:

Met Lys Asp Ala Ile Glu Gly Met Asn Gly Gln Asp Leu Asp Gly Arg
1 5 10 15
Ser Ile Thr Val Asn Glu Ala Gln Ser Arg Gly Ser Gly Gly Gly Gly
20 25 30
Gly His Arg Gly Gly Gly Gly Tyr Arg Ser Gly Gly Gly Gly
35 40 45
Gly Tyr Ser Gly Gly Gly Gly Ser Tyr Gly Gly Gly Arg Arg
50 55 60
Glu Gly Gly Gly Gly Tyr Ser Gly Gly Gly Gly Tyr Ser Ser Arg Gly
65 70 75 80
Gly Gly Gly Gly Ser Tyr Gly Gly Gly Arg Arg Glu Gly Gly Gly
85 90 95
Tyr Gly Gly Gly Glu Gly Gly Gly Tyr Gly Gly Ser Gly Gly Gly
100 105 110
Gly Trp

(2) INFORMATION FOR SEQ ID NO:1839:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 107 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..107

(D) OTHER INFORMATION: / Ceres Seq. ID 1571137

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1839:

Met Asn Gly Gln Asp Leu Asp Gly Arg Ser Ile Thr Val Asn Glu Ala
1 5 10 15
Gln Ser Arg Gly Ser Gly Gly Gly Gly His Arg Gly Gly Gly Gly
20 25 30
Gly Gly Tyr Arg Ser Gly Gly Gly Gly Tyr Ser Gly Gly Gly Gly
35 40 45
Ser Tyr Gly Gly Gly Gly Gly Arg Arg Glu Gly Gly Gly Tyr Ser
50 55 60
Gly Gly Gly Gly Tyr Ser Ser Arg Gly Gly Gly Gly Ser Tyr Gly
65 70 75 80
Gly Gly Arg Arg Glu Gly Gly Gly Tyr Gly Gly Gly Glu Gly
85 90 95
Gly Tyr Gly Gly Ser Gly Gly Gly Gly Trp

100 105

(2) INFORMATION FOR SEQ ID NO:1840:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 873 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..873

(D) OTHER INFORMATION: / Ceres Seq. ID 1571138

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1840:

gaaacacaaa	caaacacaaa	aatcaaaaagg	ggtcatttac	tatcttttaa	gagacgacat	60
atatagtctt	cgaccaagaa	aagaaaaagg	ggtagacctga	gttctctcaac	acataacata	120
atggcgaggag	ttttcaaaaac	gggttacgttt	cttgtttttg	ttttcgctgc	cggtgtgttc	180
ttcgcgaggag	actacgatgt	tggtagatgt	acggaatgga	cgagacctat	ggaccgccgag	240
ttctatacta	cttgggctac	cggtaaaact	ttcgtgttag	gcgacgagct	cgaatttgat	300
ttcgctgctg	ggaggcatga	tgtggcagtt	gtatcagaag	ctgcatttga	aaactgtgag	360
aaagagaaac	ccattagcca	catgaccggt	cTcccggtca	aaattatgct	aaacaccact	420
ggaccacaat	actttatctg	caccgtcggt	gaccattgtc	gttttggtca	aaaactttcc	480
atcactgtag	ttgctgctgg	tgcaactgga	ggtgctactc	ctgggtcgcg	tgctacccca	540
gcacctggat	caaccccaa	tactggagga	accactcctc	ccactgcggg	tgggaccaca	600
acaccttcag	gctctagcgg	aaccactact	ccagctggaa	atgcccgctc	ctcattaggt	660
ggtgtcaact	ttctgtgtcg	ttttgtttct	gctgtgtgtg	ctctcttttg	agtcacactc	720
gaaacctagt	tatgtgtttg	ttttacctta	ctctccttat	ttaaatagtc	atgtatttga	780
ttatttgtga	gaataaggac	ttgttttcaa	gtcattataa	acgtcttata	cttgtgatta	840
gtattgagtt	tcaatatatg	attattcggt	tgc			

(2) INFORMATION FOR SEQ ID NO:1841:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 196 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..196

(D) OTHER INFORMATION: / Ceres Seq. ID 1571139

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1841:

Met	Ala	Gly	Val	Phe	Lys	Thr	Val	Thr	Phe	Leu	Val	Leu	Val	Phe	Ala	
1				5				10						15		
Ala	Val	Val	Val	Phe	Ala	Glu	Asp	Tyr	Asp	Val	Gly	Asp	Asp	Thr	Glu	
				20				25						30		
Trp	Thr	Arg	Pro	Met	Asp	Pro	Glu	Phe	Tyr	Thr	Thr	Trp	Ala	Thr	Gly	
				35				40						45		
Lys	Thr	Phe	Arg	Val	Gly	Asp	Glu	Leu	Glu	Phe	Asp	Phe	Ala	Ala	Gly	
				50				55						60		
Arg	His	Asp	Val	Ala	Val	Val	Ser	Glu	Ala	Ala	Phe	Glu	Asn	Cys	Glu	
				65				70						75		
Lys	Glu	Lys	Pro	Ile	Ser	His	Met	Thr	Val	Pro	Pro	Val	Lys	Ile	Met	
				85				90						95		
Leu	Asn	Thr	Thr	Gly	Pro	Gln	Tyr	Phe	Ile	Cys	Thr	Val	Gly	Asp	His	
				100				105						110		
Cys	Arg	Gly	Gly	Gln	Lys	Leu	Ser	Ile	Thr	Val	Val	Ala	Ala	Gly	Ala	
				115				120						125		
Thr	Gly	Gly	Ala	Thr	Pro	Gly	Ala	Gly	Ala	Thr	Pro	Ala	Pro	Gly	Ser	
				130				135						140		
Thr	Pro	Ser	Thr	Gly	Gly	Thr	Thr	Pro	Pro	Thr	Ala	Gly	Gly	Thr	Thr	
				145				150						155		
Thr	Pro	Ser	Gly	Ser	Ser	Gly	Thr	Thr	Thr	Pro	Ala	Gly	Asn	Ala	Ala	

	165		170		175
Ser Ser Leu Gly	Gly Ala Thr Phe	Leu Val Ala Phe	Val Ser Ala Val		
	180	185	190		
Val Ala Leu Phe					
	195				

(2) INFORMATION FOR SEQ ID NO:1842:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 160 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..160
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571140

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1842:

Met Asp Pro Glu Phe Tyr Thr Thr Trp	Ala Thr Gly Lys Thr Phe Arg
1	5 10 15
Val Gly Asp Glu Leu Glu Phe Asp Phe	Ala Ala Gly Arg His Asp Val
	20 25 30
Ala Val Val Ser Glu Ala Ala Phe Glu Asn Cys	Glu Lys Glu Lys Pro
	35 40 45
Ile Ser His Met Thr Val Pro Pro Val Lys	Ile Met Leu Asn Thr Thr
	50 55 60
Gly Pro Gln Tyr Phe Ile Cys Thr Val Gly	Asp His Cys Arg Phe Gly
	65 70 75 80
Gln Lys Leu Ser Ile Thr Val Val Ala Ala	Gly Ala Thr Gly Gly Ala
	85 90 95
Thr Pro Gly Ala Gly Ala Thr Pro Ala Pro	Gly Ser Thr Pro Ser Thr
	100 105 110
Gly Gly Thr Thr Pro Pro Thr Ala Gly Gly	Thr Thr Pro Ser Gly
	115 120 125
Ser Ser Gly Thr Thr Thr Pro Ala Gly Asn	Ala Ala Ser Ser Leu Gly
	130 135 140
Gly Ala Thr Phe Leu Val Ala Phe Val Ser	Ala Val Val Ala Leu Phe
145	150 155 160

(2) INFORMATION FOR SEQ ID NO:1843:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 109 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..109
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571141

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1843:

Met Thr Val Pro Pro Val Lys Ile Met Leu Asn Thr	Thr Gly Pro Gln
1	5 10 15
Tyr Phe Ile Cys Thr Val Gly Asp His Cys Arg	Phe Gly Gln Lys Leu
	20 25 30
Ser Ile Thr Val Val Ala Ala Gly Ala Thr Gly	Gly Ala Thr Pro Gly
	35 40 45
Ala Gly Ala Thr Pro Ala Pro Gly Ser Thr Pro	Ser Thr Gly Gly Thr
	50 55 60
Thr Pro Pro Thr Ala Gly Gly Thr Thr Thr Pro	Ser Gly Ser Ser Gly
65	70 75 80

Thr Thr Thr Pro Ala Gly Asn Ala Ala Ser Ser Leu Gly Gly Ala Thr
85 90 95
Phe Leu Val Ala Phe Val Ser Ala Val Val Ala Leu Phe
100 105

(2) INFORMATION FOR SEQ ID NO:1844:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 620 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..620
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571153

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1844:

ctcgtagca	atctgGatct	aatccaccac	tctctccaat	tgctcattcac	tccggtttttg	60
ctatttccaa	ggagagaaag	atgatagctg	tgatcggatt	gcttctgggt	tttctagtat	120
cagcattgtt	cttaatccaa	ggaaagcgaa	gaagaacaaa	cgacaatcaa	gagaagaaga	180
gatctagcag	tgagccctga	gaagatgtgg	taagaccaaa	aagtaccagc	aagagtgaag	240
tcgcagtaca	taacaaaagg	aacgattgtt	ggatcataat	caaagataaa	gtctatgata	300
ttactttcta	ttgtgaagaa	catcctgggtg	gtgacgctat	tcttgatcat	gctgggtgatg	360
atttcaactga	tggctttctc	ggacctcaac	acgccactcg	tgttttcgac	atgattgaag	420
attttacat	cggggaact	cattagtaaa	agcttaaaga	tttgagattt	gattgaagat	480
ttgagatttc	ttcttaagta	agcttaaa	tggtttttt	aattctcttc	tcattgaaga	540
tttgagattg	cattacctt	ttgtcttget	agtgtAacac	ttctctcttc	attgtattgc	600
caaagtttcc	tcatttctcc					

(2) INFORMATION FOR SEQ ID NO:1845:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 147 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..147
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571154

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1845:

Arg	Gln	Gln	Ser	Gly	Ser	Asn	Pro	Pro	Leu	Ser	Pro	Ile	Val	Ile	His
1			5					10					15		
Ser	Gly	Phe	Ala	Ile	Ser	Lys	Glu	Arg	Lys	Met	Ile	Ala	Val	Ile	Gly
			20					25					30		
Leu	Leu	Leu	Gly	Phe	Leu	Val	Ser	Ala	Leu	Phe	Leu	Ile	Gln	Gly	Lys
			35					40					45		
Arg	Arg	Arg	Thr	Asn	Asp	Asn	Gln	Glu	Lys	Lys	Arg	Ser	Ser	Ser	Glu
			50					55					60		
Pro	Val	Glu	Asp	Val	Val	Arg	Pro	Lys	Ser	Tyr	Ser	Lys	Ser	Glu	Val
								70						80	
Ala	Val	His	Asn	Lys	Arg	Asn	Asp	Cys	Trp	Ile	Ile	Ile	Lys	Asp	Lys
								90					95		
Val	Tyr	Asp	Ile	Thr	Ser	Tyr	Val	Glu	Glu	His	Pro	Gly	Gly	Asp	Ala
								105					110		
Ile	Leu	Asp	His	Ala	Gly	Asp	Asp	Ser	Thr	Asp	Gly	Phe	Gly	Pro	
								120					125		
Gln	His	Ala	Thr	Arg	Val	Phe	Asp	Met	Ile	Glu	Asp	Phe	Tyr	Ile	Gly
								135					140		
Glu	Leu	His													
145															

(2) INFORMATION FOR SEQ ID NO:1846:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 121 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..121
(D) OTHER INFORMATION: / Ceres Seq. ID 1571155
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1846:
Met Ile Ala Val Ile Gly Leu Leu Leu Gly Phe Leu Val Ser Ala Leu
1 5 10 15
Phe Leu Ile Gln Gly Lys Arg Arg Arg Thr Asn Asp Asn Gln Glu Lys
20 25 30
Lys Arg Ser Ser Ser Glu Pro Val Glu Asp Val Val Arg Pro Lys Ser
35 40 45
Tyr Ser Lys Ser Glu Val Ala Val His Asn Lys Arg Asn Asp Cys Trp
50 55 60
Ile Ile Ile Lys Asp Lys Val Tyr Asp Ile Thr Ser Tyr Val Glu Glu
65 70 75 80
His Pro Gly Gly Asp Ala Ile Leu Asp His Ala Gly Asp Asp Ser Thr
85 90 95
Asp Gly Phe Phe Gly Pro Gln His Ala Thr Arg Val Phe Asp Met Ile
100 105 110
Glu Asp Phe Tyr Ile Gly Glu Leu His
115 120

(2) INFORMATION FOR SEQ ID NO:1847:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 290 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -
(B) LOCATION: 1..290
(D) OTHER INFORMATION: / Ceres Seq. ID 1571159

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1847:

aaaaWaWaga aatgatgact tgcataaacc ggaagttagc tcaacccccg gaaggtaacg 60
aggaagctag ggcagatcca aaaggaccag ctaaattgtt tgtgatgtga agagaggttg 120
gtgggaatca gctatttgta ttaatagaag gaacagtgtatataaaacat catttgaagc 180
tttgaatttc cctacaacct cctaattgta tagtcttggt tgagaatata tatatgtccc 240
ccaaaaacag ttgatgatta ttttaataaa cctcatctct accttctctt

(2) INFORMATION FOR SEQ ID NO:1848:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 35 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1..35
(D) OTHER INFORMATION: / Ceres Seq. ID 1571160

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1848:

Xaa Xaa Glu Met Met Thr Ser His Asn Arg Lys Leu Ala Gln Pro Pro
1 5 10 15
Glu Gly Asn Glu Glu Ala Arg Ala Asp Pro Lys Gly Pro Ala Lys Cys
20 25 30
Cys Val Met
35

(2) INFORMATION FOR SEQ ID NO:1849:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 32 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..32
(D) OTHER INFORMATION: / Ceres Seq. ID 1571161

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1849:

Met	Met	Thr	Ser	His	Asn	Arg	Lys	Leu	Ala	Gln	Pro	Pro	Glu	Gly	Asn
1			5					10			15				
Glu	Glu	Ala	Arg	Ala	Asp	Pro	Lys	Gly	Pro	Ala	Lys	Cys	Cys	Val	Met
		20						25						30	

(2) INFORMATION FOR SEQ ID NO:1850:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 36 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..36
(D) OTHER INFORMATION: / Ceres Seq. ID 1571162

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1850:

Met	Leu	Cys	Asp	Val	Lys	Arg	Gly	Trp	Trp	Glu	Ser	Ala	Ile	Cys	Ile
1			5					10			15				
Asn	Arg	Arg	Asn	Ser	Val	Tyr	Lys	Thr	Ser	Phe	Glu	Ala	Leu	Lys	Phe
			20					25					30		
Pro	Thr	Thr	Ser												
			35												

(2) INFORMATION FOR SEQ ID NO:1851:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 560 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..560
(D) OTHER INFORMATION: / Ceres Seq. ID 1571163

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1851:

atcaaaaaaa	gtaataaagt	aaagtatttc	gccgtgagag	aaagaacaat	caccatcgtc	60
taggggtttca	attcattggt	ccagtaacctc	atcgtagcgc	cgctcctctc	ttgtccagac	120
tccagaagat	tcaatggcac	ccaagaaaga	caaagtctct	cctccgtcct	ctaaaccgcc	180
caaatccggt	ggcggaagc	aaaagaaaaa	gaagtggagc	aaaggaagac	aaaaggagaa	240
agtgaacaa	atggttttgt	ttgaccaagc	aacttacgac	aagcttctct	ctgaggctcc	300
caagttcaaa	cttatcactc	cttctatcct	ctctgaccgt	ttgaggatca	atggatcgct	360
tgctagaagg	gcgatcaag	aattgatggc	taagggaaca	atcaggatgg	tctctgctca	420
ctcaagccag	catagctaca	ctagggcaac	ccacggctaa	cttcctctga	atgttttagt	480
tgttttcttg	tattttactc	aattgtctta	tgaaccatta	tctttctaga	atgcaccttt	540
acttgcaaac	attggtctac					

(2) INFORMATION FOR SEQ ID NO:1852:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 108 amino acids

(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..108
 (D) OTHER INFORMATION: / Ceres Seq. ID 1571164
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1852:
Met Ala Pro Lys Lys Asp Lys Val Pro Pro Pro Ser Ser Lys Pro Ala
1 5 10 15
Lys Ser Gly Gly Gly Lys Gln Lys Lys Lys Trp Ser Lys Gly Lys
 20 25 30
Gln Lys Glu Lys Val Asn Asn Met Val Leu Phe Asp Gln Ala Thr Tyr
 35 40 45
Asp Lys Leu Leu Ser Glu Ala Pro Lys Phe Lys Leu Ile Thr Pro Ser
 50 55 60
Ile Leu Ser Asp Arg Leu Arg Ile Asn Gly Ser Leu Ala Arg Arg Ala
65 70 75 80
Ile Arg Glu Leu Met Ala Lys Gly Thr Ile Arg Met Val Ser Ala His
 85 90 95
Ser Ser Gln Gln Ile Tyr Thr Arg Ala Thr His Gly
 100 105

(2) INFORMATION FOR SEQ ID NO:1853:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 69 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..69
 (D) OTHER INFORMATION: / Ceres Seq. ID 1571165
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1853:
Met Val Leu Phe Asp Gln Ala Thr Tyr Asp Lys Leu Leu Ser Glu Ala
1 5 10 15
Pro Lys Phe Lys Leu Ile Thr Pro Ser Ile Leu Ser Asp Arg Leu Arg
 20 25 30
Ile Asn Gly Ser Leu Ala Arg Arg Ala Ile Arg Glu Leu Met Ala Lys
 35 40 45
Gly Thr Ile Arg Met Val Ser Ala His Ser Ser Gln Gln Ile Tyr Thr
50 55 60
Arg Ala Thr His Gly
65

(2) INFORMATION FOR SEQ ID NO:1854:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 748 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
 (A) NAME/KEY: -
 (B) LOCATION: 1..748
 (D) OTHER INFORMATION: / Ceres Seq. ID 1571166
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1854:
aaccaaaaaca aaacaaaaca aaaaaaacac gagtggaagc ttttaaacaa aattagaaaa 60
agagagagag aaatggcgac gtcgggaaca tacgtgacgg aggtgccgct aaaaggaagc 120
gtggagaaac acttcaagag gtacaggaac gagaactatc tcttcctga cactatcgcc 180
caccacatcc aaagtgttac tgttcacgat ggcgaatggg acactcaagg aggcacaaag 240

atttggaaat	acacactcgg	agatggaaa	gaggaggat	tcaaggagag	gagagagata	300
gacgatgaca	ataagatagt	aaaggttgt	ggattggaag	gtcacgtgat	ggagcagttc	360
aaggtgtatg	agattgactt	ccaattttat	cccaagctcg	aagaagattg	cgtctgcaaa	420
atcactatga	tatgggagaa	gcgcaacgat	gatttcccg	aaccaagcag	ctacatgcaa	480
ctcctcaaga	gtatggttat	tgatatggag	gaccacgtcc	ttaaagctta	ataaatatca	540
caaccaccac	catoatcaca	accaccatca	tcatactcct	atatgtttat	taaattgttt	600
tcatttatat	ataatagact	agataagaac	ctgtataatg	tgccgggataa	aatgattgaa	660
ataaattatt	atgcgtaaac	ttattgtatg	agatatcata	tatgtttgta	tacaagaaaa	720
tatgtaatta	aagtBttttg	ttttattt				

(2) INFORMATION FOR SEQ ID NO:1855:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 176 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..176

(D) OTHER INFORMATION: / Ceres Seq. ID 1571167

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1855:

Asn	Gln	Asn	Lys	Thr	Lys	Gln	Lys	Lys	His	Glu	Trp	Lys	Leu	Leu	Asn	
1		5							10					15		
Lys	Ile	Arg	Lys	Arg	Glu	Arg	Glu	Met	Ala	Thr	Ser	Gly	Thr	Tyr	Val	
		20						25					30			
Thr	Glu	Val	Pro	Leu	Lys	Gly	Thr	Val	Glu	Lys	His	Phe	Lys	Arg	Tyr	
		35					40					45				
Arg	Asn	Glu	Asn	Tyr	Leu	Phe	Pro	Asp	Thr	Ile	Gly	His	His	Ile	Gln	
		50				55					60					
Ser	Val	Thr	Val	His	Asp	Gly	Glu	Trp	Asp	Thr	Gln	Gly	Gly	Ile	Lys	
		65			70				75					80		
Ile	Trp	Asn	Tyr	Thr	Leu	Gly	Asp	Gly	Lys	Glu	Glu	Val	Phe	Lys	Glu	
			85					90						95		
Arg	Arg	Glu	Ile	Asp	Asp	Asp	Asn	Lys	Ile	Val	Lys	Val	Val	Gly	Leu	
			100					105						110		
Glu	Gly	His	Val	Met	Glu	Gln	Phe	Lys	Val	Tyr	Glu	Ile	Asp	Phe	Gln	
		115					120					125				
Phe	Ile	Pro	Lys	Ser	Glu	Glu	Asp	Cys	Val	Cys	Lys	Ile	Thr	Met	Ile	
		130				135					140					
Trp	Glu	Lys	Arg	Asn	Asp	Asp	Phe	Pro	Glu	Pro	Ser	Ser	Tyr	Met	Gln	
		145			150				155					160		
Leu	Leu	Lys	Ser	Met	Val	Ile	Asp	Met	Glu	Asp	His	Val	Leu	Lys	Ala	
			165					170						175		

(2) INFORMATION FOR SEQ ID NO:1856:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 152 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..152

(D) OTHER INFORMATION: / Ceres Seq. ID 1571168

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1856:

Met	Ala	Thr	Ser	Gly	Thr	Tyr	Val	Thr	Glu	Val	Pro	Leu	Lys	Gly	Thr	
1			5						10				15			
Val	Glu	Lys	His	Phe	Lys	Arg	Tyr	Arg	Asn	Glu	Asn	Tyr	Leu	Phe	Pro	
			20					25					30			

```

Asp Thr Ile Gly His His Ile Gln Ser Val Thr Val His Asp Gly Glu
    35                      40                      45
Trp Asp Thr Gln Gly Gly Ile Lys Ile Trp Asn Tyr Thr Leu Gly Asp
    50                      55                      60
Gly Lys Glu Glu Val Phe Lys Glu Arg Arg Glu Ile Asp Asp Asp Asn
    65                      70                      75                      80
Lys Ile Val Lys Val Val Gly Leu Glu Gly His Val Met Glu Gln Phe
    85                      90                      95
Lys Val Tyr Glu Ile Asp Phe Gln Phe Ile Pro Lys Ser Glu Glu Asp
    100                      105                      110
Cys Val Cys Lys Ile Thr Met Ile Trp Glu Lys Arg Asn Asp Asp Phe
    115                      120                      125
Pro Glu Pro Ser Ser Tyr Met Gln Leu Leu Lys Ser Met Val Ile Asp
    130                      135                      140
Met Glu Asp His Val Leu Lys Ala
    145                      150

```

(2) INFORMATION FOR SEQ ID NO:1857:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1066 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1066
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571206

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1857:

```

aagactctgt tttttcccaa gatgtctggt ttctcttttt gtttcgtcca aatctctact    60
tttagggat cttgtccctc ttctttctgc tgattaaaac cctcgaattt gctccaattc    120
gacgcgaaaa agggcattga gatggtgaat ggagaatcat caactagtac gtcttactct    180
gataataaca atgacacaaa tgaatcaagga ggagactttg aatgtaacat ttgtttcgaa    240
ctagctcaag atccogattgt cactctctgt ggccatctct tttgctggcc ttgcttatac    300
cgttggcttc accaccattc acattctcaa gaatgtccgg tttgtaaagc cgtggttcaa    360
gacgataaag ttgttctctc ttacggtaga ggcaagaacc agactgacc gagatcaaaa    420
cgttatccgg gtttacggat tcttaaccga ccaacaggtc aaagacctga gactgctgct    480
cctcctcctc agcctgaagc tgcgagtaat tttttcaact acggtattgg tttgatgggt    540
ggaattatgc cgatgatggc gactacgagg tttgggaatt tcagtatggg gtttggtggt    600
ttgtttacott ctttggttaa ctttcagttt catggatttc atgatgCtac gctttatggt    660
tcaaacacgg gttatcotta cgggtggttat cataacggtt tccgtggagt tctctcctgt    720
ggacaagagc gctctatggc tctgtggagg aaccacaaag atgcatttct gaagaatatc    780
ctcttttttg ttggaactct tgtggtgata ttctcatct ggtgaaaacg aatcaacatt    840
gggtgatctc caggatgatg caaacttact tacttggtgc aagttgtgta tgtaaatatg    900
gtaatatgctg agtgtacttg tctgctattt cgacgttgtt attgtatttt tgttttgaag    960
atgaaccatg agtctacaag cttttttaca caactctttt gttgcttttg tgttttgtct    1020
aagcatctta tgaaaactag ttgtgaaata aatggtgctg gttatg

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(2) INFORMATION FOR SEQ ID NO:1858:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 227 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..227
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571207

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1858:

```

Met Val Asn Gly Glu Ser Ser Thr Ser Tyr Ser Asp Asn Asn
  1           5           10           15
Asn Asp Thr Asn Asp Gln Gly Gly Asp Phe Glu Cys Asn Ile Cys Phe

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20	25	30
Glu Leu Ala Gln Asp Pro	Ile Val Thr Leu Cys Gly	His Leu Phe Cys
35	40	45
Trp Pro Cys Leu Tyr Arg	Trp Leu His His His	Ser His Gln Glu
50	55	60
Cys Pro Val Cys Lys Ala	Val Val Gln Asp Asp	Lys Leu Val Pro Leu
65	70	75
Tyr Gly Arg Gly Lys	Asn Gln Thr Asp	Pro Arg Ser Lys Arg Tyr Pro
85	90	95
Gly Leu Arg Ile Pro	Asn Arg Pro Thr	Gly Gln Arg Pro Glu Thr Ala
100	105	110
Ala Pro Pro Gln Pro	Glu Ala Ser Asn Phe	Phe Asn Tyr Gly
115	120	125
Ile Gly Leu Met Gly	Gly Ile Met Pro Met	Met Ala Thr Thr Arg Phe
130	135	140
Gly Asn Phe Ser Met	Gly Phe Gly Gly Leu	Leu Pro Ser Leu Phe Asn
145	150	155
Phe Gln Phe His Gly	Phe His Asp Ala Thr	Leu Tyr Gly Ser Thr Pro
165	170	175
Gly Tyr Pro Tyr Gly	Gly Tyr His Asn Gly	Phe Arg Gly Val Pro Pro
180	185	190
Arg Gly Gln Glu Arg	Pro Met Ala Arg	Gly Gly Asn Gln Ser Asp Ala
195	200	205
Phe Leu Lys Asn Ile	Leu Phe Phe Val Gly	Ile Cys Val Val Ile Phe
210	215	220
Leu Ile Trp		
225		

(2) INFORMATION FOR SEQ ID NO:1859:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 520 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..520
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571220

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1859:

aagttctaaa	gtcctcaaat	cccgcaaaagc	tttttcagct	tctttgttga	attgcgagca	60
gaggtagaaa	tcagcaggaa	acaaaaatgt	tgttcttttc	ttacttcaag	gatttggttg	120
gacaagaagt	gacggttgag	ctgaagaatg	atttagccat	aagaggaaact	cttcaactaag	180
ttgatcagta	tctgaatatc	aagctcgaga	acactagggt	tgtagaccag	gaagtaccct	240
cacatgcttt	cagtgagaaa	ctgtttcatt	agaggatctg	tgttaaggta	cgtgcagtta	300
cctaaagatg	gagtcgatgt	tgatttgcct	ccagcgccag	Ctagaagaga	agctagggggt	360
ggctgattct	gaatatcttt	tgtagctcca	aaacttgat	acttttcatt	cggcgtaagt	420
gctttataat	gaattattcc	ctgatgtaga	gccaatggta	tgcccatgaa	tcttgtttcca	480
ttttattaac	aatggataat	ttaatttctt	ttctcgctcc			

(2) INFORMATION FOR SEQ ID NO:1860:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 72 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..72
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571221

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1860:

Met Leu Phe Phe Ser Tyr Phe Lys Asp Leu Val Gly Gln Glu Val Thr

1 5 10 15
Val Glu Leu Lys Asn Asp Leu Ala Ile Arg Gly Thr Leu His Ser Val
20 25 30
Asp Gln Tyr Leu Asn Ile Lys Leu Glu Asn Thr Arg Val Val Asp Gln
35 40 45
Glu Val Pro Ser His Ala Phe Ser Glu Lys Leu Phe His Gln Arg Ile
50 55 60
Cys Gly Lys Val Arg Ala Val Thr
65 70

(2) INFORMATION FOR SEQ ID NO:1861:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..40
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571222
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1861:

Met Leu Ser Val Arg Asn Cys Phe Ile Arg Gly Ser Val Val Arg Tyr
1 5 10 15
Val Gln Leu Pro Lys Asp Gly Val Asp Val Asp Leu Leu His Gly Ala
20 25 30
Ala Arg Arg Glu Ala Arg Gly Gly
35 40

(2) INFORMATION FOR SEQ ID NO:1862:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..36
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571223
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1862:

Met Glu Ser Met Leu Ile Cys Phe Thr Ala Gln Leu Glu Glu Lys Leu
1 5 10 15
Gly Val Ala Asp Ser Glu Ile Ser Leu Tyr Leu Gln Asn Leu Asn Thr
20 25 30
Phe His Ser Ala
35

(2) INFORMATION FOR SEQ ID NO:1863:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2401 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..2401
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571228
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1863:

acaaatcttt	ctctttctct	ttctctctct	aacacaattt	agaacaaaaa	tttcttcttt	60
ctctctcccc	gagaggccct	tcgctgttca	ttgaagttct	cttagaattt	tcatacaact	120
tggttctgta	atttgcaaaa	cagacaacaa	tggttgagcg	tggaagagg	actcaacaat	180
gtttcagaga	caacaacaat	gacaacaacc	ggaatcaaa	gagaagactt	tcttacgaat	240

cogaagaaaa	aaagatcgat	aacaaagacg	atctcgttgt	tgtttacaga	atcttatgcc	300
caagtgggtg	catgggaagt	gttatagcca	aaagtggcaa	agttattaac	ttgattaggc	360
aagaaactag	agctaggagt	aaagtgtgtg	atcctttttc	aggttgtagc	gaaagagctc	420
taacgatctt	ttgctcggtt	tcggagaaga	aagacattgt	tgacatttag	tatagtgaat	480
tggattactc	tggtcctttg	tggtctgtct	aaagctgtct	tcttaaagtc	catgatgcta	540
ttgtgggttc	tttagctact	gctgctgaga	acactaaagt	tgatagagat	gacttttaga	600
aatgtcgtct	tttagttccg	tctagtcagt	gttctattgt	catttggtaaa	tctgggtcga	660
ttattaagaa	cattagaggt	agaactagag	ctaacgttaa	ggttgtctct	aaagatgctt	720
ctgatccttc	tcacacttgt	gccatggatt	ttgacaacat	tggttatgata	tctgggtgaga	780
McTtgaatcc	gtgaagaagg	cactttttcg	tgttttcgca	atcatgtaca	aagtcaagtc	840
tcgagaacag	attcctctcg	atacaactgt	ccaagaagtt	cccgctagta	ttataattcc	900
gtctgatctg	tctatctatg	cacaagccgg	tttataccoc	agtcaggatt	ctattttcca	960
acatgggggc	aatgttttcat	cgttttatcg	tacactacct	cagggtcatg	gagaaaatgc	1020
tgcaaatcca	ctgcgggttt	tttctgtctc	tgctcttctc	gtggttcaatg	gtttttggtg	1080
gtcttcaga	tcagaaaaagt	tggtctataa	agttatttgc	gctttctcca	aaattggtcg	1140
tggtatcggg	aaaggaggat	taaccattaa	gggaataaga	caagcaagcg	ggctctcatat	1200
cgaaagttaat	gactcgagag	caaatcatga	tgatgactgt	gttatcactg	tcactgctac	1260
agagttctct	gatgatttga	agtcctatgc	gggttgaagct	gttcttctac	ttcaagagaa	1320
aattaatgat	gaagcagcgg	acaaagttaa	aatgcaactc	cttgatctct	ctaaggttaat	1380
agggatgcatt	atagggaataa	gtggctcaat	cataagtgaa	atcagcaaaa	ggacaagaagc	1440
tgatattctat	attctcgaaag	gaaataatac	gctcaagagc	tgatcccaat	gatgactctg	1500
ttcgagatgc	tggtgaagta	agcaatgtga	gagatgctct	tattcagata	gttctgagcg	1560
ttcgagatga	tggttttaag	gatagagaga	ctgggttccag	gaatcaacct	ctcgcaagat	1620
ctgagataaa	caattttctc	tttccaagta	tgatgaatac	tggtcttgca	cttctctcaat	1680
ctttctatgc	ttctgttccg	caagttgctt	ctgtagattt	cgataggaga	ccagaataacc	1740
ggagcagcat	gaagcatgct	ctctcgagt	gtggaatac	gttttatgga	agttttccgg	1800
tgggcaaatc	aagttatgga	tccaactctc	cttaactcat	caatctatat	ggaggattgc	1860
ctcagctctac	tactatggag	gttcgaatcc	cagcaaatgc	agtggttgtaa	gttatgggca	1920
gaggagagag	caactgtggc	aacataagaa	ggatatacag	agccatgata	gaaatttctc	1980
attccaaaagg	ttcccatggc	ggtgcgcttg	ctctcatctc	cgggacattc	gaacagaaGc	2040
gtaccgcaga	gaactgtgtc	caagctttta	tcatgtccac	ttgaataatt	tgctctgccc	2100
cttaatacct	ttccatggaa	gtgtgttcca	tcaatctacc	ttctcttgat	tttctttgat	2160
cggtgtttct	aggttttctc	ctctccatca	agctcatgtt	tagatatggt	tgcatctctc	2220
atcaaacatt	tcggtatctc	atctcgactc	agttactttt	ggttctctgt	gctagacatt	2280
tttagtgtct	tcaggaccat	tcttttcccc	tttctctgog	agctgttctg	actataacta	2340
cttatctccg	tcgagtaaaa	caaaatcggt	cttatatcaa	tcaaaacttg	cttattctSc	2400

(2) INFORMATION FOR SEQ ID NO:1864:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 214 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..214

(D) OTHER INFORMATION: / Ceres Seq. ID 1571229

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1864:

Met	Val	Glu	Arg	Gly	Lys	Arg	Thr	His	Asn	Arg	Phe	Arg	Asp	Asn	Asn
1				5				10					15		
Asn	Asp	Asn	Asn	Arg	Asn	Gln	Arg	Arg	Arg	Leu	Ser	Tyr	Glu	Ser	Glu
				20				25					30		
Glu	Lys	Lys	Ile	Asp	Asn	Lys	Asp	Asp	Leu	Val	Val	Val	Tyr	Arg	Ile
				35				40					45		
Leu	Cys	Pro	Ser	Gly	Val	Met	Gly	Ser	Val	Ile	Gly	Lys	Ser	Gly	Lys
				50				55					60		
Val	Ile	Asn	Leu	Ile	Arg	Gln	Glu	Thr	Arg	Ala	Arg	Ile	Lys	Val	Val
				65				70					75		
Asp	Pro	Phe	Pro	Gly	Cys	Ser	Glu	Arg	Val	Ile	Thr	Ile	Phe	Cys	Ser
				85				90					95		

Val Ser Glu Lys Lys Asp Ile Val Asp Ile Glu Tyr Ser Glu Leu Asp
100 105 110
Tyr Ser Val Pro Leu Cys Ser Ala Gln Ala Ala Leu Lys Val His
115 120 125
Asp Ala Ile Val Ala Ser Leu Ala Thr Ala Ala Glu Asn Thr Lys Ile
130 135 140
Asp Arg Asp Asp Phe Arg Glu Cys Arg Leu Leu Val Pro Ser Ser Gln
145 150 155 160
Cys Ser Ile Val Ile Gly Lys Ser Gly Ser Ile Ile Lys Asn Ile Arg
165 170 175
Gly Arg Thr Arg Ala Asn Val Lys Val Val Ser Lys Asp Ala Ser Asp
180 185 190
Pro Ser His Thr Cys Ala Met Asp Phe Asp Asn Ile Val Met Ile Ser
195 200 205
Gly Glu Xaa Leu Asn Pro
210

(2) INFORMATION FOR SEQ ID NO:1865:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 160 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..160

(D) OTHER INFORMATION: / Ceres Seq. ID 1571230

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1865:

Met Gly Ser Val Ile Gly Lys Ser Gly Lys Val Ile Asn Leu Ile Arg
1 5 10 15
Gln Glu Thr Arg Ala Arg Ile Lys Val Val Asp Pro Phe Pro Gly Cys
20 25 30
Ser Glu Arg Val Ile Thr Ile Phe Cys Ser Val Ser Glu Lys Lys Asp
35 40 45
Ile Val Asp Ile Glu Tyr Ser Glu Leu Asp Tyr Ser Val Pro Leu Cys
50 55 60
Ser Ala Gln Ala Ala Leu Leu Lys Val His Asp Ala Ile Val Ala Ser
65 70 75 80
Leu Ala Thr Ala Ala Glu Asn Thr Lys Ile Asp Arg Asp Asp Phe Arg
85 90 95
Glu Cys Arg Leu Leu Val Pro Ser Ser Gln Cys Ser Ile Val Ile Gly
100 105 110
Lys Ser Gly Ser Ile Ile Lys Asn Ile Arg Gly Arg Thr Arg Ala Asn
115 120 125
Val Lys Val Val Ser Lys Asp Ala Ser Asp Pro Ser His Thr Cys Ala
130 135 140
Met Asp Phe Asp Asn Ile Val Met Ile Ser Gly Glu Xaa Leu Asn Pro
145 150 155 160

(2) INFORMATION FOR SEQ ID NO:1866:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 219 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..219

(D) OTHER INFORMATION: / Ceres Seq. ID 1571231

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1866:

Met	Tyr	Lys	Val	Ser	Pro	Arg	Glu	Gln	Ile	Pro	Leu	Asp	Thr	Thr	Val
1			5					10						15	
Gln	Glu	Val	Pro	Ala	Ser	Ile	Ile	Ile	Pro	Ser	Asp	Leu	Ser	Ile	Tyr
			20				25						30		
Pro	Gln	Ala	Gly	Leu	Tyr	Pro	Ser	Gln	Asp	Ser	Ile	Phe	Gln	His	Gly
			35				40					45			
Ala	Asn	Val	Ser	Ser	Phe	Ile	Gly	Thr	Leu	Pro	Gln	Gly	Tyr	Gly	Glu
			50				55				60				
Asn	Ala	Ala	Asn	Pro	Leu	Pro	Val	Phe	Ser	Ala	Ser	Ala	Leu	Pro	Val
				70					75				80		
Val	His	Gly	Phe	Gly	Gly	Ser	Ser	Arg	Ser	Glu	Lys	Leu	Ala	Ile	Lys
				85					90				95		
Val	Ile	Cys	Ala	Ser	Ser	Lys	Ile	Gly	Arg	Val	Ile	Gly	Lys	Gly	Gly
			100				105					110			
Leu	Thr	Ile	Lys	Gly	Ile	Arg	Gln	Ala	Ser	Gly	Ser	His	Ile	Glu	Val
			115				120					125			
Asn	Asp	Ser	Arg	Thr	Asn	His	Asp	Asp	Asp	Cys	Val	Ile	Thr	Val	Thr
			130				135				140				
Ala	Thr	Glu	Ser	Pro	Asp	Asp	Leu	Lys	Ser	Met	Ala	Val	Glu	Ala	Val
				150					155					160	
Leu	Leu	Leu	Gln	Glu	Lys	Ile	Asn	Asp	Glu	Asp	Glu	Asp	Lys	Val	Lys
				165					170				175		
Met	Gln	Leu	Leu	Val	Ser	Ser	Lys	Val	Ile	Gly	Cys	Ile	Ile	Gly	Lys
				180				185					190		
Ser	Gly	Ser	Ile	Ile	Ser	Glu	Ile	Arg	Lys	Arg	Thr	Lys	Ala	Asp	Ile
				195				200				205			
His	Ile	Ser	Lys	Gly	Asn	Asn	Thr	Pro	Lys	Ser					
			210				215								

(2) INFORMATION FOR SEQ ID NO:1867:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 731 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..731
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571235

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1867:

aaaaacacaa	actctctata	ctcacaaat	tgtttaactc	atctttctaa	gttggtttcg	60
attcaagaat	atcacaaagt	ctaagtgttc	ccttctatt	ctcgtctctc	cggtttgtt	120
ccttgtcttt	atttcatcgt	ccctcttggt	ccctacacct	agttttgtgt	ctagagtta	180
ctattctctg	gtgcaagaag	aggtcaaaaa	ggttcacaga	tacacagaac	ctgaggagcc	240
ggaagttcca	gaagagccgg	agctgccttc	accgaggagg	ctcgagattc	cagaagagcc	300
tgaattccca	gaagagcctg	aggttctctg	agaacccgaa	gttcctgaag	agcccgaaga	360
accagaagag	ccagcagggt	caacatttga	atttccatca	tggtttcoga	gctttcccat	420
tcccgggtgt	aatggcgggt	tgccaaagac	tgaaaagaca	aaacctacat	caacagttga	480
agaggttaac	gtttctaaca	agaagccata	gatcaatggg	taagaacgtg	caaatgatta	540
tataaaactat	atatgcaatt	atagtttttg	ttgtttttg	gttaaatgat	agagattaca	600
tatgtattac	agttattagag	tcttcacatt	gtcatgattg	agttctctaa	cgctcctgat	660
ataactctgt	actaattctc	tcttgtaaca	tgtatatctc	ttgtggtaca	aaaaatatat	720
ataataactct	t					

(2) INFORMATION FOR SEQ ID NO:1868:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 144 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..144
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571236

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1868:

Met	Thr	Asn	Val	Arg	Leu	Pro	Ile	Leu	Val	Ser	Ser	Val	Leu	Phe	Leu
1				5					10				15		
Val	Phe	Ile	Ser	Ser	Ser	Leu	Leu	Phe	Pro	Thr	Pro	Ser	Phe	Ala	Ala
			20					25					30		
Arg	Val	Ser	His	Ser	Ser	Leu	Val	Gln	Glu	Glu	Val	Lys	Lys	Val	Pro
			35					40				45			
Tyr	Thr	Glu	Pro	Glu	Glu	Pro	Pro	Glu	Val	Pro	Glu	Glu	Pro	Glu	Leu
			50			55					60				
Ser	Pro	Glu	Glu	Pro	Glu	Ile	Pro	Glu	Glu	Pro	Glu	Ile	Pro	Glu	Glu
			65			70				75				80	
Pro	Glu	Val	Pro	Gly	Glu	Pro	Glu	Val	Pro	Glu	Glu	Pro	Glu	Glu	Pro
			85					90						95	
Glu	Glu	Pro	Ala	Gly	Ser	Thr	Phe	Glu	Phe	Pro	Ser	Trp	Phe	Pro	Ser
			100					105					110		
Phe	Pro	Ile	Pro	Gly	Val	Asn	Gly	Gly	Leu	Pro	Lys	Thr	Glu	Lys	Thr
			115				120					125			
Lys	Pro	Thr	Ser	Thr	Val	Glu	Glu	Val	Asn	Val	Ser	Asn	Lys	Lys	Pro
			130			135					140				

(2) INFORMATION FOR SEQ ID NO:1869:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 941 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..941
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571241

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1869:

atagaatata	aaagtttgcta	aatttgatta	aagatatgga	caaagttcca	agattttttg	60
tttgtaaact	ttaaaatggt	ttatgttatt	acttggtttt	ggtttttgta	ggagttctcg	120
gtgatggatt	tatggctcgt	gatttaacta	tagagaacac	ggcaggagca	gatgcgcacc	180
aagcggttgc	gttttagatca	gacagtgatt	tttcggtact	tgaaaactgc	gagtttcttg	240
ggaaccaaga	cactctttat	gctcactctc	tcctgcagtt	ctacaaacaa	tgtcgaaatcc	300
aaggcaacct	agacttcact	tttggttaact	cagctgcctg	attccaaagt	tgtgatatcc	360
taatcgctgc	aaaacactcc	aaactcgagc	aaggcggctgc	aaacaaacgc	atcacagcac	420
acgggaggat	tgatcgctcg	cagtcocagg	gattttgtgt	tttgaactgt	tcgatttaacg	480
gaacagaggga	atacatgaag	gagtttcaag	ctaaccctga	aaggcataag	aactctcttg	540
gaagaccgtg	gaaggagttt	tcgaggacgg	ttttttgtaa	ctgtaactct	gagttcttga	600
ttagtctctga	tggatggatg	ccttggaaag	gggatttcgc	attgaagact	ttgtattacg	660
gtgatataaa	gaatacgggt	ccgggatcgg	ttagatcgag	tagggttcca	tggagtagtg	720
agataccaga	gaagcatggt	gatgtttact	ctgttgccaa	ttttattcag	gctgatgagt	780
gggtctccac	gactgcttga	ttttttTtaa	aggaaacatg	aggtttttag	attttgaaaa	840
gaagagaaga	gaagtctgtca	ttgttaacttt	attgtagtgt	caaatattag	tgtggtttct	900
ttatcgctca	ttgggggattc	ataatagatt	aataattgaa	g		

(2) INFORMATION FOR SEQ ID NO:1870:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 222 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..222
(D) OTHER INFORMATION: / Ceres Seq. ID 1571242

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1870:

```
Met Ala Arg Asp Leu Thr Ile Glu Asn Thr Ala Gly Ala Asp Ala His
1      5      10      15
Gln Ala Val Ala Phe Arg Ser Asp Ser Asp Phe Ser Val Leu Glu Asn
20     25     30
Cys Glu Phe Leu Gly Asn Gln Asp Thr Leu Tyr Ala His Ser Leu Arg
35     40     45
Gln Phe Tyr Lys Gln Cys Arg Ile Gln Gly Asn Val Asp Phe Ile Phe
50     55     60
Gly Asn Ser Ala Ala Val Phe Gln Asp Cys Asp Ile Leu Ile Ala Ser
65     70     75     80
Lys His Ser Lys Leu Glu Gln Gly Gly Ala Asn Asn Ala Ile Thr Ala
85     90     95
His Gly Arg Ile Asp Ala Ser Gln Ser Thr Gly Phe Val Phe Leu Asn
100    105    110
Cys Ser Ile Asn Gly Thr Glu Glu Tyr Met Lys Glu Phe Gln Ala Asn
115    120    125
Pro Glu Arg His Lys Asn Phe Leu Gly Arg Pro Trp Lys Glu Phe Ser
130    135    140
Arg Thr Val Phe Val Asn Cys Asn Leu Glu Ser Leu Ile Ser Pro Asp
145    150    155    160
Gly Trp Met Pro Trp Asn Gly Asp Phe Ala Leu Lys Thr Leu Tyr Tyr
165    170    175
Gly Glu Tyr Lys Asn Thr Gly Pro Gly Ser Val Arg Ser Ser Arg Val
180    185    190
Pro Trp Ser Ser Glu Ile Pro Glu Lys His Val Asp Val Tyr Ser Val
195    200    205
Ala Asn Phe Ile Gln Ala Asp Glu Trp Ala Ser Thr Thr Ala
210    215    220
```

(2) INFORMATION FOR SEQ ID NO:1871:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 543 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..543
(D) OTHER INFORMATION: / Ceres Seq. ID 1571243

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1871:

```
ctcagaacat ctcaaatctca attgaaatct taaaatccaa aattttcccg agaaaaatta 60
aagtttccgt agaaaatgtc aggtcgtggg aaggaggcca aaggattggg caaaggagga 120
gctaaacgtc acaggaagggt tctgagagac aacatccaag gaatcactaa gccgcgcgatt 180
cggagattgg ctgctagagg tggagtcaag cgtattagtg gtttdRatct acgaggagac 240
acgtggcggt ctcaagatct ttttgagaa tggtatccgt gacgccgtta cttacactga 300
gcaagctcgg aggaagaagg tgactgctat ggatgttgtt tatgctotta agagacaagg 360
aagaactctc tacggattcg gcggctaggg tttttgattg ttgttttttg tgttttctacg 420
ttttatagga ttgtaatttt cagaatttgg tgttaacttc gaaaaaatta aagaattgaa 480
ggttgttgtt gcaatttcgt gattgttgaa ggtgttgttg caaacttyya gtaatttcag 540
ttt
```

(2) INFORMATION FOR SEQ ID NO:1872:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..68

(D) OTHER INFORMATION: / Ceres Seq. ID 1571244

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1872:

Met Ser Gly Arg Gly Lys Gly Gly Lys Gly Leu Gly Lys Gly Gly Ala
1 5 10 15
Lys Arg His Arg Lys Val Leu Arg Asp Asn Ile Gln Gly Ile Thr Lys
20 25 30
Pro Ala Ile Arg Arg Leu Ala Arg Arg Gly Gly Val Lys Arg Ile Ser
35 40 45
Gly Xaa Xaa Leu Arg Gly Asp Thr Trp Arg Ser Gln Asp Leu Phe Gly
50 55 60
Glu Cys Tyr Pro
65

(2) INFORMATION FOR SEQ ID NO:1873:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2135 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..2135

(D) OTHER INFORMATION: / Ceres Seq. ID 1571245

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1873:

atcacctctc	tcttctctcg	aaatcacccat	gagtatggaa	gcaacggagc	tacaagatct	60
ctctgacgac	gcgcattacg	ccgcttctca	acaacaagga	tcggctagta	tgatgcgtaS	120
cgatagcgga	aagagaagtt	tacaaaagtga	acacgaagac	gctgtattga	tttatttgaa	180
agataacgtt	gcaattcatc	ctacacagtt	cgcatctgag	aggattagtg	gtagattgaa	240
gttgactaag	caagattctg	tctctttct	gtcgtggatt	ccgtacaagg	gacaaacatc	300
aaatgcaaa	ctatcagaga	aagacaggag	tctttatacc	atcacccggc	ttccgtttac	360
tgaagtga	tcattagga	gacacactcc	tgctctcgga	tgccagtagt	taattgttgt	420
ccgtgtctct	ggacttgcat	ttccacctct	gtacttctac	aatggaggag	tcaggaggatt	480
tctggccatg	gtgaagcagc	atgtttttct	tgcaaggtcg	tcagaagatc	aaaatgtgtt	540
catttgtaat	gatttttcaga	gtcccttgca	gagaactttg	tcttcattgg	agtgccaa	600
ttcaactgct	gtagcaagtg	gacaatccgt	atacccatga	gacggagggt	ctcttagtga	660
aaatcaaa	agaaacagtt	cagatgttgg	taataagata	tctagtgttt	ccagctctgg	720
cttcagaaa	caaaagagtc	atgatccaac	tcgggatctt	tcaatccatc	tactagagaa	780
gtttctctg	gtttaccaat	ttgctcgaga	tacaactact	cagctgtttt	cggaacaa	840
tggtcttggt	tcatttgaca	agagatggaa	taacaaaccc	gtacatagtt	atcctgaaaa	900
gttgctgaac	atcgttgagg	aaaaagcatca	tgaactccgt	catagttatt	ctgaaaatga	960
ccctctcaag	gatgacgaaa	tttcttatat	tgatgtccct	gctgatccct	tagagtttga	1020
taaatataag	ttgatgtggg	gaaaaccaa	gcaaccacca	atggggcgata	aagagtctaac	1080
agcattgttg	gattctgaag	ggcaggttgt	ggaatcaaaa	gctcttcagg	agagagtgtt	1140
ctatggaggc	attgagcacc	agttgcgtag	agaggatagg	cccttctctc	tgggatatta	1200
tgcatatgat	tcgacatatg	cagagagaga	atatcttcga	tctgtcaaac	ggatggaaata	1260
tgcaacattg	aaacagcaat	ggcagagcat	ttcccttgaa	caagcaaaaa	gggttcacaaa	1320
atatacggag	agaaaaggat	tgatagataa	agatgtggta	agaactgata	gggcatttga	1380
atactatgaa	ggggatgaca	atctacatgt	caatagcatg	cgatgatatt	tggtgaccta	1440
ctctctctac	aaattttgac	tggtgttactg	ccagggaatg	agtgattatc	tgctctcatat	1500
cttgtctcgt	atggaggatg	aatcagaatc	tttttggtgW	ttcRtgccac	tgatggaaacg	1560
acttgaccac	aaactttaac	gtgaccagaa	tggaatgcac	actcagctct	ctgcactctc	1620
aaagctggta	gagttgctcg	atagcccgtc	acataaattac	tttaaggaga	atgactgctt	1680
gaattacttc	ttctgttttc	gctggtattct	gattcagttt	aaaagggaat	ttgagtatga	1740
gaagacaatg	cagctgtggg	aggtgatgtg	gacccactac	ctctcagaac	attttcacct	1800
atatgtttgt	gtggcggctc	tgaagcgatg	ccgcagcaag	ataatgggag	aacagatgga	1860
ttttgatact	ctcttaaatg	tctcaatgta	gtctctggg	catattgata	tcgattcaac	1920
agtcagagat	ccgcagaacac	tttccataga	agctggtgaa	aatggtgctg	ctagcattcc	1980
tccaggaaac	ctcctctctc	tacccttga	tgacggtacc	ttatatctc	aggaagatga	2040

tgttttgtaa gtaatacgac ttttcttttt tcttctggac atgttaccaa aatttggatt 2100
gcttttacta gaaatcccat acaatgatta agggc

(2) INFORMATION FOR SEQ ID NO:1874:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 682 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..682
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571246

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1874:

Ser	Pro	Leu	Ser	Ser	Pro	Glu	Ile	Thr	Met	Ser	Met	Glu	Ala	Thr	Glu
1			5						10					15	
Leu	Gln	Asp	Leu	Ser	Asp	Asp	Ala	Asp	Tyr	Ala	Ala	Ser	Gln	Gln	Gln
			20					25					30		
Gly	Ser	Ala	Ser	Met	Met	Arg	Xaa	Asp	Ser	Gly	Lys	Arg	Ser	Leu	Gln
			35				40					45			
Ser	Glu	His	Glu	Asp	Ala	Val	Leu	Ile	Tyr	Leu	Lys	Asp	Asn	Val	Ala
			50			55					60				
Ile	His	Pro	Thr	Gln	Phe	Ala	Ser	Glu	Arg	Ile	Ser	Gly	Arg	Leu	Lys
65				70						75				80	
Leu	Thr	Lys	Gln	Asp	Ser	Val	Leu	Phe	Leu	Ser	Trp	Ile	Pro	Tyr	Lys
			85					90						95	
Gly	Gln	Thr	Ser	Asn	Ala	Lys	Leu	Ser	Glu	Lys	Asp	Arg	Ser	Leu	Tyr
			100					105						110	
Thr	Ile	Thr	Ala	Val	Pro	Phe	Thr	Glu	Val	Arg	Ser	Ile	Arg	Arg	His
			115				120					125			
Thr	Pro	Ala	Leu	Gly	Trp	Gln	Tyr	Val	Ile	Val	Val	Leu	Ser	Ser	Gly
			130			135					140				
Leu	Ala	Phe	Pro	Pro	Leu	Tyr	Phe	Tyr	Asn	Gly	Gly	Val	Arg	Glu	Phe
145				150					155					160	
Leu	Ala	Met	Val	Lys	Gln	His	Val	Phe	Leu	Ala	Arg	Ser	Ser	Glu	Asp
			165						170					175	
Gln	Asn	Val	Phe	Ile	Val	Asn	Asp	Phe	Gln	Ser	Pro	Leu	Gln	Arg	Thr
			180				185						190		
Leu	Ser	Ser	Leu	Glu	Leu	Pro	Ser	Ser	Leu	Pro	Val	Ala	Ser	Gly	Gln
			195			200					205				
Ser	Val	Tyr	Pro	Leu	Asp	Gly	Gly	Ser	Ser	Ser	Glu	Asn	Gln	Arg	Arg
			210			215					220				
Thr	Ser	Ser	Asp	Val	Gly	Asn	Arg	Val	Ser	Ser	Val	Ser	Gln	Ser	Gly
225				230						235				240	
Phe	Arg	Lys	Gln	Lys	Ser	His	Asp	Pro	Thr	Arg	Asp	Leu	Ser	Ile	His
			245						250					255	
Leu	Leu	Glu	Lys	Phe	Ser	Leu	Val	Thr	Lys	Phe	Ala	Arg	Asp	Thr	Thr
			260				265						270		
Thr	Gln	Leu	Phe	Ser	Glu	Asn	Asn	Gly	Phe	Gly	Ser	Ile	Asp	Lys	Arg
			275				280					285			
Trp	Asn	Asn	Gln	Pro	Val	His	Ser	Tyr	Pro	Glu	Lys	Leu	Ser	Asn	Ile
			290			295					300				
Ala	Glu	Glu	Lys	His	His	Glu	Ile	Arg	His	Ser	Tyr	Ser	Glu	Asn	Asp
305				310						315				320	
Leu	Leu	Lys	Asp	Asp	Glu	Ile	Ser	Tyr	Ile	Asp	Val	Pro	Ala	Asp	Pro
			325						330					335	
Leu	Glu	Phe	Asp	Lys	Leu	Ser	Leu	Met	Trp	Gly	Lys	Pro	Arg	Gln	Pro
			340				345					350			
Pro	Met	Gly	His	Lys	Glu	Phe	Thr	Ala	Leu	Leu	Asp	Ser	Glu	Gly	Arg
			355			360					365				
Val	Val	Glu	Ser	Lys	Ala	Leu	Arg	Glu	Arg	Val	Phe	Tyr	Gly	Gly	Ile

Met	Ser	Met	Glu	Ala	Thr	Glu	Leu	Gln	Asp	Leu	Ser	Asp	Asp	Ala	Asp
1			5					10						15	
Tyr	Ala	Ala	Ser	Gln	Gln	Gln	Gly	Ser	Ala	Ser	Met	Met	Arg	Xaa	Asp
			20					25					30		
Ser	Gly	Lys	Arg	Ser	Leu	Gln	Ser	Glu	His	Glu	Asp	Ala	Val	Leu	Ile
		35					40					45			
Tyr	Leu	Lys	Asp	Asn	Val	Ala	Ile	His	Pro	Thr	Gln	Phe	Ala	Ser	Glu
	50					55					60				
Arg	Ile	Ser	Gly	Arg	Leu	Lys	Leu	Thr	Lys	Gln	Asp	Ser	Val	Leu	Phe
65				70						75				80	

Leu Ser Trp Ile Pro Tyr Lys Gly Gln Thr Ser Asn Ala Lys Leu Ser
85 90 95
Glu Lys Asp Arg Ser Leu Tyr Thr Ile Thr Ala Val Pro Phe Thr Glu
100 105 110
Val Arg Ser Ile Arg Arg His Thr Pro Ala Leu Gly Trp Gln Tyr Val
115 120 125
Ile Val Val Leu Ser Ser Gly Leu Ala Phe Pro Pro Leu Tyr Phe Tyr
130 135 140
Asn Gly Gly Val Arg Glu Phe Leu Ala Met Val Lys Gln His Val Phe
145 150 155 160
Leu Ala Arg Ser Ser Glu Asp Gln Asn Val Phe Ile Val Asn Asp Phe
165 170 175
Gln Ser Pro Leu Gln Arg Thr Leu Ser Ser Leu Glu Leu Pro Ser Ser
180 185 190
Leu Pro Val Ala Ser Gly Gln Ser Val Tyr Pro Leu Asp Gly Gly Ser
195 200 205
Ser Ser Glu Asn Gln Arg Arg Thr Ser Ser Asp Val Gly Asn Arg Val
210 215 220
Ser Ser Val Ser Gln Ser Gly Phe Arg Lys Gln Lys Ser His Asp Pro
225 230 235 240
Thr Arg Asp Leu Ser Ile His Leu Leu Glu Lys Phe Ser Leu Val Thr
245 250 255
Lys Phe Ala Arg Asp Thr Thr Thr Gln Leu Phe Ser Glu Asn Asn Gly
260 265 270
Phe Gly Ser Ile Asp Lys Arg Trp Asn Asn Gln Pro Val His Ser Tyr
275 280 285
Pro Glu Lys Leu Ser Asn Ile Ala Glu Glu Lys His His Glu Ile Arg
290 295 300
His Ser Tyr Ser Glu Asn Asp Leu Leu Lys Asp Asp Glu Ile Ser Tyr
305 310 315 320
Ile Asp Val Pro Ala Asp Pro Leu Glu Phe Asp Lys Leu Ser Leu Met
325 330 335
Trp Gly Lys Pro Arg Gln Pro Pro Met Gly His Lys Glu Phe Thr Ala
340 345 350
Leu Leu Asp Ser Glu Gly Arg Val Val Glu Ser Lys Ala Leu Arg Glu
355 360 365
Arg Val Phe Tyr Gly Gly Ile Glu His Gln Leu Arg Arg Glu Val Trp
370 375 380
Pro Phe Leu Leu Gly Tyr Tyr Ala Tyr Asp Ser Thr Tyr Ala Glu Arg
385 390 395 400
Glu Tyr Leu Arg Ser Val Lys Arg Met Glu Tyr Tyr Ala Thr Leu Lys Gln
405 410 415
Gln Trp Gln Ser Ile Ser Pro Glu Gln Ala Lys Arg Phe Thr Lys Tyr
420 425 430
Arg Glu Arg Lys Gly Leu Ile Asp Lys Asp Val Val Arg Thr Asp Arg
435 440 445
Ala Phe Glu Tyr Tyr Glu Gly Asp Asp Asn Leu His Val Asn Ser Met
450 455 460
Arg Asp Ile Leu Leu Thr Tyr Ser Phe Tyr Asn Phe Asp Leu Gly Tyr
465 470 475 480
Cys Gln Gly Met Ser Asp Tyr Leu Ser Pro Ile Leu Phe Val Met Glu
485 490 495
Asp Glu Ser Glu Ser Phe Trp Xaa Phe Xaa Ala Leu Met Glu Arg Leu
500 505 510
Gly Pro Asn Phe Asn Arg Asp Gln Asn Gly Met His Thr Gln Leu Phe
515 520 525
Ala Leu Ser Lys Leu Val Glu Leu Leu Asp Ser Pro Leu His Asn Tyr
530 535 540
Phe Lys Glu Asn Asp Cys Leu Asn Tyr Phe Phe Cys Phe Arg Trp Ile
545 550 555 560
Leu Ile Gln Phe Lys Arg Glu Phe Glu Tyr Glu Lys Thr Met Gln Leu

										565											570											575		
Trp	Glu	Val	Met	Trp	Thr	His	Tyr	Leu	Ser	Glu	His	Phe	His	Leu	Tyr																			
										580											585											590		
Val	Cys	Val	Ala	Val	Leu	Lys	Arg	Cys	Arg	Ser	Lys	Ile	Met	Gly	Glu																			
										595											600											605		
Gln	Met	Asp	Phe	Asp	Thr	Leu	Leu	Lys	Phe	Ile	Asn	Glu	Leu	Ser	Gly																			
										610											615											620		
His	Ile	Asp	Leu	Asp	Ser	Thr	Val	Arg	Asp	Ala	Glu	Ala	Leu	Cys	Ile																			
										625											630											635		
Glu	Ala	Gly	Glu	Asn	Gly	Ala	Ala	Ser	Ile	Pro	Pro	Gly	Thr	Pro	Pro																			
										645											650											655		
Ser	Leu	Pro	Leu	Asp	Asp	Gly	Thr	Leu	Tyr	Pro	Gln	Glu	Asp	Val																				
										660											665											670		

Leu

(2) INFORMATION FOR SEQ ID NO:1876:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 671 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..671

(D) OTHER INFORMATION: / Ceres Seq. ID 1571248

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1876:

Met	Glu	Ala	Thr	Glu	Leu	Gln	Asp	Leu	Ser	Asp	Asp	Ala	Asp	Tyr	Ala																			
1																																		
										5											10											15		
Ala	Ser	Gln	Gln	Gln	Gly	Ser	Ala	Ser	Met	Met	Arg	Xaa	Asp	Ser	Gly																			
										20											25											30		
Lys	Arg	Ser	Leu	Gln	Ser	Glu	His	Glu	Asp	Ala	Val	Leu	Ile	Tyr	Leu																			
										35											40											45		
Lys	Asp	Asn	Val	Ala	Ile	His	Pro	Thr	Gln	Phe	Ala	Ser	Glu	Arg	Ile																			
										50											55											60		
Ser	Gly	Arg	Leu	Lys	Leu	Thr	Lys	Gln	Asp	Ser	Val	Leu	Phe	Leu	Ser																			
										65											70											75		
Trp	Ile	Pro	Tyr	Lys	Gly	Gln	Thr	Ser	Asn	Ala	Lys	Leu	Ser	Glu	Lys																			
										85											90											95		
Asp	Arg	Ser	Leu	Tyr	Thr	Ile	Thr	Ala	Val	Pro	Phe	Thr	Glu	Val	Arg																			
										100											105											110		
Ser	Ile	Arg	Arg	His	Thr	Pro	Ala	Leu	Gly	Trp	Gln	Tyr	Val	Ile	Val																			
										115											120											125		
Val	Leu	Ser	Ser	Gly	Leu	Ala	Phe	Pro	Pro	Leu	Tyr	Phe	Tyr	Asn	Gly																			
										130											135											140		
Gly	Val	Arg	Glu	Phe	Leu	Ala	Met	Val	Lys	Gln	His	Val	Phe	Leu	Ala																			
										145											150											155		
Arg	Ser	Ser	Glu	Asp	Gln	Asn	Val	Phe	Ile	Val	Asn	Asp	Phe	Gln	Ser																			
										165											170											175		
Pro	Leu	Gln	Arg	Thr	Leu	Ser	Ser	Leu	Glu	Leu	Pro	Ser	Ser	Leu	Pro																			
										180											185											190		
Val	Ala	Ser	Gly	Gln	Ser	Val	Tyr	Pro	Leu	Asp	Gly	Gly	Ser	Ser	Ser																			
										195											200											205		
Glu	Asn	Gln	Arg	Arg	Thr	Ser	Ser	Asp	Val	Gly	Asn	Arg	Val	Ser	Ser																			
										210											215											220		
Val	Ser	Gln	Ser	Gly	Phe	Arg	Lys	Gln	Lys	Ser	His	Asp	Pro	Thr	Arg																			
										225											230											235		
Asp	Leu	Ser	Ile	His	Leu	Leu	Glu	Lys	Phe	Ser	Leu	Val	Thr	Lys	Phe																			
										245											250											255		
Ala	Arg	Asp	Thr	Thr	Gln	Leu	Phe	Ser	Glu	Asn	Asn	Gly	Phe	Gly																				
										260											265											270		

Ser Ile Asp Lys Arg Trp Asn Asn Gln Pro Val His Ser Tyr Pro Glu
275 280 285
Lys Leu Ser Asn Ile Ala Glu Glu Lys His His Glu Ile Arg His Ser
290 295 300
Tyr Ser Glu Asn Asp Leu Leu Lys Asp Asp Glu Ile Ser Tyr Ile Asp
305 310 315 320
Val Pro Ala Asp Pro Leu Glu Phe Asp Lys Leu Ser Leu Met Trp Gly
325 330 335
Lys Pro Arg Gln Pro Pro Met Gly His Lys Glu Phe Thr Ala Leu Leu
340 345 350
Asp Ser Glu Gly Arg Val Val Glu Ser Lys Ala Leu Arg Glu Arg Val
355 360 365
Phe Tyr Gly Gly Ile Glu His Gln Leu Arg Arg Glu Val Trp Pro Phe
370 375 380
Leu Leu Gly Tyr Tyr Ala Tyr Asp Ser Thr Tyr Ala Glu Arg Glu Tyr
385 390 395 400
Leu Arg Ser Val Lys Arg Met Glu Tyr Ala Thr Leu Lys Gln Gln Trp
405 410 415
Gln Ser Ile Ser Pro Glu Gln Ala Lys Arg Phe Thr Lys Tyr Arg Glu
420 425 430
Arg Lys Gly Leu Ile Asp Lys Asp Val Val Arg Thr Asp Arg Ala Phe
435 440 445
Glu Tyr Tyr Glu Gly Asp Asp Asn Leu His Val Asn Ser Met Arg Asp
450 455 460
Ile Leu Leu Thr Tyr Ser Phe Tyr Asn Phe Asp Leu Gly Tyr Cys Gln
465 470 475 480
Gly Met Ser Asp Tyr Leu Ser Pro Ile Leu Phe Val Met Glu Asp Glu
485 490 495
Ser Glu Ser Phe Trp Xaa Phe Xaa Ala Leu Met Glu Arg Leu Gly Pro
500 505 510
Asn Phe Asn Arg Asp Gln Asn Gln Met His Thr Gln Leu Phe Ala Leu
515 520 525
Ser Lys Leu Val Glu Leu Leu Asp Ser Pro Leu His Asn Tyr Phe Lys
530 535 540
Glu Asn Asp Cys Leu Asn Tyr Phe Phe Cys Phe Arg Trp Ile Leu Ile
545 550 555 560
Gln Phe Lys Arg Glu Phe Glu Tyr Glu Lys Thr Met Gln Leu Trp Glu
565 570 575
Val Met Trp Thr His Tyr Leu Ser Glu His Phe His Leu Tyr Val Cys
580 585 590
Val Ala Val Leu Lys Arg Cys Arg Ser Lys Ile Met Gly Glu Gln Met
595 600 605
Asp Phe Asp Thr Leu Leu Lys Phe Ile Asn Glu Leu Ser Gly His Ile
610 615 620
Asp Leu Asp Ser Thr Val Arg Asp Ala Glu Ala Leu Cys Ile Glu Ala
625 630 635 640
Gly Glu Asn Gly Ala Ala Ser Ile Pro Pro Gly Thr Pro Pro Ser Leu
645 650 655
Pro Leu Asp Asp Gly Thr Leu Tyr Pro Gln Glu Asp Asp Val Leu
660 665 670

(2) INFORMATION FOR SEQ ID NO:1877:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 726 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..726
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571257

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1877:

aagagatcac	ttctccgacg	cagaaatgac	gaagtTcagg	aagcttggtc	ggccggcggg	60
tcaccgtatg	ttccatgctta	ggactatggt	ttctcagttg	gtgaagcacg	agcgatttga	120
gaccactgtc	actaaggcta	aagagggttcg	tcgtcttgct	gataaatatg	ttcaactcgg	180
caaagagggg	tcactctctg	ctgcaaggcg	agcagctggt	tttgtgagag	gagatgatgt	240
ctttacaag	attttcacag	aactggcaca	tagatacaaa	gataagagctg	gtggatacac	300
aagatgctta	cgtactcgca	tacgagttgg	tgatgctgct	cctatggcct	atatcgagtt	360
tattgcacga	gagaaagcag	ttaggcaatc	aaaaccagca	acacotcaac	caccgcaacg	420
agtgccattg	gaccatggg	aaagatctctg	gctcaccagg	cagttcgCtc	cgccataagga	480
ggagaaaaatc	cctgattctg	agctgtaatg	tggcataagc	aatttccctc	tggtcaccaa	540
atatcttgct	tctgtctcaa	aaatgtattt	tcgtgatcat	ttatcatatg	ccacaatatg	600
ttttcacaga	aggaacacaa	taagttagct	ttttcatttg	tttgaacatt	gaaagtgtac	660
tcttgaaaac	attaacagcg	ttagagagac	tctttctttg	cctatctacc	tatgaactaa	720

actggt

(2) INFORMATION FOR SEQ ID NO:1878:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 168 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..168
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571258

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1878:

Arg	Asp	His	Phe	Ser	Asp	Ala	Glu	Met	Thr	Lys	Phe	Arg	Lys	Leu	Gly
1			5						10					15	
Arg	Pro	Ala	Gly	His	Arg	Met	Ser	Met	Leu	Arg	Thr	Met	Val	Ser	Gln
			20					25					30		
Leu	Val	Lys	His	Glu	Arg	Ile	Glu	Thr	Thr	Val	Thr	Lys	Ala	Lys	Glu
			35				40					45			
Val	Arg	Arg	Leu	Ala	Asp	Asn	Met	Ile	Gln	Leu	Gly	Lys	Glu	Gly	Ser
			50				55					60			
Leu	Ser	Ala	Ala	Arg	Arg	Ala	Ala	Gly	Phe	Val	Arg	Gly	Asp	Asp	Val
			65			70			75				80		
Leu	His	Lys	Ile	Phe	Thr	Glu	Leu	Ala	His	Arg	Tyr	Lys	Asp	Arg	Ala
			85						90				95		
Gly	Gly	Tyr	Thr	Arg	Leu	Leu	Arg	Thr	Arg	Ile	Arg	Val	Gly	Asp	Ala
			100				105						110		
Ala	Pro	Met	Ala	Tyr	Ile	Glu	Phe	Ile	Asp	Arg	Glu	Asn	Glu	Leu	Arg
			115				120					125			
Gln	Ser	Lys	Pro	Ala	Thr	Pro	Gln	Pro	Pro	Gln	Arg	Val	Pro	Leu	Asp
			130				135					140			
Pro	Trp	Glu	Arg	Ser	Arg	Leu	Thr	Arg	Gln	Phe	Ala	Pro	Pro	Lys	Glu
			145			150			155					160	
Glu	Lys	Ile	Pro	Asp	Ser	Glu	Leu								
			165												

(2) INFORMATION FOR SEQ ID NO:1879:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 160 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..160
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571259

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1879:

Met Thr Lys Phe Arg Lys Leu Gly Arg Pro Ala Gly His Arg Met Ser

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 576 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: DNA (genomic)
 (ix) FEATURE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1881:

(2) INFORMATION FOR SEQ ID NO:1882:

(A) LENGTH: 115 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

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(ix) FEATURE:
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(D) OTHER INFORMATION: / Ceres Seq. ID 1571262

[illegible]

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 112 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

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(ix) FEATURE:
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(A) NAME/KEY: peptide

(B) LOCATION: 1..112

(D) OTHER INFORMATION: / Ceres Seq. ID 1571264

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1883:

Met	Pro	Tyr	Ser	Gln	Pro	Met	Ser	Ala	Gly	Gln	Leu	Ala	Thr	Ser	Leu
1			5						10					15	
Ala	Asn	Ala	Thr	Pro	Ala	Gln	Gln	Arg	Thr	Leu	Leu	Gly	Glu	Ser	Leu
			20					25					30		
Tyr	Pro	Leu	Val	Asp	Gln	Ile	Glu	Ser	Glu	His	Ala	Ala	Lys	Val	Thr
		35					40					45			
Gly	Met	Leu	Leu	Glu	Met	Asp	Gln	Thr	Glu	Val	Leu	His	Leu	Leu	Glu

50	55	60
Ser Pro Glu Ala Leu Asn Ala Lys Val Ser Glu Ala Leu Asp Val Leu		
65	70	75
Arg Asn Val Asn Gln Pro Ser Ser Gln Gly Ser Glu Gly Asn Lys Ser		80
85	90	95
Gly Ser Pro Ser Asp Leu Leu Ala Ser Leu Ser Ile Asn Asp His Leu		
100	105	110

(2) INFORMATION FOR SEQ ID NO:1884:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 632 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..632
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571265

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1884:

attccccatc	gcacagacc	gcctaagaat	ccgagagaga	agaagagata	atgcagatct	60
togtcaaaac	cctcaccggc	aaaactataa	ccctagaggt	tgagagcagc	gacaccatcg	120
acaatgttaa	agccaaaatc	caggacaaat	agggcatacc	acctgatcaa	cagaggctga	180
tttttgctgg	taagcaattg	gaagatggcc	ggaccttagc	tgactacaac	atccagaaga	240
agtcactctc	tcactctgtc	ctcagggtca	gaggtggaac	catgatcaag	gtgaagacac	300
tcactgtaaa	agaaatcgag	attgatctcg	aaccaaccca	cactattgat	cggatcaaa	360
aacgtgttga	agagaaagaa	ggcatccctc	ctgttcaaca	aaggctcctc	tatgccggaa	420
aacagcttgc	tgatgacaaa	acggccaaag	attatgcgat	agagggaggg	tctgttcttc	480
atttggttct	tgctcttagg	ggtggtcttc	tctgatctga	ataaataagc	ttttcaacaa	540
acatctttcc	cctcactatt	gtcctccttt	tgtggaAttc	atgacacaca	aaaattgcta	600
tgggaaaattg	gaatattatg	atgttttttc	tc			

(2) INFORMATION FOR SEQ ID NO:1885:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 77 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..77
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571266

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1885:

Met Ile Lys Val Lys Thr Leu Thr Gly Lys Glu Ile Glu Ile Asp Ile		
1	5	10
Glu Pro Thr Asp Thr Ile Asp Arg Ile Lys Glu Arg Val Glu Glu Lys		15
20	25	30
Glu Gly Ile Pro Pro Val Gln Gln Arg Leu Ile Tyr Ala Gly Lys Gln		
35	40	45
Leu Ala Asp Asp Lys Thr Ala Lys Asp Tyr Ala Ile Glu Gly Gly Ser		
50	55	60
Val Leu His Leu Val Leu Ala Leu Arg Gly Gly Leu Leu		
65	70	75

(2) INFORMATION FOR SEQ ID NO:1886:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1120 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1120

(D) OTHER INFORMATION: / Ceres Seq. ID 1571271

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1886:

aaaactcaag	gggttgattt	ttctttctca	actacggttaa	gattttctct	acacttttct	60
ttttcccggt	attctctttt	agtcctcgat	tctctacgcg	tttcagcgctc	agtccttcta	120
gatctctaaa	gccttcgtgc	tcgccaatat	aaatctctga	gatcggtccc	gtaaaaatcg	180
attcgcgctg	tttttgagta	aaaaaaatgg	cgcaacaatc	gttgatctac	agtttcgtcg	240
ctcggtgtac	cggtatcttc	gttgagttca	cagattttcaa	aggcaatttc	acatcaaatg	300
ctgctcagtg	ccttcagaag	cttccttctt	ctaacacaaa	gtttacctac	aactgcgcat	360
gtcacacgtt	caattacctc	gtcgaaaatg	gattcaccta	ttgtgttgtt	gcagttgatt	420
ctgctgggag	gcagattcct	atggctttct	tggaacgagt	taaggaggat	tcaacaaga	480
gatatggttg	tggaagggtc	gcaactgctc	aagcaaacag	cttgaataaa	gaatttgggt	540
cgaaactgaa	agagcatatg	cagtattgca	tgatcatccc	tgatgagatt	agcaagcttg	600
ctaagggttaa	agctcaagtg	tctgaagtta	aaggtgttat	gatggaaaaa	attgagaagg	660
ttcttgaccg	tggtgagaag	attgagcttt	tggttgacaa	aacagaaaaa	cttcgctcac	720
agggcgcaaga	ttttagaaca	caaggaaactc	aaatgagaag	aaagatgtgg	tttcagaaca	780
tgaagataaa	gctcattgtc	cttgcaatta	tcattgcctt	gattctcatc	atcatcctct	840
caatttgtgg	gggattcaac	tcgcgttaaat	aagtcgtgaa	catttcttcc	cgccggttat	900
gactgcgctc	tgtgcttccc	aagatctctg	agaatatctt	cattcagttc	gttgcgtcac	960
cttttttttt	ttWttgtttt	tgwgatttct	atattctcat	actatatgtt	tctctctaga	1020
ttgtactttt	tgaattttgt	ttgtatagg	ctatatatat	tatatatata	tgtatgcatt	1080
ttcgacaatc	tgcaattgtg	ctattgctgg	tactgacact			

(2) INFORMATION FOR SEQ ID NO:1887:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 221 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..221

(D) OTHER INFORMATION: / Ceres Seq. ID 1571272

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1887:

Met	Ala	Gln	Gln	Ser	Leu	Ile	Tyr	Ser	Phe	Val	Ala	Arg	Gly	Thr	Val
1				5					10					15	
Ile	Leu	Val	Glu	Phe	Thr	Asp	Phe	Lys	Gly	Asn	Phe	Thr	Ser	Ile	Ala
			20						25				30		
Ala	Gln	Cys	Leu	Gln	Lys	Leu	Pro	Ser	Ser	Asn	Asn	Lys	Phe	Thr	Tyr
			35				40					45			
Asn	Cys	Asp	Gly	His	Thr	Phe	Asn	Tyr	Leu	Val	Glu	Asn	Gly	Phe	Thr
			50				55					60			
Tyr	Cys	Val	Val	Ala	Val	Asp	Ser	Ala	Gly	Arg	Gln	Ile	Pro	Met	Ala
						70				75				80	
Phe	Leu	Glu	Arg	Val	Lys	Glu	Asp	Phe	Asn	Lys	Arg	Tyr	Gly	Gly	Gly
						85				90				95	
Lys	Ala	Ala	Thr	Ala	Gln	Ala	Asn	Ser	Leu	Asn	Lys	Glu	Phe	Gly	Ser
						100				105				110	
Lys	Leu	Lys	Glu	His	Met	Gln	Tyr	Cys	Met	Asp	His	Pro	Asp	Glu	Ile
						115				120				125	
Ser	Lys	Leu	Ala	Lys	Val	Lys	Ala	Gln	Val	Ser	Glu	Val	Lys	Gly	Val
						130				135				140	
Met	Met	Glu	Asn	Ile	Glu	Lys	Val	Leu	Asp	Gly	Glu	Lys	Ile	Glu	
						145				150				155	
Leu	Leu	Val	Asp	Lys	Thr	Glu	Asn	Leu	Arg	Ser	Gln	Ala	Gln	Asp	Phe
						165				170				175	
Arg	Thr	Gln	Gly	Thr	Gln	Met	Arg	Arg	Lys	Met	Trp	Phe	Gln	Asn	Met
						180				185				190	
Lys	Ile	Lys	Leu	Ile	Val	Leu	Ala	Ile	Ile	Ile	Ala	Leu	Ile	Leu	Ile

195 200 205
Ile Ile Leu Ser Ile Cys Gly Gly Phe Asn Cys Gly Lys
210 215 220

(2) INFORMATION FOR SEQ ID NO:1888:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 143 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..143
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571273
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1888:

Met	Ala	Phe	Leu	Glu	Arg	Val	Lys	Glu	Asp	Phe	Asn	Lys	Arg	Tyr	Gly
1			5					10					15		
Gly	Gly	Lys	Ala	Ala	Thr	Ala	Gln	Ala	Asn	Ser	Leu	Asn	Lys	Glu	Phe
			20				25					30			
Gly	Ser	Lys	Leu	Lys	Glu	His	Met	Gln	Tyr	Cys	Met	Asp	His	Pro	Asp
			35			40						45			
Glu	Ile	Ser	Lys	Leu	Ala	Lys	Val	Lys	Ala	Gln	Val	Ser	Glu	Val	Lys
			50			55				60					
Gly	Val	Met	Met	Glu	Asn	Ile	Glu	Lys	Val	Leu	Asp	Arg	Gly	Glu	Lys
			65			70				75				80	
Ile	Glu	Leu	Leu	Val	Asp	Lys	Thr	Glu	Asn	Leu	Arg	Ser	Gln	Ala	Gln
			85					90						95	
Asp	Phe	Arg	Thr	Gln	Gly	Thr	Gln	Met	Arg	Arg	Lys	Met	Trp	Phe	Gln
			100					105					110		
Asn	Met	Lys	Ile	Lys	Leu	Ile	Val	Leu	Ala	Ile	Ile	Ile	Ala	Leu	Ile
			115			120							125		
Leu	Ile	Ile	Leu	Ser	Ile	Cys	Gly	Gly	Phe	Asn	Cys	Gly	Lys		
			130			135						140			

(2) INFORMATION FOR SEQ ID NO:1889:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1348 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1348
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571291
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1889:

aaacacGcaa	caacaaacaat	gtctctctct	ctccgatcta	ccaccgcgcg	ttctcttthc	60
ctccgcctcct	cctcctcctc	ctccagatcc	actctcaact	tctccgcttc	ctctctcttc	120
tccttcgtca	gatctctcgt	ctctctctcc	cgctctctct	ctctctcaac	ctctctcag	180
aaatgctgaa	ttgcgtcggt	gaatcggagt	ttcaactcca	ccaccgcgcg	tactaaatct	240
tcattctcag	atcctgatca	gttgaagaac	gctagagaag	atatcaaaga	gctctctcag	300
accaaattct	gccatccgat	tttgtttaga	ttaggttgcc	atgatgtcgg	tacgtataac	360
aagaaacatta	aggaatggcc	acaaagaggt	ggagctaagt	gaagtttgag	attcgatatt	420
gagcttaaac	atactgctaa	tgctggtctt	gtgaatgctt	taaaactgat	taaggatatt	480
aaagagaaat	actctgggat	cagttatgct	gatttgttcc	agttagctag	tgctactgtc	540
atagagggaag	ctggaggacc	gaaaaatccc	atgaaatgat	gtagagttag	tgctctgtgt	600
ctctgaggatt	gtccagaaga	aggaagacct	ccagatgctg	gtcctctctc	gctctgctat	660
catctcagag	aagtgttttt	cagaatggga	ttagatgaca	aggacatagt	tgcatattct	720
ggtgctcaca	cggttagaag	attctaggcca	gaacgtagtg	gttgggggaa	gctcgagacg	780
aagtacacga	aagaaggacc	tggagacca	ggaggacagt	catggacacc	agagtggcgt	840
aagtttgata	attcgtactt	caaggagatc	aaggaaaaga	gagatgaaga	tctctctgtc	900
ctaccacagt	atgctgccat	ctctgaagat	tcttctttca	aggtctatgc	tgaaaagtat	960

gctgcagatc aggatgcatt tttcaaggat tacgctgtag cgcctgcgaa actcagcaat 1020
cttggcgcag aatttaaccc tcggaggagt atcattatct aatggggcac ctaatttact 1080
caaccagact tatgatttta gagaacgta gtccaataat gaaagagaag aaaaagtga 1140
cgagagaact ttcacgcgac tacttttcga gatacctttt ggacaaaatgt tctggctgt 1200
tcaaaggatt ttgttttagcc gaaagtattt gatcgttttc atggttttgt gctttcatgt 1260
ttttttcttg taataaattg cggaagtgat tatccaaaat ctatacaaat ttgtctgga 1320
attgaattat tttatcgatg ttataact

(2) INFORMATION FOR SEQ ID NO:1890:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 353 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..353

(D) OTHER INFORMATION: / Ceres Seq. ID 1571292

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1890:

Lys	Xaa	Ala	Thr	Thr	Thr	Met	Ser	Ser	Ser	Ser	Leu	Arg	Ser	Thr	Thr	Ala
1			5						10						15	
Ala	Ser	Leu	Xaa	Leu	Arg	Ser	Ser	Ser	Ser	Ser	Ser	Arg	Ser	Thr	Leu	
			20					25					30			
Thr	Leu	Ser	Ala	Ser	Ser	Ser	Leu	Ser	Phe	Val	Arg	Ser	Leu	Val	Ser	
			35				40					45				
Ser	Pro	Arg	Leu	Ser	Ser	Ser	Ser	Pro	Leu	Ser	Gln	Lys	Cys	Arg	Ile	
			50				55				60					
Ala	Ser	Val	Asn	Arg	Ser	Phe	Asn	Ser	Thr	Thr	Ala	Ala	Thr	Lys	Ser	
65				70					75					80		
Ser	Ser	Ser	Asp	Pro	Asp	Gln	Leu	Lys	Asn	Ala	Arg	Glu	Asp	Ile	Lys	
			85					90					95			
Glu	Leu	Leu	Ser	Thr	Lys	Phe	Cys	His	Pro	Ile	Leu	Val	Arg	Leu	Gly	
			100				105					110				
Trp	His	Asp	Ala	Gly	Thr	Tyr	Asn	Lys	Asn	Ile	Lys	Glu	Trp	Pro	Gln	
			115				120					125				
Arg	Gly	Gly	Ala	Asn	Gly	Ser	Leu	Arg	Phe	Asp	Ile	Glu	Leu	Lys	His	
			130			135					140					
Thr	Ala	Asn	Ala	Gly	Leu	Val	Asn	Ala	Leu	Asn	Leu	Ile	Lys	Asp	Ile	
145				150						155				160		
Lys	Glu	Lys	Tyr	Ser	Gly	Ile	Ser	Tyr	Ala	Asp	Leu	Phe	Gln	Leu	Ala	
			165						170					175		
Ser	Ala	Thr	Ala	Ile	Glu	Glu	Ala	Gly	Gly	Pro	Lys	Ile	Pro	Met	Lys	
			180					185					190			
Tyr	Gly	Arg	Val	Asp	Ala	Ser	Gly	Pro	Glu	Asp	Cys	Pro	Glu	Glu	Gly	
			195				200					205				
Arg	Leu	Pro	Asp	Ala	Gly	Pro	Pro	Ser	Pro	Ala	Thr	His	Leu	Arg	Glu	
			210			215					220					
Val	Phe	Tyr	Arg	Met	Gly	Leu	Asp	Asp	Lys	Asp	Ile	Val	Ala	Leu	Ser	
225				230					235					240		
Gly	Ala	His	Thr	Leu	Gly	Arg	Ser	Arg	Pro	Glu	Arg	Ser	Gly	Trp	Gly	
			245					250					255			
Lys	Pro	Glu	Thr	Lys	Tyr	Thr	Lys	Glu	Gly	Pro	Gly	Ala	Pro	Gly	Gly	
			260				265					270				
Gln	Ser	Trp	Thr	Pro	Glu	Trp	Leu	Lys	Phe	Asp	Asn	Ser	Tyr	Phe	Lys	
			275				280				285					
Glu	Ile	Lys	Glu	Lys	Arg	Asp	Glu	Asp	Leu	Leu	Val	Leu	Pro	Thr	Asp	
			290			295					300					
Ala	Ala	Ile	Phe	Glu	Asp	Ser	Ser	Phe	Lys	Val	Tyr	Ala	Glu	Lys	Tyr	
305				310					315					320		
Ala	Ala	Asp	Gln	Asp	Ala	Phe	Phe	Lys	Asp	Tyr	Ala	Val	Ala	His	Ala	
			325					330						335		

Lys Leu Ser Asn Leu Gly Ala Glu Phe Asn Pro Pro Glu Gly Ile Ile
340 345 350
Ile

(2) INFORMATION FOR SEQ ID NO:1891:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 347 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..347
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571293

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1891:

Met	Ser	Ser	Ser	Leu	Arg	Ser	Thr	Thr	Ala	Ala	Ser	Leu	Xaa	Leu	Arg
1				5					10					15	
Ser	Ser	Ser	Ser	Ser	Ser	Arg	Ser	Thr	Leu	Thr	Leu	Ser	Ala	Ser	Ser
				20				25					30		
Ser	Leu	Ser	Phe	Val	Arg	Ser	Leu	Val	Ser	Ser	Pro	Arg	Leu	Ser	Ser
				35				40				45			
Ser	Ser	Pro	Leu	Ser	Gln	Lys	Cys	Arg	Ile	Ala	Ser	Val	Asn	Arg	Ser
				50			55				60				
Phe	Asn	Ser	Thr	Thr	Ala	Ala	Thr	Lys	Ser	Ser	Ser	Asp	Pro	Asp	
65				70				75				80			
Gln	Leu	Lys	Asn	Ala	Arg	Glu	Asp	Ile	Lys	Glu	Leu	Leu	Ser	Thr	Lys
				85				90				95			
Phe	Cys	His	Pro	Ile	Leu	Val	Arg	Leu	Gly	Trp	His	Asp	Ala	Gly	Thr
				100				105				110			
Tyr	Asn	Lys	Asn	Ile	Lys	Glu	Trp	Pro	Gln	Arg	Gly	Gly	Ala	Asn	Gly
				115			120					125			
Ser	Leu	Arg	Phe	Asp	Ile	Glu	Leu	Lys	His	Thr	Ala	Asn	Ala	Gly	Leu
				130			135				140				
Val	Asn	Ala	Leu	Asn	Leu	Ile	Lys	Asp	Ile	Lys	Glu	Lys	Tyr	Ser	Gly
145				150				155				160			
Ile	Ser	Tyr	Ala	Asp	Leu	Phe	Gln	Leu	Ala	Ser	Ala	Thr	Ala	Ile	Glu
				165				170				175			
Glu	Ala	Gly	Gly	Pro	Lys	Ile	Pro	Met	Lys	Tyr	Gly	Arg	Val	Asp	Ala
				180				185				190			
Ser	Gly	Pro	Glu	Asp	Cys	Pro	Glu	Glu	Gly	Arg	Leu	Pro	Asp	Ala	Gly
				195			200				205				
Pro	Pro	Ser	Pro	Ala	Thr	His	Leu	Arg	Glu	Val	Phe	Tyr	Arg	Met	Gly
				210			215				220				
Leu	Asp	Asp	Lys	Asp	Ile	Val	Ala	Leu	Ser	Gly	Ala	His	Thr	Leu	Gly
225				230				235				240			
Arg	Ser	Arg	Pro	Glu	Arg	Ser	Gly	Trp	Gly	Lys	Pro	Glu	Thr	Lys	Tyr
				245				250				255			
Thr	Lys	Glu	Gly	Pro	Gly	Ala	Pro	Gly	Gly	Gln	Ser	Trp	Thr	Pro	Glu
				260				265				270			
Trp	Leu	Lys	Phe	Asp	Asn	Ser	Tyr	Phe	Lys	Glu	Ile	Lys	Glu	Lys	Arg
				275			280				285				
Asp	Glu	Asp	Leu	Leu	Val	Leu	Pro	Thr	Asp	Ala	Ala	Ile	Phe	Glu	Asp
				295				300				305			
Ser	Ser	Phe	Lys	Val	Tyr	Ala	Glu	Lys	Tyr	Ala	Ala	Asp	Gln	Asp	Ala
310				315				320							
Phe	Phe	Lys	Asp	Tyr	Ala	Val	Ala	His	Ala	Lys	Leu	Ser	Asn	Leu	Gly
				325				330				335			
Ala	Glu	Phe	Asn	Pro	Pro	Glu	Gly	Ile	Ile	Ile					
				340			345								

(2) INFORMATION FOR SEQ ID NO:1892:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1532 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1532

(D) OTHER INFORMATION: / Ceres Seq. ID 1571304

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1892:

atatataagc	tcacaggtctt	gtacatcttc	atcatctgat	ctcggggaag	ctccgatctg	60
agtttttttt	agcaatggcg	aaaatgattc	ctagcctcgt	ctctctaatt	cttatcggct	120
ttgttgogat	cgctcccgcc	gcagtttatt	tcgaggagcg	ctttgatgat	ggctggggaga	180
acagatgggt	taaatctggag	tggagaagg	atgataacac	tgctggggag	tggaaagcaca	240
ctgcgggaaa	ttggctcgtg	gacgctaaag	ataaaggat	ccagaccagt	gaagactaca	300
gattctacgc	catttcagct	gagttccctg	aattcagtaa	caaggacaag	accttagtgt	360
ttcaattctc	agtcacaagc	gagcaaaaag	ttgactgcgg	tggtgggtac	atgaagctac	420
taagtgggtg	tggtgaccaa	aagaatttgg	gtggagacac	accatacagt	atcattgtttg	480
gtcctgatat	ctgtggctac	agcacaaaag	aagtgcattg	tatccttacc	tataatgaag	540
ccaaccacct	gatcaagaaa	gatgttccat	gtgAaactga	ccagctcacc	catgtgtaca	600
catatttact	cgccccaagt	gctacttaca	gcattctcat	cgacaatgtt	gagaaacaaa	660
ctggtagcct	ttactctgac	tgggatcttc	tcccacccaa	gaagatcaag	gaccccgagc	720
ccaagaagcc	tgaggactgg	gacgaacaag	aatacatctt	tgaccttgaa	gacaaagaa	780
ctgacgggta	cgatgatatt	cctaaggaga	tcccagacac	cgactcaag	aagcctgagg	840
actgggagta	tgaagaagat	gtgagtgga	ctgccccaac	aatccccaac	ccctgagtaca	900
tggttggaatg	gaagcctaag	caaatcaaga	acccccaaact	caaggggcaag	tggggagctc	960
catgtattga	caaccctgac	ttcaaggatg	accacagagct	ctacgtcttc	cccaagctga	1020
aatatgttgg	actcgaattg	tggcaggtga	aatcaggatc	atgtgtcgac	aatgtcttga	1080
tctgcgatga	cccagactat	gccaaagaat	tggcagatga	aacatggggg	aagctcaagg	1140
atcgcgagaa	agcagctctt	gatgaggctg	agaagaagaa	tgaggaaag	gaatccaagg	1200
acgcaCctgc	ggaattctgat	gctgaagacg	aaccagagga	tgatgaagga	ggagatgatt	1260
ccgattctga	atctaaagcc	gaggagacca	aatcagaaga	tagcgaggaa	acctctgaga	1320
aagacgcac	cgctcatgat	gagctatagg	tgaagggttg	aagatttgaa	gaccaaagtt	1380
ttcagtcctc	ttattgtttt	atcgtttttt	tttgaagtat	tttagcatct	agtttgtcgg	1440
agatagaaac	aagtttttag	aaaactaaaa	gggggatata	atgtctgtca	gatgtcatt	1500
ttagacttta	aaaaaccatg	aagaagtttt	gc			

(2) INFORMATION FOR SEQ ID NO:1893:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 424 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..424

(D) OTHER INFORMATION: / Ceres Seq. ID 1571305

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1893:

Met	Ala	Lys	Met	Ile	Pro	Ser	Leu	Val	Ser	Leu	Ile	Leu	Ile	Gly	Leu
1			5					10			15				
Val	Ala	Ile	Ala	Ser	Ala	Ala	Val	Ile	Phe	Glu	Glu	Arg	Phe	Asp	Asp
			20				25				30				
Gly	Trp	Glu	Asn	Arg	Trp	Val	Lys	Ser	Glu	Trp	Lys	Lys	Asp	Asp	Asn
			35				40				45				
Thr	Ala	Gly	Glu	Trp	Lys	His	Thr	Ala	Gly	Asn	Trp	Ser	Gly	Asp	Ala
			50				55				60				
Asn	Asp	Lys	Gly	Ile	Gln	Thr	Ser	Glu	Asp	Trp	Arg	Phe	Tyr	Ala	Ile
			65				70				75			80	
Ser	Ala	Glu	Phe	Pro	Glu	Phe	Ser	Asn	Lys	Lys	Thr	Leu	Val	Phe	
			85				90				95				

Gln Phe Ser Val Lys His Glu Gln Lys Leu Asp Cys Gly Gly Gly Tyr
100 105 110
Met Lys Leu Leu Ser Gly Asp Val Asp Gln Lys Lys Phe Gly Gly Asp
115 120 125
Thr Pro Tyr Ser Ile Met Phe Gly Pro Asp Ile Cys Gly Tyr Ser Thr
130 135 140
Lys Lys Val His Ala Ile Leu Thr Tyr Asn Glu Ala Asn His Leu Ile
145 150 155 160
Lys Lys Asp Val Pro Cys Glu Thr Asp Gln Leu Thr His Val Tyr Thr
165 170 175
Phe Ile Leu Arg Pro Asp Ala Thr Tyr Ser Ile Leu Ile Asp Asn Val
180 185 190
Glu Lys Gln Thr Gly Ser Leu Tyr Ser Asp Trp Asp Leu Leu Pro Pro
195 200 205
Lys Lys Ile Lys Asp Pro Ser Ala Lys Lys Pro Glu Asp Trp Asp Glu
210 215 220
Gln Glu Tyr Ile Ser Asp Pro Glu Asp Lys Lys Pro Asp Gly Tyr Asp
225 230 235 240
Asp Ile Pro Lys Glu Ile Pro Asp Thr Asp Ser Lys Lys Pro Glu Asp
245 250 255
Trp Asp Asp Glu Glu Asp Gly Glu Trp Thr Ala Pro Thr Ile Pro Asn
260 265 270
Pro Glu Tyr Met Gly Glu Trp Lys Pro Lys Gln Ile Lys Asn Pro Asn
275 280 285
Tyr Lys Gly Lys Trp Glu Ala Pro Leu Ile Asp Asn Pro Asp Phe Lys
290 295 300
Asp Asp Pro Glu Leu Tyr Val Phe Pro Lys Leu Lys Tyr Val Gly Leu
305 310 315 320
Glu Leu Trp Gln Val Lys Ser Gly Ser Leu Phe Asp Asn Val Leu Ile
325 330 335
Cys Asp Asp Pro Asp Tyr Ala Lys Lys Leu Ala Asp Glu Thr Trp Gly
340 345 350
Lys Leu Lys Asp Ala Glu Lys Ala Ala Phe Asp Glu Ala Glu Lys Lys
355 360 365
Asn Glu Glu Glu Glu Ser Lys Asp Ala Pro Ala Glu Ser Asp Ala Glu
370 375 380
Asp Glu Pro Glu Asp Asp Glu Gly Gly Asp Asp Ser Asp Ser Glu Ser
385 390 395 400
Lys Ala Glu Glu Thr Lys Ser Glu Asp Ser Glu Glu Thr Ser Glu Lys
405 410 415
Asp Ala Thr Ala His Asp Glu Leu
420

(2) INFORMATION FOR SEQ ID NO:1894:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 421 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..421

(D) OTHER INFORMATION: / Ceres Seq. ID 1571306

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1894:

Met Ile Pro Ser Leu Val Ser Leu Ile Leu Ile Gly Leu Val Ala Ile
1 5 10 15
Ala Ser Ala Ala Val Ile Phe Glu Glu Arg Phe Asp Asp Gly Trp Glu
20 25 30
Asn Arg Trp Val Lys Ser Glu Trp Lys Lys Asp Asp Asn Thr Ala Gly
35 40 45
Glu Trp Lys His Thr Ala Gly Asn Trp Ser Gly Asp Ala Asn Asp Lys

Met Lys Leu Leu Ser Gly Asp Val Asp Gln Lys Lys Phe Gly Gly Asp
1 5 10 15

```

Thr Pro Tyr Ser Ile Met Phe Gly Pro Asp Ile Cys Gly Tyr Ser Thr
      20      25      30
Lys Lys Val His Ala Ile Leu Thr Tyr Asn Glu Ala Asn His Leu Ile
      35      40      45
Lys Lys Asp Val Pro Cys Glu Thr Asp Gln Leu Thr His Val Tyr Thr
      50      55      60
Phe Ile Leu Arg Pro Asp Ala Thr Tyr Ser Ile Leu Ile Asp Asn Val
      65      70      75      80
Glu Lys Gln Thr Gly Ser Leu Tyr Ser Asp Trp Asp Leu Leu Pro Pro
      85      90      95
Lys Lys Ile Lys Asp Pro Ser Ala Lys Lys Pro Glu Asp Trp Asp Glu
      100      105      110
Gln Glu Tyr Ile Ser Asp Pro Glu Asp Lys Lys Pro Asp Gly Tyr Asp
      115      120      125
Asp Ile Pro Lys Glu Ile Pro Asp Thr Asp Ser Lys Lys Pro Glu Asp
      130      135      140
Trp Asp Asp Glu Glu Asp Gly Glu Trp Thr Ala Pro Thr Ile Pro Asn
      145      150      155      160
Pro Glu Tyr Met Gly Glu Trp Lys Pro Lys Gln Ile Lys Asn Pro Asn
      165      170      175
Tyr Lys Gly Lys Trp Glu Ala Pro Leu Ile Asp Asn Pro Asp Phe Lys
      180      185      190
Asp Asp Pro Glu Leu Tyr Val Phe Pro Lys Leu Lys Tyr Val Gly Leu
      195      200      205
Glu Leu Trp Gln Val Lys Ser Gly Ser Leu Phe Asp Asn Val Leu Ile
      210      215      220
Cys Asp Asp Pro Asp Tyr Ala Lys Lys Leu Ala Asp Glu Thr Trp Gly
      225      230      235      240
Lys Leu Lys Asp Ala Glu Lys Ala Ala Phe Asp Glu Ala Glu Lys Lys
      245      250      255
Asn Glu Glu Glu Glu Ser Lys Asp Ala Pro Ala Glu Ser Asp Ala Glu
      260      265      270
Asp Glu Pro Glu Asp Asp Glu Gly Gly Asp Asp Ser Asp Ser Glu Ser
      275      280      285
Lys Ala Glu Glu Thr Lys Ser Glu Asp Ser Glu Glu Thr Ser Glu Lys
      290      295      300
Asp Ala Thr Ala His Asp Glu Leu
      305      310

```

(2) INFORMATION FOR SEQ ID NO:1896:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1257 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1257
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571312

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1896:

```

acactcgtct taccaaaact tctctacac aaccaaiaac atctctttgc aacaaaactt      60
gttgtaactc atctcttctc tctcttctc catcacagac tcataacaaa tgggagaagt      120
ttcagtggtg gagaacaaga aagtgatact aaagaattat gtatagtgta ttctctacaga      180
aacagacatg gaagtgaaac tcggagaaac aattgagcta aaagcaccaa aaggatcttc      240
ttgtttcttc gtcaaaaaat tatacttgtc ttgtgatcct tacatgagag gtgctatgcg      300
tgattttcac ggttctctatc tcccgccctt tgttctctgc caacgtatcg aaggggttgg      360
tttagcaaga gtgatagatt ctgatgatac taattataag cccggcgata tagctctcgg      420
tatcatctgt tgggaagaat acagtttgct acgtaGttca gataacctac agttgagaaa      480
tattcaatta gacgacgaca ttcgcttttc ttatcatctc ggacttctcg ggaatggctgg      540
atttacagca tatgcagggt ttaatgagat atgttgtctc aagaaagggg acagtgtttt      600
tgtctctgca gcatgtggag cagtttgaca acttggttgt cagctagcta agttgcacgg      660

```

ctgctatgtt	gttggttagcg	ccggtagtaa	gcaaaaggtt	gagatcctta	aaaacgagct	720
tggatatgat	gaagccttta	actacaagga	agaggctgat	cttgatactg	ctttgaagag	780
gtacttccca	gaggggatcg	atatctactt	cgataacgtg	ggtggatcca	tgcttgatgc	840
agcactctc	aacatgaagg	ttcgtggaag	aatcgcgctc	tgtggaatgg	tgctttatac	900
aagcctctca	acttcacac	aaggaatcaa	gaacctatac	agcgctatct	acaaacgctt	960
aaggctagaa	gggttcttgc	agagtgatta	ccttcatac	ttcccacagt	ttcttgaaaa	1020
tgtaagagaa	tattacaaga	aaggcaagat	tgctacatc	gaagatatat	ctgaagcctc	1080
cgaccAtcgc	tcNccgcgtc	actgtttggg	ctgttttccg	ggaaaaatat	cggtaaaacg	1140
gtgtgtcggg	ttgctaaga	gtgattgttt	ctaaaaagta	tattgtaagt	gacttaaaac	1200
agacattata	tgaataaaag	ccgccataag	ttcttatagg	aaaaacgtta	gttaaatc	

(2) INFORMATION FOR SEQ ID NO:1897:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 354 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..354

(D) OTHER INFORMATION: / Ceres Seq. ID 1571313

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1897:

Met	Gly	Glu	Val	Ser	Val	Val	Glu	Asn	Lys	Lys	Val	Ile	Leu	Lys	Asn
1			5					10						15	
Tyr	Val	Asp	Gly	Ile	Pro	Thr	Glu	Thr	Asp	Met	Glu	Val	Lys	Leu	Gly
			20					25					30		
Glu	Thr	Ile	Glu	Leu	Lys	Ala	Pro	Lys	Gly	Ser	Ser	Cys	Phe	Leu	Val
			35				40					45			
Lys	Asn	Leu	Tyr	Leu	Ser	Cys	Asp	Pro	Tyr	Met	Arg	Gly	Arg	Met	Arg
			50			55					60				
Asp	Phe	His	Gly	Ser	Tyr	Leu	Pro	Pro	Phe	Val	Pro	Gly	Gln	Arg	Ile
			65			70				75				80	
Glu	Gly	Phe	Gly	Leu	Ala	Arg	Val	Ile	Asp	Ser	Asp	Asp	Thr	Asn	Tyr
			85						90				95		
Lys	Pro	Gly	Asp	Ile	Val	Ser	Gly	Ile	Ile	Gly	Trp	Glu	Glu	Tyr	Ser
			100				105						110		
Leu	Leu	Arg	Ser	Ser	Asp	Asn	Leu	Gln	Leu	Arg	Asn	Ile	Gly	Leu	Asp
			115			120					125				
Asp	Asp	Ile	Pro	Leu	Ser	Tyr	His	Leu	Gly	Leu	Leu	Gly	Met	Ala	Gly
			130			135					140				
Phe	Thr	Ala	Tyr	Ala	Gly	Phe	Asn	Glu	Ile	Cys	Cys	Pro	Lys	Lys	Gly
			145			150				155				160	
Asp	Ser	Val	Phe	Val	Ser	Ala	Ala	Cys	Gly	Ala	Val	Gly	Gln	Leu	Val
			165						170				175		
Gly	Gln	Leu	Ala	Lys	Leu	His	Gly	Cys	Tyr	Val	Val	Gly	Ser	Ala	Gly
			180				185						190		
Ser	Lys	Gln	Lys	Val	Glu	Ile	Leu	Lys	Asn	Glu	Leu	Gly	Tyr	Asp	Glu
			195				200					205			
Ala	Phe	Asn	Tyr	Lys	Glu	Glu	Ala	Asp	Leu	Asp	Thr	Ala	Leu	Lys	Arg
			210			215					220				
Tyr	Phe	Pro	Glu	Gly	Ile	Asp	Ile	Tyr	Phe	Asp	Asn	Val	Gly	Gly	Ser
			225			230				235				240	
Met	Leu	Asp	Ala	Ala	Leu	Leu	Asn	Met	Lys	Val	Arg	Gly	Arg	Ile	Ala
			245						250					255	
Leu	Cys	Gly	Met	Val	Ser	Leu	Gln	Ser	Leu	Ser	Thr	Ser	Ser	Gln	Gly
			260				265						270		
Ile	Lys	Asn	Leu	Tyr	Ser	Ala	Ile	Tyr	Lys	Arg	Leu	Arg	Leu	Glu	Gly
			275				280					285			
Phe	Leu	Gln	Ser	Asp	Tyr	Leu	His	Ile	Phe	Pro	Gln	Phe	Leu	Glu	Asn
			290				295				300				
Val	Lys	Arg	Tyr	Tyr	Lys	Glu	Gly	Lys	Ile	Val	Tyr	Ile	Glu	Asp	Ile

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(2) INFORMATION FOR SEQ ID NO:1898:

(A) LENGTH: 328 amino acids

(C) STRANDEDNESS:

(D) TOPOLOGY: \lim

(D) TOPOLOGY: linear
MOLECULE TYPE: peptid

(11) MOLECULE TYPE: peptide
(12) FEATURE:

(ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1 328

(B) LOCATION: 1..328

(D) OTHER INFORMATION: / Ceres Seq. ID 1571314

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1898:

[illegible]

(2) INFORMATION FOR SEQ ID NO:1899:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 296 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..296

(D) OTHER INFORMATION: / Ceres Seq. ID 1571315

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1899:

Met Arg Gly Arg Met Arg Asp Phe His Gly Ser Tyr Leu Pro Pro Phe
1 5 10 15
Val Pro Gly Gln Arg Ile Glu Gly Phe Gly Leu Ala Arg Val Ile Asp
20 25 30
Ser Asp Asp Thr Asn Tyr Lys Pro Gly Asp Ile Val Ser Gly Ile Ile
35 40 45
Gly Trp Gly Glu Tyr Ser Leu Leu Arg Ser Ser Asp Asn Leu Gln Leu
50 55 60
Arg Asn Ile Gln Leu Asp Asp Asp Ile Pro Leu Ser Tyr His Leu Gly
65 70 75 80
Leu Leu Gly Met Ala Gly Phe Thr Ala Tyr Ala Gly Phe Asn Glu Ile
85 90 95
Cys Cys Pro Lys Lys Gly Asp Ser Val Phe Val Ser Ala Ala Cys Gly
100 105 110
Ala Val Gly Gln Leu Val Gly Gln Leu Ala Lys Leu His Gly Cys Tyr
115 120 125
Val Val Gly Ser Ala Gly Ser Lys Gln Lys Val Glu Ile Leu Lys Asn
130 135 140
Glu Leu Gly Tyr Asp Glu Ala Phe Asn Tyr Lys Glu Glu Ala Asp Leu
145 150 155 160
Asp Thr Ala Leu Lys Arg Tyr Phe Pro Glu Gly Ile Asp Ile Tyr Phe
165 170 175
Asp Asn Val Gly Gly Ser Met Leu Asp Ala Ala Leu Leu Asn Met Lys
180 185 190
Val Arg Gly Arg Ile Ala Leu Cys Gly Met Val Ser Leu Gln Ser Leu
195 200 205
Ser Thr Ser Ser Gln Gly Ile Lys Asn Leu Tyr Ser Ala Ile Tyr Lys
210 215 220
Arg Leu Arg Leu Glu Gly Phe Leu Gln Ser Asp Tyr Leu His Ile Phe
225 230 235 240
Pro Gln Phe Leu Glu Asn Val Lys Arg Tyr Tyr Lys Glu Gly Lys Ile
245 250 255
Val Tyr Ile Glu Asp Ile Ser Glu Gly Leu Asp His Arg Xaa Pro Leu
260 265 270
His Leu Leu Gly Cys Phe Pro Gly Lys Ile Ser Val Asn Arg Leu Phe
275 280 285
Gly Leu Leu Lys Ser Asp Cys Phe
290 295

(2) INFORMATION FOR SEQ ID NO:1900:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1766 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1766

(D) OTHER INFORMATION: / Ceres Seq. ID 1571333

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1900:

ctaaccattgg	attcagagctc	tctagtgaag	aatccgccat	ggctgtttcca	tttctaagct	60
cttctcttaca	actcacaccc	acttctccga	ttctcttcac	taaagtaaca	ccaacaccaa	120
taatccacaa	ccacagatca	acatgcacta	taccacacaa	gcctcgtcta	cgtctcctcc	180
gccgcctccg	cgtcgttgga	acgcgcgtat	ctgatcaaac	agaaggaagt	ggagatgttc	240
ttttaaacc	tgaagaagag	aaacgtgttg	agggtgggga	ttatgattgg	acagaggaat	300
gggatccatt	gtacttaact	aaaaacgtcc	ctgaagatgc	gcctcttgcc	ctcaccgtct	360
acgatcgcta	aattgttttg	tataaagacg	gYgaaggaac	acttcgttgt	tacgaagatc	420
gggtctccta	tcggttggct	aagtgtgtctg	aaggacaatt	gattgatggg	agattggaat	480
gtttgtatca	ttggttgcaa	tttgaaggag	aggcgaaatg	tgtcaagatt	cctcagcttc	540
ctgcaagtgc	taagattcca	aaggctgctt	gtgtgaagac	gtatgaggtg	aaggattcac	600
aaggagtgtg	gtgggtgtgt	atgtcaacaa	agacacctcc	aaacctctga	aggcttccct	660
gggttgagaa	tttcgctaga	cccggttttt	tcgacatttc	gactactcat	gagcttccct	720
atgaccattc	cattctttta	gagaatctga	tgatcctgc	tcattgtcct	atctctcatg	780
atagaacgga	tttcaactgc	aaaaaagaaa	atgctcagcc	tttggttttc	gaggtcacag	840
agcgaagtga	tcggggtttc	gcaggagactt	ggggccgaga	gagagaaggt	gggaaagga	900
gtataattact	tcgggttgat	gtcctctgtg	ttctgcagaa	caatcgagag	ttcgaggga	960
aggatggagt	gaagaactat	ttttcagggc	tgtttctttg	tagacctaca	gggcaagga	1020
agtcctatgc	tattgttagg	tttggggtca	caaaaagatc	gcctttgggt	tcggtgttac	1080
ctcaatgggt	ctggcatcag	aatgcctgca	agggttttga	acaagacatg	gggtttctat	1140
cgctctcaaaa	acgaggttct	gatgaaggag	aaagtaccaa	ctaagctatt	gtatttgaat	1200
ctaaagtcat	cggacacatg	ggctcgctgaa	tagaaagtgg	atggacaaag	ttgtgcattg	1260
gatgccttac	catttcgggc	ataggacctat	atctctcccc	aaagtcctcc	ctgtcgtgga	1320
acatgcgccg	gcaggcctca	ttgcagctct	ctctgcttct	taccctgcaa	aaggcggaat	1380
tgggactatg	catgctccca	atttggctaa	ccggtacttc	agacatatta	ttcattgtag	1440
aaagtcgagc	aatgtgatca	aatcttttga	gcctcgaaaa	aatatcctct	ctgcacggcg	1500
agtggtcttg	acggcttttg	ccattcttgt	gggttagtaga	cagtgggaag	ctgtccttgt	1560
agtggtcaga	gcatttgtct	cagccgcgac	ttatacctgc	ttaaagagcta	taaatctaaa	1620
caccaataaac	ttcattagaa	cacacagaag	acatgaaaaa	tgtatagtgt	catgttctct	1680
ctctttccaa	caaatgtgat	ttcatgaaat	aaatttttgc	ttgtaaacgc	aatatatata	1740
ttcagaaggt	ttcaatgttt	gccagc				

(2) INFORMATION FOR SEQ ID NO:1901:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 393 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..393
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571334

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1901:

Asn	Ile	Gly	Phe	Glu	Leu	Ser	Ser	Glu	Glu	Ser	Ala	Met	Ala	Val	Pro
1			5					10						15	
Phe	Leu	Ser	Ser	Ser	Leu	Gln	Leu	Thr	Pro	Thr	Ser	Pro	Ile	Leu	Phe
			20					25					30		
Thr	Lys	Val	Thr	Pro	Thr	Pro	Ile	Ile	His	Asn	His	Arg	Ser	Thr	Cys
			35				40					45			
Thr	Ile	Pro	Thr	Lys	Pro	Arg	Leu	Arg	Leu	Arg	Arg	Ser	Ala	Val	
			50				55				60				
Ala	Gly	Thr	Ala	Val	Ser	Asp	Gln	Thr	Glu	Gly	Gly	Gly	Asp	Val	Leu
			65				70			75				80	
Leu	Asn	Pro	Glu	Glu	Lys	Arg	Val	Glu	Val	Ala	Asp	Tyr	Asp	Trp	
			85					90				95			
Thr	Glu	Glu	Trp	Tyr	Pro	Leu	Tyr	Leu	Thr	Lys	Asn	Val	Pro	Glu	Asp
			100					105				110			
Ala	Pro	Leu	Gly	Leu	Thr	Val	Tyr	Asp	Arg	Gln	Ile	Val	Leu	Tyr	Lys
			115				120					125			
Asp	Xaa	Glu	Gly	Thr	Leu	Arg	Cys	Tyr	Glu	Asp	Arg	Cys	Pro	His	Arg
			130				135					140			

Leu Ala Lys Leu Ser Glu Gly Gln Leu Ile Asp Gly Arg Leu Glu Cys
145 150 155 160
Leu Tyr His Gly Trp Gln Phe Glu Gly Glu Gly Lys Cys Val Lys Ile
165 170 175
Pro Gln Leu Pro Ala Ser Ala Lys Ile Pro Lys Ala Ala Cys Val Lys
180 185 190
Thr Tyr Glu Val Lys Asp Ser Gln Gly Val Val Trp Val Trp Met Ser
195 200 205
Thr Lys Thr Pro Pro Asn Pro Glu Lys Leu Pro Trp Phe Glu Asn Phe
210 215 220
Ala Arg Pro Gly Phe Phe Asp Ile Ser Thr Thr His Glu Leu Pro Tyr
225 230 235 240
Asp His Ser Ile Leu Leu Glu Asn Leu Met Asp Pro Ala His Val Pro
245 250 255
Ile Ser His Asp Arg Thr Asp Phe Thr Ala Lys Arg Lys Asp Ala Gln
260 265 270
Pro Leu Val Phe Glu Val Thr Glu Arg Ser Asn Arg Gly Phe Ala Gly
275 280 285
Thr Trp Gly Arg Glu Arg Glu Gly Gly Lys Ser Asn Leu Leu Arg
290 295 300
Phe Asp Ala Pro Cys Val Leu Gln Asn Asn Arg Glu Phe Glu Gly Lys
305 310 315 320
Asp Gly Val Lys Asn Tyr Phe Ser Gly Leu Phe Leu Cys Arg Pro Thr
325 330 335
Gly Gln Gly Lys Ser Met Leu Ile Val Arg Phe Gly Val Thr Lys Arg
340 345 350
Ser Pro Leu Val Ser Val Leu Pro Gln Trp Phe Trp His Gln Asn Ala
355 360 365
Cys Lys Val Phe Glu Gln Asp Met Gly Phe Leu Ser Ser Gln Lys Arg
370 375 380
Gly Ser Asp Glu Gly Glu Ser Thr Asn
385 390

(2) INFORMATION FOR SEQ ID NO:1902:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 381 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..381
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571335

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1902:

Met Ala Val Pro Phe Leu Ser Ser Ser Leu Gln Leu Thr Pro Thr Ser
1 5 10 15
Pro Ile Leu Phe Thr Lys Val Thr Pro Thr Pro Ile Ile His Asn His
20 25 30
Arg Ser Thr Cys Thr Ile Pro Thr Lys Pro Arg Leu Arg Leu Leu Arg
35 40 45
Arg Ser Ala Val Ala Gly Thr Ala Val Ser Asp Gln Thr Glu Gly Gly
50 55 60
Gly Asp Val Leu Leu Asn Pro Glu Glu Glu Lys Arg Val Glu Val Ala
65 70 75 80
Asp Tyr Asp Trp Thr Glu Glu Trp Tyr Pro Leu Tyr Leu Thr Lys Asn
85 90 95
Val Pro Glu Asp Ala Pro Leu Gly Leu Thr Val Tyr Asp Arg Gln Ile
100 105 110
Val Leu Tyr Lys Asp Xaa Glu Gly Thr Leu Arg Cys Tyr Glu Asp Arg
115 120 125
Cys Pro His Arg Leu Ala Lys Leu Ser Glu Gly Gln Leu Ile Asp Gly

130	135	140
Arg Leu Glu Cys Leu Tyr His Gly Trp Gln Phe Glu Gly Glu Gly Lys		
145	150	155
Cys Val Lys Ile Pro Gln Leu Pro Ala Ser Ala Lys Ile Pro Lys Ala		
	165	170
Ala Cys Val Lys Thr Tyr Glu Val Lys Asp Ser Gln Gly Val Val Trp		
	180	185
Val Trp Met Ser Thr Lys Thr Pro Pro Asn Pro Glu Lys Leu Pro Trp		
	195	200
Phe Glu Asn Phe Ala Arg Pro Gly Phe Phe Asp Ile Ser Thr Thr His		
	210	215
Glu Leu Pro Tyr Asp His Ser Ile Leu Leu Glu Asn Leu Met Asp Pro		
225	230	235
Ala His Val Pro Ile Ser His Asp Arg Thr Asp Phe Thr Ala Lys Arg		
	245	250
Lys Asp Ala Gln Pro Leu Val Phe Glu Val Thr Glu Arg Ser Asn Arg		
	260	265
Gly Phe Ala Gly Thr Trp Gly Arg Glu Arg Glu Gly Gly Lys Gly Ser		
	275	280
Asn Leu Leu Arg Phe Asp Ala Pro Cys Val Leu Gln Asn Asn Arg Glu		
	290	295
Phe Glu Gly Lys Asp Gly Val Lys Asn Tyr Phe Ser Gly Leu Phe Leu		
305	310	315
Cys Arg Pro Thr Gly Gln Gly Lys Ser Met Leu Ile Val Arg Phe Gly		
	325	330
Val Thr Lys Arg Ser Pro Leu Val Ser Val Leu Pro Gln Trp Phe Trp		
	340	345
His Gln Asn Ala Cys Lys Val Phe Glu Gln Asp Met Gly Phe Leu Ser		
	355	360
Ser Gln Lys Arg Gly Ser Asp Glu Gly Glu Ser Thr Asn		
	370	375
		380

(2) INFORMATION FOR SEQ ID NO:1903:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1486 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1486

(D) OTHER INFORMATION: / Ceres Seq. ID 1571340

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1903:

atcacaaattt	ttctacggctc	agagattcaa	aagagtctct	tctctctatc	ttattctccg	60
atcatcatga	tgcaagcagcc	accacccgga	ggtatccttc	cacatcacgc	tcctcctcct	120
ttctgcgcac	aacagtagcg	ttaccaacaa	cottacggga	ttgctggagc	tgctccacca	180
ccaccacaga	tgtggaatcc	toaagcggcg	gcgcgcgc	Cat	cagttcacgc	240
gcagagatcc	ggactctttg	gctcggggac	ttacagtatt	ggatggatga	gaatttcctc	300
tacgggttgc	ttgctcatat	cggagagatg	gtttctgcta	aagtgtatgc	taacaagcaa	360
accggtcaa	ttgaaggata	cgttttcatt	gaatttcgat	ctcatgctgc	tgctgaagaa	420
gtcttcacaa	cattcaacaa	cgctcctatc	ccgagcttct	ctgatcagct	ctttagacgt	480
mactggggat	cattgagttc	aggagataaa	cgagacgatt	caccggacta	cacgatattt	540
gtcgggtgat	tgagctgtga	tgttacggat	tatatcttac	ttgagacgtt	cagagcctct	600
tatccgtcag	tgaagggtgc	aaaggttggt	attaacagag	tcactggagc	tacaaaaagg	660
tatgggtttg	ttagggtttc	tgatgaaagt	gaacagatcc	gtgctatgac	ggagatgaat	720
ggcggtctct	gtctctactag	acctatgaga	attggtcccg	ctgctagcaa	gaaaggtgta	780
atcggtcaca	gagattcata	ccagagctct	gctgcagggg	taacaaactga	taatgatcca	840
aataacacaa	ctgtttttgt	tggtgggata	gatgcactcg	tcacggatga	tcactctgaag	900
aatgtcttta	gcgaatatgg	tgagattgtg	catgtgaaaa	taccocgtcg	aaagcgctgt	960
ggattcgttc	agttttccga	gaagagctgt	gcagagggaag	ctcttagaat	gctgaatgga	1020
gtgcaattag	gcggaacaa	cgctcagctc	tcatggggcg	gaagtctctc	gaacaaacag	1080

tcgggggagc	cgagccagtt	ttactacggt	gggtatggac	aaggacagga	gcagtatggg	1140
tacacgatgc	ctcaagacc	taatgcatat	tacggaggct	actctggtgg	aggatacagc	1200
gggtggttacc	agcagacacc	acaggcagga	cagcaaccac	cacaacagcc	accacagcag	1260
caacaagtgc	ggtttagcta	ctaaccocga	gagtattgct	tgagttaatg	tcactctgct	1320
tgttggttgc	gtactttggt	atgaacttgc	ttctgcgtgc	cttggttatg	atattttccc	1380
aaacacaggt	tatttgtctt	tgcttttctc	taggtgtgtg	ttgagttttt	aactcttaat	1440
aatgtttctg	cgatgcttct	gtttttaatg	ttttcatcac	cttttg		

(2) INFORMATION FOR SEQ ID NO:1904:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 427 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..427

(D) OTHER INFORMATION: / Ceres Seq. ID 1571341

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1904:

Ile	Thr	Ile	Phe	Leu	Arg	Ser	Glu	Ile	Gln	Lys	Ser	Ser	Phe	Ser	Leu
1			5						10					15	
Ser	Tyr	Ser	Pro	Ile	Ile	Met	Met	Gln	Gln	Pro	Pro	Pro	Gly	Gly	Ile
			20					25					30		
Leu	Pro	His	His	Ala	Pro	Pro	Pro	Ser	Ala	Gln	Gln	Gln	Tyr	Gly	Tyr
			35				40					45			
Gln	Gln	Pro	Tyr	Gly	Ile	Ala	Gly	Ala	Ala	Pro	Pro	Pro	Pro	Gln	Met
			50			55					60				
Trp	Asn	Pro	Gln	Ala	Ala	Ala	Pro	Pro	Ser	Val	Gln	Pro	Thr	Thr	Ala
65				70					75					80	
Asp	Glu	Ile	Arg	Thr	Leu	Trp	Ile	Gly	Asp	Leu	Gln	Tyr	Trp	Met	Asp
			85					90					95		
Glu	Asn	Phe	Leu	Tyr	Gly	Cys	Phe	Ala	His	Thr	Gly	Glu	Met	Val	Ser
			100					105					110		
Ala	Lys	Val	Ile	Arg	Asn	Lys	Gln	Thr	Gly	Gln	Val	Glu	Gly	Tyr	Gly
			115				120					125			
Phe	Ile	Glu	Phe	Ala	Ser	His	Ala	Ala	Ala	Glu	Arg	Val	Leu	Gln	Thr
			130				135					140			
Phe	Asn	Asn	Ala	Pro	Ile	Pro	Ser	Phe	Pro	Asp	Gln	Leu	Phe	Arg	Leu
145				150						155				160	
Xaa	Trp	Ala	Ser	Leu	Ser	Ser	Gly	Asp	Lys	Arg	Asp	Asp	Ser	Pro	Asp
			165						170					175	
Tyr	Thr	Ile	Phe	Val	Gly	Asp	Leu	Ala	Ala	Asp	Val	Thr	Asp	Tyr	Ile
			180					185					190		
Leu	Leu	Glu	Thr	Phe	Arg	Ala	Ser	Tyr	Pro	Ser	Val	Lys	Gly	Ala	Lys
			195					200				205			
Val	Val	Ile	Asn	Arg	Val	Thr	Gly	Arg	Thr	Lys	Gly	Tyr	Gly	Phe	Val
			210			215					220				
Arg	Phe	Ser	Asp	Glu	Ser	Glu	Gln	Ile	Arg	Ala	Met	Thr	Glu	Met	Asn
225				230						235				240	
Gly	Val	Pro	Cys	Ser	Thr	Arg	Pro	Met	Arg	Ile	Gly	Pro	Ala	Ala	Ser
			245						250				255		
Lys	Lys	Gly	Val	Thr	Gly	Gln	Arg	Asp	Ser	Tyr	Gln	Ser	Ser	Ala	Ala
			260					265					270		
Gly	Val	Thr	Thr	Asp	Asn	Asp	Pro	Asn	Asn	Thr	Thr	Val	Phe	Val	Gly
			275				280					285			
Gly	Leu	Asp	Ala	Ser	Val	Thr	Asp	Asp	His	Leu	Lys	Asn	Val	Phe	Ser
			290				295				300				
Gln	Tyr	Gly	Glu	Ile	Val	His	Val	Lys	Ile	Pro	Ala	Gly	Lys	Arg	Cys
305				310						315				320	
Gly	Phe	Val	Gln	Phe	Ser	Glu	Lys	Ser	Cys	Ala	Glu	Glu	Ala	Leu	Arg
			325						330					335	

Met Leu Asn Gly Val Gln Leu Gly Gly Thr Thr Val Arg Leu Ser Trp
340 345 350
Gly Arg Ser Pro Ser Asn Lys Gln Ser Gly Asp Pro Ser Gln Phe Tyr
355 360 365
Tyr Gly Gly Tyr Gly Gln Gly Gln Glu Gln Tyr Gly Tyr Thr Met Pro
370 375 380
Gln Asp Pro Asn Ala Tyr Tyr Gly Gly Tyr Ser Gly Gly Tyr Ser
385 390 395 400
Gly Gly Tyr Gln Gln Thr Pro Gln Ala Gly Gln Gln Pro Pro Gln Gln
405 410 415
Pro Pro Gln Gln Gln Gln Val Gly Phe Ser Tyr
420 425

(2) INFORMATION FOR SEQ ID NO:1905:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 405 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..405
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571342

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1905:

Met Met Gln Gln Pro Pro Pro Gly Gly Ile Leu Pro His His Ala Pro
1 5 10 15
Pro Pro Ser Ala Gln Gln Gln Tyr Gly Tyr Gln Gln Pro Tyr Gly Ile
20 25 30
Ala Gly Ala Ala Pro Pro Pro Pro Gln Met Trp Asn Pro Gln Ala Ala
35 40 45
Ala Pro Pro Ser Val Gln Pro Thr Thr Ala Asp Glu Ile Arg Thr Leu
50 55 60
Trp Ile Gly Asp Leu Gln Tyr Trp Met Asp Glu Asn Phe Leu Tyr Gly
65 70 75 80
Cys Phe Ala His Thr Gly Glu Met Val Ser Ala Lys Val Ile Arg Asn
85 90 95
Lys Gln Thr Gly Gln Val Glu Gly Tyr Gly Phe Ile Glu Phe Ala Ser
100 105 110
His Ala Ala Ala Glu Arg Val Leu Gln Thr Phe Asn Asn Ala Pro Ile
115 120 125
Pro Ser Phe Pro Asp Gln Leu Phe Arg Leu Xaa Trp Ala Ser Leu Ser
130 135 140
Ser Gly Asp Lys Arg Asp Ser Pro Asp Tyr Thr Ile Phe Val Gly
145 150 155 160
Asp Leu Ala Ala Asp Val Thr Asp Tyr Ile Leu Leu Glu Thr Phe Arg
165 170 175
Ala Ser Tyr Pro Ser Val Lys Gly Ala Lys Val Val Ile Asn Arg Val
180 185 190
Thr Gly Arg Thr Lys Gly Tyr Gly Phe Val Arg Phe Ser Asp Glu Ser
195 200 205
Glu Gln Ile Arg Ala Met Thr Glu Met Asn Gly Val Pro Cys Ser Thr
210 215 220
Arg Pro Met Arg Ile Gly Pro Ala Ala Ser Lys Lys Gly Val Thr Gly
225 230 235 240
Gln Arg Asp Ser Tyr Gln Ser Ser Ala Ala Gly Val Thr Thr Asp Asn
245 250 255
Asp Pro Asn Asn Thr Thr Val Phe Val Gly Gly Leu Asp Ala Ser Val
260 265 270
Thr Asp Asp His Leu Lys Asn Val Phe Ser Gln Tyr Gly Glu Ile Val
275 280 285
His Val Lys Ile Pro Ala Gly Lys Arg Cys Gly Phe Val Gln Phe Ser

290	295	300
Glu Lys Ser Cys Ala	Glu Glu Ala Leu Arg	Met Leu Asn Gly Val Gln
305	310	315
Leu Gly Gly Thr Thr	Val Arg Leu Ser Trp	Gly Arg Ser Pro Ser Asn
325	330	335
Lys Gln Ser Gly Asp	Pro Ser Gln Phe Tyr	Tyr Gly Gly Tyr Gly Gln
340	345	350
Gly Gln Glu Gln Tyr	Gly Tyr Thr Met Pro	Gln Asp Pro Asn Ala Tyr
355	360	365
Tyr Gly Gly Tyr Ser	Gly Gly Gly Tyr Ser	Gly Gly Tyr Gln Gln Thr
370	375	380
Pro Gln Ala Gly Gln	Gln Gln Gln Gln Pro	Gln Gln Gln Gln Gln
385	390	395
Val Gly Phe Ser Tyr		400

(2) INFORMATION FOR SEQ ID NO:1906:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 404 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..404

(D) OTHER INFORMATION: / Ceres Seq. ID 1571343

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1906:

Met	Gln	Gln	Pro	Pro	Pro	Gly	Gly	Ile	Leu	Pro	His	Ala	Pro	Pro
1			5					10					15	
Pro	Ser	Ala	Gln	Gln	Tyr	Gly	Tyr	Gln	Gln	Pro	Tyr	Gly	Ile	Ala
			20					25				30		
Gly	Ala	Ala	Pro	Pro	Pro	Gln	Met	Trp	Asn	Pro	Gln	Ala	Ala	Ala
			35					40				45		
Pro	Pro	Ser	Val	Gln	Pro	Thr	Ala	Asp	Glu	Ile	Arg	Thr	Leu	Trp
			50					55				60		
Ile	Gly	Asp	Leu	Gln	Tyr	Trp	Met	Asp	Glu	Asn	Phe	Leu	Tyr	Gly
			65					70				75		80
Phe	Ala	His	Thr	Gly	Glu	Met	Val	Ser	Ala	Lys	Val	Ile	Arg	Asn
			85					90				95		Lys
Gln	Thr	Gly	Gln	Val	Glu	Gly	Tyr	Gly	Phe	Ile	Glu	Phe	Ala	Ser
			100					105				110		His
Ala	Ala	Ala	Glu	Arg	Val	Leu	Gln	Thr	Phe	Asn	Asn	Ala	Pro	Ile
			115					120				125		Pro
Ser	Phe	Pro	Asp	Gln	Leu	Phe	Arg	Leu	Xaa	Trp	Ala	Ser	Leu	Ser
			130					135				140		Ser
Gly	Asp	Lys	Arg	Asp	Asp	Ser	Pro	Asp	Tyr	Thr	Ile	Phe	Val	Gly
			145					150				155		Asp
Leu	Ala	Ala	Asp	Val	Thr	Asp	Tyr	Ile	Leu	Leu	Glu	Thr	Phe	Arg
			165					170				175		Ala
Ser	Tyr	Pro	Ser	Val	Lys	Gly	Ala	Lys	Val	Val	Ile	Asn	Arg	Val
			180					185				190		Thr
Gly	Arg	Thr	Lys	Gly	Tyr	Gly	Phe	Val	Arg	Phe	Ser	Asp	Glu	Ser
			195					200				205		Glu
Gln	Ile	Arg	Ala	Met	Thr	Glu	Met	Asn	Gly	Val	Pro	Cys	Ser	Thr
			210					215				220		Arg
Pro	Met	Arg	Ile	Gly	Pro	Ala	Ala	Ser	Lys	Lys	Gly	Val	Thr	Gly
			225					230				235		Gln
Arg	Asp	Ser	Tyr	Gln	Ser	Ser	Ala	Ala	Gly	Val	Thr	Thr	Asp	Asn
			245					250				255		Asp
Pro	Asn	Asn	Thr	Thr	Val	Phe	Val	Gly	Gly	Leu	Asp	Ala	Ser	Val
			260					265				270		Thr

Asp Asp His Leu Lys Asn Val Phe Ser Gln Tyr Gly Glu Ile Val His
275 280 285
Val Lys Ile Pro Ala Gly Lys Arg Cys Gly Phe Val Gln Phe Ser Glu
290 295 300
Lys Ser Cys Ala Glu Glu Ala Leu Arg Met Leu Asn Gly Val Gln Leu
305 310 315 320
Gly Gly Thr Thr Val Arg Leu Ser Trp Gly Arg Ser Pro Ser Asn Lys
325 330 335
Gln Ser Gly Asp Pro Ser Gln Phe Tyr Tyr Gly Tyr Gly Gln Gly
340 345 350
Gln Glu Gln Tyr Gly Tyr Thr Met Pro Gln Asp Pro Asn Ala Tyr Tyr
355 360 365
Gly Gly Tyr Ser Gly Gly Gly Tyr Ser Gly Gly Tyr Gln Gln Thr Pro
370 375 380
Gln Ala Gly Gln Gln Pro Pro Gln Gln Pro Pro Gln Gln Gln Val
385 390 395 400
Gly Phe Ser Tyr

(2) INFORMATION FOR SEQ ID NO:1907:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 481 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..481
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571348

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1907:

atcttctctt	cttttgcttc	tcctttcttt	gagtgcttc	acttctcttg	catccttcaa	60
atctatccac	agcaaggaat	ggcgacagCa	gcagcaccag	cagtgatttc	atggacaaga	120
tcaggcatgt	tgcccaaat	oggacaaacc	cagaagaaat	ctgagatgaa	agtttcttac	180
ataactggac	ttaaactcata	tggttggttc	aaggcacaga	acaacaaggt	tgcttcaatg	240
ggatcaccac	ctgcacacaga	acagtgtttt	gctaacgttg	tgatgtctct	caaaaggaaga	300
agagttggat	tcgttcttct	tcgaatcgaa	acttctgttg	aagaagctga	agcagagtaa	360
atagagtaaa	ttgctgctct	tataattata	tatttttggt	tattgttgtt	gtcaagcttt	420
ggtaaaactt	gatggataca	tgttacattt	gtttatgaag	aagctctttt	cttggttagat	480

(2) INFORMATION FOR SEQ ID NO:1908:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..119
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571349

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1908:

Ile	Phe	Ser	Ser	Phe	Ala	Ser	Pro	Phe	Phe	Glu	Ser	Leu	His	Phe	Ser
1				5					10					15	
Cys	Ile	Leu	Gln	Thr	His	Pro	Gln	Gln	Gly	Met	Ala	Thr	Ala	Ala	Ala
			20					25					30		
Pro	Ala	Val	Ile	Ser	Trp	Thr	Arg	Ser	Gly	Ile	Val	Ser	Lys	Ser	Gly
			35				40				45				
Gln	Thr	Gln	Lys	Lys	Ser	Glu	Met	Lys	Val	Ser	Tyr	Ile	Thr	Gly	Leu
	50				55					60					
Asn	Ser	Tyr	Gly	Gly	Leu	Lys	Ala	Gln	Asn	Asn	Lys	Val	Val	Ser	Met
65				70				75						80	

Gly Ser Pro Leu Cys Thr Glu Gln Cys Phe Ala Asn Val Val Met Ser
85 90 95
Leu Lys Gly Arg Arg Val Gly Phe Val Leu Leu Arg Ile Glu Thr Ser
100 105 110
Val Glu Glu Ala Glu Ala Glu
115

(2) INFORMATION FOR SEQ ID NO:1909:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 93 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..93

(D) OTHER INFORMATION: / Ceres Seq. ID 1571350

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1909:

Met Ala Thr Ala Ala Pro Ala Val Ile Ser Trp Thr Arg Ser Gly
1 5 10 15
Ile Val Ser Lys Ser Gly Gln Thr Gln Lys Lys Ser Glu Met Lys Val
20 25 30
Ser Tyr Ile Thr Gly Leu Asn Ser Tyr Gly Gly Leu Lys Ala Gln Asn
35 40 45
Asn Lys Val Val Ser Met Gly Ser Pro Leu Cys Thr Glu Gln Cys Phe
50 55 60
Ala Asn Val Val Met Ser Leu Lys Gly Arg Arg Val Gly Phe Val Leu
65 70 75 80
Leu Arg Ile Glu Thr Ser Val Glu Glu Ala Glu Ala Glu
85 90

(2) INFORMATION FOR SEQ ID NO:1910:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 64 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..64

(D) OTHER INFORMATION: / Ceres Seq. ID 1571351

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1910:

Met Lys Val Ser Tyr Ile Thr Gly Leu Asn Ser Tyr Gly Gly Leu Lys
1 5 10 15
Ala Gln Asn Asn Lys Val Val Ser Met Gly Ser Pro Leu Cys Thr Glu
20 25 30
Gln Cys Phe Ala Asn Val Val Met Ser Leu Lys Gly Arg Arg Val Gly
35 40 45
Phe Val Leu Leu Arg Ile Glu Thr Ser Val Glu Glu Ala Glu Ala Glu
50 55 60

(2) INFORMATION FOR SEQ ID NO:1911:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 426 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1..51
(D) OTHER INFORMATION: / Ceres Seq. ID 1571363
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1914:
Met Lys Pro Lys Pro Gly Lys Pro Lys Ala Val Gly Asp Thr Lys Pro
1 5 10 15
Lys Glu Glu Lys Lys Lys Glu Val Lys Lys Glu Glu Ile Lys Lys Glu
20 25 30
Glu Lys Lys Glu Glu Lys Lys Glu Glu Lys Lys Glu Thr Lys Ala Glu
35 40 45
Lys Ala Glu
50

(2) INFORMATION FOR SEQ ID NO:1915:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 754 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..754

(D) OTHER INFORMATION: / Ceres Seq. ID 1571364

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1915:

aagtgactgc	gagcgccgaa	aatcgcaatg	ggtgcgtaca	aatacgtgtc	ggagctatgg	60
aggaagaagc	agtcggatgt	gatgagggtt	cttcagaggg	ttaggtgttg	ggagtatcgc	120
cagcagcctt	ccattgttgc	tctgtgtcgt	cccaactcgc	ccgacaaggc	tcgtcgtctc	180
ggctacaagg	ccaagcaggg	gtttgttgtc	taccgtgttc	gagtcagacg	tgggtggacg	240
aaagagccag	tgcctaaggg	tatcgtgtac	ggtaaaaccca	ccaaccaggg	agtgacacag	300
ctcaaattcc	agcgtagtta	gagatcgttt	gctgaggaaac	gtgctggtcg	caaacctggga	360
ggccttaggg	ttgttaactc	ctactggctc	aatgaggact	ctacctacaa	gtactacgag	420
attatccctg	tagaccctgc	acacaaatgcc	gtccgaaatg	atccaaggat	caactggatc	480
tgcaaccctg	tgacacaagca	cagagaactc	agaggctctca	ccctccgaaGg	aagaagaagt	540
cggtgtcttc	gtggaaaagg	tcacaacaac	cacaagaaca	gaccttcccc	cagggaacac	600
tggaagaaga	acaacagtat	ctctctccgt	cgttaccggt	gatcagtttt	atgtttttgt	660
ttttctcgaa	ctggtatatt	tacagtgtgg	attgtgtttc	ggaattctgg	aattacattg	720
ggatggaaga	ctttcacatt	caagagtttg	tttc			

(2) INFORMATION FOR SEQ ID NO:1916:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 204 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..204

(D) OTHER INFORMATION: / Ceres Seq. ID 1571365

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1916:

Met Gly Ala Tyr Lys Tyr Val Ser	Glu Leu Trp Arg Lys Lys Gln Ser	
1 5 10 15		
Asp Val Met Arg Phe Leu Gln Arg Val Arg Cys Trp Glu Tyr Arg Gln		
20 25 30		
Gln Pro Ser Ile Val Arg Leu Val Arg Pro Thr Arg Pro Asp Lys Ala		
35 40 45		
Arg Arg Leu Gly Tyr Lys Ala Lys Gln Gly Phe Val Val Tyr Arg Val		
50 55 60		
Arg Val Arg Arg Gly Gly Arg Lys Arg Pro Val Pro Lys Gly Ile Val		
65 70 75 80		
Tyr Gly Lys Pro Thr Asn Gln Gly Val Thr Gln Leu Lys Phe Gln Arg		
85 90 95		

Ser Lys Arg Ser Val Ala Glu Glu Arg Ala Gly Arg Lys Leu Gly Gly
100 105 110
Leu Arg Val Val Asn Ser Tyr Trp Leu Asn Glu Asp Ser Thr Tyr Lys
115 120 125
Tyr Tyr Glu Ile Ile Leu Val Asp Pro Ala His Asn Ala Val Arg Asn
130 135 140
Asp Pro Arg Ile Asn Trp Ile Cys Asn Pro Val His Lys His Arg Glu
145 150 155 160
Leu Arg Gly Leu Thr Ser Glu Gly Lys Lys Asn Arg Gly Leu Arg Gly
165 170 175
Lys Gly His Asn Asn His Lys Asn Arg Pro Ser Arg Arg Ala Thr Trp
180 185 190
Lys Lys Asn Asn Ser Ile Ser Leu Arg Arg Tyr Arg
195 200

(2) INFORMATION FOR SEQ ID NO:1917:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 186 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..186
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571366

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1917:

Met Arg Phe Leu Gln Arg Val Arg Cys Trp Glu Tyr Arg Gln Gln Pro
1 5 10 15
Ser Ile Val Arg Leu Val Arg Pro Thr Arg Pro Asp Lys Ala Arg Arg
20 25 30
Leu Gly Tyr Lys Ala Lys Gln Gly Phe Val Val Tyr Arg Val Arg Val
35 40 45
Arg Arg Gly Gly Arg Lys Arg Pro Val Pro Lys Gly Ile Val Tyr Gly
50 55 60
Lys Pro Thr Asn Gln Gly Val Thr Gln Leu Lys Phe Gln Arg Ser Lys
65 70 75 80
Arg Ser Val Ala Glu Glu Arg Ala Gly Arg Lys Leu Gly Gly Leu Arg
85 90 95
Val Val Asn Ser Tyr Trp Leu Asn Glu Asp Ser Thr Tyr Lys Tyr Tyr
100 105 110
Glu Ile Ile Leu Val Asp Pro Ala His Asn Ala Val Arg Asn Asp Pro
115 120 125
Arg Ile Asn Trp Ile Cys Asn Pro Val His Lys His Arg Glu Leu Arg
130 135 140
Gly Leu Thr Ser Glu Gly Lys Lys Asn Arg Gly Leu Arg Gly Lys Gly
145 150 155 160
His Asn Asn His Lys Asn Arg Pro Ser Arg Arg Ala Thr Trp Lys Lys
165 170 175
Asn Asn Ser Ile Ser Leu Arg Arg Tyr Arg
180 185

(2) INFORMATION FOR SEQ ID NO:1918:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 103 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..103
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571367

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1918:

Met Pro Ser Glu Met Ile Gln Gly Ser Thr Gly Ser Ala Thr Leu Cys
1 5 10 15
Thr Ser Thr Glu Asn Ser Glu Val Ser Pro Pro Lys Glu Arg Arg Ile
20 25 30
Val Val Phe Val Glu Arg Val Thr Thr Thr Arg Thr Asp Leu Pro
35 40 45
Ala Gly Gln Pro Gly Arg Arg Thr Thr Val Ser Leu Ser Val Val Thr
50 55 60
Gly Asp Gln Phe Tyr Val Leu Phe Phe Leu Glu Leu Val Tyr Leu Gln
65 70 75 80
Cys Gly Leu Cys Phe Gly Ile Leu Glu Leu His Trp Asp Gly Arg Leu
85 90 95
Ser His Ser Arg Val Cys Phe
100

(2) INFORMATION FOR SEQ ID NO:1919:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 651 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..651
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571372

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1919:

aaaagttccc ttctgttggtc atcggaatcc ctagaacact cgatttcagc aaaatcaaat 60
cggtattcagt gatcaaaagt caatttggtc gagaagaagt tgagcgttga agatgacgga 120
ggcgtatgata agaaataaagc caggaatggc gagtgtgaag gatatgccgc tgcttcagga 180
tggtccgccca cggggtgggt tcgcaccggt ccgatatgcc ccgccgatat ccaataccgg 240
tctagtgcga atggccaagt tctttgccgt ttctgggtgcc ttgtctggg gaattgacca 300
ggtcggccag ggaacaaaaa tccgcagggc attgaaggaa gagaatatg ctgctcgtag 360
aacaatactt cccattcttc aagcagaaga agatgaaagg ttgtgtctgt agtggaaaaa 420
gtatctggaa tatgaggtcg atgtaatgaa agatgttccg ggaatggaaa tgggcgagaa 480
tgtgtacaat tctggtcgct ggatGcctcc ggctactggg gaactccgtc ctgatgtgtg 540
gtgatcttct agtttctctc aaatgcataat gatgatgat aatgatgttt cgctgaggat 600
tgatatgttc ttgttatatc ttttttctt cgggtaataa gagaatgatt c

(2) INFORMATION FOR SEQ ID NO:1920:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 143 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..143
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571373

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1920:

Met Thr Glu Ala Met Ile Arg Asn Lys Pro Gly Met Ala Ser Val Lys
1 5 10 15
Asp Met Pro Leu Leu Gln Asp Gly Pro Pro Pro Gly Gly Phe Ala Pro
20 25 30
Val Arg Tyr Ala Arg Arg Ile Ser Asn Thr Gly Pro Ser Ala Met Ala
35 40 45
Met Phe Leu Ala Val Ser Gly Ala Phe Ala Trp Gly Met Tyr Gln Val
50 55 60
Gly Gln Gly Asn Lys Ile Arg Arg Ala Leu Lys Glu Glu Lys Tyr Ala
65 70 75 80
Ala Arg Arg Thr Ile Leu Pro Ile Leu Gln Ala Glu Glu Asp Glu Arg

	85		90		95
Phe Val Ser Glu Trp Lys Lys Tyr	Leu Glu Tyr Glu Ala Asp Val Met				
100	105		110		
Lys Asp Val Pro Gly Trp Lys Val Gly Glu Asn Val Tyr Asn Ser Gly					
115	120		125		
Arg Trp Met Pro Pro Ala Thr Gly Glu Leu Arg Pro Asp Val Trp					
130	135		140		

(2) INFORMATION FOR SEQ ID NO:1921:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 139 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..139

(D) OTHER INFORMATION: / Ceres Seq. ID 1571374

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1921:

Met Ile Arg Asn Lys Pro Gly Met Ala Ser Val Lys Asp Met Pro Leu					
1	5		10		15
Leu Gln Asp Gly Pro Pro Pro Gly Gly Phe Ala Pro Val Arg Tyr Ala					
20	25		30		
Arg Arg Ile Ser Asn Thr Gly Pro Ser Ala Met Ala Met Phe Leu Ala					
35	40		45		
Val Ser Gly Ala Phe Ala Trp Gly Met Tyr Gln Val Gly Gln Gly Asn					
50	55		60		
Lys Ile Arg Arg Ala Leu Lys Glu Glu Lys Tyr Ala Ala Arg Arg Thr					
65	70		75		80
Ile Leu Pro Ile Leu Gln Ala Glu Glu Asp Gly Arg Phe Val Ser Gly					
85	90		95		
Trp Lys Lys Tyr Leu Glu Tyr Glu Ala Asp Val Met Lys Asp Val Pro					
100	105		110		
Gly Trp Lys Val Gly Glu Asn Val Tyr Asn Ser Gly Arg Trp Met Pro					
115	120		125		
Pro Ala Thr Gly Glu Leu Arg Pro Asp Val Trp					
130	135				

(2) INFORMATION FOR SEQ ID NO:1922:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 132 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..132

(D) OTHER INFORMATION: / Ceres Seq. ID 1571375

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1922:

Met Ala Ser Val Lys Asp Met Pro Leu Leu Gln Asp Gly Pro Pro Pro					
1	5		10		15
Gly Gly Phe Ala Pro Val Arg Tyr Ala Arg Arg Ile Ser Asn Thr Gly					
20	25		30		
Pro Ser Ala Met Ala Met Phe Leu Ala Val Ser Gly Ala Phe Ala Trp					
35	40		45		
Gly Met Tyr Gln Val Gly Gln Gly Asn Lys Ile Arg Arg Ala Leu Lys					
50	55		60		
Glu Glu Lys Tyr Ala Ala Arg Arg Thr Ile Leu Pro Ile Leu Gln Ala					
65	70		75		80
Glu Glu Asp Glu Arg Phe Val Ser Glu Trp Lys Lys Tyr Leu Glu Tyr					
85	90		95		

Glu Ala Asp Val Met Lys Asp Val Pro Gly Trp Lys Val Gly Glu Asn
100 105 110
Val Tyr Asn Ser Gly Arg Trp Met Pro Pro Ala Thr Gly Glu Leu Arg
115 120 125
Pro Asp Val Trp
130

(2) INFORMATION FOR SEQ ID NO:1923:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1755 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1755

(D) OTHER INFORMATION: / Ceres Seq. ID 1571376

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1923:

acatctatct	ctttctctct	ctttccttgc	aaattttcag	ctctcaaaaga	gttaagaggtt	60
agagagagag	aggatgtgcca	ttagggaaaat	caaagatgta	gagagggggtg	aaatagtgaa	120
taaggtagaa	gatcttggga	aaccattttt	gactcatgaa	gatgatgaaa	aaagagagtga	180
gaataaagaa	tcaatattga	tggttctctt	cagtactttt	gttgctgtct	gtggctcctt	240
tgagttggcg	tctgtgtgtg	gatactcagc	gcctactcag	tcatctataa	gacaagatct	300
caatctctcc	cttgcagagt	tctccatggt	ttgatccatc	ttaactatcg	gtgcaatgct	360
tggtgctgtt	atgagtggga	aaatttcaga	tttctccggc	cgaaaaaggg	caatgaggac	420
gtcagcttgc	ttctgcatta	caggttggct	cgctgtcttc	ttcaccaagg	gggcatgttt	480
acttgatgta	ggaaagttct	ttacaggata	tggaaattga	gttttttctt	atgtgggtccc	540
tggtgacatt	gctgagatga	ctcccaagaa	tctccagagt	ggactcacaa	cactgaacca	600
actcatgatt	gtgacggctc	catgggtttc	tttcttgatc	ggactctcca	tttcttgtaa	660
aactctgtgc	ctaaccgtac	tgtctccctg	catgtgtttg	ctctttggct	tggtcttcac	720
acccgaatct	cctcgatggc	tggcaaaaag	aggccatgag	aaagagtttc	gcgtagccct	780
gcaaaagctg	cgaggaaaaag	atgcagatat	cacaaatgaa	gcagacggta	ttcaactctc	840
gattcaagct	ctagagattc	ttccaaaagc	agaattccaa	gcaccttgtg	ccaagaaata	900
tggtcgatct	gtcatcattg	gtgtttccct	gatggtatcc	caacagtttg	ttggaatacaa	960
tgggatcgga	ttctacgcaa	gtgaaacggt	tgtaaaagcc	ggatttacct	ctgggaaact	1020
aggaacaatc	gctatcgctt	gttcaggtgc	caataactgt	tcttggaaca	atcttgatag	1080
ataaatctgg	acgaaggcca	ctaattatga	tttcagctgg	tggtatcttc	ttgggatgca	1140
tactcacagg	cacatctttc	ttactcaagg	gacagagctt	gttgcttgaa	tggtgctcct	1200
ccttagccgt	tggaggtgta	cttatctatg	tagctgcttt	ctccatcgga	atgggacctg	1260
ttccttgggt	gataatgtct	gagatatctc	cgataaaact	aaaggggaac	gcagggaagct	1320
tagtggtaact	agtgaatttg	tctggtgctt	gggctgtttc	ttacactttc	aaacttccca	1380
tgagctggag	ctctccaggt	acattctatt	tgtactcggc	ttttgcagct	gcgcagataa	1440
tatttctggc	gaagatgggt	ccagagacga	aaggggaagc	actggaagag	atccaaagctt	1500
gtattcgaa	agaaacataa	gaagaaagat	acaatcaatg	ttatgggaat	gttatcaaat	1560
gaaaagactc	gaactattcc	cgttgggtgag	ctcaaaagtg	agtagagtaa	aaattatcgc	1620
cgggagataa	cgttgaaagt	ccgatgatga	ggcataaagg	ttttgcatga	atgttatgag	1680
aataggttta	cttttatgta	ttgttctcag	ttttTaagtt	ttcatcaaat	aggtttttga	1740
wtggtaaaaa	aaacc					

(2) INFORMATION FOR SEQ ID NO:1924:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 336 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..336

(D) OTHER INFORMATION: / Ceres Seq. ID 1571377

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1924:

Met Ala Ile Arg Glu Ile Lys Asp Val Glu Arg Gly Glu Ile Val Asn

1	5	10	15
Lys Val Glu Asp	Leu Gly Lys Pro	Phe Leu Thr His	Glu Asp Asp Glu
20	25	30	35
Lys Glu Ser Glu	Asn Asn Glu Ser	Tyr Leu Met Val	Leu Phe Ser Thr
40	45	50	55
Phe Val Ala Val	Cys Gly Ser Phe	Glu Phe Gly Ser	Cys Val Gly Tyr
60	65	70	75
Ser Ala Pro Thr	Gln Ser Ser Ile	Arg Gln Asp Leu	Asn Leu Ser Leu
80	85	90	95
Ala Glu Phe Ser	Met Phe Gly Ser	Ile Leu Thr Ile	Gly Ala Met Leu
100	105	110	115
Gly Ala Val Met	Ser Gly Lys Ile	Ser Asp Phe Ser	Gly Arg Lys Gly
120	125	130	135
Ala Met Arg Thr	Ser Ala Cys Phe	Cys Ile Thr Gly	Trp Leu Ala Val
140	145	150	155
Phe Phe Thr Lys	Gly Ala Leu Leu	Asp Val Gly Arg	Phe Phe Thr
160	165	170	175
Gly Tyr Gly Ile	Gly Val Phe Ser	Tyr Val Val Pro	Val Tyr Ile Ala
180	185	190	195
Glu Ile Ser Pro	Lys Asn Leu Arg	Gly Gly Leu Thr	Thr Leu Asn Gln
200	205	210	215
Leu Met Ile Val	Ile Gly Ser Ser	Val Ser Phe Leu	Ile Gly Ser Leu
220	225	230	235
Ile Ser Trp Lys	Thr Leu Ala Leu	Thr Val Leu Ala	Pro Cys Ile Val
240	245	250	255
Leu Leu Phe Gly	Leu Cys Phe Ile	Pro Glu Ser Pro	Arg Trp Leu Ala
260	265	270	275
Lys Ala Gly His	Glu Lys Glu Phe	Arg Val Ala Leu	Gln Lys Leu Arg
280	285	290	295
Gly Lys Asp Ala	Asp Ile Thr Asn	Glu Ala Asp Gly	Ile Gln Val Ser
300	305	310	315
Ile Gln Ala Leu	Glu Ile Leu Pro	Lys Ala Arg Ile	Gln Asp Leu Val
320	325	330	335
Ser Lys Lys Tyr	Gly Arg Ser Val	Ile Ile Gly Val	Ser Leu Met Val
340	345	350	355
Phe Gln Gln Phe	Val Gly Ile Asn	Gly Ile Gly Phe	Tyr Ala Ser Glu
360	365	370	375
Thr Phe Val Lys	Ala Gly Phe Thr	Ser Gly Lys Leu	Gly Thr Ile Ala
380	385	390	395
Ile Ala Cys Ser	Gly Ala Asn Asn	Cys Ser Trp Asn	Asn Leu Asp Arg

(2) INFORMATION FOR SEQ ID NO:1925:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 294 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..294

(D) OTHER INFORMATION: / Ceres Seq. ID 1571378

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1925:

Met Val Leu Phe	Ser Thr Phe Val	Ala Val Cys	Gly Ser Phe Glu Phe
1	5	10	15
Gly Ser Cys Val	Gly Tyr Ser Ala	Pro Thr Gln Ser	Ser Ile Arg Gln
20	25	30	35
Asp Leu Asn Leu	Ser Leu Ala Glu	Phe Ser Met Phe	Gly Ser Ile Leu
35	40	45	

Thr Ile Gly Ala Met Leu Gly Ala Val Met Ser Gly Lys Ile Ser Asp
50 55 60
Phe Ser Gly Arg Lys Gly Ala Met Arg Thr Ser Ala Cys Phe Cys Ile
65 70 75 80
Thr Gly Trp Leu Ala Val Phe Phe Thr Lys Gly Ala Leu Leu Leu Asp
85 90 95
Val Gly Arg Phe Phe Thr Gly Tyr Gly Ile Gly Val Phe Ser Tyr Val
100 105 110
Val Pro Val Tyr Ile Ala Glu Ile Ser Pro Lys Asn Leu Arg Gly Gly
115 120 125
Leu Thr Thr Leu Asn Gln Leu Met Ile Val Ile Gly Ser Ser Val Ser
130 135 140
Phe Leu Ile Gly Ser Leu Ile Ser Trp Lys Thr Leu Ala Leu Thr Val
145 150 155 160
Leu Ala Pro Cys Ile Val Leu Leu Phe Gly Leu Cys Phe Ile Pro Glu
165 170 175
Ser Pro Arg Trp Trp Leu Ala Lys Ala Gly His Glu Lys Glu Phe Arg Val
180 185 190
Ala Leu Gln Lys Leu Arg Gly Lys Asp Ala Asp Ile Thr Asn Glu Ala
195 200 205
Asp Gly Ile Gln Val Ser Ile Gln Ala Leu Glu Ile Leu Pro Lys Ala
210 215 220
Arg Ile Gln Asp Leu Val Ser Lys Lys Tyr Gly Arg Ser Val Ile Ile
225 230 235 240
Gly Val Ser Leu Met Val Phe Gln Gln Phe Val Gly Ile Asn Gly Ile
245 250 255
Gly Phe Tyr Ala Ser Glu Thr Phe Val Lys Ala Gly Phe Thr Ser Gly
260 265 270
Lys Leu Gly Thr Ile Ala Ile Ala Cys Ser Gly Ala Asn Asn Cys Ser
275 280 285
Trp Asn Asn Leu Asp Arg
290

(2) INFORMATION FOR SEQ ID NO:1926:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 252 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..252
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571379

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1926:

Met Phe Gly Ser Ile Leu Thr Ile Gly Ala Met Leu Gly Ala Val Met
1 5 10 15
Ser Gly Lys Ile Ser Asp Phe Ser Gly Arg Lys Gly Ala Met Arg Thr
20 25 30
Ser Ala Cys Phe Cys Ile Thr Gly Trp Leu Ala Val Phe Phe Thr Lys
35 40 45
Gly Ala Leu Leu Leu Asp Val Gly Arg Phe Phe Thr Gly Tyr Gly Ile
50 55 60
Gly Val Phe Ser Tyr Val Val Pro Val Tyr Ile Ala Glu Ile Ser Pro
65 70 75 80
Lys Asn Leu Arg Gly Gly Leu Thr Thr Leu Asn Gln Leu Met Ile Val
85 90 95
Ile Gly Ser Ser Val Ser Phe Leu Ile Gly Ser Leu Ile Ser Trp Lys
100 105 110
Thr Leu Ala Leu Thr Val Leu Ala Pro Cys Ile Val Leu Leu Phe Gly
115 120 125
Leu Cys Phe Ile Pro Glu Ser Pro Arg Trp Leu Ala Lys Ala Gly His

130 135 140
Glu Lys Glu Phe Arg Val Ala Leu Gln Lys Leu Arg Gly Lys Asp Ala
145 150 155 160
Asp Ile Thr Asn Glu Ala Asp Gly Ile Gln Val Ser Ile Gln Ala Leu
165 170 175
Glu Ile Leu Pro Lys Ala Arg Ile Gln Asp Leu Val Ser Lys Lys Tyr
180 185 190
Gly Arg Ser Val Ile Ile Gly Val Ser Leu Met Val Phe Gln Gln Phe
195 200 205
Val Gly Ile Asn Gly Ile Gly Phe Tyr Ala Ser Glu Thr Phe Val Lys
210 215 220
Ala Gly Phe Thr Ser Gly Lys Leu Gly Thr Ile Ala Ile Ala Cys Ser
225 230 235 240
Gly Ala Asn Asn Cys Ser Trp Asn Asn Leu Asp Arg
245 250

(2) INFORMATION FOR SEQ ID NO:1927:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 580 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..580
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571387

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1927:

ctgggtggtc	ttaactctctt	tatccgcttg	actaaagaaa	attggcgctgc	agtgatagag	60
acgaagaaga	agaagaaaaat	gccgtgcctc	aacctctcca	ccaacgttaa	ccttgacggc	120
gtcgatacat	cttcattctt	ctcggaagct	tctccaccg	tcgcgaaaaat	catcggaag	180
cctgagaact	atgtgatgat	tgtcttgaaa	ggctcagtcg	ctatgtcatt	tggcgggacc	240
gaggatcctg	cagcttatgt	tgaattagtt	tctatcggtg	gccttaatgc	ggatgtgaac	300
aagaagctaa	gcgctgctgt	tccgcctatt	cttgagacta	agctatcggt	gcccaagtct	360
cgattctctc	tcaagtttta	tgacaccaag	ggatccttct	ttggttgga	cgggcggaact	420
ctttaattcc	gtggtagggt	attagtgtga	ttgtcttaaa	atgtatgatc	tactctcacc	480
gatcaagtaa	ctttgaactA	cttcgtattg	taaacatact	taagggttga	tggagttgca	540
taaagaataa	acattttatgc	tatatatgat	gtcacaactc			

(2) INFORMATION FOR SEQ ID NO:1928:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 141 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..141
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571388

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1928:

Leu Gly Gly Leu Thr Leu Phe Ile Arg Leu Thr Lys Glu Asn Trp Arg	
1 5 10 15	
Arg Val Ile Glu Thr Lys Lys Lys Lys Lys Met Pro Cys Leu Asn Leu	
20 25 30	
Ser Thr Asn Val Asn Leu Asp Gly Val Asp Thr Ser Ser Ile Leu Ser	
35 40 45	
Glu Ala Ser Ser Thr Val Ala Lys Ile Ile Gly Lys Pro Glu Asn Tyr	
50 55 60	
Val Met Ile Val Leu Lys Gly Ser Val Pro Met Ser Phe Gly Gly Thr	
65 70 75 80	
Glu Asp Pro Ala Ala Tyr Gly Glu Leu Val Ser Ile Gly Gly Leu Asn	
85 90 95	

Ala Asp Val Asn Lys Lys Leu Ser Ala Ala Val Ser Ala Ile Leu Glu
100 105 110
Thr Lys Leu Ser Val Pro Lys Ser Arg Phe Phe Leu Lys Phe Tyr Asp
115 120 125
Thr Lys Gly Ser Phe Phe Gly Trp Asn Gly Ala Thr Leu
130 135 140

(2) INFORMATION FOR SEQ ID NO:1929:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..115

(D) OTHER INFORMATION: / Ceres Seq. ID 1571389

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1929:

Met Pro Cys Leu Asn Leu Ser Thr Asn Val Asn Leu Asp Gly Val Asp
1 5 10 15
Thr Ser Ser Ile Leu Ser Glu Ala Ser Ser Thr Val Ala Lys Ile Ile
20 25 30
Gly Lys Pro Glu Asn Tyr Val Met Ile Val Leu Lys Gly Ser Val Pro
35 40 45
Met Ser Phe Gly Gly Thr Glu Asp Pro Ala Ala Tyr Gly Glu Leu Val
50 55 60
Ser Ile Gly Gly Leu Asn Ala Asp Val Asn Lys Lys Leu Ser Ala Ala
65 70 75 80
Val Ser Ala Ile Leu Glu Thr Lys Leu Ser Val Pro Lys Ser Arg Phe
85 90 95
Phe Leu Lys Phe Tyr Asp Thr Lys Gly Ser Phe Phe Gly Trp Asn Gly
100 105 110
Ala Thr Leu
115

(2) INFORMATION FOR SEQ ID NO:1930:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 76 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..76

(D) OTHER INFORMATION: / Ceres Seq. ID 1571390

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1930:

Met Ile Val Leu Lys Gly Ser Val Pro Met Ser Phe Gly Gly Thr Glu
1 5 10 15
Asp Pro Ala Ala Tyr Gly Glu Leu Val Ser Ile Gly Gly Leu Asn Ala
20 25 30
Asp Val Asn Lys Lys Leu Ser Ala Ala Val Ser Ala Ile Leu Glu Thr
35 40 45
Lys Leu Ser Val Pro Lys Ser Arg Phe Phe Leu Lys Phe Tyr Asp Thr
50 55 60
Lys Gly Ser Phe Phe Gly Trp Asn Gly Ala Thr Leu
65 70 75

(2) INFORMATION FOR SEQ ID NO:1931:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1332 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single


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(A) NAME/KEY: -
(B) LOCATION: 1..1332
(D) OTHER INFORMATION: / Ceres Seq. ID 1571391
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acgacactttt	gtttctctct	tctctattaa	tactatagtt	tctctcaaac	tctctgatta	60
gctcctaattt	actcaaacgg	tgtgacattt	ttttctgata	aacaatcata	ggcaaggcta	120
ctcttggttgt	aggaagacgg	gtgacgaaaa	gggccactgga	caatctgaag	aggaacgaag	180
ctgtgttgact	atatccaggaa	actcgtgttat	ggtaactgga	gacacctccc	caaaaattgcc	240
ctttctgcaga	gagtggtgcaa	aagttgttagg	ttaaggtgga	ctaattatcg	ccgacagagt	300
ataaagcggg	gaaggtttctc	ttttgagagaa	gaagaaacca	ttatctagct	tcatgctctc	360
ttaagaaaca	agtggtctgc	gattgcggcg	cggtttaccg	tgaaacagca	tatgagatct	420
aagaactttt	ggaaactctca	tataaagaag	aagctactta	gaatggggat	tgatccaagt	480
actccacgtc	cacgactoga	tctctctgat	atctcatcca	tcttagcttc	atctctatac	540
aattatctct	cacatcacat	gaacatgtca	agactcatga	tggtactcaa	tcgtcgtcat	600
cgagcgcaac	atccattggt	taaccccgag	atactcaagc	tgcctacttc	tctctctctt	660
caaaatcaaa	accaaGaacc	tgtgtgtgga	ctatgactcg	agaaactcaag	aaagacaaac	720
agttttataga	caaacccggag	taaaccaata	ccaaaccgac	caatattatcg	agaaacagct	780
ctcttaagaa	ctccaactct	catcgccaac	attcccacat	gaagctctac	agtttaacaa	840
catggaatct	cacttcaatg	gtttttgga	acaaaattct	gtttaaactt	ctatcactgc	900
agtcacaagt	tgctataatc	cgctactcaa	cgtatttcca	agttcaaaat	ttgtcttgga	960
tctcttttat	tcggatcaga	gcttcaactt	cgcaaattcg	gtcttaaaac	cgccatctct	1020
ggcgcgcgag	cgcgactaogt	taaaactcgag	ttacataaat	agtagcagtt	gcagcactga	1080
ggatgaataa	gaagactatt	cgagtaattc	catgaagttt	gatatctccg	atttcttggg	1140
cgttaaaggt	ttatttatatt	aaatccaaga	acaaaataaa	actctcagat	ggatcactgt	1200
ttctttttat	ttctttgtgt	taatttaaga	cttttttttt	tgtttttcog	atttgtttac	1260
ttgtgaataa	ctggttttgt	tttgttgtta	atttgttata	ttctctcaga	tctttatagct	1320
aatacattct	tt					

[illegible]

145 150 155 160
Asn Arg Arg His His Gln Gln His Pro Leu Val Asn Pro Glu Ile Leu
165 170 175
Lys Leu Ala Thr Ser Leu Phe Ser Gln Asn Gln Asn Gln Glu Pro Cys
180 185 190
Gly Gly Ser
195

(2) INFORMATION FOR SEQ ID NO:1933:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..119
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571393

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1933:

Met Pro Pro Phe Pro Asn Glu Ala His Gln Phe Asn Asn Met Asp His
1 5 10 15
His Phe Asn Gly Phe Gly Glu Gln Asn Leu Val Ser Thr Ser Thr Thr
20 25 30
Ser Val Gln Asp Cys Tyr Asn Pro Ser Phe Asn Asp Tyr Ser Ser Ser
35 40 45
Asn Phe Val Leu Asp Pro Ser Tyr Ser Asp Gln Ser Phe Asn Phe Ala
50 55 60
Asn Ser Val Leu Asn Thr Pro Ser Ser Ser Pro Ser Pro Thr Thr Leu
65 70 75 80
Asn Ser Ser Tyr Ile Asn Ser Ser Ser Cys Ser Thr Glu Asp Glu Ile
85 90 95
Glu Ser Tyr Cys Ser Asn Leu Met Lys Phe Asp Ile Pro Asp Phe Leu
100 105 110
Asp Val Asn Gly Phe Ile Ile
115

(2) INFORMATION FOR SEQ ID NO:1934:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 106 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..106
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571394

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1934:

Met Asp His His Phe Asn Gly Phe Gly Glu Gln Asn Leu Val Ser Thr
1 5 10 15
Ser Thr Thr Ser Val Gln Asp Cys Tyr Asn Pro Ser Phe Asn Asp Tyr
20 25 30
Ser Ser Ser Asn Phe Val Leu Asp Pro Ser Tyr Ser Asp Gln Ser Phe
35 40 45
Asn Phe Ala Asn Ser Val Leu Asn Thr Pro Ser Ser Ser Pro Ser Pro
50 55 60
Thr Thr Leu Asn Ser Ser Tyr Ile Asn Ser Ser Cys Ser Thr Glu
65 70 75 80
Asp Glu Ile Glu Ser Tyr Cys Ser Asn Leu Met Lys Phe Asp Ile Pro
85 90 95
Asp Phe Leu Asp Val Asn Gly Phe Ile Ile
100 105

(2) INFORMATION FOR SEQ ID NO:1935:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1461 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1461
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571395

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1935:

actcaactct	ctttcgaaac	tcaatcctta	tataacacat	cccatGttaa	gcctataagc	60
tacaacatc	agctctctca	caaaaataaa	atggaggga	gccagtgac	cagtgctcagg	120
ctctctctgg	tgggtgcctgc	tctctgtgga	ggtgagaa	agccacgaca	gctcacaccc	180
atggagctag	ccatgaagct	ccactacgtc	cgagccgtct	acttcttcaa	gggtgcacgt	240
gacttcaact	tcgcccagct	gaagaacacc	atgtttactc	tacagtctct	actccaatct	300
tatcaccaac	tctcaggtcg	gatccggatg	tccgacaacg	acaacgacac	ttcagctgcga	360
gccataacct	caactcgtct	caacgacagt	ggcatacgcg	tggtcgaggc	caacgtcga	420
gagttccacg	tggagaagtg	gctcaggttg	gacgacgggt	ccattgacca	ccgatttctt	480
gtctacgac	acgttctctg	tcttgatctt	acottctcgc	cactcgtttt	ctccagata	540
actcagttta	aattgtgtgg	gctctgtatt	gggttgagtt	gggcccatat	tcttggagac	600
gtgttttcag	catcaacgtt	catgaaaaa	cttggacagc	tggtagtcgg	tcatgcccca	660
acaaaacggg	tttaccgcga	aacccccgaa	ctaacctctc	atgctcgtta	tgatggtgaa	720
gctattttcca	tfgaaaagat	agattcgggt	ggcgagttat	ggttacttac	caataaatcg	780
aagatggggga	gacacatttt	taatttttgc	ctcaaccaca	ttgatagctt	gatggccaa	840
tacacccacg	gagaccaaac	ttctctggag	gttgatattt	tgatgacatt	gatattgga	900
tcgctactga	atattccggg	cgaaacaaac	acgaattgta	taacaatttg	tgacgtgaa	960
aagttttcaa	ctgtgtggaa	cgaggacttg	gtaataacgc	tagtggaata	gaatgacgaa	1020
atggtttggg	tactcgaact	actgtcactg	attgctggtg	aaaaaagaga	agaaaacggt	1080
gcgatcaaga	ggatgataga	acaagataaa	ggctcttcgg	attttttcac	gtacgggtga	1140
aatttaacgt	ttgtgaatct	tgatgatatg	gaattgagat	caacggaggg	caacggaggg	1200
aagccggatt	tcgtaaaact	cacgattcat	gggttcggag	acaaggtgtg	tgttttggtt	1260
tttcccaacg	aaaactttgc	aaggattgta	agtgtagtga	tgccctgaaga	agaccttgca	1320
aaactcaagg	aggaggtgac	taatatgatt	atataacttt	gtatctctct	cttgttgtaa	1380
tacataaatg	ctgtttttta	ctctttgtaa	tttcattatc	gaattgttgg	gaagcctatc	1440
aataaattgt	ttgaactggt	t				

(2) INFORMATION FOR SEQ ID NO:1936:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 451 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..451
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571396

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1936:

Thr	Gln	Leu	Ser	Phe	Glu	Thr	Gln	Ser	Leu	Tyr	Asn	Thr	Ser	His	Val
1				5				10				15			
Lys	Pro	Ile	Ser	Tyr	Thr	Tyr	Gln	Leu	Ser	His	Lys	Asn	Lys	Met	Glu
				20				25				30			
Gly	Ser	Pro	Val	Thr	Ser	Val	Arg	Leu	Ser	Ser	Val	Pro	Ala	Ser	
				35				40				45			
Val	Val	Gly	Glu	Asn	Lys	Pro	Arg	Gln	Leu	Thr	Pro	Met	Asp	Leu	Ala
				50				55				60			
Met	Lys	Leu	His	Tyr	Val	Arg	Ala	Val	Tyr	Phe	Phe	Lys	Gly	Ala	Arg
				65				70				75			80
Asp	Phe	Thr	Val	Thr	Ala	Asp	Val	Lys	Asn	Thr	Met	Phe	Thr	Leu	Gln
				85				90				95			

Leu Leu Gln Ser Tyr His His Val Ser Gly Arg Ile Arg Met Ser Asp
100 105 110
Asn Asp Asn Asp Thr Ser Ala Ala Ala Ile Pro Tyr Ile Arg Cys Asn
115 120 125
Asp Ser Gly Ile Arg Val Val Glu Ala Asn Val Glu Phe Thr Val
130 135 140
Glu Lys Trp Leu Glu Leu Asp Asp Arg Ser Ile Asp His Arg Phe Leu
145 150 155 160
Val Tyr Asp His Val Leu Gly Pro Asp Leu Thr Phe Ser Pro Leu Val
165 170 175
Phe Leu Gln Ile Thr Gln Phe Lys Cys Gly Gly Leu Cys Ile Gly Leu
180 185 190
Ser Trp Ala His Ile Leu Gly Asp Val Phe Ser Ala Ser Thr Phe Met
195 200 205
Lys Thr Leu Gly Gln Leu Val Ser Gly His Ala Pro Thr Lys Pro Val
210 215 220
Tyr Pro Lys Thr Pro Glu Leu Thr Ser His Ala Arg Asn Asp Gly Glu
225 230 235 240
Ala Ile Ser Ile Glu Lys Ile Asp Ser Val Gly Glu Tyr Trp Leu Leu
245 250 255
Thr Asn Lys Cys Lys Met Gly Arg His Ile Phe Asn Phe Ser Leu Asn
260 265 270
His Ile Asp Ser Leu Met Ala Lys Tyr Thr Thr Arg Asp Gln Pro Phe
275 280 285
Ser Glu Val Asp Ile Leu Tyr Ala Leu Ile Trp Lys Ser Leu Leu Asn
290 295 300
Ile Arg Gly Glu Thr Asn Thr Asn Val Ile Thr Ile Cys Asp Arg Lys
305 310 315 320
Lys Ser Ser Thr Cys Trp Asn Glu Asp Leu Val Ile Ser Val Val Glu
325 330 335
Lys Asn Asp Glu Met Val Gly Ile Ser Glu Leu Ala Ala Leu Ile Ala
340 345 350
Gly Glu Lys Arg Glu Glu Asn Gly Ala Ile Lys Arg Met Ile Glu Gln
355 360 365
Asp Lys Gly Ser Ser Asp Phe Phe Thr Tyr Gly Ala Asn Leu Thr Phe
370 375 380
Val Asn Leu Asp Glu Ile Asp Met Tyr Glu Leu Glu Ile Asn Gly Gly
385 390 395 400
Lys Pro Asp Phe Val Asn Tyr Thr Ile His Gly Val Gly Asp Lys Gly
405 410 415
Val Val Leu Val Phe Pro Lys Gln Asn Phe Ala Arg Ile Val Ser Val
420 425 430
Val Met Pro Glu Glu Asp Leu Ala Lys Leu Lys Glu Glu Val Thr Asn
435 440 445
Met Ile Ile
450

(2) INFORMATION FOR SEQ ID NO:1937:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 421 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..421

(D) OTHER INFORMATION: / Ceres Seq. ID 1571397

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1937:

Met Glu Gly Ser Pro Val Thr Ser Val Arg Leu Ser Ser Val Val Pro
1 5 10 15
Ala Ser Val Val Gly Glu Asn Lys Pro Arg Gln Leu Thr Pro Met Asp

(B) LOCATION: 1..391

(D) OTHER INFORMATION: / Ceres Seq. ID 1571398

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1938:

Met	Asp	Leu	Ala	Met	Lys	Leu	His	Tyr	Val	Arg	Ala	Val	Tyr	Phe	Phe
1				5				10						15	
Lys	Gly	Ala	Arg	Asp	Phe	Thr	Val	Ala	Asp	Val	Lys	Asn	Thr	Met	Phe
				20				25						30	
Thr	Leu	Gln	Ser	Leu	Leu	Gln	Ser	Tyr	His	His	Val	Ser	Gly	Arg	Ile
				35				40						45	
Arg	Met	Ser	Asp	Asn	Asp	Asn	Asp	Thr	Ser	Ala	Ala	Ala	Ile	Pro	Tyr
				50				55						60	
Ile	Arg	Cys	Asn	Asp	Ser	Gly	Ile	Arg	Val	Val	Glu	Ala	Asn	Val	Glu
65					70				75					80	
Glu	Phe	Thr	Val	Glu	Lys	Trp	Leu	Glu	Leu	Asp	Asp	Arg	Ser	Ile	Asp
				85					90					95	
His	Arg	Phe	Leu	Val	Tyr	Asp	His	Val	Leu	Gly	Pro	Asp	Leu	Thr	Phe
				100				105						110	
Ser	Pro	Leu	Val	Phe	Leu	Gln	Ile	Thr	Gln	Phe	Lys	Cys	Gly	Gly	Leu
				115				120						125	
Cys	Ile	Gly	Leu	Ser	Trp	Ala	His	Ile	Leu	Gly	Asp	Val	Phe	Ser	Ala
				130				135						140	
Ser	Thr	Phe	Met	Lys	Thr	Leu	Gly	Gln	Leu	Val	Ser	Gly	His	Ala	Pro
145					150					155				160	
Thr	Lys	Pro	Val	Tyr	Pro	Lys	Thr	Pro	Glu	Leu	Thr	Ser	His	Ala	Arg
				165					170					175	
Asn	Asp	Gly	Glu	Ala	Ile	Ser	Ile	Glu	Lys	Ile	Asp	Ser	Val	Gly	Glu
				180				185						190	
Tyr	Trp	Leu	Leu	Thr	Asn	Lys	Cys	Lys	Met	Gly	Arg	His	Ile	Phe	Asn
				195				200						205	
Phe	Ser	Leu	Asn	His	Ile	Asp	Ser	Leu	Met	Ala	Lys	Tyr	Thr	Thr	Arg
				210				215						220	
Asp	Gln	Pro	Phe	Ser	Glu	Val	Asp	Ile	Leu	Tyr	Ala	Leu	Ile	Trp	Lys
225					230					235				240	
Ser	Leu	Leu	Asn	Ile	Arg	Gly	Glu	Thr	Asn	Thr	Asn	Val	Ile	Thr	Ile
				245					250					255	
Cys	Asp	Arg	Lys	Lys	Ser	Ser	Thr	Cys	Trp	Asn	Glu	Asp	Leu	Val	Ile
				260				265						270	
Ser	Val	Val	Glu	Lys	Asn	Asp	Glu	Met	Val	Gly	Ile	Ser	Glu	Leu	Ala
				275				280						285	
Ala	Leu	Ile	Ala	Gly	Glu	Lys	Arg	Glu	Glu	Asn	Gly	Ala	Ile	Lys	Arg
				290				295						300	
Met	Ile	Glu	Gln	Asp	Lys	Gly	Ser	Ser	Asp	Phe	Phe	Thr	Tyr	Gly	Ala
305					310					315				320	
Asn	Leu	Thr	Phe	Val	Asn	Leu	Asp	Glu	Ile	Asp	Met	Tyr	Glu	Leu	Glu
				325					330					335	
Ile	Asn	Gly	Gly	Lys	Pro	Asp	Phe	Val	Asn	Tyr	Thr	Ile	His	Gly	Val
				340				345						350	
Gly	Asp	Lys	Gly	Val	Val	Leu	Val	Phe	Pro	Lys	Gln	Asn	Phe	Ala	Arg
				355				360						365	
Ile	Val	Ser	Val	Val	Met	Pro	Glu	Glu	Asp	Leu	Ala	Lys	Leu	Lys	Glu
				370				375						380	
Glu	Val	Thr	Asn	Met	Ile	Ile									
385					390										

(2) INFORMATION FOR SEQ ID NO:1939:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1193 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1193

(D) OTHER INFORMATION: / Ceres Seq. ID 1571418

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1939:

ctcttttagca	aaaaatctca	gaactcaRaa	aaaaaaCaSR	tcacaaccca	aagacaatgS	60
gagatgagtt	tgcgtctcgc	tcatottcca	acctcaaaac	caattgtgtc	actaaacct	120
ggaaaaaac	ttaatttccc	aatccgaaac	catagaatcc	ctaaaaatc	gaaaccttt	180
tgcgttaggt	cttcaatgag	cttgctcaaa	ccaccagac	aaactctatc	tagtaactgg	240
gatgtatcta	gtctctccat	tgattccggt	gtcactctc	cttcaagact	cccaagtttc	300
gaagaactcg	ataccaccaa	catgttgctc	cgtcaaaagaa	tcgtctttt	gggttctcag	360
gttgatgata	tgacggcgga	tttggttata	agtcaagctat	tgttactaga	tgcgtaggac	420
tcagaaagag	acattacgct	ttttatcaat	tcaccgggtg	gatctattac	tgcgtggatg	480
ggaatatatg	atgcaatgaa	acaatgtaag	gcggatgtat	ctactgtttg	cttaggggta	540
gctgcattcta	tggtgtcggt	tcttcttgct	tctggttcaa	aagggaacg	gtattgtgat	600
ctcaactcta	aagttaigtat	ccatcagcca	cttggtactg	ctggaggcaa	agcaacggaa	660
atgagcatac	gtataagaga	aatgatgtac	cacaagatta	aacttaacaa	aatcttctct	720
agaatcactg	ggagacgtga	atcagagatc	gaaagtgaac	cagaccgtga	taacttcttg	780
aatccatggg	aggcgaaaga	atatggtttg	atcgacgctg	taatcgatga	tgggaaaccg	840
ggactaatcg	ctccaattgg	agatggtact	cctctctcta	aaaccaaagt	ctggggtctt	900
tggaagagtc	aaggaaccaa	gaaagacaa	actaacttgc	catctgagcg	ctccatgaca	960
cagaaatggt	atgccgccat	tgaatagaac	tgttggtgca	gcgtttacgc	cttttatatg	1020
tatttctggt	ggtacctgtg	accatataac	gttgcaattc	ctgtgtttgt	accatttctc	1080
tgatagattt	tgtgaataat	tgaaggcaa	aagatagatt	atttgtgtga	gaagaagcta	1140
caaaatttaa	tgattaaatt	gaatcataac	gccatgagaa	gctttgtgtt	ttc	

(2) INFORMATION FOR SEQ ID NO:1940:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 328 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..328

(D) OTHER INFORMATION: / Ceres Seq. ID 1571419

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1940:

Leu	Phe	Ser	Lys	Lys	Ser	Gln	Asn	Ser	Xaa	Lys	Lys	Xaa	Xaa	Gln	His
1			5				10							15	
Gln	Arg	Gln	Xaa	Glu	Met	Ser	Leu	Arg	Leu	Ala	Ser	Ser	Ser	Thr	Ser
			20				25							30	
Asn	Pro	Ile	Cys	Leu	Leu	Asn	Pro	Gly	Lys	Asn	Leu	Asn	Phe	Pro	Ile
			35				40					45			
Arg	Asn	His	Arg	Ile	Pro	Lys	Thr	Ser	Lys	Pro	Phe	Cys	Val	Arg	Ser
			50				55					60			
Ser	Met	Ser	Leu	Ser	Lys	Pro	Pro	Arg	Gln	Thr	Leu	Ser	Ser	Asn	Trp
			65				70					75			80
Asp	Val	Ser	Ser	Phe	Ser	Ile	Asp	Ser	Val	Ala	Gln	Ser	Pro	Ser	Arg
			85				90							95	
Leu	Pro	Ser	Phe	Glu	Glu	Leu	Asp	Thr	Thr	Asn	Met	Leu	Leu	Arg	Gln
			100				105							110	
Arg	Ile	Val	Phe	Leu	Gly	Ser	Gln	Val	Asp	Asp	Met	Thr	Ala	Asp	Leu
			115				120							125	
Val	Ile	Ser	Gln	Leu	Leu	Leu	Leu	Asp	Ala	Glu	Asp	Ser	Glu	Arg	Asp
			130				135							140	
Ile	Thr	Leu	Phe	Ile	Asn	Ser	Pro	Gly	Ser	Gly	Ile	Thr	Ala	Gly	Met
			145				150							155	160
Gly	Ile	Tyr	Asp	Ala	Met	Lys	Gln	Cys	Lys	Ala	Asp	Val	Ser	Thr	Val
			165				170							175	
Cys	Leu	Gly	Leu	Ala	Ala	Ser	Met	Gly	Ala	Phe	Leu	Leu	Ala	Ser	Gly
			180				185							190	
Ser	Lys	Gly	Lys	Arg	Tyr	Cys	Met	Pro	Asn	Ser	Lys	Val	Met	Ile	His
			195				200							205	

Gln	Pro	Leu	Gly	Thr	Ala	Gly	Gly	Lys	Ala	Thr	Glu	Met	Ser	Ile	Arg	
210						215					220					
Ile	Arg	Glu	Met	Met	Tyr	His	Lys	Ile	Lys	Leu	Asn	Lys	Ile	Phe	Ser	
225					230					235					240	
Arg	Ile	Thr	Gly	Lys	Pro	Glu	Ser	Glu	Ile	Glu	Ser	Asp	Thr	Asp	Arg	
			245						250					255		
Asp	Asn	Phe	Leu	Asn	Pro	Trp	Glu	Ala	Lys	Glu	Tyr	Gly	Leu	Ile	Asp	
			260					265					270			
Ala	Val	Ile	Asp	Asp	Gly	Lys	Pro	Gly	Leu	Ile	Ala	Pro	Ile	Gly	Asp	
		275					280					285				
Gly	Thr	Pro	Pro	Pro	Lys	Thr	Lys	Val	Trp	Asp	Leu	Trp	Lys	Val	Glu	
290					295						300					
Gly	Thr	Lys	Lys	Asp	Asn	Thr	Asn	Leu	Pro	Ser	Glu	Arg	Ser	Met	Thr	
305					310					315					320	
Gln	Asn	Gly	Tyr	Ala	Ala	Ile	Glu									
					325											

(2) INFORMATION FOR SEQ ID NO:1941:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 307 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..307
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571420

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1941:

Met	Ser	Leu	Arg	Leu	Ala	Ser	Ser	Ser	Thr	Ser	Asn	Pro	Ile	Cys	Leu	
1				5					10					15		
Leu	Asn	Pro	Gly	Lys	Asn	Leu	Asn	Phe	Pro	Ile	Arg	Asn	His	Arg	Ile	
			20					25					30			
Pro	Lys	Thr	Ser	Lys	Pro	Phe	Cys	Val	Arg	Ser	Ser	Met	Ser	Leu	Ser	
		35				40						45				
Lys	Pro	Pro	Arg	Gln	Thr	Leu	Ser	Ser	Asn	Trp	Asp	Val	Ser	Ser	Phe	
	50				55					60						
Ser	Ile	Asp	Ser	Val	Ala	Gln	Ser	Pro	Ser	Arg	Leu	Pro	Ser	Phe	Glu	
65				70					75					80		
Glu	Leu	Asp	Thr	Thr	Asn	Met	Leu	Leu	Arg	Gln	Arg	Ile	Val	Phe	Leu	
			85					90					95			
Gly	Ser	Gln	Val	Asp	Asp	Met	Thr	Ala	Asp	Leu	Val	Ile	Ser	Gln	Leu	
		100					105					110				
Leu	Leu	Leu	Asp	Ala	Glu	Asp	Ser	Glu	Arg	Asp	Ile	Thr	Leu	Phe	Ile	
		115				120					125					
Asn	Ser	Pro	Gly	Gly	Ser	Ile	Thr	Ala	Gly	Met	Gly	Ile	Tyr	Asp	Ala	
		130				135					140					
Met	Lys	Gln	Cys	Lys	Ala	Asp	Val	Ser	Thr	Val	Cys	Leu	Gly	Leu	Ala	
145				150					155					160		
Ala	Ser	Met	Gly	Ala	Phe	Leu	Leu	Ala	Ser	Gly	Ser	Lys	Gly	Lys	Arg	
			165						170				175			
Tyr	Cys	Met	Pro	Asn	Ser	Lys	Val	Met	Ile	His	Gln	Pro	Leu	Gly	Thr	
		180					185						190			
Ala	Gly	Gly	Lys	Ala	Thr	Glu	Met	Ser	Ile	Arg	Ile	Arg	Glu	Met	Met	
	195					200						205				
Tyr	His	Lys	Ile	Lys	Leu	Asn	Lys	Ile	Phe	Ser	Arg	Ile	Thr	Gly	Lys	
	210					215					220					
Pro	Glu	Ser	Glu	Ile	Glu	Ser	Asp	Thr	Asp	Arg	Asp	Asn	Phe	Leu	Asn	
225					230				235					240		
Pro	Trp	Glu	Ala	Lys	Glu	Tyr	Gly	Leu	Ile	Asp	Ala	Val	Ile	Asp	Asp	
			245					250					255			
Gly	Lys	Pro	Gly	Leu	Ile	Ala	Pro	Ile	Gly	Asp	Gly	Thr	Pro	Pro	Pro	

(2) INFORMATION FOR SEQ ID NO:1942:

(A) LENGTH: 263 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..263
(D) OTHER INFORMATION: / Ceres Seq. ID 1571421

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1942:

(2) INFORMATION FOR SEQ ID NO:1943:

(A) LENGTH: 1191 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -
(B) LOCATION: 1.1191
(D) OTHER INFORMATION: / Ceres Seq. ID 1571422

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1943:

taccattctt	ctgaaaaatga	acacctcaga	agccctaagc	accacaatga	ttttgggcac	60
cacactagaa	aaccacagcg	tgctgtgaag	cctgatgctt	tgaaggagcc	tcacattatt	120
gatgtgcctg	cattgtcatt	ggatgatgtg	aaagaaaaga	ccgataacct	tggatcaaaag	180
tcattgattg	gtgaaggatc	ttacggcaga	gcctattatg	caaccttgaa	agatggaaaag	240
gctgtgcggg	tgaagaagct	tgacaatgca	gcggaacctg	aatcaaatgt	tgagtctctt	300
actcaggtct	cgagggtttc	caagctgaag	cacgataatt	ttgttgagct	cttcgggtat	360
tgcgttgaag	ggaatttcgc	cattcttcgc	tatgagtttg	ctactatggg	atctttacat	420
gacatcttac	acggggaggaa	aggagtcaca	ggagcacac	caggtcactg	gcttgacttg	480
atccaaaggg	tcagaataga	atttgatgca	gctagaggac	ttgagtattt	gcatgagaaa	540
gttcaacctg	cagtaataca	cagagatatt	cgatctagca	atgtgctctt	ctttgaagat	600
tttaaaagcca	agatcgctga	ttttaatcta	tcgaaccaat	ctcctgatat	ggctgctcgt	660
cttcattcta	ccagagtttt	gggaatcttc	ggttaccacg	caccagagta	tgcgatgact	720
ggtaacatga	cacagaagag	fgatgtttat	agtttttggt	tggtgctttt	ggagctcttg	780
actggtagga	aaccgcctga	tcatacgatg	cctcgtgtgc	aacaaagtct	tgttactctg	840
gctactccaa	ggctaaagtga	agacaaagt	aagcaatgtg	ttgatccaaa	actaaaggaa	900
gaatatcctc	ctaaagctgt	tgcaaaagct	gctgcagtag	cagcattgtg	tgtgcaaat	960
gaatcagagt	ttagggcaaa	cattgcagct	gtggtaaaag	ctctcaacc	attgtgtgag	1020
tcatacaacg	cagcagctgt	accagtcag	gaagcctgat	tcttctgtgc	aatagcaaca	1080
atgggaagatt	gggttcgggt	tcagttgttg	ccataccgta	taaatgtgtt	cttaaagaga	1140
gtctttttgt	cgaggctttt	cttcagttaa	gagctccaaa	agcaccacac	c	

(2) INFORMATION FOR SEQ ID NO:1944:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 352 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1.352
(D) OTHER INFORMATION: / Ceres Seq. ID 1571423

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1944:

Tyr	His	Ser	Ser	Glu	Asn	Glu	His	Leu	Arg	Ser	Pro	Lys	His	His	Asn
1				5					10					15	
Asp	Phe	Gly	His	His	Thr	Arg	Lys	Pro	Gln	Ala	Ala	Val	Lys	Pro	Asp
			20					25				30			
Ala	Leu	Lys	Glu	Pro	Pro	Ser	Ile	Asp	Val	Pro	Ala	Leu	Ser	Leu	Asp
		35					40				45				
Glu	Leu	Lys	Glu	Lys	Thr	Asp	Asn	Phe	Gly	Ser	Lys	Ser	Leu	Ile	Gly
		50				55				60					
Glu	Gly	Ser	Tyr	Gly	Arg	Ala	Tyr	Tyr	Ala	Thr	Leu	Lys	Asp	Gly	Lys
		65			70				75					80	
Ala	Val	Ala	Val	Lys	Lys	Leu	Asp	Asn	Ala	Ala	Glu	Pro	Glu	Ser	Asn
			85					90					95		
Val	Glu	Phe	Leu	Thr	Gln	Val	Ser	Arg	Val	Ser	Lys	Leu	Lys	His	Asp
			100					105					110		
Asn	Phe	Val	Glu	Leu	Phe	Gly	Tyr	Cys	Val	Glu	Gly	Asn	Phe	Arg	Ile
		115				120						125			
Leu	Ala	Tyr	Glu	Phe	Ala	Thr	Met	Gly	Ser	Leu	His	Asp	Ile	Leu	His
		130				135					140				
Gly	Arg	Lys	Gly	Val	Gln	Gly	Ala	Gln	Pro	Gly	Pro	Thr	Leu	Asp	Trp
		145			150				155					160	
Ile	Gln	Arg	Val	Arg	Ile	Ala	Val	Asp	Ala	Ala	Arg	Gly	Leu	Glu	Tyr
			165					170					175		
Leu	His	Glu	Lys	Val	Gln	Pro	Ala	Val	Ile	His	Arg	Asp	Ile	Arg	Ser
		180					185					190			
Ser	Asn	Val	Leu	Leu	Phe	Glu	Asp	Phe	Lys	Ala	Lys	Ile	Ala	Asp	Phe

195	200	205
Asn Leu Ser Asn Gln Ser Pro Asp Met Ala Ala Arg Leu His Ser Thr		
210	215	220
Arg Val Leu Gly Xaa Phe Gly Tyr His Ala Pro Glu Tyr Ala Met Thr		
225	230	235
Gly Gln Leu Thr Gln Lys Ser Asp Val Tyr Ser Phe Gly Val Val Leu		
	245	250
Leu Glu Leu Leu Thr Gly Arg Lys Pro Val Asp His Thr Met Pro Arg		
	260	265
Gly Gln Gln Ser Leu Val Thr Trp Ala Thr Pro Arg Leu Ser Glu Asp		
	275	280
Lys Val Lys Gln Cys Val Asp Pro Lys Leu Lys Gly Glu Tyr Pro Pro		
	290	295
Lys Ala Val Ala Lys Leu Ala Ala Val Ala Ala Leu Cys Val Gln Tyr		
305	310	315
Glu Ser Glu Phe Arg Pro Asn Met Ser Ile Val Val Lys Ala Leu Gln		
	325	330
Pro Leu Leu Arg Ser Ser Thr Ala Ala Ala Val Pro Val Gln Glu Ala		
	340	345
		350

(2) INFORMATION FOR SEQ ID NO:1945:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 217 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..217

(D) OTHER INFORMATION: / Ceres Seq. ID 1571424

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1945:

Met Gly Ser Leu His Asp Ile Leu His Gly Arg Lys Gly Val Gln Gly	
1	5 10 15
Ala Gln Pro Gly Pro Thr Leu Asp Trp Ile Gln Arg Val Arg Ile Ala	
	20 25 30
Val Asp Ala Ala Arg Gly Leu Glu Tyr Leu His Glu Lys Val Gln Pro	
	35 40 45
Ala Val Ile His Arg Asp Ile Arg Ser Ser Asn Val Leu Leu Phe Glu	
	50 55 60
Asp Phe Lys Ala Lys Ile Ala Asp Phe Asn Leu Ser Asn Gln Ser Pro	
65	70 75 80
Asp Met Ala Ala Arg Leu His Ser Thr Arg Val Leu Gly Xaa Phe Gly	
	85 90 95
Tyr His Ala Pro Glu Tyr Ala Met Thr Gly Gln Leu Thr Gln Lys Ser	
	100 105 110
Asp Val Tyr Ser Phe Gly Val Val Leu Leu Glu Leu Thr Gly Arg	
	115 120 125
Lys Pro Val Asp His Thr Met Pro Arg Gly Gln Gln Ser Leu Val Thr	
	130 135 140
Trp Ala Thr Pro Arg Leu Ser Glu Asp Lys Val Lys Gln Cys Val Asp	
145	150 155 160
Pro Lys Leu Lys Gly Glu Tyr Pro Pro Lys Ala Val Ala Lys Leu Ala	
	165 170 175
Ala Val Ala Ala Leu Cys Val Gln Tyr Glu Ser Glu Phe Arg Pro Asn	
	180 185 190
Met Ser Ile Val Val Lys Ala Leu Gln Pro Leu Leu Arg Ser Ser Thr	
	195 200 205
Ala Ala Ala Val Pro Val Gln Glu Ala	
	210 215

(2) INFORMATION FOR SEQ ID NO:1946:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1500 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1500
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571425

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1946:

aacgcttgcga	cagctctctac	accgctcatga	acactgaatc	agttgtcgag	ttccttggga	60
atgtgacctt	gttcgacggg	ttacctagtt	cctctctgaa	gagaatctcc	gaagtctgtt	120
ctctcaaaag	ttatgacaga	ggtgattatg	tggttcgtga	aaatcaaaat	gtggatggag	180
tttatttttc	cttgcaagga	caggctcagg	ttctgagatc	agccgaagag	gaaaaactac	240
aagagttccc	tttgaacga	tatgatttct	tcggccatgg	tattttcggg	gatgtttaact	300
cagcagatgt	tggtgctgtg	acagagctta	cctgcttgct	gttgatgtct	gatcatcgtg	360
ctttacttga	aataaagtca	gtctcggatt	cgataaagga	acgctgtctt	gtggaagaca	420
tactatatct	agaaccatta	gatttgaatg	tataccgggg	gttcacccca	cctaagctc	480
caacctatgg	aaagggtttat	ggaggccaat	tagttggaca	ggcacttgcc	gcagcatcaa	540
aaactgttga	aactatgaag	atagtcacata	attttcattg	ctatttccct	cttgttggag	600
atataaatat	tcccatcata	tatgatgtta	acogcttacg	tgacggcaac	aaacttgcga	660
ccagaaagtgt	agatgctaga	cagaaaaggaa	aaactatatt	acccttgctc	gcgtcatttc	720
agaaaaagca	acaaagtttt	attcaccagg	agtcgaccat	gcctcataca	ccagctcctg	780
aaacgcttct	accaaaggag	gagatgcttg	aacggcttgg	tactgacctt	ctgtcactcta	840
gggattaccg	aaaccaaagt	gcaactgaaa	ttagtgttcc	attccctata	gatatttcgat	900
tttgtgagcg	aaactcgttcc	actaaacaga	ataagctctc	tcacaagacta	aaatatttgtt	960
ttagagcaaa	gggaaaaact	tctgatgatg	atcaagcttt	gcacagatgt	gtgggttgcat	1020
ttgtctccga	tttgatactc	gccactatca	gtttaaaccc	tcaccggaga	gagggcatga	1080
gtgtagctgc	tcttagcctg	gaccactcga	tgtgtgtcca	ccgacctgtg	agagcagatg	1140
attgggtgtg	gtttgtgtga	gtccaactgc	gacctaaagc	cgcggttttg	caactgggcaa	1200
aatgttcaac	agaaaaggag	agctgggtgt	atcattgacg	caagaagctg	tgtaaagaga	1260
agctgtgact	atgaagccat	ccttcggggc	caagctatga	agccatagga	ttttgatagt	1320
gagagaattg	ctgcactctg	tactcctcac	ggtcacattc	caaaagctcg	tcacttatca	1380
tacattttgca	tatgtttttc	gatccacaat	tattattttc	ccctctaaaa	gggtctacac	1440
atcatgttgt	ttgtaaccac	gataatgttt	caacagcaat	gaaaaagcaa	acagtgtgtc	1500

(2) INFORMATION FOR SEQ ID NO:1947:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 385 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..385
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571426

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1947:

Arg	Phe	Asp	Ser	Leu	Tyr	Thr	Val	Met	Asn	Thr	Glu	Ser	Val	Val	Glu
1			5						10				15		
Phe	Leu	Gly	Asn	Val	Thr	Leu	Leu	Gln	Arg	Leu	Pro	Ser	Ser	Ser	Leu
			20					25				30			
Lys	Arg	Ile	Ser	Glu	Val	Val	Val	Phe	Lys	Gly	Tyr	Asp	Arg	Gly	Asp
			35					40				45			
Tyr	Val	Val	Arg	Glu	Asn	Gln	Asn	Val	Asp	Gly	Val	Tyr	Phe	Leu	Leu
			50				55				60				
Gln	Gly	Gln	Ala	Gln	Val	Leu	Arg	Ser	Ala	Glu	Glu	Glu	Asn	Tyr	Gln
			65				70			75			80		
Glu	Phe	Pro	Leu	Lys	Arg	Tyr	Asp	Phe	Phe	Gly	His	Gly	Ile	Phe	Gly

Val
385

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 377 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ix) FEATURE:

(B) LOCATION: 1..377

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1948:

Met	Asn	Thr	Glu	Ser	Val	Val	Glu	Phe	Leu	Gly	Asn	Val	Thr	Leu	Leu
1				5					10					15	
Gln	Arg	Leu	Pro	Ser	Ser	Ser	Leu	Lys	Arg	Ile	Ser	Glu	Val	Val	Val
			20					25					30		
Phe	Lys	Gly	Tyr	Asp	Arg	Gly	Asp	Tyr	Val	Val	Arg	Glu	Asn	Gln	Asn
		35					40					45			
Val	Asp	Gly	Val	Tyr	Phe	Leu	Leu	Gln	Gly	Gln	Ala	Gln	Val	Leu	Arg
	50					55					60				
Ser	Ala	Glu	Glu	Glu	Asn	Tyr	Gln	Glu	Phe	Pro	Leu	Lys	Arg	Tyr	Asp
65					70					75				80	

Phe Phe Gly His Gly Ile Phe Gly Asp Val Tyr Ser Ala Asp Val Val
85 90 95
Ala Val Thr Glu Leu Thr Cys Leu Leu Met Ser Asp His Arg Ala
100 105 110
Leu Leu Glu Ile Lys Ser Val Ser Asp Ser Asp Lys Glu Arg Cys Leu
115 120 125
Val Glu Asp Ile Leu Tyr Leu Glu Pro Leu Asp Leu Asn Val Tyr Arg
130 135 140
Gly Phe Thr Pro Pro Asn Ala Pro Thr Tyr Gly Lys Val Tyr Gly Gly
145 150 155 160
Gln Leu Val Gly Gln Ala Leu Ala Ala Ser Lys Thr Val Glu Thr
165 170 175
Met Lys Ile Val His Asn Phe His Cys Tyr Phe Leu Leu Val Gly Asp
180 185 190
Ile Asn Ile Pro Ile Ile Tyr Asp Val Asn Arg Leu Arg Asp Gly Asn
195 200 205
Asn Phe Ala Thr Arg Ser Val Asp Ala Arg Gln Lys Gly Lys Thr Ile
210 215 220
Phe Thr Leu Phe Ala Ser Phe Gln Lys Lys Gln Gln Gly Phe Ile His
225 230 235 240
Gln Glu Ser Thr Met Pro His Thr Pro Ala Pro Glu Thr Leu Leu Pro
245 250 255
Arg Glu Glu Met Leu Glu Arg Leu Val Thr Glu Pro Leu Leu Pro Arg
260 265 270
Asp Tyr Arg Asn Gln Val Ala Thr Glu Ile Ser Val Pro Phe Pro Ile
275 280 285
Asp Ile Arg Phe Cys Glu Pro Asn Arg Ser Thr Lys Gln Asn Lys Ser
290 295 300
Pro Pro Arg Leu Lys Tyr Trp Phe Arg Ala Lys Gly Lys Leu Ser Asp
305 310 315 320
Asp Asp Gln Ala Leu His Arg Cys Val Val Ala Phe Ala Ser Asp Leu
325 330 335
Ile Phe Ala Thr Ile Ser Leu Asn Pro His Arg Arg Glu Gly Met Ser
340 345 350
Val Ala Ala Leu Ser Leu Asp His Ser Met Trp Phe His Arg Pro Val
355 360 365
Arg Ala Asp Asp Trp Leu Leu Phe Val
370 375

(2) INFORMATION FOR SEQ ID NO:1949:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 271 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..271
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571428

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1949:

Met Ser Asp His Arg Ala Leu Leu Glu Ile Lys Ser Val Ser Asp Ser
1 5 10 15
Asp Lys Glu Arg Cys Leu Val Glu Asp Ile Leu Tyr Leu Glu Pro Leu
20 25 30
Asp Leu Asn Val Tyr Arg Gly Phe Thr Pro Pro Asn Ala Pro Thr Tyr
35 40 45
Gly Lys Val Tyr Gly Gly Gln Leu Val Gly Gln Ala Leu Ala Ala Ala
50 55 60
Ser Lys Thr Val Glu Thr Met Lys Ile Val His Asn Phe His Cys Tyr
65 70 75 80
Phe Leu Leu Val Gly Asp Ile Asn Ile Pro Ile Ile Tyr Asp Val Asn

(2) INFORMATION FOR SEQ ID NO:1950:

(A) LENGTH: 1974 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

MOLECULE TYPE: DNA (α

(ii) MOLECULE TYPE: DNA (genomic)

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(ix) FEATURE:
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(A) NAME/KEY: -

(B) LOCATION: 1..1974

(D) OTHER INFORMATION: / Ceres Seq. ID 1571432

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1950:

aaaaaagaat	acacagaca	gtctctcgtg	gctcgttaat	ggcgattctc	aaattctgat	60
ctcgtacaaa	caatggcgca	aacctcgga	ccagtcaacg	cgacgatgc	ccaggattgt	120
cactcgtctc	ttctctctcc	ggcgaggagg	ttctcgtctc	gtaattacgt	cgaaagcgtg	180
aaagtgtgac	gctgtttagg	gaagaagaat	ggatttgtatt	tttcagctcg	tttgctggga	240
ccgtgtcagc	gggttaactc	acagctgggt	gaagtcacac	acgagctctc	ttcgaaagtt	300
ggtttttgaa	ttgtttttgt	gtcaggtgat	gaggatgaag	agtcatttgg	agattatttg	360
agtaaatgac	ctcgtctcgc	ttgttcgttt	actgatctgg	aaacccgtga	ccgtttggat	420
gagtttgttta	aggttagggg	aatcatctca	ctagtgtatg	ttgatgatgc	tgcttaaaatt	480
gtgaatgaca	atggtgtgtg	gcttcacaga	agctatggag	ctgatgctta	ttttttacaa	540
ccagagaaaa	tgaagagcat	caaaaggagt	gaagatagag	ctcgaggaga	acagacctta	600
agatctgaac	ttgttgactc	ttccagagct	tttgtgtatt	cgctcagcgc	aaacacggta	660
cccgatcacg	agcttgaggg	aaaaaccatt	ggcctctctc	ttctctgtgc	ctctcacagg	720
aaatgcacag	agcttaactc	aaagcttgtt	ggcttttata	cgaagctgaa	gggaataaag	780
gaggttttgt	agatttgttt	gatattctct	gaagatagat	aggagctttc	taatcaagac	840
ttcaagacca	agcattgctc	gactctgcgc	ttcaacgaca	aaagtgtgat	aaaattggct	900
cggcatttca	tgctgtcaac	actaccgaca	cttgctcatt	tcggcctgta	tggaaaaaat	960
cgtcacctga	atgtcgtgta	agctattggc	gactattggg	ttcttcgcta	ctctttcaat	1020
ccagagaagc	ttcaagaact	caaggagcta	gaaaagscac	aggttagagg	tcaaacgcgc	1080
gagtcacttc	ttgtctcagg	tgactctaac	taagttctac	gaaaaggatg	ggcaaaagtg	1140
cttgtttcgc	attcgtgtgg	gaagaactat	cttttgtact	ttctcagcta	ctggtgtctc	1200
ccctgtcgcg	tttttaacc	aaagcttgtt	gaagtatata	acgagataaa	ggagcggaat	1260
gacagcgttt	aattgatctt	ctctcctagc	gacgcgtacc	aggaataatt	ctgatgatgc	1320
tttgtccaaa	tgccgtgctc	ggctcttcca	tttgtgtatc	ctaggaaagt	actcctggta	1380
aaaaaccttta	agctttgttg	atcccaaatc	tagcagctat	gggacacatt	gggcaaaagg	1440
taacaaaaga	acgaaggagc	cttgtctgag	cccatggagc	cgtgatctta	ccctctttac	1500
ttgcgaagac	ttgaagctta	ttgaagctta	ctcatgatag	atagcaaaag	attggcttaa	1560

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gaagggtgaaa catgtttctcc atgaagaaca tgagctagaa ctaactcgtg ttcagggttta 1620
cacatgcgat aagtggtgagg aagaaggagc aatatggtga ccattgcgac gaatgcgact 1680
ttgatcttca cgccaagtgt gctttaaacg agtacacaaa agaaaaacgc gatgaggctg 1740
tgaaagttgg tggcAgacga gtccaaagat gggtgggttt gtgaaggaaa cgtatgcacc 1800
aaggcctgat aggtagcttc aggcacagtt atgtcactat gtgtatgcaa agctatttcc 1860
ttcttttgta taattgctaa tagtgagaat gtgtgggtac aacttgatat ctgattaaga 1920
ccttgagat aaactctgtt aatctaaagt agtaataaaa gaattcttt attt

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(2) INFORMATION FOR SEQ ID NO:1951:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 470 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..470

(D) OTHER INFORMATION: / Ceres Seq. ID 1571433

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1951:

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Lys Lys Glu Tyr Thr Asp Gln Ser Ser Cys Ala Arg Asn Trp Arg Phe
1      5      10      15
Ser Asn Ser Ile Ser Val Gln Thr Met Ala Glu Thr Ser Lys Gln Val
20     25     30
Asn Gly Asp Asp Ala Gln Asp Leu His Ser Leu Leu Ser Ser Pro Ala
35     40     45
Arg Asp Phe Leu Val Arg Asn Asp Gly Glu Gln Val Lys Val Asp Ser
50     55     60
Leu Leu Gly Lys Lys Ile Gly Leu Tyr Phe Ser Ala Ala Trp Cys Gly
65     70     75     80
Pro Cys Gln Arg Phe Thr Pro Gln Leu Val Glu Val Tyr Asn Glu Leu
85     90     95
Ser Ser Lys Val Gly Phe Glu Ile Val Phe Val Ser Gly Asp Glu Asp
100    105    110
Glu Glu Ser Phe Gly Asp Tyr Phe Ser Lys Met Pro Trp Leu Ala Val
115    120    125
Pro Phe Thr Asp Ser Glu Thr Arg Asp Arg Leu Asp Glu Leu Phe Lys
130    135    140
Val Arg Gly Ile Pro Asn Leu Val Met Val Asp Asp His Gly Lys Leu
145    150    155    160
Val Asn Glu Asn Gly Val Gly Val Ile Arg Ser Tyr Gly Ala Asp Ala
165    170    175
Tyr Pro Phe Thr Pro Glu Lys Met Lys Glu Ile Lys Glu Asp Glu Asp
180    185    190
Arg Ala Arg Arg Glu Gln Thr Leu Arg Ser Val Leu Val Thr Pro Ser
195    200    205
Arg Asp Phe Val Ile Ser Pro Asp Gly Asn Lys Val Pro Val Ser Glu
210    215    220
Leu Glu Gly Lys Thr Ile Gly Leu Leu Phe Ser Val Ala Ser Tyr Arg
225    230    235    240
Lys Cys Thr Glu Leu Thr Pro Lys Leu Val Glu Phe Tyr Thr Lys Leu
245    250    255
Lys Glu Asn Lys Glu Asp Phe Glu Ile Val Leu Ile Ser Leu Glu Asp
260    265    270    275
Asp Glu Glu Ser Phe Asn Gln Asp Phe Lys Thr Lys Pro Trp Leu Ala
280    285
Leu Pro Phe Asn Asp Lys Ser Gly Ser Lys Leu Ala Arg His Phe Met
290    295    300
Leu Ser Thr Leu Pro Thr Leu Val Ile Leu Gly Pro Asp Gly Lys Ile
305    310    315    320
Arg His Ser Asn Val Ala Glu Ala Ile Asp Asp Tyr Gly Val Leu Ala
325    330    335

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Tyr Pro Phe Thr Pro Glu Lys Phe Gln Glu Leu Lys Glu Leu Glu Lys
340 345 350
Ala Lys Val Glu Ala Gln Thr Leu Glu Ser Leu Leu Val Ser Gly Asp
355 360 365
Leu Asn Tyr Val Leu Gly Lys Asp Gly Ala Lys Val Leu Val Ser Asp
370 375 380
Leu Val Gly Lys Thr Ile Leu Met Tyr Phe Ser Ala His Trp Cys Pro
385 390 395 400
Pro Cys Arg Ala Phe Thr Pro Lys Leu Val Glu Val Tyr Lys Gln Ile
405 410 415
Lys Glu Arg Asn Glu Ala Phe Glu Leu Ile Phe Ile Ser Ser Asp Arg
420 425 430
Asp Gln Glu Ser Phe Asp Glu Tyr Tyr Ser Gln Met Pro Trp Leu Ala
435 440 445
Leu Pro Phe Gly Asp Pro Arg Lys Ala Ser Leu Ala Lys Thr Phe Lys
450 455 460
Val Gly Gly Ser Gln Cys
465 470

(2) INFORMATION FOR SEQ ID NO:1952:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 446 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..446

(D) OTHER INFORMATION: / Ceres Seq. ID 1571434

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1952:

Met Ala Glu Thr Ser Lys Gln Val Asn Gly Asp Asp Ala Gln Asp Leu
1 5 10 15
His Ser Leu Leu Ser Ser Pro Ala Arg Asp Phe Leu Val Arg Asn Asp
20 25 30
Gly Glu Gln Val Lys Val Asp Ser Leu Leu Gly Lys Lys Ile Gly Leu
35 40 45
Tyr Phe Ser Ala Ala Trp Cys Gly Pro Cys Gln Arg Phe Thr Pro Gln
50 55 60
Leu Val Glu Val Tyr Asn Glu Leu Ser Ser Lys Val Gly Phe Glu Ile
65 70 75 80
Val Phe Val Ser Gly Asp Glu Asp Glu Ser Phe Gly Asp Tyr Phe
85 90 95
Ser Lys Met Pro Trp Leu Ala Val Pro Phe Thr Asp Ser Glu Thr Arg
100 105 110
Asp Arg Leu Asp Glu Leu Phe Lys Val Arg Gly Ile Pro Asn Leu Val
115 120 125
Met Val Asp Asp His Gly Lys Leu Val Asn Glu Asn Gly Val Gly Val
130 135 140
Ile Arg Ser Tyr Gly Ala Asp Ala Tyr Pro Phe Thr Pro Glu Lys Met
145 150 155 160
Lys Glu Ile Lys Glu Asp Glu Asp Arg Ala Arg Arg Glu Gln Thr Leu
165 170 175
Arg Ser Val Leu Val Thr Pro Ser Arg Asp Phe Val Ile Ser Pro Asp
180 185 190
Gly Asn Lys Val Pro Val Ser Glu Leu Glu Gly Lys Thr Ile Gly Leu
195 200 205
Leu Phe Ser Val Ala Ser Tyr Arg Lys Cys Thr Glu Leu Thr Pro Lys
210 215 220
Leu Val Glu Phe Tyr Thr Lys Leu Lys Glu Asn Lys Glu Asp Phe Glu
225 230 235 240
Ile Val Leu Ile Ser Leu Glu Asp Asp Glu Glu Ser Phe Asn Gln Asp

Met	Pro	Trp	Leu	Ala	Val	Pro	Phe	Thr	Asp	Ser	Glu	Thr	Arg	Asp	Arg
1				5					10					15	
Leu	Asp	Glu	Leu	Phe	Lys	Val	Arg	Gly	Ile	Pro	Asn	Leu	Val	Met	Val
			20					25					30		
Asp	Asp	His	Gly	Lys	Leu	Val	Asn	Glu	Asn	Gly	Val	Gly	Val	Ile	Arg
		35					40					45			
Ser	Tyr	Gly	Ala	Asp	Ala	Tyr	Pro	Phe	Thr	Pro	Glu	Lys	Met	Lys	Glu
	50					55					60				
Ile	Lys	Glu	Asp	Glu	Asp	Arg	Ala	Arg	Arg	Glu	Gln	Thr	Leu	Arg	Ser
65					70					75				80	
Val	Leu	Val	Thr	Pro	Ser	Arg	Asp	Phe	Val	Ile	Ser	Pro	Asp	Gly	Asn
				85					90					95	
Lys	Val	Pro	Val	Ser	Glu	Leu	Glu	Gly	Lys	Thr	Ile	Gly	Leu	Leu	Phe
			100					105					110		
Ser	Val	Ala	Ser	Tyr	Arg	Lys	Cys	Thr	Glu	Leu	Thr	Pro	Lys	Leu	Val
		115					120					125			
Glu	Phe	Tyr	Thr	Lys	Leu	Lys	Glu	Asn	Lys	Glu	Asp	Phe	Glu	Ile	Val
	130					135					140				
Leu	Ile	Ser	Leu	Glu	Asp	Asp	Glu	Glu	Ser	Phe	Asn	Gln	Asp	Phe	Lys
145					150					155				160	
Thr	Lys	Pro	Trp	Leu	Ala	Leu	Pro	Phe	Asn	Asp	Lys	Ser	Gly	Ser	Lys
			165						170					175	
Leu	Ala	Arg	His	Phe	Met	Leu	Ser	Thr	Leu	Pro	Thr	Leu	Val	Ile	Leu
			180						185				190		

Gly Pro Asp Gly Lys Ile Arg His Ser Asn Val Ala Glu Ala Ile Asp
195 200 205
Asp Tyr Gly Val Leu Ala Tyr Pro Phe Thr Pro Glu Lys Phe Gln Glu
210 215 220
Leu Lys Glu Leu Glu Lys Ala Lys Val Glu Ala Gln Thr Leu Glu Ser
225 230 235 240
Leu Leu Val Ser Gly Asp Leu Asn Tyr Val Leu Gly Lys Asp Gly Ala
245 250 255
Lys Val Leu Val Ser Asp Leu Val Gly Lys Thr Ile Leu Met Tyr Phe
260 265 270
Ser Ala His Trp Cys Pro Pro Cys Arg Ala Phe Thr Pro Lys Leu Val
275 280 285
Glu Val Tyr Lys Gln Ile Lys Glu Arg Asn Glu Ala Phe Glu Leu Ile
290 295 300
Phe Ile Ser Ser Asp Arg Asp Gln Glu Ser Phe Asp Glu Tyr Tyr Ser
305 310 315 320
Gln Met Pro Trp Leu Ala Leu Pro Phe Gly Asp Pro Arg Lys Ala Ser
325 330 335
Leu Ala Lys Thr Phe Lys Val Gly Gly Ser Gln Cys
340 345

(2) INFORMATION FOR SEQ ID NO:1954:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1146 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1146
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571440

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1954:

ctctgctaaa	tctgtgtcga	tctaaaaaat	caacgaacac	aaaactcatc	aaagctcctc	60
aaaaaccctaa	acacagctctc	tccatcttct	tcaactctct	tctcgctcgg	attctcatct	120
cttcttctgg	tttcagattg	agtcttggta	ctgtgtttca	taagactalt	gaagttaaga	180
tgtctggagc	attgaatatg	actcttggat	agattgttaa	gaggggtaaa	actgcaaggt	240
ctggggggaag	agggaattct	cgtgggcgtg	gtcgtggacg	tgtgtgtgtg	ggaagaggag	300
ctggaccctgc	tagaagaggt	cctcttgcTG	gtgaatgctc	gtccatcatc	tttcaccatt	360
aacaagcctg	tcgtaSggt	caggagcttg	ccatggcmaa	gcggttttgt	tgaagatggc	420
ctaagagctg	ccggggcatc	aggagttgaa	gttggaacca	ggctccatgt	tacaaatctg	480
gaccaggtg	tgacaaatga	agatataaag	gaactcttct	ctgagattgt	ggaggtagag	540
cgttatgcga	ttcattatga	caaaaatggg	cgtccaagtg	gcacagctga	agtgtgtgat	600
ccaaagaagaa	gtgattcatt	tcaagctctg	aagaaatata	acaatgtgct	attgtagtga	660
aggccaatga	gacttgagat	tttgggtggc	aacaattctt	ccgaggctcc	tttatcttgt	720
cgctggaatg	tgaatgtcac	tggactcaat	ggaaggctga	agaggacggt	tgttatccaa	780
caaggaggag	gagggagagg	aggaagaggt	ccagctccta	ctgtcactgc	ccgccttcca	840
attcataacc	agcagggagg	agggatgaga	ggaggaagag	gcgggttttg	tgtatagagg	900
cgtggtaata	gtggccctgg	tctgtgtgtg	ggaagaggaa	atggaaaaga	gccagtgga	960
aagtcatctg	ctgatcttga	caaagatctt	gagagctatc	acgctgatgc	catgaacacc	1020
tcttaaatcg	tgtttgtgtg	ttcttactaa	actagtttca	gatgaaatca	tgcttctctt	1080
tttttcatgc	tcttcgttgg	ttttgttgga	tgttgattgt	aaagtaaatg	gaagcctttt	1140

(2) INFORMATION FOR SEQ ID NO:1955:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 272 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide

(B) LOCATION: 1..272
(D) OTHER INFORMATION: / Ceres Seq. ID 1571441
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1955:

```

Met Arg Leu Leu Arg Gly Val Lys Leu Gln Gly Leu Gly Glu Glu Gly
1      5      10      15
Phe Leu Val Gly Val Val Val Asp Val Val Val Val Glu Glu Glu Leu
20     25     30
Asp Leu Leu Glu Glu Val Leu Leu Val Val Asn Ala Arg Pro Ser Ser
35     40     45
Phe Thr Ile Asn Lys Pro Val Arg Xaa Val Arg Ser Leu Pro Trp Gln
50     55     60
Ser Gly Leu Phe Glu Asp Gly Leu Arg Ala Ala Gly Ala Ser Gly Val
65     70     75     80
Glu Val Gly Thr Arg Leu His Val Thr Asn Leu Asp Gln Gly Val Thr
85     90     95
Asn Glu Asp Ile Arg Glu Leu Phe Ser Glu Ile Gly Glu Val Glu Arg
100    105    110
Tyr Ala Ile His Tyr Asp Lys Asn Gly Arg Pro Ser Gly Thr Ala Glu
115    120    125
Val Val Tyr Pro Arg Arg Ser Asp Ala Phe Gln Ala Leu Lys Lys Tyr
130    135    140
Asn Asn Val Leu Leu Asp Gly Arg Pro Met Arg Leu Glu Ile Leu Gly
145    150    155    160
Gly Asn Asn Ser Ser Glu Ala Pro Leu Ser Gly Arg Val Asn Val Asn
165    170    175
Val Thr Gly Leu Asn Gly Arg Leu Lys Arg Thr Val Val Ile Gln Gln
180    185    190
Gly Gly Gly Gly Arg Gly Gly Arg Gly Pro Ala Pro Thr Val Ser Arg
195    200    205
Arg Leu Pro Ile His Asn Gln Gln Gly Gly Gly Met Arg Gly Gly Arg
210    215    220
Gly Gly Phe Arg Ala Arg Gly Arg Gly Asn Gly Gly Arg Gly Arg Gly
225    230    235    240
Gly Gly Arg Gly Asn Gly Lys Lys Pro Val Glu Lys Ser Ala Ala Asp
245    250    255
Leu Asp Lys Asp Leu Glu Ser Tyr His Ala Asp Ala Met Asn Thr Ser
260    265    270

```

(2) INFORMATION FOR SEQ ID NO:1956:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1569 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..1569

(D) OTHER INFORMATION: / Ceres Seq. ID 1571445

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1956:

```

aaaaaaacaa aaacagagcc aggaataatg tcagtcttcc tctgtttcct ctgcctcttta      60
ccoccttatct taattctctt gaaaaatctc aaaccatcga aatggaagct tcctccaggcc      120
ccaaagaagc ttccgatcat cgggaactta caccaacgcc gggaattaca tcccaggaac      180
agtcggaatc ttctcgaaaa gtacggacca atcgtgtttc tccgatacgg attcgtcccc      240
gtggtcgtga tctcgtcaaa agaagcagca gaggaagttc tcaagaccac gatcttgagt      300
gttgtagccg accagagacg gttgggacca gagcaatctc ttacaacttt aaagacatcg      360
gattcgcaac gtgcggtgaa gattggagaa cgatgcggaa gctctcgggt gtcgagctct      420
tcagctcgaa aaagcttcaa tctttcaggt atatcagaga ggaagagaac gacttctgtg      480
tcaagaaact ctctgattta gcttcagac gatctttggt gaatcttgag aaaaaccttt      540
ttacttttagt cggaagtata gtgtgtagga taggggtttg gataaatctc cgtgagtgtg      600

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agtctgttga	tgaagatagc	atcgatgac	ttgtgcacaa	gtctgaagat	gtcataagga	660
attctatctt	ctctgtattc	tttcccggt	taatgggtag	gtctcatgag	tggatctcca	720
gtgagaggaa	gagattgaat	agactttact	cggaaagtaga	cactttcttt	cagaatattc	780
ttgatgatca	tctcaagcct	ggaagagaga	gctctgatata	catcgatgtg	atgattgata	840
tgatgaagaa	gcaagagaaa	gagggagact	ctttcaagtt	caccactgat	catctcaaa	900
ggatgatctc	ggacatatct	ctagcaggag	ttggaacaag	ctccactaca	ttgatatggg	960
cgatgaccga	gctgatccaga	aacccgagag	tgatgaagaa	agttcaagac	gagattcgga	1020
caacacttgg	ggacaagaag	gagagaatca	cagaagaaga	tttaaacacc	cttcactact	1080
tcaagctcat	ggctcaagag	atatccaggt	tacatccagc	agctccaact	ttgctcccaa	1140
gagagacatt	gtctcatgtc	aagatccaag	gtctacgat	tcctgtctaa	acacagatca	1200
tgatcaaaCG	ttacgcgatt	gcacgtgatc	caaaactatg	gacaaaccc	gatgagttta	1260
accctgatag	gttcccttgc	agctccatag	attacagagg	actgaacttt	gagctattac	1320
cgtttggtac	tggtaggagg	atatgtccag	ggatgacaat	ggggatcgcc	attgttgaat	1380
tgggactatt	gaatttgcct	tactttcttc	actgggggct	accagagaag	gaagaagcca	1440
aggagatcat	caccgggaat	gaagttgtct	ttgacctgtt	tcaagttttt	ctccactgaa	1500
tatgtgtttt	ggttatgcaa	tgtttgtact	acactaagct	tgattctaaa	ttaataacat	1560
cttacaagc						

(2) INFORMATION FOR SEQ ID NO:1957:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 498 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..498

(D) OTHER INFORMATION: / Ceres Seq. ID 1571446

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1957:

Lys	Asn	Lys	Asn	Arg	Ala	Arg	Asn	Asn	Val	Ser	Leu	Pro	Leu	Phe	Pro
1			5					10						15	
Leu	Pro	Leu	Thr	Pro	Tyr	Leu	Asn	Leu	Leu	Glu	Lys	Ser	Gln	Thr	Ile
			20					25					30		
Glu	Met	Glu	Ala	Ser	Ser	Arg	Pro	Lys	Glu	Ala	Ser	Asp	His	Arg	Glu
			35				40					45			
Leu	Thr	Pro	Thr	Pro	Gly	Ile	Thr	Ser	Gln	Glu	Gln	Ser	Glu	Ser	Phe
			50			55					60				
Arg	Lys	Val	Arg	Thr	Asn	Arg	Val	Ser	Pro	Ile	Arg	Ile	Arg	Pro	Arg
65					70				75					80	
Gly	Arg	Asp	Leu	Val	Lys	Arg	Ser	Ser	Arg	Gly	Ser	Ser	Gln	Asp	His
			85					90					95		
Asp	Leu	Glu	Cys	Cys	Ser	Arg	Pro	Glu	Thr	Val	Gly	Thr	Arg	Ala	Ile
			100					105					110		
Ser	Tyr	Asn	Phe	Lys	Asp	Ile	Gly	Phe	Ala	Pro	Cys	Gly	Glu	Asp	Trp
		115				120					125				
Arg	Thr	Met	Arg	Lys	Leu	Ser	Val	Val	Glu	Leu	Phe	Ser	Ser	Lys	Lys
		130			135						140				
Leu	Gln	Ser	Phe	Arg	Tyr	Ile	Arg	Glu	Glu	Glu	Asn	Asp	Leu	Cys	Val
145				150					155					160	
Lys	Lys	Leu	Ser	Asp	Leu	Ala	Ser	Arg	Arg	Ser	Leu	Val	Asn	Leu	Glu
			165					170					175		
Lys	Thr	Leu	Phe	Thr	Leu	Val	Gly	Ser	Ile	Val	Cys	Arg	Ile	Gly	Phe
			180			185						190			
Gly	Ile	Asn	Leu	Arg	Glu	Cys	Glu	Phe	Val	Asp	Glu	Asp	Ser	Ile	Asp
		195				200					205				
Asp	Leu	Val	His	Lys	Ser	Glu	Asp	Val	Ile	Arg	Asn	Ser	Ile	Phe	Ser
		210			215					220					
Asp	Phe	Phe	Pro	Gly	Leu	Met	Gly	Arg	Leu	Ile	Glu	Trp	Ile	Phe	Ser
225				230					235					240	
Glu	Arg	Lys	Arg	Leu	Asn	Arg	Leu	Tyr	Ser	Glu	Val	Asp	Thr	Phe	Phe
			245					250					255		

```

Gln Asn Ile Leu Asp Asp His Leu Lys Pro Gly Arg Glu Ser Ser Asp
      260      265      270
Ile Ile Asp Val Met Ile Asp Met Met Lys Lys Gln Glu Lys Glu Gly
      275      280      285
Asp Ser Phe Lys Phe Thr Thr Asp His Leu Lys Gly Met Ile Ser Asp
      290      295      300
Ile Phe Leu Ala Gly Val Gly Thr Ser Ser Thr Thr Leu Ile Trp Ala
      305      310      315      320
Met Thr Glu Leu Ile Arg Asn Pro Arg Val Met Lys Lys Val Gln Asp
      325      330      335
Glu Ile Arg Thr Thr Leu Gly Asp Lys Lys Glu Arg Ile Thr Glu Glu
      340      345      350
Asp Leu Asn Gln Leu His Tyr Phe Lys Leu Met Val Lys Glu Ile Phe
      355      360      365
Arg Leu His Pro Ala Ala Pro Leu Leu Pro Arg Glu Thr Leu Ser
      370      375      380
His Val Lys Ile Gln Gly Tyr Asp Ile Pro Ala Lys Thr Gln Ile Met
      385      390      395      400
Ile Asn Ala Tyr Ala Ile Ala Arg Asp Pro Lys Leu Trp Thr Asn Pro
      405      410      415
Asp Glu Phe Asn Pro Asp Arg Phe Leu Asp Ser Ser Ile Asp Tyr Arg
      420      425      430
Gly Leu Asn Phe Glu Leu Leu Pro Phe Gly Ser Gly Arg Arg Ile Cys
      435      440      445
Pro Gly Met Thr Met Gly Ile Ala Ile Val Glu Leu Gly Leu Leu Asn
      450      455      460
Leu Leu Tyr Phe Phe Asp Trp Gly Leu Pro Glu Lys Glu Glu Ala Lys
      465      470      475      480
Glu Ile Ile Thr Gly Asn Glu Val Ala Leu Asp Leu Val Gln Val Phe
      485      490      495
Leu His

```

(2) INFORMATION FOR SEQ ID NO:1958:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 465 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..465
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571447

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1958:

```

Met Glu Ala Ser Ser Arg Pro Lys Glu Ala Ser Asp His Arg Glu Leu
1      5      10
Thr Pro Thr Pro Gly Ile Thr Ser Gln Glu Gln Ser Glu Ser Phe Arg
      20      25      30
Lys Val Arg Thr Asn Arg Val Ser Pro Ile Arg Ile Arg Pro Arg Gly
      35      40      45
Arg Asp Leu Val Lys Arg Ser Ser Arg Gly Ser Ser Gln Asp His Asp
      50      55      60
Leu Glu Cys Cys Ser Arg Pro Glu Thr Val Gly Thr Arg Ala Ile Ser
      65      70      75      80
Tyr Asn Phe Lys Asp Ile Gly Phe Ala Pro Cys Gly Glu Asp Trp Arg
      85      90      95
Thr Met Arg Lys Leu Ser Val Val Glu Leu Phe Ser Ser Lys Lys Leu
      100      105      110
Gln Ser Phe Arg Tyr Ile Arg Glu Glu Glu Asn Asp Leu Cys Val Lys
      115      120      125
Lys Leu Ser Asp Leu Ala Ser Arg Arg Ser Leu Val Asn Leu Glu Lys

```

130	135	140
Thr Leu Phe Thr Leu Val Gly Ser Ile Val Cys Arg Ile Gly Phe Gly		
145	150	155
Ile Asn Leu Arg Glu Cys Glu Phe Val Asp Glu Asp Ser Ile Asp Asp		
	165	170
Leu Val His Lys Ser Ser Glu Asp Val Ile Arg Asn Ser Ile Phe Ser Asp		
	180	185
Phe Phe Pro Gly Leu Met Gly Arg Leu Ile Glu Trp Ile Phe Ser Glu		
	195	200
Arg Lys Arg Leu Asn Arg Leu Tyr Ser Glu Val Asp Thr Phe Phe Gln		
	210	215
Asn Ile Leu Asp Asp His Leu Lys Pro Gly Arg Glu Ser Ser Asp Ile		
225	230	235
Ile Asp Val Met Ile Asp Met Met Lys Lys Gln Glu Lys Glu Gly Asp		
	245	250
Ser Phe Lys Phe Thr Thr Asp His Leu Lys Gly Met Ile Ser Asp Ile		
	260	265
Phe Leu Ala Gly Val Gly Thr Ser Ser Thr Thr Leu Ile Trp Ala Met		
	275	280
Thr Glu Leu Ile Arg Asn Pro Arg Val Met Lys Lys Val Gln Asp Glu		
	290	295
Ile Arg Thr Thr Leu Gly Asp Lys Lys Glu Arg Ile Thr Glu Glu Asp		
305	310	315
Leu Asn Gln Leu His Tyr Phe Lys Leu Met Val Lys Glu Ile Phe Arg		
	325	330
Leu His Pro Ala Ala Pro Leu Leu Leu Pro Arg Glu Thr Leu Ser His		
	340	345
Val Lys Ile Gln Gly Tyr Asp Ile Pro Ala Lys Thr Gln Ile Met Ile		
	355	360
Asn Ala Tyr Ala Ile Ala Arg Asp Pro Lys Leu Trp Thr Asn Pro Asp		
	370	375
Glu Phe Asn Pro Asp Arg Phe Leu Asp Ser Ser Ile Asp Tyr Arg Gly		
385	390	395
Leu Asn Phe Glu Leu Leu Pro Phe Gly Ser Gly Arg Arg Ile Cys Pro		
	405	410
Gly Met Thr Met Gly Ile Ala Ile Val Glu Leu Gly Leu Leu Asn Leu		
	420	425
Leu Tyr Phe Phe Asp Trp Gly Leu Pro Glu Lys Glu Glu Ala Lys Glu		
	435	440
Ile Ile Thr Gly Asn Glu Val Ala Leu Asp Leu Val Gln Val Phe Leu		
	450	455
		460

His
465

(2) INFORMATION FOR SEQ ID NO:1959:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 368 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..368
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571448

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1959:

Met Arg Lys Leu Ser Val Val Glu Leu Phe Ser Ser Lys Lys Leu Gln	
1	5
Ser Phe Arg Tyr Ile Arg Glu Glu Glu Asn Asp Leu Cys Val Lys Lys	
	20
Leu Ser Asp Leu Ala Ser Arg Arg Ser Leu Val Asn Leu Glu Lys Thr	
	35
	40
	45

Leu	Phe	Thr	Leu	Val	Gly	Ser	Ile	Val	Cys	Arg	Ile	Gly	Phe	Gly	Ile
50						55					60				
Asn	Leu	Arg	Glu	Cys	Glu	Phe	Val	Asp	Glu	Asp	Ser	Ile	Asp	Asp	Leu
65					70					75				80	
Val	His	Lys	Ser	Glu	Asp	Val	Ile	Arg	Asn	Ser	Ile	Phe	Ser	Asp	Phe
			85						90					95	
Phe	Pro	Gly	Leu	Met	Gly	Arg	Leu	Ile	Glu	Trp	Ile	Phe	Ser	Glu	Arg
			100					105					110		
Lys	Arg	Leu	Asn	Arg	Leu	Tyr	Ser	Glu	Val	Asp	Thr	Phe	Phe	Gln	Asn
		115					120					125			
Ile	Leu	Asp	Asp	His	Leu	Lys	Pro	Gly	Arg	Glu	Ser	Ser	Asp	Ile	Ile
	130					135					140				
Asp	Val	Met	Ile	Asp	Met	Met	Lys	Lys	Gln	Glu	Lys	Glu	Gly	Asp	Ser
145					150					155					160
Phe	Lys	Phe	Thr	Thr	Asp	His	Leu	Lys	Gly	Met	Ile	Ser	Asp	Ile	Phe
			165						170					175	
Leu	Ala	Gly	Val	Gly	Thr	Ser	Ser	Thr	Thr	Leu	Ile	Trp	Ala	Met	Thr
	180							185					190		
Glu	Leu	Ile	Arg	Asn	Pro	Arg	Val	Met	Lys	Lys	Val	Gln	Asp	Glu	Ile
	195						200					205			
Arg	Thr	Thr	Leu	Gly	Asp	Lys	Lys	Glu	Arg	Ile	Thr	Glu	Glu	Asp	Leu
	210					215					220				
Asn	Gln	Leu	His	Tyr	Phe	Lys	Leu	Met	Val	Lys	Glu	Ile	Phe	Arg	Leu
225					230					235					240
His	Pro	Ala	Ala	Pro	Leu	Leu	Leu	Pro	Arg	Glu	Thr	Leu	Ser	His	Val
			245						250					255	
Lys	Ile	Gln	Gly	Tyr	Asp	Ile	Pro	Ala	Lys	Thr	Gln	Ile	Met	Ile	Asn
			260					265						270	
Ala	Tyr	Ala	Ile	Ala	Arg	Asp	Pro	Lys	Leu	Trp	Thr	Asn	Pro	Asp	Glu
	275						280					285			
Phe	Asn	Pro	Asp	Arg	Phe	Leu	Asp	Ser	Ser	Ile	Asp	Tyr	Arg	Gly	Leu
	290					295					300				
Asn	Phe	Glu	Leu	Leu	Pro	Phe	Gly	Ser	Gly	Arg	Arg	Ile	Cys	Pro	Gly
305					310					315					320
Met	Thr	Met	Gly	Ile	Ala	Ile	Val	Glu	Leu	Gly	Leu	Leu	Asn	Leu	Leu
			325						330					335	
Tyr	Phe	Phe	Asp	Trp	Gly	Leu	Pro	Glu	Lys	Glu	Glu	Ala	Lys	Glu	Ile
			340					345				350			
Ile	Thr	Gly	Asn	Glu	Val	Ala	Leu	Asp	Leu	Val	Gln	Val	Phe	Leu	His
	355						360					365			

(2) INFORMATION FOR SEQ ID NO:1960:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1221 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1221
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571460

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1960:

atattttcttc	ttctcttccaa	tttacagttc	tctgcacctt	ttactttccc	ctgttttttg	60
atcctcaatc	accaaaacct	agcttggtct	tctgttgatt	atttcgaaaa	gggggtttgt	120
ttgtttttctg	ggaatcagca	aaaatcacga	aatggttgcc	ttaatatctc	aatcgggata	180
aaatcgatcg	aaaatgagtc	agccttctgt	gattcttgct	acggttagct	atgatcacac	240
catccgattc	tgggaagccg	aamctggctg	ctgttacccg	accattcagt	atctcgattc	300
gcattgaaat	aggcttgaga	taaccccgaga	taagcattat	ctagctgcag	cttgcaatcc	360
tcataattcga	ctctttgatg	tcaattccaa	tagtctccaa	cctgtgatga	cttacgattc	420


```

acacaccaac  aatgtttatg  cagtaggatt  tcaatgtgat  gcaaaatgga  tgtattcagg  480
atcagaagat  ggcacagtta  agatctggga  ctttaagggt  ccgggttgcc  aaaaggagta  540
tgaaagtgtt  gcagcggtta  atacagttgt  ttacacccca  aatcagactg  aattgatata  600
tggagaccac  aatggaataa  tacgtgtatg  ggatctcaga  gcaaatctgt  gtactgtgga  660
actggtacca  gaagttgata  cagctgtacg  gtctttaact  gttatgtggg  atgggacaat  720
ggtagtcgct  gctaacaacc  gtggCaacat  gttatgtatg  gcgcttgttg  cgtggghaaac  780
agacaatgac  agagtttgag  ccccttcata  agctgcaagc  tcataatggc  cacatcccta  840
aatgtctcct  ctctcctgca  aacaaatata  tagcgactgc  atcatctgat  aaaactgtca  900
aaatatggaa  cgtcgatggt  ttcaaaactg  agaaaagttt  aacaggacat  caaagatggg  960
tttGggactg  cgtctctcca  gtggatggag  aatttcttgt  aacagcatca  tcggacatga  1020
cggctagatt  gtggtcgatg  ccagcaggca  aagaagttaa  agtataccac  ggctatcaca  1080
aagccactgt  gtgctgtgca  ctccacgact  aaaaccttaa  taagaatgaa  agctaaatta  1140
tgaacaaact  acgattgtgt  ttttgtgt  ttagttaaact  ctgtacatt  tcaatcgaat  1200
tcgttcaaat  tgctcttatg  t

```

(2) INFORMATION FOR SEQ ID NO:1961:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 201 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..201

(D) OTHER INFORMATION: / Ceres Seq. ID 1571461

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1961:

```

Met Ser Gln Pro Ser Val Ile Leu Ala Thr Ala Ser Tyr Asp His Thr
1      5      10      15
Ile Arg Phe Trp Glu Ala Glu Xaa Gly Arg Cys Tyr Arg Thr Ile Gln
      20      25      30
Tyr Pro Asp Ser His Val Asn Arg Leu Glu Ile Thr Pro Asp Lys His
      35      40      45
Tyr Leu Ala Ala Ala Cys Asn Pro His Ile Arg Leu Phe Asp Val Asn
50      55      60
Ser Asn Ser Pro Gln Pro Val Met Thr Tyr Asp Ser His Thr Asn Asn
65      70      75
Val Met Ala Val Gly Phe Gln Cys Asp Ala Lys Trp Met Tyr Ser Gly
      85      90      95
Ser Glu Asp Gly Thr Val Lys Ile Trp Asp Leu Arg Ala Pro Gly Cys
      100     105     110
Gln Lys Glu Tyr Glu Ser Val Ala Ala Val Asn Thr Val Val Leu His
      115     120     125
Pro Asn Gln Thr Glu Leu Ile Ser Gly Asp Gln Asn Gly Asn Ile Arg
130     135     140
Val Trp Asp Leu Arg Ala Asn Ser Cys Ser Cys Glu Leu Val Pro Glu
145     150     155     160
Val Asp Thr Ala Val Arg Ser Leu Thr Val Met Trp Asp Gly Thr Met
      165     170     175
Val Val Ala Ala Asn Asn Arg Gly Asn Met Leu Cys Met Ala Leu Val
      180     185     190
Ala Trp Xaa Thr Asp Asn Asp Arg Val
      195     200

```

(2) INFORMATION FOR SEQ ID NO:1962:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 130 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide

(B) LOCATION: 1..130

(D) OTHER INFORMATION: / Ceres Seq. ID 1571462

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1962:

```
Met Thr Tyr Asp Ser His Thr Asn Asn Val Met Ala Val Gly Phe Gln
1      5      10      15
Cys Asp Ala Lys Trp Met Tyr Ser Gly Ser Glu Asp Gly Thr Val Lys
      20      25      30
Ile Trp Asp Leu Arg Ala Pro Gly Cys Gln Lys Glu Tyr Glu Ser Val
      35      40      45
Ala Ala Val Asn Thr Val Val Leu His Pro Asn Gln Thr Glu Leu Ile
      50      55      60
Ser Gly Asp Gln Asn Gly Asn Ile Arg Val Trp Asp Leu Arg Ala Asn
      65      70      75      80
Ser Cys Ser Cys Glu Leu Val Pro Glu Val Asp Thr Ala Val Arg Ser
      85      90      95
Leu Thr Val Met Trp Asp Gly Thr Met Val Val Ala Ala Asn Asn Arg
      100      105      110
Gly Asn Met Leu Cys Met Ala Leu Val Ala Trp Xaa Thr Asp Asn Asp
      115      120      125
Arg Val
      130
```

(2) INFORMATION FOR SEQ ID NO:1963:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 120 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..120

(D) OTHER INFORMATION: / Ceres Seq. ID 1571463

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1963:

```
Met Ala Val Gly Phe Gln Cys Asp Ala Lys Trp Met Tyr Ser Gly Ser
1      5      10      15
Glu Asp Gly Thr Val Lys Ile Trp Asp Leu Arg Ala Pro Gly Cys Gln
      20      25      30
Lys Glu Tyr Glu Ser Val Ala Ala Val Asn Thr Val Val Leu His Pro
      35      40      45
Asn Gln Thr Glu Leu Ile Ser Gly Asp Gln Asn Gly Asn Ile Arg Val
      50      55      60
Trp Asp Leu Arg Ala Asn Ser Cys Ser Cys Glu Leu Val Pro Glu Val
      65      70      75      80
Asp Thr Ala Val Arg Ser Leu Thr Val Met Trp Asp Gly Thr Met Val
      85      90      95
Val Ala Ala Asn Asn Arg Gly Asn Met Leu Cys Met Ala Leu Val Ala
      100      105      110
Trp Xaa Thr Asp Asn Asp Arg Val
      115      120
```

(2) INFORMATION FOR SEQ ID NO:1964:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1636 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1636

(D) OTHER INFORMATION: / Ceres Seq. ID 1571464

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1964:

```

acttctctttt gttccccaaa ttctcgaaat cgaaacacga cttaaaacga aaaagacgag      60
acttttaaca ctcagacact aaccaacact ctctctcttt ctatctctct ctgcgcgcatc      120
ggaagcagat ttctctcaaa aggtggattt caacgaagct tagtgagta aaggtcttca      180
tcgatcaaat caagtctgac ccttcccttc tcaactactcc ttcaactctcc ttcttccgtg      240
actatctcga gagtcttggg gctaagatac ctactggtgt ccatgaagaa gacaaagaca      300
ctaagccgag gagtttctga gtggaagaga gtgatgatga tatggatgaa actgaagaag      360
taaaacacgaa agtggaggaa gaagaagaag aggtatgagat tgttgaatct gatgtagagc      420
ttgaaggaga cactgttgag cctgataatg atctctctca gaagatgggg gattcatcag      480
tgagggtgac tgatgagaat cgtgaagctg ctcaagaagc taaggggcaaa gcCatggagg      540
ccctttctga aggaaacttt gatgaagcaa ttgagcattt aactcgggca ataacgttga      600
accgcacttc agctattatg tatgaaaca gagctagtgt ctacattaa ttgaagaagc      660
caaacctgc tttcogagat gcaaacgcag cattggagat taacctgat ttgtccaag      720
gatacaagtc acgaggtatg gctcgtgcca tgcttgaga atgggcagag gctgcaaaag      780
accttcacct tgcactctac atagactatg atgaggaaat tagtgctgtt ctcaaaaag      840
ttgaacctaa tgcacataag cttgaggagc accgtagaaa gtatgacaga ttacgttaag      900
aaaagagaga caaaaaagct gaacgggata gattactctg ccgtgctgaa gcacagcgtg      960
cctatgataa agctaagaaa caagaacagt catcacttag cagaccatca ggagcggtt      1020
tccaggagg tatgcccggt ggtttccca gaggatgccc cgggtggatt ccaggaggaa      1080
tgaggagcat gcccgcgga ttcccgagg gaattgggtg tatggcggtt atggccggtg      1140
gattccagag aggaatgggc ggtggtatgc ctgcaggaaat gggcggtggt atggccggaa      1200
tgggcggtgg taatgcctgt ggaatgggtg gtggcggtat gccagggtga ggcggtggt      1260
tgccgtggtg tgccggtatg cctggtggtg tggaacttcag caaaatatgt aatgatcctg      1320
agctaatagc ggcatttagc gaacctgaag tcatggctgc ttctcaagat gtgatgaaga      1380
accctgcgaa cctagcgaa catcaggcga atccgaaggt ggctcccggt attgcaaga      1440
tgatggcga atttgacaga cctcagtaaa caaaacaaga agcttgcttt tctttgcgaa      1500
ttctgtggt taattgcgtg agataagaga tatgttggag aacttttttt ttcttttat      1560
ttgtcgttc agaggaactt taacaggaac aaaactcttt ttcttctggt agtaactcac      1620
ctctctctct tttttt

```

(2) INFORMATION FOR SEQ ID NO:1965:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 441 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..441

(D) OTHER INFORMATION: / Ceres Seq. ID 1571465

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1965:

```

Met Asp Ser Thr Lys Leu Ser Glu Leu Lys Val Phe Ile Asp Gln Cys
1           5           10           15
Lys Ser Asp Pro Ser Leu Leu Thr Thr Pro Ser Leu Ser Phe Phe Arg
20           25           30
Asp Tyr Leu Glu Ser Leu Gly Ala Lys Ile Pro Thr Gly Val His Glu
35           40           45
Glu Asp Lys Asp Thr Lys Pro Arg Ser Phe Val Val Glu Glu Ser Asp
50           55           60
Asp Asp Met Asp Glu Thr Glu Glu Val Lys Pro Lys Val Glu Glu Glu
65           70           75           80
Glu Glu Glu Asp Glu Ile Val Glu Ser Asp Val Glu Leu Glu Gly Asp
85           90           95
Thr Val Glu Pro Asp Asn Asp Pro Pro Gln Lys Met Gly Asp Ser Ser
100          105          110
Val Glu Val Thr Asp Glu Asn Arg Glu Ala Ala Gln Glu Ala Lys Gly
115          120          125
Lys Ala Met Glu Ala Leu Ser Glu Gly Asn Phe Asp Glu Ala Ile Glu
130          135          140
His Leu Thr Arg Ala Ile Thr Leu Asn Pro Thr Ser Ala Ile Met Tyr
145          150          155          160
Gly Asn Arg Ala Ser Val Tyr Ile Lys Leu Lys Lys Pro Asn Ala Ala

```

(2) INFORMATION FOR SEQ ID NO:1966:

(A) LENGTH: 375 amino acids

(C) STRANDEDNESS:

MOLECULE TYPE: peptid

FEATURE:

(B) LOCATION: 1..375

(D) OTHER INFORMATION: / Ceres Seq. ID 1571466

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1966:

Met	Asp	Glu	Thr	Glu	Glu	Val	Lys	Pro	Lys	Val	Glu	Glu	Glu	Glu	Glu
1				5					10					15	
Glu	Asp	Glu	Ile	Val	Glu	Ser	Asp	Val	Glu	Leu	Glu	Gly	Asp	Thr	Val
			20					25					30		
Glu	Pro	Asp	Asn	Asp	Pro	Pro	Gln	Lys	Met	Gly	Asp	Ser	Ser	Val	Glu
		35					40					45			
Val	Thr	Asp	Glu	Asn	Arg	Glu	Ala	Gln	Glu	Ala	Lys	Gly	Lys	Ala	
		50				55				60					
Met	Glu	Ala	Leu	Ser	Glu	Gly	Asn	Phe	Asp	Glu	Ala	Ile	Glu	His	Leu
65				70					75					80	
Thr	Arg	Ala	Ile	Thr	Leu	Asn	Pro	Thr	Ser	Ala	Ile	Met	Tyr	Gly	Asn
				85					90				95		
Arg	Ala	Ser	Val	Tyr	Ile	Lys	Leu	Lys	Lys	Pro	Asn	Ala	Ala	Ile	Arg
			100					105					110		

Asp Ala Asn Ala Ala Leu Glu Ile Asn Pro Asp Ser Ala Lys Gly Tyr
115 120 125
Lys Ser Arg Gly Met Ala Arg Ala Met Leu Gly Glu Trp Ala Glu Ala
130 135 140
Ala Lys Asp Leu His Leu Ala Ser Thr Ile Asp Tyr Asp Glu Glu Ile
145 150 155 160
Ser Ala Val Leu Lys Lys Val Glu Pro Asn Ala His Lys Leu Glu Glu
165 170 175
His Arg Arg Lys Tyr Asp Arg Leu Arg Lys Glu Arg Glu Asp Lys Lys
180 185 190
Ala Glu Arg Asp Arg Leu Arg Arg Ala Glu Ala Gln Ala Ala Tyr
195 200 205
Asp Lys Ala Lys Lys Glu Glu Gln Ser Ser Ser Ser Arg Pro Ser Gly
210 215 220
Gly Gly Phe Pro Gly Gly Met Pro Gly Gly Phe Pro Gly Gly Met Pro
225 230 235 240
Gly Gly Phe Pro Gly Gly Met Gly Gly Met Pro Gly Gly Phe Pro Gly
245 250 255
Gly Met Gly Gly Met Gly Gly Met Pro Gly Gly Phe Pro Gly Gly Met
260 265 270
Gly Gly Gly Met Pro Ala Gly Met Gly Gly Met Pro Gly Met Gly
275 280 285
Gly Gly Met Pro Ala Gly Met Gly Gly Gly Gly Met Pro Gly Ala Gly
290 295 300
Gly Gly Met Pro Gly Gly Gly Met Pro Gly Gly Met Asp Phe Ser
305 310 315 320
Lys Ile Leu Asn Asp Pro Glu Leu Met Thr Ala Phe Ser Asp Pro Glu
325 330 335
Val Met Ala Ala Leu Gln Asp Val Met Lys Asn Pro Ala Asn Leu Ala
340 345 350
Lys His Gln Ala Asn Pro Lys Val Ala Pro Val Ile Ala Lys Met Met
355 360 365
Gly Lys Phe Ala Gly Pro Gln
370 375

(2) INFORMATION FOR SEQ ID NO:1967:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 334 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..334
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571467

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1967:

Met Gly Asp Ser Ser Val Glu Val Thr Asp Glu Asn Arg Glu Ala Ala
1 5 10 15
Gln Glu Ala Lys Gly Lys Ala Met Glu Ala Leu Ser Glu Gly Asn Phe
20 25 30
Asp Glu Ala Ile Glu His Leu Thr Arg Ala Ile Thr Leu Asn Pro Thr
35 40 45
Ser Ala Ile Met Tyr Gly Asn Arg Ala Ser Val Tyr Ile Lys Leu Lys
50 55 60
Lys Pro Asn Ala Ala Ile Arg Asp Ala Asn Ala Ala Leu Glu Ile Asn
65 70 75 80
Pro Asp Ser Ala Lys Gly Tyr Lys Ser Arg Gly Met Ala Arg Ala Met
85 90 95
Leu Gly Glu Trp Ala Glu Ala Ala Lys Asp Leu His Leu Ala Ser Thr
100 105 110
Ile Asp Tyr Asp Glu Glu Ile Ser Ala Val Leu Lys Lys Val Glu Pro

115	120	125
Asn Ala His Lys Leu Glu Glu His Arg Arg Lys Tyr Asp Arg Leu Arg		
130	135	140
Lys Glu Arg Glu Asp Lys Lys Ala Glu Arg Asp Arg Leu Arg Arg Arg		
145	150	155
Ala Glu Ala Gln Ala Ala Tyr Asp Lys Ala Lys Lys Glu Glu Gln Ser		
165	170	175
Ser Ser Ser Arg Pro Ser Gly Gly Gly Phe Pro Gly Gly Met Pro Gly		
180	185	190
Gly Phe Pro Gly Gly Met Pro Gly Gly Phe Pro Gly Gly Met Gly Gly		
195	200	205
Met Pro Gly Gly Phe Pro Gly Gly Met Gly Gly Met Gly Met Pro		
210	215	220
Gly Gly Phe Pro Gly Gly Met Gly Gly Gly Met Pro Ala Gly Met Gly		
225	230	235
Gly Gly Met Pro Gly Met Gly Gly Gly Met Pro Ala Gly Met Gly Gly		
245	250	255
Gly Gly Met Pro Gly Ala Gly Gly Gly Met Pro Gly Gly Gly Gly Met		
260	265	270
Pro Gly Gly Met Asp Phe Ser Lys Ile Leu Asn Asp Pro Glu Leu Met		
275	280	285
Thr Ala Phe Ser Asp Pro Glu Val Met Ala Ala Leu Gln Asp Val Met		
290	295	300
Lys Asn Pro Ala Asn Leu Ala Lys His Gln Asn Pro Lys Val Ala		
305	310	315
Pro Val Ile Ala Lys Met Met Gly Lys Phe Ala Gly Pro Gln		
325	330	

(2) INFORMATION FOR SEQ ID NO:1968:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1132 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1132
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571468

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1968:

acattcctca	ccaaaccctc	tccaaaacac	accacacagt	acgcacacac	acaaagacaa	60
tgctcccttt	caaaatatct	ttcttcacga	ctctctctgt	gcggcggttt	tcagtgctcg	120
ctgtcgattt	caacactgac	gtcaacgtag	cttggggaaa	tgcccggtgg	aagatactca	180
acaaagccca	gcttcttact	ctctccttag	acaaatcctc	tggttccggt	tttcaatcca	240
aaacagagta	tttgtttgga	aagattgata	tgcagattaa	gcttgttctc	ggtaactctg	300
caggaaacgt	cacaactttt	taoctgaggt	tatatatttt	ctttaggagt	tttaagtgat	360
tttggaattg	gtttttatat	tgagacttca	tcttgacatt	tttgtgtatt	tgacgtctaa	420
atccgaagga	tccacttggt	atgagattga	ttttgagttc	tttgggtaata	tgagtggaga	480
tccttatact	ttcacactta	atgttttac	tcaaggtaaa	ggtagcagaag	agcaacaatt	540
ccatctctgg	ttgaccccaa	cgcgcaatt	ccacacttac	tcaatctctc	ggaacccctca	600
aagaatcata	ttgaccgtcg	atgacacacc	cattagagag	tttaaaaaat	atgagtctct	660
cggtgtcttg	tttccaagaa	acaagccgat	gaggatgtac	gcgagtttat	ggaacgcaga	720
cgattggcca	acaagaggcg	gtcttgttaa	aactgattgg	tctaaagctc	cattcatggc	780
ttcttacaga	aacattaa	ttgactcgaa	accaaaactc	aattgtgtaca	ctcaagaaat	840
ggattcaaca	agccaagcta	gactcaaatg	ggttcagaag	aattacatga	tctacaatta	900
ttgtactgac	catagagggt	ttccacaggg	agctcctaag	gaatgcacaa	caagctcata	960
gaactcga	ttatatctta	tttatttatc	tacacttctc	ctcttctctt	tatgtgaaaa	1020
tttgtaatgc	tetgtttcta	gcttgtctat	tatgtccog	aatttctttt	tctgtttttg	1080
attcttttgc	ttgtakatct	ttgtccarta	aaggaaatga	tgtgtcttta	cc	

(2) INFORMATION FOR SEQ ID NO:1969:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 118 amino acids

(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..118
(D) OTHER INFORMATION: / Ceres Seq. ID 1571469
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1969:
Ile Pro His Gln Thr Leu Ser Lys Thr His Pro His Val Arg Thr His
1 5 10 15
Thr Lys Thr Met Ser Pro Phe Lys Ile Phe Phe Thr Thr Leu Leu
20 25 30
Val Ala Ala Phe Ser Val Ser Ala Ala Asp Phe Asn Thr Asp Val Asn
35 40 45
Val Ala Trp Gly Asn Gly Arg Gly Lys Ile Leu Asn Asn Gly Gln Leu
50 55 60
Leu Thr Leu Ser Leu Asp Lys Ser Ser Gly Ser Gly Phe Gln Ser Lys
65 70 75 80
Thr Glu Tyr Leu Phe Gly Lys Ile Asp Met Gln Ile Lys Leu Val Pro
85 90 95
Gly Asn Ser Ala Gly Thr Val Thr Thr Phe Tyr Val Ser Leu Tyr Ile
100 105 110
Xaa Phe Arg Ser Phe Lys
115

(2) INFORMATION FOR SEQ ID NO:1970:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 99 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..99
(D) OTHER INFORMATION: / Ceres Seq. ID 1571470
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1970:
Met Ser Pro Phe Lys Ile Phe Phe Phe Thr Thr Leu Leu Val Ala Ala
1 5 10 15
Phe Ser Val Ser Ala Ala Asp Phe Asn Thr Asp Val Asn Val Ala Trp
20 25 30
Gly Asn Gly Arg Gly Lys Ile Leu Asn Asn Gly Gln Leu Leu Thr Leu
35 40 45
Ser Leu Asp Lys Ser Ser Gly Ser Gly Phe Gln Ser Lys Thr Glu Tyr
50 55 60
Leu Phe Gly Lys Ile Asp Met Gln Ile Lys Leu Val Pro Gly Asn Ser
65 70 75 80
Ala Gly Thr Val Thr Thr Phe Tyr Val Ser Leu Tyr Ile Xaa Phe Arg
85 90 95
Ser Phe Lys

(2) INFORMATION FOR SEQ ID NO:1971:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 163 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..163

(D) OTHER INFORMATION: / Ceres Seq. ID 1571471

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1971:

Met	Ser	Gly	Asp	Pro	Tyr	Thr	Leu	His	Thr	Asn	Val	Tyr	Thr	Gln	Gly
1			5						10					15	
Lys	Gly	Asp	Lys	Glu	Gln	Gln	Phe	His	Leu	Trp	Phe	Asp	Pro	Thr	Ala
			20				25					30			
Asn	Phe	His	Thr	Tyr	Ser	Ile	Leu	Trp	Asn	Pro	Gln	Arg	Ile	Ile	Leu
			35			40						45			
Thr	Val	Asp	Asp	Thr	Pro	Ile	Arg	Glu	Phe	Lys	Asn	Tyr	Glu	Ser	Leu
	50				55					60					
Gly	Val	Leu	Phe	Pro	Lys	Asn	Lys	Pro	Met	Arg	Met	Tyr	Ala	Ser	Leu
65			70						75					80	
Trp	Asn	Ala	Asp	Asp	Trp	Ala	Thr	Arg	Gly	Gly	Leu	Val	Lys	Thr	Asp
			85						90					95	
Trp	Ser	Lys	Ala	Pro	Phe	Met	Ala	Ser	Tyr	Arg	Asn	Ile	Lys	Ile	Asp
			100				105						110		
Ser	Lys	Pro	Asn	Ser	Asn	Trp	Tyr	Thr	Gln	Glu	Met	Asp	Ser	Thr	Ser
			115				120					125			
Gln	Ala	Arg	Leu	Lys	Trp	Val	Gln	Lys	Asn	Tyr	Met	Ile	Tyr	Asn	Tyr
	130				135						140				
Cys	Thr	Asp	His	Arg	Arg	Phe	Pro	Gln	Gly	Ala	Pro	Lys	Glu	Cys	Thr
145				150					155					160	
Thr	Ser	Ser													

(2) INFORMATION FOR SEQ ID NO:1972:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 733 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..733

(D) OTHER INFORMATION: / Ceres Seq. ID 1571472

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1972:

cccggttcaa	aaacccaaaa	ttctagagat	agaggacggc	aatgcgatgg	gggtcatcttt	60
ctcgcgcctcc	tttactaaact	ccaccaccgc	cgccgcgcgtt	cctcctccgt	cgccaccccttc	120
atcgccgtca	cgttccaaatg	taaaatctaa	cggagaagag	agacctcgtt	tcttcgatggg	180
aaaggcgaag	aacaagtgtc	gggctaatagc	tgacatcgta	cctggctcgac	atcccgcagag	240
gtggcgtaaa	gacgtcgccg	gtaacatagt	ctgcaaacgc	ttcggaattt	gcaatgggttg	300
tctctgtttc	gagtatgata	acattgtttc	ttattccaaa	gggtggagagt	cgaatagcggg	360
gaattgtcag	attcttccaa	caagagttaa	caagattcaaa	tcagctccaag	aaaatggttga	420
tgccaccact	cttaagagtg	gtGgcggaag	ctacggtgtg	ggaagacggt	arggaggagg	480
atacgggtgtg	ggtgaaggag	gaggttacgg	aggaagcggt	gggtgtggag	gatggtaatt	540
cttttaatta	ggTtttggga	ttaccaatga	atgttctctc	tctcgcttgt	tatgtcttcta	600
cttgggtttt	tgtgtttctc	attttgtttc	gggtctgctt	tagatttgat	gtaacagcttc	660
gtgattaggt	attttgggat	ctggaaacgt	aattttaagt	cacttgatcat	tctctaaata	720
acaaatttct	tgc					

(2) INFORMATION FOR SEQ ID NO:1973:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 178 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..178

(D) OTHER INFORMATION: / Ceres Seq. ID 1571473

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1973:

Pro Val Gln Lys Pro Lys Ile Leu Glu Ile Glu Asp Gly Asn Ala Met
1 5 10 15
Gly Ser Ser Phe Ser Ala Ser Phe Thr Asn Ser Thr Thr Ala Ala Ala
20 25 30
Val Pro Pro Pro Ser Pro Ser Pro Ser Arg Ser Asn Val Lys
35 40 45
Ser Asn Gly Glu Glu Arg Pro Arg Phe Phe Asp Gly Lys Ala Lys Asn
50 55 60
Lys Cys Trp Ala Asn Ala Asp Ile Val Pro Gly Arg His Pro Glu Arg
65 70 75 80
Trp Arg Lys Asp Val Ala Gly Asn Ile Val Cys Lys Arg Phe Gly Asn
85 90 95
Cys Asn Gly Cys Leu Cys Phe Glu Tyr Asp His Ile Val Pro Tyr Ser
100 105 110
Lys Gly Gly Glu Ser Ile Ala Glu Asn Cys Gln Ile Leu Gln Thr Arg
115 120 125
Val Asn Arg Phe Lys Ser Ala Gln Glu Asn Val Asp Ala Thr Thr Leu
130 135 140
Lys Ser Gly Gly Gly Ser Tyr Gly Gly Gly Arg Arg Xaa Gly Gly Gly
145 150 155 160
Tyr Gly Gly Gly Glu Gly Gly Tyr Gly Gly Ser Gly Gly Gly Gly
165 170 175
Gly Trp

(2) INFORMATION FOR SEQ ID NO:1974:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 163 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..163

(D) OTHER INFORMATION: / Ceres Seq. ID 1571474

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1974:

Met Gly Ser Ser Phe Ser Ala Ser Phe Thr Asn Ser Thr Thr Ala Ala
1 5 10 15
Ala Val Pro Pro Pro Ser Pro Pro Ser Ser Pro Ser Arg Ser Asn Val
20 25 30
Lys Ser Asn Gly Glu Glu Arg Pro Arg Phe Phe Asp Gly Lys Ala Lys
35 40 45
Asn Lys Cys Trp Ala Asn Ala Asp Ile Val Pro Gly Arg His Pro Glu
50 55 60
Arg Trp Arg Lys Asp Val Ala Gly Asn Ile Val Cys Lys Arg Phe Gly
65 70 75 80
Asn Cys Asn Gly Cys Leu Cys Phe Glu Tyr Asp His Ile Val Pro Tyr
85 90 95
Ser Lys Gly Gly Glu Ser Ile Ala Glu Asn Cys Gln Ile Leu Gln Thr
100 105 110
Arg Val Asn Arg Phe Lys Ser Ala Gln Glu Asn Val Asp Ala Thr Thr
115 120 125
Leu Lys Ser Gly Gly Gly Ser Tyr Gly Gly Gly Arg Arg Xaa Gly Gly
130 135 140
Gly Tyr Gly Gly Gly Glu Gly Gly Gly Tyr Gly Gly Ser Gly Gly Gly
145 150 155 160
Gly Gly Trp

(2) INFORMATION FOR SEQ ID NO:1975:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1406 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1406

(D) OTHER INFORMATION: / Ceres Seq. ID 1571479

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1975:

aatttttttga	gtttttgtct	cgaaaccgg	tttaaccocaa	gaaccccaag	atctctctct	60
atttggtttgc	ctttctcttt	ctttctgact	caaacctctta	aatcaattct	cgcgatttaag	120
caaaacoccta	gatttattct	actcttcgaa	gtcgatttca	atggaagggt	cctcgtcagc	180
catcgcgagg	aagacatggg	agctagagaa	caacattctc	cgagtggaa	caaccgattc	240
agcctccgac	agtatattcc	actacgagca	cgcttcacaa	gcacaaatcc	agcaggagaa	300
gccatggggc	tcggatcccta	actacttcaa	gcgcgttcc	atctcagccc	ttgctctctt	360
caagatgggt	gttcacgcgt	gctccgggtg	cacaatcgag	atcatgggtc	ttatgcaggg	420
taaaacgcag	gggtatatac	tcactggttt	ggatgctttt	gctttgctgt	ttgaaggtac	480
tgagactagg	gttaatgctc	agtctgatgc	ctatgagtat	atgggttgat	actctcagac	540
cagcaagctg	gctggggagg	tgagaaacgt	tgttggtggg	tatcactctc	acccctgggt	600
tggatgtttg	ctctcgggta	ttgatgtttc	gacacagatg	cttaaccaac	agtatcagga	660
gccattctta	gctgtttgta	ttgatccaac	aaggactgtt	tcggctggta	aggttgagat	720
tgggggcattc	agaacatatt	cagagggaca	taagatctcg	gatgatcatg	ttctgagta	780
tcagactatc	cctcttaaca	agattgagga	ctttggtgta	ctttgcaaac	agactactc	840
attggacatc	acttatttca	agtcactctc	cgatagtcac	catttgagtc	tcctttggaa	900
caagtatctg	gtgaacactc	ttctctcttc	cccactgttg	ggcaaatggg	actatgttgc	960
cgggcaaatc	tcagactttg	ctgagaagct	cgagcaagcg	gagagtacgc	tcgttaactc	1020
ccggtatggA	aggaattcgc	Cccagccgtg	caccAaaagg	aggaagagg	atgagctcA	1080
aactccgcaa	gataactcgc	gatagtgcaa	agataactgt	cgacagctc	atggactaa	1140
tgtcacaggt	tatcaagag	atctgtttca	attccgctcg	tcagccaag	aagtctgctg	1200
acgactcatc	agatccagag	cccatgatta	ctcgtgaag	ttggtctatt	ctttgttttt	1260
ttggctcgcg	aaattgacta	tcggtttgac	ccggtttatg	agggcaatgc	cattgttccc	1320
tatatctcta	gtgtagtatt	tgcttcagac	aaagatcttt	gggttattaa	atgacattaa	1380
cataaatcga	cttaattggt	tttgcg				

(2) INFORMATION FOR SEQ ID NO:1976:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 314 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..314

(D) OTHER INFORMATION: / Ceres Seq. ID 1571480

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1976:

Met	Glu	Gly	Ser	Ser	Ser	Ala	Ile	Ala	Arg	Lys	Thr	Trp	Glu	Leu	Glu	
1				5					10					15		
Asn	Asn	Ile	Leu	Arg	Val	Glu	Pro	Thr	Asp	Ser	Ala	Ser	Asp	Ser	Ile	
			20				25						30			
Phe	His	Tyr	Asp	Asp	Ala	Ser	Gln	Ala	Lys	Ile	Gln	Gln	Glu	Lys	Pro	
			35				40					45				
Trp	Ala	Ser	Asp	Pro	Asn	Tyr	Phe	Lys	Arg	Val	His	Ile	Ser	Ala	Leu	
			50				55				60					
Ala	Leu	Leu	Lys	Met	Val	Val	His	Ala	Arg	Ser	Gly	Gly	Thr	Ile	Glu	
			65				70				75			80		
Ile	Met	Gly	Leu	Met	Gln	Gly	Lys	Thr	Glu	Gly	Asp	Thr	Ile	Ile	Val	
			85				90							95		
Met	Asp	Ala	Phe	Ala	Leu	Pro	Val	Glu	Gly	Thr	Glu	Thr	Arg	Val	Asn	
			100				105						110			
Ala	Gln	Ser	Asp	Ala	Tyr	Glu	Tyr	Met	Val	Glu	Tyr	Ser	Gln	Thr	Ser	
			115				120						125			

Lys Leu Ala Gly Arg Leu Glu Asn Val Val Gly Trp Tyr His Ser His
130 135 140
Pro Gly Tyr Gly Cys Trp Leu Ser Gly Ile Asp Val Ser Thr Gln Met
145 150 155 160
Leu Asn Gln Gln Tyr Gln Glu Pro Phe Leu Ala Val Val Ile Asp Pro
165 170 175
Thr Arg Thr Val Ser Ala Gly Lys Val Glu Ile Gly Ala Phe Arg Thr
180 185 190
Tyr Pro Glu Gly His Lys Ile Ser Asp Asp His Val Ser Glu Tyr Gln
195 200 205
Thr Ile Pro Leu Asn Lys Ile Glu Asp Phe Gly Val His Cys Lys Gln
210 215 220
Tyr Tyr Ser Leu Asp Ile Thr Tyr Phe Lys Ser Ser Leu Asp Ser His
225 230 235 240
Leu Leu Asp Leu Leu Trp Asn Lys Tyr Trp Val Asn Thr Leu Ser Ser
245 250 255
Ser Pro Leu Leu Gly Asn Gly Asp Tyr Val Ala Gly Gln Ile Ser Asp
260 265 270
Leu Ala Glu Lys Leu Glu Gln Ala Glu Ser Gln Leu Ala Asn Ser Arg
275 280 285
Tyr Gly Arg Asn Cys Ala Gln Pro Val Thr Lys Arg Arg Lys Glu Asp
290 295 300
Glu Pro Gln Thr Arg Glu Asp Asn Ser Gly
305 310

(2) INFORMATION FOR SEQ ID NO:1977:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 246 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..246

(D) OTHER INFORMATION: / Ceres Seq. ID 1571481

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1977:

Met Val Val His Ala Arg Ser Gly Gly Thr Ile Glu Ile Met Gly Leu
1 5 10 15
Met Gln Gly Lys Thr Glu Gly Asp Thr Ile Ile Val Met Asp Ala Phe
20 25 30
Ala Leu Pro Val Glu Gly Thr Glu Thr Arg Val Asn Ala Gln Ser Asp
35 40 45
Ala Tyr Glu Tyr Met Val Glu Tyr Ser Gln Thr Ser Lys Leu Ala Gly
50 55 60
Arg Leu Glu Asn Val Val Gly Trp Tyr His Ser His Pro Gly Tyr Gly
65 70 75 80
Cys Trp Leu Ser Gly Ile Asp Val Ser Thr Gln Met Leu Asn Gln Gln
85 90 95
Tyr Gln Glu Pro Phe Leu Ala Val Val Ile Asp Pro Thr Arg Thr Val
100 105 110
Ser Ala Gly Lys Val Glu Ile Gly Ala Phe Arg Thr Tyr Pro Glu Gly
115 120 125
His Lys Ile Ser Asp Asp His Val Ser Glu Tyr Gln Thr Ile Pro Leu
130 135 140
Asn Lys Ile Glu Asp Phe Gly Val His Cys Lys Gln Tyr Tyr Ser Leu
145 150 155 160
Asp Ile Thr Tyr Phe Lys Ser Ser Leu Asp Ser His Leu Leu Asp Leu
165 170 175
Leu Trp Asn Lys Tyr Trp Val Asn Thr Leu Ser Ser Ser Pro Leu Leu
180 185 190
Gly Asn Gly Asp Tyr Val Ala Gly Gln Ile Ser Asp Leu Ala Glu Lys

	195		200		205
Leu	Glu	Gln	Ala	Glu	Ser
210				Gln	Leu
				215	
Cys	Ala	Gln	Pro	Val	Thr
225					230
					235
Arg	Glu	Asp	Asn	Ser	Gly
					245

(2) INFORMATION FOR SEQ ID NO:1978:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 233 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..233

(D) OTHER INFORMATION: / Ceres Seq. ID 1571482

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1978:

Met	Gly	Leu	Met	Gln	Gly	Lys	Thr	Glu	Gly	Asp	Thr	Ile	Ile	Val	Met
1			5						10					15	
Asp	Ala	Phe	Ala	Leu	Pro	Val	Glu	Gly	Thr	Glu	Thr	Arg	Val	Asn	Ala
			20						25					30	
Gln	Ser	Asp	Ala	Tyr	Glu	Tyr	Met	Val	Glu	Tyr	Ser	Gln	Thr	Ser	Lys
			35						40					45	
Leu	Ala	Gly	Arg	Leu	Glu	Asn	Val	Val	Gly	Trp	Tyr	His	Ser	His	Pro
			50						55					60	
Gly	Tyr	Gly	Cys	Trp	Leu	Ser	Gly	Ile	Asp	Val	Ser	Thr	Gln	Met	Leu
			65						70					75	
Asn	Gln	Gln	Tyr	Gln	Glu	Pro	Phe	Leu	Ala	Val	Val	Ile	Asp	Pro	Thr
			85						90					95	
Arg	Thr	Val	Ser	Ala	Gly	Lys	Val	Glu	Ile	Gly	Ala	Phe	Arg	Thr	Tyr
			100						105					110	
Pro	Glu	Gly	His	Lys	Ile	Ser	Asp	Asp	His	Val	Ser	Glu	Tyr	Gln	Thr
			115						120					125	
Ile	Pro	Leu	Asn	Lys	Ile	Glu	Asp	Phe	Gly	Val	His	Cys	Lys	Gln	Tyr
			130						135					140	
Tyr	Ser	Leu	Asp	Ile	Thr	Tyr	Phe	Lys	Ser	Ser	Leu	Asp	Ser	His	Leu
			145						150					155	
Leu	Asp	Leu	Leu	Trp	Asn	Lys	Tyr	Trp	Val	Asn	Thr	Leu	Ser	Ser	Ser
			165						170					175	
Pro	Leu	Leu	Gly	Asn	Gly	Asp	Tyr	Val	Ala	Gly	Gln	Ile	Ser	Asp	Leu
			180						185					190	
Ala	Glu	Lys	Leu	Glu	Gln	Ala	Glu	Ser	Gln	Leu	Ala	Asn	Ser	Arg	Tyr
			195						200					205	
Gly	Arg	Asn	Cys	Ala	Gln	Pro	Val	Thr	Lys	Arg	Arg	Lys	Glu	Asp	Glu
			210						215					220	
Pro	Gln	Thr	Arg	Glu	Asp	Asn	Ser	Gly							
			225						230						

(2) INFORMATION FOR SEQ ID NO:1979:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1654 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1654

(D) OTHER INFORMATION: / Ceres Seq. ID 1571483

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1979:

acmatwacyt	agaacatcct	aatcaaaact	gcttcgcgca	ttgctcgaaa	atcgcgctctt	60
ctgacaatgt	gctgaactgt	agtcacgtgc	cgagtttagca	aagtgaact	tcgaagatttc	120
tcttacctta	atctcaaggtt	tctgcagttt	taagaaacgc	cgtttacaaa	atgttcaagt	180
tgaagcaatg	gttgatttat	ttggtgtatt	cgtttagtaat	aatgaacaca	gaaggactgt	240
ttgtcaaat	tacatttgtt	cgaaacgcag	tcgttaaaag	ggcgttgtt	ttagatggaa	300
gtccaccagc	ttatcatttg	gatagaggtt	ctggaactgg	aatcaatagt	tggttgatac	360
agcttgaggg	aggaggatgg	tgcaataatg	taacaaattg	cgtttagtcg	atgcatactc	420
gattagggtc	atcgaaagaa	atgggtggga	accttgcttt	ctcagctatt	cttagcaata	480
agaaaacaata	taactcctgat	ttttacaatt	ggaatagagt	gaaagttaga	tactgtgacg	540
gggcactcatt	cacaggagat	gtagaagcag	tgaacctgcg	tactaatctt	cacttcagag	600
gtgctgcagt	ttggttagcc	gttatgcaag	agctgctagc	taaaagcgatg	ataaacgcgc	660
agaattcgctg	ttgtctgtgc	ttgtctgctg	gcgggttagc	ttcgctgatg	ctattgtgata	720
gtttccgtgc	tctattaccg	atgggaacca	aagtaaaatg	tctttcagat	gctgggtttt	780
ttctcaacac	aagagacgct	tcaggagctc	aatacattaa	aacatacttc	gaagatgttg	840
ttactcttca	tggatcagca	aagaacttgc	cgaggctcatg	cacatcaaga	tttaactcctg	900
caatgtgttt	ctttccgcgaa	tatgtggctc	gccagattag	aactcctctg	ttcattctta	960
atgcccgttta	tgaactcttg	cagataaaga	acattttggc	tcgcgcgagca	gctgatccct	1020
acggaaaattg	gcaaaagtgt	caactagaca	tcaagaattg	ccatccaagt	cagatcaaa	1080
ttatgcaaga	tttcagggtta	gagttcttga	gtgcagtgat	aggtttagg	agatcttcat	1140
caagagggat	gttcatagat	tcttgctaca	ctcaactgca	aaccagagca	caaatcttcat	1200
ggttcttgcca	agattctcca	attctaaacc	gaacgacaa	agcaaaagct	gttgagagatt	1260
gggtttatga	cagaaacattg	tttcagaaga	tagattgtcc	ttacccttgt	aacctactct	1320
gccaccacag	ggTttttcac	tctctagat	gctcctccaa	tttaagtgat	tctaccatat	1380
acagatagata	tttattatta	ttttgaaaag	aaaattttgct	tataaatatg	tcatttgtta	1440
gatacatata	gtgaaatatt	cctagggttt	agctatagaa	gatgaaaaag	aaaaagagt	1500
tgataattc	ttgagtggtg	agaataagca	ataggagtaa	ttttcttcag	cactgttctt	1560
gtgtgctgtt	taattgtctc	tgtttctctt	ctattctgat	gtaaaatgca	aattgttacc	1620

(2) INFORMATION FOR SEQ ID NO:1980:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 411 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..411

(D) OTHER INFORMATION: / Ceres Seq. ID 1571484

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1980:

Met	Phe	Lys	Leu	Lys	Gln	Trp	Leu	Ile	Tyr	Leu	Val	Tyr	Ser	Leu	Val
1			5					10						15	
Ile	Met	Asn	Thr	Glu	Gly	Leu	Phe	Val	Asn	Ile	Thr	Phe	Val	Arg	Asn
			20					25						30	
Ala	Val	Ala	Lys	Gly	Ala	Val	Cys	Leu	Asp	Gly	Ser	Pro	Pro	Ala	Tyr
			35					40						45	
His	Leu	Asp	Arg	Gly	Ser	Gly	Thr	Gly	Ile	Asn	Ser	Trp	Leu	Ile	Gln
			50					55						60	
Leu	Glu	Gly	Gly	Gly	Trp	Cys	Asn	Asn	Val	Thr	Asn	Cys	Val	Ser	Arg
65					70				75					80	
Met	His	Thr	Arg	Leu	Gly	Ser	Ser	Lys	Lys	Met	Val	Glu	Asn	Leu	Ala
					85				90					95	
Phe	Ser	Ala	Ile	Leu	Ser	Asn	Lys	Lys	Gln	Tyr	Asn	Pro	Asp	Phe	Tyr
					100				105					110	
Asn	Trp	Asn	Arg	Val	Lys	Val	Arg	Tyr	Cys	Asp	Gly	Ala	Ser	Phe	Thr
					115				120					125	
Gly	Asp	Val	Glu	Ala	Val	Asn	Pro	Ala	Thr	Asn	Leu	His	Phe	Arg	Gly
					130				135					140	
Ala	Arg	Val	Trp	Leu	Ala	Val	Met	Gln	Glu	Leu	Leu	Ala	Lys	Gly	Met
145						150				155				160	
Ile	Asn	Ala	Glu	Asn	Ala	Val	Leu	Ser	Gly	Cys	Ser	Ala	Gly	Gly	Leu

(2) INFORMATION FOR SEQ ID NO:1981:

(A) LENGTH: 394 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: lipid

MOLECULE TYPE: pentide

(11) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..394

(D) OTHER INFORMATION: / Ceres Seq. ID 1571485

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1981:

Met	Asn	Thr	Glu	Gly	Leu	Phe	Val	Asn	Ile	Thr	Phe	Val	Arg	Asn	Ala
1			5						10					15	
Val	Ala	Lys	Gly	Ala	Val	Cys	Leu	Asp	Gly	Ser	Pro	Pro	Ala	Tyr	His
		20						25					30		
Leu	Asp	Arg	Gly	Ser	Gly	Thr	Gly	Ile	Asn	Ser	Trp	Leu	Ile	Gln	Leu
		35					40					45			
Glu	Gly	Gly	Gly	Trp	Cys	Asn	Asn	Val	Thr	Asn	Cys	Val	Ser	Arg	Met
		50				55					60				
His	Thr	Arg	Leu	Gly	Ser	Lys	Lys	Met	Val	Glu	Asn	Leu	Ala	Phe	
65					70				75					80	
Ser	Ala	Ile	Leu	Ser	Asn	Lys	Lys	Gln	Tyr	Asn	Pro	Asp	Phe	Tyr	Asn
				85					90					95	
Trp	Asn	Arg	Val	Lys	Val	Arg	Tyr	Cys	Asp	Gly	Ala	Ser	Phe	Thr	Gly
			100					105					110		
Asp	Val	Glu	Ala	Val	Asn	Pro	Ala	Thr	Asn	Leu	His	Phe	Arg	Gly	Ala
		115					120					125			
Arg	Val	Trp	Leu	Ala	Val	Met	Gln	Glu	Leu	Leu	Ala	Lys	Gly	Met	Ile
		130				135						140			

Asn	Ala	Glu	Asn	Ala	Val	Leu	Ser	Gly	Cys	Ser	Ala	Gly	Gly	Leu	Ala
145					150					155					160
Ser	Leu	Met	His	Cys	Asp	Ser	Phe	Arg	Ala	Leu	Leu	Pro	Met	Gly	Thr
				165					170						175
Lys	Val	Lys	Cys	Leu	Ser	Asp	Ala	Gly	Phe	Phe	Leu	Asn	Thr	Arg	Asp
				180					185					190	
Val	Ser	Gly	Val	Gln	Tyr	Ile	Lys	Thr	Tyr	Phe	Glu	Asp	Val	Val	Thr
				195				200					205		
Leu	His	Gly	Ser	Ala	Lys	Asn	Leu	Pro	Arg	Ser	Cys	Thr	Ser	Arg	Leu
				210				215				220			
Thr	Pro	Ala	Met	Cys	Phe	Phe	Pro	Gln	Tyr	Val	Ala	Arg	Gln	Ile	Arg
225					230					235					240
Thr	Pro	Leu	Phe	Ile	Leu	Asn	Ala	Ala	Tyr	Asp	Ser	Trp	Gln	Ile	Lys
				245					250						255
Asn	Ile	Leu	Ala	Pro	Arg	Ala	Ala	Asp	Pro	Tyr	Gly	Lys	Trp	Gln	Ser
				260				265					270		
Cys	Gln	Leu	Asp	Ile	Lys	Asn	Cys	His	Pro	Ser	Gln	Ile	Lys	Val	Met
				275				280					285		
Gln	Asp	Phe	Arg	Leu	Glu	Phe	Leu	Ser	Ala	Val	Ile	Gly	Leu	Gly	Arg
				290				295				300			
Ser	Ser	Ser	Arg	Gly	Met	Phe	Ile	Asp	Ser	Cys	Tyr	Thr	His	Cys	Gln
305					310					315					320
Thr	Glu	Thr	Gln	Thr	Ser	Trp	Phe	Trp	Gln	Asp	Ser	Pro	Ile	Leu	Asn
				325					330						335
Arg	Thr	Thr	Ile	Ala	Lys	Ala	Val	Gly	Asp	Trp	Val	Tyr	Asp	Arg	Thr
				340					345						
Leu	Phe	Gln	Lys	Ile	Asp	Cys	Pro	Tyr	Pro	Cys	Asn	Pro	Thr	Cys	His
				355				360					365		
His	Arg	Val	Phe	His	Ser	Ser	Arg	Cys	Ser	Ser	Asn	Leu	Ser	Asp	Ser
				370				375				380			
Thr	Ile	Tyr	Ser	Ile	Asp	Leu	Leu	Leu	Phe						
385					390										

(2) INFORMATION FOR SEQ ID NO:1982:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 331 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..331

(D) OTHER INFORMATION: / Ceres Seq. ID 1571486

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1982:

Met	His	Thr	Arg	Leu	Gly	Ser	Ser	Lys	Lys	Met	Val	Glu	Asn	Leu	Ala
1				5				10					15		
Phe	Ser	Ala	Ile	Leu	Ser	Asn	Lys	Lys	Gln	Tyr	Asn	Pro	Asp	Phe	Tyr
				20				25					30		
Asn	Trp	Asn	Arg	Val	Lys	Val	Arg	Tyr	Cys	Asp	Gly	Ala	Ser	Phe	Thr
				35				40					45		
Gly	Asp	Val	Glu	Ala	Val	Asn	Pro	Ala	Thr	Asn	Leu	His	Phe	Arg	Gly
				50				55					60		
Ala	Arg	Val	Trp	Leu	Ala	Val	Met	Gln	Glu	Leu	Leu	Ala	Lys	Gly	Met
				65				70					75		80
Ile	Asn	Ala	Glu	Asn	Ala	Val	Leu	Ser	Gly	Cys	Ser	Ala	Gly	Gly	Leu
				85				90					95		
Ala	Ser	Leu	Met	His	Cys	Asp	Ser	Phe	Arg	Ala	Leu	Leu	Pro	Met	Gly
				100				105					110		
Thr	Lys	Val	Lys	Cys	Leu	Ser	Asp	Ala	Gly	Phe	Phe	Leu	Asn	Thr	Arg
				115				120					125		
Asp	Val	Ser	Gly	Val	Gln	Tyr	Ile	Lys	Thr	Tyr	Phe	Glu	Asp	Val	Val

130	135	140
Thr Leu His Gly Ser	Ala Lys Asn Leu Pro Arg	Ser Cys Thr Ser Arg
145	150	155
Leu Thr Pro Ala Met	Cys Phe Phe Pro Gln Tyr	Val Ala Arg Gln Ile
165	170	175
Arg Thr Pro Leu Phe	Ile Leu Asn Ala Ala Tyr	Asp Ser Trp Gln Ile
180	185	190
Lys Asn Ile Leu Ala	Pro Arg Ala Ala Asp Pro	Tyr Gly Lys Trp Gln
195	200	205
Ser Cys Gln Leu Asp	Ile Lys Asn Cys His Pro	Ser Gln Ile Lys Val
210	215	220
Met Gln Asp Phe Arg	Leu Glu Phe Leu Ser Ala	Val Ile Gly Leu Gly
225	230	235
Arg Ser Ser Ser Arg	Gly Met Phe Ile Asp Ser	Cys Tyr Thr His Cys
245	250	255
Gln Thr Glu Thr Gln	Thr Ser Trp Phe Trp	Gln Asp Ser Pro Ile Leu
260	265	270
Asn Arg Thr Thr Ile	Ala Lys Ala Val Gly Asp	Trp Val Tyr Asp Arg
275	280	285
Thr Leu Phe Gln Lys	Ile Asp Cys Pro Tyr Pro	Cys Asn Pro Thr Cys
290	295	300
His His Arg Val Phe	His Ser Ser Arg Cys Ser	Asn Leu Ser Asp
305	310	315
Ser Thr Ile Tyr Ser	Ile Asp Leu Leu Leu Phe	
325	330	

(2) INFORMATION FOR SEQ ID NO:1983:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1649 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1649

(D) OTHER INFORMATION: / Ceres Seq. ID 1571487

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1983:

tccatttaata	ctctctctccc	ctcatcctct	cttctctctct	catcatcatc	ttctttcttca	60
atggcccttca	cgcgtttttct	ctctctctct	ttcttcctatg	ccgccggtt	ctctctccta	120
ctccgcgcta	caactttaccg	tccgatgggt	cttctctcgg	gaagccttgg	ttctctctat	180
ataggagaga	cttttccagct	gatcgagct	tacaaaacag	agaacccctga	gcctttctatc	240
gacgagagag	tagccccggt	cGgttcgggt	ttcatgacgc	atcttttttg	tgaaccgacg	300
attttctcag	ctgaccgcga	aacgaaccgg	ttgtgtcttc	agaacgaagg	gaagcttttt	360
gagtgttctt	atcctgtcttc	catttgtaac	cttttgggga	aaactctct	gcttcttatg	420
aaaggtctct	tgcataaacg	tatgcactct	ctcaccatga	gctttgtctaa	ttcttcaact	480
attaaagacc	atctctatgct	tgatattgac	cggttagtcc	ggtttaactc	tgattctctg	540
ctctctctgt	ttctctctcat	ggaagaagcc	aaaaagataa	cgtttgagct	aacggtgaag	600
cagttgatga	gcctttgatcc	aggggaattg	agtgaagagt	taaggaaaaga	gtatctctct	660
gtcatcgaa	gcctctctctc	ctctctctct	ccaccactta	ccgcaaaagc		720
atccaagcgc	ggaggaaggt	tgacgggtg	tggtgatgaa	aaggaggagg		780
gaggaggaag	aaggagcgga	gagaaagaaa	gatattgctt	cgccggttgc	tcggcggagt	840
gatggatttt	cogatgaaga	gattgttgac	ttcttgggtg	cttactgtg	cgcccggttat	900
gaaacaacct	ccaagatcat	gaactctgcc	gtcaaatctc	tcaccgagac	ttcttttagct	960
cttgcctca	ctcaaggaaga	gcattgaaag	attagggcac	tgaaagattg	ttcgttatagt	1020
cttgattgga	gtgattacaa	gtcaatgcc	ttcacacaa	gtgtgggttaa	tgagacgcta	1080
cgagtggtca	acatcatcgg	cggtgttttc	agacgtgcac	tgacgagatt	tgagatcaaa	1140
ggttataaaa	ttccaaaagc	gttcaaatga	ttctcatcgt	ttagacgggt	ctatttagac	1200
ccaaacacct	tcgaagatgc	tcgcactttc	aacccttgga	ggtgcacag	caactcggta	1260
acgacagggc	cttctaatgc	ttctcacacc	tttggtggag	ggccaaggtc	atgtcccggt	1320
tacgagctgg	ctaggggttc	actctctgtt	ttctctcacc	gcctagtgc	aggcttcaat	1380
tgggttctcg	cagagcaaga	caagctgggt	ttctttccaa	ctacaagaac	gcagaaacgg	1440

(2) INFORMATION FOR SEO ID NO:1984:

(1) SEQUENCE CHARACTERISTICS:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 492 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..492

(D) OTHER INFORMATION: / Ceres Seq. ID 1571488

```
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1984:
```

1	er	le	Asn	Thr	5	eu	Ser	Pro	Ser	Ser	Ser	10	Leu	Leu	Leu	Ser	Ser	Ser
1	Ser	Ser	Ser	Ser	20	Met	Ala	Phe	Thr	Ala	Phe	25	Leu	Leu	Leu	Leu	Ser	Ser
Ile	Ala	Ala	Ala	Gly		Phe	Leu	Leu	Leu	Leu	Arg		Arg	Thr	Arg	45	Tyr	Arg
Met	Gly	Leu	Pro	Pro	Gly		Ser	Leu	Gly	Leu	Pro	Leu	60	Ile	Gly		Glu	Thr
Phe	Gln	Leu	Ile	Gly	Ala	70	Tyr	Lys	Thr	Glu	Asn	75	Phe	Met	Thr	His	Leu	Phe
Asp	Glu	Arg	Val	Ala	Arg	85	Tyr	Gly	Ser	Val	90	Phe	Met	Thr	His	Leu	Phe	
Gly	Glu	Pro	Thr	Ile	Phe		Ser	Ala	Asp	Pro	Glu	Thr	Asn	Arg	110	Phe	Val	
Leu	Gln	Asn	Glu	Gly	Lys		Leu	Phe	Glu	Cys	Ser	Tyr	Pro	Ala	Ser	Ile		
Cys	Asn	Leu	Leu	Gly	Lys		His	Ser	Leu	Leu	Leu	Met	140	Lys	Gly	Ser	Leu	
His	Lys	Arg	Met	His	Ser	150	Leu	Thr	Met	Ser	Phe	Ala	Asn	Ser	Ser	Ile		
Ile	Lys	Asp	His	Leu	Met	165	Leu	Asp	Ile	Asp	Arg	Leu	Val	Arg	Phe	Asn		
Leu	Asp	Ser	Trp	Ser	Ser	180	Arg	Val	Leu	Leu	Met	Glu	Glu	Ala	Lys	Lys		
Ile	Thr	Phe	Glu	Leu	Thr	195	Val	Lys	Gln	Leu	Met	Ser	Phe	Asp	Pro	Gly		
Glu	Trp	Ser	Glu	Ser	Leu	210	Arg	Lys	Glu	Tyr	Leu	Leu	Val	Ile	Glu	Gly		
Phe	Phe	Ser	Leu	Pro	Leu	225	Pro	Leu	Phe	Ser	Thr	Thr	Tyr	Arg	Lys	Ala		
Ile	Gln	Ala	Arg	Arg	Lys	240	Val	Ala	Glu	Ala	Leu	Thr	Val	Val	Val	Met		
Lys	Arg	Arg	Glu	Glu	Glu	260	Glu	Glu	Gly	Ala	Glu	Arg	Lys	Lys	Asp	Met		
Leu	Ala	Ala	Leu	Leu	Ala	275	Ala	Asp	Asp	Gly	Phe	Ser	Asp	Glu	Glu	Ile		
Val	Asp	Phe	Leu	Val	Ala	290	Leu	Leu	Val	Ala	Gly	Tyr	Glu	Thr	Thr	Ser		
Thr	Ile	Met	Thr	Leu	Ala	305	Val	Lys	Phe	Leu	Thr	315	Glu	Thr	Pro	Leu	Ala	
Leu	Ala	Gln	Leu	Lys	Glu	325	Glu	His	Glu	Lys	330	Ile	Arg	Ala	Met	Lys	Ser	
Asp	Ser	Tyr	Ser	Leu	Glu	340	Trp	Ser	Asp	Tyr	Lys	Ser	Met	Pro	Phe	Thr		
Gln	Cys	Val	Val	Asn	Glu	355	Thr	Leu	Arg	Val	Ala	Asn	Ile	Ile	Gly	Gly		

(2) INFORMATION FOR SEQ ID NO:1985:

(A) LENGTH: 472 amino acids

(C) STRANDEDNESS:

(ii) MOLECULE TYPE: peptide

(A) NAME/KEY: peptide

(D) OTHER INFORMATION

SEQUENCE DESCRIPTION: SEQ ID NO:1985:

Ala Phe Thr Ala Phe Leu Leu Leu Leu Ser Se

1	Phe	Leu	Leu	Leu	Leu	Arg	Arg	Thr	Arg	Tyr	Arg	Arg	Met	Gly	Leu	Pro
			20						25					30		
Pro	Gly	Ser	Leu	Gly	Leu	Pro	Leu	Ile	Gly	Glu	Thr	Phe	Gln	Leu	Ile	
		35					40					45				
Gly	Ala	Tyr	Lys	Thr	Glu	Asn	Pro	Glu	Pro	Phe	Ile	Asp	Glu	Arg	Val	
	50					55				60						
Ala	Arg	Tyr	Gly	Ser	Val	Phe	Met	Thr	His	Leu	Phe	Gly	Glu	Pro	Thr	
	65				70					75					80	
Ile	Phe	Ser	Ala	Asp	Pro	Glu	Thr	Asn	Arg	Phe	Val	Leu	Gln	Asn	Glu	
				85					90					95		
Gly	Lys	Leu	Phe	Glu	Cys	Ser	Tyr	Pro	Ala	Ser	Ile	Cys	Asn	Leu	Leu	
		100						105					110			
Gly	Lys	His	Ser	Leu	Leu	Leu	Met	Lys	Gly	Ser	Leu	His	Lys	Arg	Met	
		115					120					125				
His	Ser	Leu	Thr	Met	Ser	Phe	Ala	Asn	Ser	Ser	Ile	Ile	Lys	Asp	His	
	130					135					140					
Leu	Met	Leu	Asp	Ile	Asp	Arg	Leu	Val	Arg	Phe	Asn	Leu	Asp	Ser	Trp	
	145				150					155					160	
Ser	Ser	Arg	Val	Leu	Leu	Met	Glu	Glu	Ala	Lys	Lys	Ile	Thr	Phe	Glu	
			165						170					175		
Leu	Thr	Val	Lys	Gln	Leu	Met	Ser	Phe	Asp	Pro	Gly	Glu	Trp	Ser	Glu	
			180					185					190			
Ser	Leu	Arg	Lys	Glu	Tyr	Leu	Leu	Val	Ile	Glu	Gly	Phe	Phe	Ser	Leu	
		195					200					205				
Pro	Leu	Pro	Leu	Phe	Ser	Thr	Thr	Tyr	Arg	Lys	Ala	Ile	Gln	Ala	Arg	
	210					215					220					
Arg	Lys	Val	Ala	Glu	Ala	Leu	Thr	Val	Val	Val	Met	Lys	Arg	Arg	Glu	
	225				230					235					240	
Glu	Glu	Glu	Glu	Gly	Ala	Glu	Arg	Lys	Lys	Asp	Met	Leu	Ala	Ala	Leu	
				245					250					255		

Leu Ala Ala Asp Asp Gly Phe Ser Asp Glu Glu Ile Val Asp Phe Leu
260 265 270
Val Ala Leu Leu Val Ala Gly Tyr Glu Thr Thr Ser Thr Ile Met Thr
275 280 285
Leu Ala Val Lys Phe Leu Thr Glu Thr Pro Leu Ala Leu Ala Gln Leu
290 295 300
Lys Glu Glu His Glu Lys Ile Arg Ala Met Lys Ser Asp Ser Tyr Ser
305 310 315 320
Leu Glu Trp Ser Asp Tyr Lys Ser Met Pro Phe Thr Gln Cys Val Val
325 330 335
Asn Glu Thr Leu Arg Val Ala Asn Ile Ile Gly Gly Val Phe Arg Arg
340 345 350
Ala Met Thr Asp Val Glu Ile Lys Gly Tyr Lys Ile Pro Lys Gly Trp
355 360 365
Lys Val Phe Ser Ser Phe Arg Ala Val His Leu Asp Pro Asn His Phe
370 375 380
Lys Asp Ala Arg Thr Phe Asn Pro Trp Arg Trp Gln Ser Asn Ser Val
385 390 395 400
Thr Thr Gly Pro Ser Asn Val Phe Thr Pro Phe Gly Gly Gly Pro Arg
405 410 415
Leu Cys Pro Gly Tyr Glu Leu Ala Arg Val Ala Leu Ser Val Phe Leu
420 425 430
His Arg Leu Val Thr Gly Phe Ser Trp Val Pro Ala Glu Gln Asp Lys
435 440 445
Leu Val Phe Phe Pro Thr Thr Arg Thr Gln Lys Arg Tyr Pro Ile Phe
450 455 460
Val Lys Arg Arg Asp Phe Ala Thr
465 470

(2) INFORMATION FOR SEQ ID NO:1986:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 444 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..444

(D) OTHER INFORMATION: / Ceres Seq. ID 1571490

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1986:

Met Gly Leu Pro Pro Gly Ser Leu Gly Leu Pro Leu Ile Gly Glu Thr
1 5 10 15
Phe Gln Leu Ile Gly Ala Tyr Lys Thr Glu Asn Pro Glu Pro Phe Ile
20 25 30
Asp Glu Arg Val Ala Arg Tyr Gly Ser Val Phe Met Thr His Leu Phe
35 40 45
Gly Glu Pro Thr Ile Phe Ser Ala Asp Pro Glu Thr Asn Arg Phe Val
50 55 60
Leu Gln Asn Glu Gly Lys Leu Phe Glu Cys Ser Tyr Pro Ala Ser Ile
65 70 75 80
Cys Asn Leu Leu Gly Lys His Ser Leu Leu Leu Met Lys Gly Ser Leu
85 90 95
His Lys Arg Met His Ser Leu Thr Met Ser Phe Ala Asn Ser Ser Ile
100 105 110
Ile Lys Asp His Leu Met Leu Asp Ile Asp Arg Leu Val Arg Phe Asn
115 120 125
Leu Asp Ser Trp Ser Ser Arg Val Leu Leu Met Glu Glu Ala Lys Lys
130 135 140
Ile Thr Phe Glu Leu Thr Val Lys Gln Leu Met Ser Phe Asp Pro Gly
145 150 155 160
Glu Trp Ser Glu Ser Leu Arg Lys Glu Tyr Leu Leu Val Ile Glu Gly

amcatccwaa	tcgaaaaaat	ttaaccagca	tatacaaaaa	acttcgcgat	ccctctagcg	60
ttctctcttc	cggcgatatt	ctctctcttc	ggctcacatt	gcacctgcctc	tcactcgatc	120
ctctgctctt	tcagggacaa	ctattctcga	aacatgcgag	tcagaaagat	tgaaacgggt	180
catgaggaca	tgttccatga	tgctcagatg	gatactactg	gaagcggatc	tgcaactgca	240
tcactgtact	gcacaatcaa	gataaccggt	gtcagcaaca	accggtggat	cgacgaacta	300
ggacataatc	cggcgccaccg	tggtctcttc	ttggaaagtgc	cgctggcgatc	cccaaaagat	360
gcacaaatca	ttgcttcgat	ctctcatgat	ggtcagatca	tactctggaa	agaaggcaac	420
cagaaccaat	ggacccaaga	ctatgttttc	acagaccaca	aatcttcagt	caactccatt	480
tcgggggctc	ctcatgatat	cgacatctac	ttggcctgcg	ggctcatctga	tggcaccatt	540
tcgtgttttc	caagcccgctc	cgacgggtgc	tgggaacacat	caaggattga	ccaagcacat	600
ccggtttgag	tcacttcagt	ctcatggggc	ccagccacac	cgcctggctgc	tcttgtgagc	660
ttctgtcttc	tcctgcctgg	ttacaaggac	gcttcttggtg	tgatctgata	tacogtgaat	720
gtgtgggaag	tcctgaacgg	gtctctggaag	atgattatgt	ttcgcactct	ctaaaagcac	780
actgatggg	tcctgatatt	gqctctggga	ccaaactctg	gtctccocaa	gtccaccata	840

gccagtggtt	cccaagatgg	gaaagttatc	atatggacag	tgggaaaaga	aggtgagcaa	900
tgggaaggtg	aggtttctca	ggacttttatg	actcctgtgt	ggcgggtctc	gtcgtcgttg	960
accggtaact	tattggccgt	atccgatggg	aacaacaacg	tgactgtgtg	gAaagaggct	1020
gttgatggag	agtgggaaca	agttacttgt	gttgagcctt	aggtttttga	tgcttttcta	1080
tctctctgct	cttctcttta	aggaactgaa	tcaaacattt	tttctttact	cttttcttag	1140
tcgggtttgg	tggtcttttt	cagggaatgt	tgaattgggt	ttcttaaaga	cttttggatt	1200
atattttttc	ttattctttt	catagagacc	attttaaaat	tcc		

(2) INFORMATION FOR SEQ ID NO:1988:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 302 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..302
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571500

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1988:

Met	Pro	Gly	Gln	Lys	Ile	Glu	Thr	Gly	His	Glu	Asp	Ile	Val	His	Asp
1			5						10					15	
Val	Gln	Met	Asp	Tyr	Tyr	Gly	Lys	Arg	Ile	Ala	Thr	Ala	Ser	Ser	Asp
			20					25					30		
Cys	Thr	Ile	Lys	Ile	Thr	Gly	Val	Ser	Asn	Asn	Gly	Gly	Ser	Gln	Gln
			35					40					45		
Leu	Ala	Thr	Leu	Thr	Gly	His	Arg	Gly	Pro	Val	Trp	Glu	Val	Ala	Trp
			50				55					60			
Ala	His	Pro	Lys	Tyr	Gly	Ser	Ile	Leu	Ala	Ser	Cys	Ser	Tyr	Asp	Gly
			65				70			75				80	
Gln	Val	Ile	Leu	Trp	Lys	Glu	Gly	Asn	Gln	Asn	Gln	Trp	Thr	Gln	Asp
			85					90						95	
His	Val	Phe	Thr	Asp	His	Lys	Ser	Ser	Val	Asn	Ser	Ile	Ala	Trp	Ala
			100					105					110		
Pro	His	Asp	Ile	Gly	Leu	Ser	Leu	Ala	Cys	Gly	Ser	Ser	Asp	Gly	Asn
			115				120						125		
Ile	Ser	Val	Phe	Thr	Ala	Arg	Ala	Asp	Gly	Gly	Trp	Asp	Thr	Ser	Arg
			130				135					140			
Ile	Asp	Gln	Ala	His	Pro	Val	Gly	Val	Thr	Ser	Val	Ser	Trp	Ala	Pro
			145				150					155			160
Ala	Thr	Ala	Pro	Gly	Ala	Leu	Val	Ser	Ser	Gly	Leu	Leu	Asp	Pro	Val
			165					170					175		
Tyr	Lys	Leu	Ala	Ser	Gly	Gly	Cys	Asp	Asn	Thr	Val	Lys	Val	Trp	Lys
			180					185					190		
Leu	Ala	Asn	Gly	Ser	Trp	Lys	Met	Asp	Cys	Phe	Pro	Ala	Leu	Gln	Lys
			195				200						205		
His	Thr	Asp	Trp	Val	Arg	Asp	Val	Ala	Trp	Ala	Pro	Asn	Leu	Gly	Leu
			210				215				220				
Pro	Lys	Ser	Thr	Ile	Ala	Ser	Gly	Ser	Gln	Asp	Gly	Lys	Val	Ile	Ile
			225				230			235				240	
Trp	Thr	Val	Gly	Lys	Glu	Gly	Glu	Gln	Trp	Glu	Gly	Lys	Val	Leu	Lys
			245					250					255		
Asp	Phe	Met	Thr	Pro	Val	Trp	Arg	Val	Ser	Ser	Ser	Leu	Thr	Gly	Asn
			260				265					270			
Leu	Leu	Ala	Val	Ser	Asp	Gly	Asn	Asn	Val	Thr	Val	Trp	Lys	Glu	
			275				280					285			
Ala	Val	Asp	Gly	Glu	Trp	Glu	Gln	Val	Thr	Ala	Val	Glu	Pro		
			290				295					300			

(2) INFORMATION FOR SEQ ID NO:1989:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 284 amino acids
- (B) TYPE: amino acid

- (C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..284
(D) OTHER INFORMATION: / Ceres Seq. ID 1571501
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1989:

```

Met Asp Tyr Tyr Gly Lys Arg Ile Ala Thr Ala Ser Ser Asp Cys Thr
1      5      10      15
Ile Lys Ile Thr Gly Val Ser Asn Asn Gly Gly Ser Gln Gln Leu Ala
20     25     30
Thr Leu Thr Gly His Arg Gly Pro Val Trp Glu Val Ala Trp Ala His
35     40     45
Pro Lys Tyr Gly Ser Ile Leu Ala Ser Cys Ser Tyr Asp Gly Gln Val
50     55     60
Ile Leu Trp Lys Glu Gly Asn Gln Asn Trp Thr Gln Asp His Val
65     70     75
Phe Thr Asp His Lys Ser Ser Val Asn Ser Ile Ala Trp Ala Pro His
85     90     95
Asp Ile Gly Leu Ser Leu Ala Cys Gly Ser Ser Asp Gly Asn Ile Ser
100    105    110
Val Phe Thr Ala Arg Ala Asp Gly Trp Asp Thr Ser Arg Ile Asp
115    120    125
Gln Ala His Pro Val Gly Val Thr Ser Val Ser Trp Ala Pro Ala Thr
130    135    140
Ala Pro Gly Ala Leu Val Ser Ser Gly Leu Leu Asp Pro Val Tyr Lys
145    150    155
Leu Ala Ser Gly Gly Cys Asp Asn Thr Val Lys Val Trp Lys Leu Ala
165    170    175
Asn Gly Ser Trp Lys Met Asp Cys Phe Pro Ala Leu Gln Lys His Thr
180    185    190
Asp Trp Val Arg Asp Val Ala Trp Ala Pro Asn Leu Gly Leu Pro Lys
195    200    205
Ser Thr Ile Ala Ser Gly Ser Gln Asp Gly Lys Val Ile Ile Trp Thr
210    215    220
Val Gly Lys Glu Gly Glu Gln Trp Glu Gly Lys Val Leu Lys Asp Phe
225    230    235
Met Thr Pro Val Trp Arg Val Ser Ser Ser Leu Thr Gly Asn Leu Leu
245    250    255
Ala Val Ser Asp Gly Asn Asn Asn Val Thr Val Trp Lys Glu Ala Val
260    265    270
Asp Gly Glu Trp Glu Gln Val Thr Ala Val Glu Pro
275    280

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(2) INFORMATION FOR SEQ ID NO:1990:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1194 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..1194
(D) OTHER INFORMATION: / Ceres Seq. ID 1571502

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1990:

```

gacaacaatg gcgccttcct cgtcgagcgg tctcacgttc aagctacatc ctctgggtgat      60
gcttaacata tccgatcact tcactagggt taaaactcag cttaatcctc ccgcgcgttc      120
ttgcgcacc  ggggaatggct ccaacaacgc cgacgcgatg ttactgcaaa accctagggt      180
ttatggctgc gtcacgggtc tccagagagg tcgtacgggt gagatcttca acagtcttca      240
gctgatattc gatcctgcgc ttgatactct cgacagatcc ttcttcgaga agaagcaaga      300

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actctataag	aaggtgttcc	ctgacttcta	cgtattggga	tggatttcta	cggaagtga	360
cgctaccgaa	tctgatatgc	atatccacaa	agctctgatg	gacattaatg	aatctctgtg	420
gtatgttctt	ttaaactcctg	ctatcaatca	tgacacagaag	gatcttctgt	tgactatcta	480
cgaaagcgaa	tttcatgtca	ttgatggaat	tctctcagtcg	atttctgtgc	ataccagcta	540
cacaattgag	acagttgaag	ctgaaaagaat	atctgttgat	catgtTgcac	atcttaagcc	600
atctgatgga	ggctcagctg	cgactcagtt	ggctgctcat	cttactggaa	tacatagtgc	660
catcaagatg	cttaaatagca	gaatcagagt	gctataccag	catattgtcg	ctatgcagaa	720
aggtgataaa	ccttgtgaga	actcagttct	gagacaagta	tctagtctgc	tcagaagtgt	780
gcctgcgcga	gaatcagaga	agttcaatga	aaatttcttg	atggagtaca	acgacaaatt	840
gctgatgtct	tacctagcaa	tgatcacgaa	ttgtaccagc	aacatgaacg	aggtgggtga	900
caaattcaac	actgcatacg	acaaacacag	cogaagaggt	ggtaggactg	cggtcaatga	960
aagattagtt	tcaatgtaaa	aaaacctttt	ctttcttttg	gtggctcggt	ccttaagtga	1020
aaatttagaa	ctcttttaag	gcatttcact	tttcggaacc	aaacaaacag	ctaggaagct	1080
tttcttctgt	ttaagctttg	tctagacaga	agctaaagtt	aggcctaact	aaattttgct	1140
acaagactgt	aaaaacaaaa	cagcttttac	cttctctcaa	tttttcattt	attc	

(2) INFORMATION FOR SEQ ID NO:1991:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 319 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..319

(D) OTHER INFORMATION: / Ceres Seq. ID 1571503

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1991:

Thr	Thr	Met	Ala	Pro	Ser	Ser	Ser	Ser	Ser	Gly	Leu	Thr	Phe	Lys	Leu	His
1				5						10					15	
Pro	Leu	Val	Met	Leu	Asn	Ile	Ser	Asp	His	Phe	Thr	Arg	Val	Lys	Thr	
				20				25						30		
Gln	Leu	Asn	Pro	Pro	Ala	Ala	Ser	Cys	Ala	Thr	Gly	Asn	Gly	Ser	Asn	
				35				40					45			
Asn	Ala	Asp	Ala	Met	Leu	Leu	Gln	Asn	Pro	Arg	Val	Tyr	Gly	Cys	Val	
				50			55					60				
Ile	Gly	Leu	Gln	Arg	Gly	Arg	Thr	Val	Glu	Ile	Phe	Asn	Ser	Phe	Glu	
65					70					75					80	
Leu	Ile	Phe	Asp	Pro	Ala	Leu	Asp	Thr	Leu	Asp	Arg	Ser	Phe	Leu	Glu	
				85					90					95		
Lys	Lys	Gln	Glu	Leu	Tyr	Lys	Lys	Val	Phe	Pro	Asp	Phe	Tyr	Val	Leu	
				100				105					110			
Gly	Trp	Tyr	Ser	Thr	Gly	Ser	Asp	Ala	Thr	Glu	Ser	Asp	Met	His	Ile	
				115				120				125				
His	Lys	Ala	Leu	Met	Asp	Ile	Asn	Glu	Ser	Pro	Val	Tyr	Val	Leu	Leu	
				130			135					140				
Asn	Pro	Ala	Ile	Asn	His	Ala	Gln	Lys	Asp	Leu	Pro	Val	Thr	Ile	Tyr	
				145			150			155				160		
Glu	Ser	Glu	Phe	His	Val	Ile	Asp	Gly	Ile	Pro	Gln	Ser	Ile	Phe	Val	
				165				170					175			
His	Thr	Ser	Tyr	Thr	Ile	Glu	Thr	Val	Glu	Ala	Glu	Arg	Ile	Ser	Val	
				180				185					190			
Asp	His	Val	Ala	His	Leu	Lys	Pro	Ser	Asp	Gly	Gly	Ser	Ala	Ala	Thr	
				195			200					205				
Gln	Leu	Ala	Ala	His	Leu	Thr	Gly	Ile	His	Ser	Ala	Ile	Lys	Met	Leu	
				210			215				220					
Asn	Ser	Arg	Ile	Arg	Val	Leu	Tyr	Gln	His	Ile	Val	Ala	Met	Gln	Lys	
				225			230			235				240		
Gly	Asp	Lys	Pro	Cys	Glu	Asn	Ser	Val	Leu	Arg	Gln	Val	Ser	Ser	Leu	
				245				250					255			
Leu	Arg	Ser	Leu	Pro	Ala	Ala	Glu	Ser	Glu	Lys	Phe	Asn	Glu	Asn	Phe	
				260			265					270				

Leu	Met	Glu	Tyr	Asn	Asp	Lys	Leu	Leu	Met	Ser	Tyr	Leu	Ala	Met	Ile
		275					280					285			
Thr	Asn	Cys	Thr	Ser	Asn	Met	Asn	Glu	Val	Val	Asp	Lys	Phe	Asn	Thr
		290				295					300				
Ala	Tyr	Asp	Lys	His	Ser	Arg	Arg	Gly	Gly	Arg	Thr	Ala	Phe	Met	
305					310					315					

(2) INFORMATION FOR SEQ ID NO:1992:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 317 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

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(A) NAME/KEY: peptide
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(B) LOCATION: 1..317

(D) OTHER INFORMATION: / Ceres Seq. ID 1571504

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1992:

Met	Ala	Pro	Ser	Ser	Ser	Ser	Gly	Leu	Thr	Phe	Lys	Leu	His	Pro	Leu
1	Val	Met	Leu	Asn	Ile	Ser	Asp	His	Phe	Thr	Arg	Val	Lys	Thr	Gln
			20					25					30		
Asn	Pro	Pro	Ala	Ala	Ser	Cys	Ala	Thr	Gly	Asn	Gly	Ser	Asn	Asn	Ala
		35					40					45			
Asp	Ala	Met	Leu	Leu	Gln	Asn	Pro	Arg	Val	Tyr	Gly	Cys	Val	Ile	Gln
	50					55					60				
Leu	Gln	Arg	Gly	Arg	Thr	Val	Glu	Ile	Phe	Asn	Ser	Phe	Glu	Leu	Ile
65					70					75					80
Phe	Asp	Pro	Ala	Leu	Asp	Thr	Leu	Asp	Arg	Ser	Phe	Leu	Glu	Lys	Lys
				85					90					95	
Gln	Glu	Leu	Tyr	Lys	Lys	Val	Phe	Pro	Asp	Phe	Tyr	Val	Leu	Gly	Trp
		100						105					110		
Tyr	Ser	Thr	Gly	Ser	Asp	Ala	Thr	Glu	Ser	Asp	Met	His	Ile	His	Lys
		115					120					125			
Ala	Leu	Met	Asp	Ile	Asn	Glu	Ser	Pro	Val	Tyr	Val	Leu	Leu	Asn	Pro
	130					135					140				
Ala	Ile	Asn	His	Ala	Gln	Lys	Asp	Leu	Pro	Val	Thr	Ile	Tyr	Glu	Ser
145					150					155					160
Glu	Phe	His	Val	Ile	Asp	Gly	Ile	Pro	Gln	Ser	Ile	Phe	Val	His	Thr
			165						170					175	
Ser	Tyr	Thr	Ile	Glu	Thr	Val	Glu	Ala	Glu	Arg	Ile	Ser	Val	Asp	His
			180					185					190		
Val	Ala	His	Leu	Lys	Pro	Ser	Asp	Gly	Gly	Ser	Ala	Ala	Thr	Gln	Leu
		195					200					205			
Ala	Ala	His	Leu	Thr	Gly	Ile	His	Ser	Ala	Ile	Lys	Met	Leu	Asn	Ser
	210					215					220				
Arg	Ile	Arg	Val	Leu	Tyr	Gln	His	Ile	Val	Ala	Met	Gln	Lys	Gly	Asp
225					230					235					240
Lys	Pro	Cys	Glu	Asn	Ser	Val	Leu	Arg	Gln	Val	Ser	Ser	Leu	Leu	Arg
			245						250					255	
Ser	Leu	Pro	Ala	Ala	Glu	Ser	Glu	Lys	Phe	Asn	Glu	Asn	Phe	Leu	Met
		260						265					270		
Glu	Tyr	Asn	Asp	Lys	Leu	Leu	Met	Ser	Tyr	Leu	Ala	Met	Ile	Thr	Asn
		275					280					285			
Cys	Thr	Ser	Asn	Met	Asn	Glu	Val	Val	Asp	Lys	Phe	Asn	Thr	Ala	Tyr
	290					295					300				
Asp	Lys	His	Ser	Arg	Arg	Gly	Gly	Arg	Thr	Ala	Phe	Met			
305					310					315					

(2) INFORMATION FOR SEQ ID NO:1993:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 300 amino acids

(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..300
(D) OTHER INFORMATION: / Ceres Seq. ID 1571505
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1993:
Met Leu Asn Ile Ser Asp His Phe Thr Arg Val Lys Thr Gln Leu Asn
1 5 10 15
Pro Pro Ala Ala Ser Cys Ala Thr Gly Asn Gly Ser Asn Asn Ala Asp
20 25 30
Ala Met Leu Leu Gln Asn Pro Arg Val Tyr Gly Cys Val Ile Gly Leu
35 40 45
Gln Arg Gly Arg Thr Val Glu Ile Phe Asn Ser Phe Glu Leu Ile Phe
50 55 60
Asp Pro Ala Leu Asp Thr Leu Asp Arg Ser Phe Leu Glu Lys Lys Gln
65 70 75 80
Glu Leu Tyr Lys Lys Val Phe Pro Asp Phe Tyr Val Leu Gly Trp Tyr
85 90 95
Ser Thr Gly Ser Asp Ala Thr Glu Ser Asp Met His Ile His Lys Ala
100 105 110
Leu Met Asp Ile Asn Glu Ser Pro Val Tyr Val Leu Leu Asn Pro Ala
115 120 125
Ile Asn His Ala Gln Lys Asp Leu Pro Val Thr Ile Tyr Glu Ser Glu
130 135 140
Phe His Val Ile Asp Gly Ile Pro Gln Ser Ile Phe Val His Thr Ser
145 150 155 160
Tyr Thr Ile Glu Thr Val Glu Ala Glu Arg Ile Ser Val Asp His Val
165 170 175
Ala His Leu Lys Pro Ser Asp Gly Gly Ser Ala Ala Thr Gln Leu Ala
180 185 190
Ala His Leu Thr Gly Ile His Ser Ala Ile Lys Met Leu Asn Ser Arg
195 200 205
Ile Arg Val Leu Tyr Gln His Ile Val Ala Met Gln Lys Gly Asp Lys
210 215 220
Pro Cys Glu Asn Ser Val Leu Arg Gln Val Ser Ser Leu Leu Arg Ser
225 230 235 240
Leu Pro Ala Ala Glu Ser Glu Lys Phe Asn Glu Asn Phe Leu Met Glu
245 250 255
Tyr Asn Asp Lys Leu Leu Met Ser Tyr Leu Ala Met Ile Thr Asn Cys
260 265 270
Thr Ser Asn Met Asn Glu Val Val Asp Lys Phe Asn Thr Ala Tyr Asp
275 280 285
Lys His Ser Arg Arg Gly Gly Arg Thr Ala Phe Met
290 295 300

(2) INFORMATION FOR SEQ ID NO:1994:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1965 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..1965
(D) OTHER INFORMATION: / Ceres Seq. ID 1571522

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1994:

aaaacacaaa catatctctt atcaaacacc aacagctcta ttctctacct catttctcat 60
catacaaaag agagagaaaa aaactatgga attgacactg aattctctga gttctcttat 120

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caaacgtaaa gatgccaa gttctagaaa ccaagaaaagt tctccaaca acatgacctt 180
tgccgaagatg aagccgcca catatcaatt ccaagcaaa aactcgggta aggaaatgaa 240
gttcactcac gagaagaact tccgcgcaga aggtgaaaacc ctgagaaact gggagaagct 300
ccacgtttctc tcataccacc actccaagaa cgacgctagc gttccgggtg tgcgtcatgt 360
accgctgcac acagtaacaa tgtcagggca ttggaacaaa ccacgagcca tgaacgctag 420
tttgatggcc ctgaaaaggag ctgggtgtgga aggtgtgatg gtggatgctt ggtggggatt 480
ggtggagaaa gatggaccta tgaattataa ctgggaagggc tatgcccagc ttatacacat 540
ggttcaaaag cagcgtctca aactccaggt cgttatgtca ttccatcaat gtggaggaaa 600
cgtaggagac tcttgacgta tcccttggc tccatgggtg cttgaagaga tcagacaaga 660
ccctgatctt gtctacacag acaaatctgg gagaaggaa cctgaatata tctccttggg 720
atgtgatctt gtgcctgtcc taagaggaag aacacctatc caggtctcat cagatttcat 780
gaggagcttc cgtgaacgtg ttgaaggcta cataggagga gttattgcgg aaattcaagt 840
aggaatggga cctgtgtgag aattgagata cccatcatac cctgagagca acgggaacctg 900
gagatctccc ggaattggag agttccagtg ctacgacaag tatatgaaat cgtcacttca 960
agcatatgct gagtcaatcg ggaaaactaa ctgggggaaca agtggaacct atgatgccgg 1020
cgagtacaag aacctccacg aagatactga atttttcagg agagacggaa catggaatag 1080
cgagtatgca aagtttttca ttgaaatggta ctccgggaag cgtctagaac atggagacca 1140
actctatctc tcagcgaaag gtatctttca aggaagcggg gcaaaagctat caggaagagt 1200
agctggaaat cactggcact acaacaccag gtcacacgca gctgagctaa ccgctggata 1260
ctacaaacca agaaatccct acgggtatct gccaatagct aagatgttca acaaacatgt 1320
agttgtgtct aacttcacct gcattggagat gaagacgggg gagcaacctg agcacggaa 1380
ttgtccacca gaaggtctgg tcaagcaagt acagaacggc acagggcagg ccggaaccga 1440
actagcaggg tagaagcggc tagaacgata tgactcaagc gcattcggag aagtggtagc 1500
aacaataagg tcgattcttg gaaatgggtt aaccgcaatt acttacctaa gaatgaacaa 1560
cgcggttatt gaggtgcaaa attggcagca gttagtggag ttgtttaa gaatgaagaa 1620
aggtggctcat gggaggagac tctcaaaaga agacacaact ggaagtggac tttagtttgg 1680
attttgcaaa ggcaagatcg ctgagaatgt ggaggaggct gctttagtgt aattccccac 1740
Rataggtaca tacatatagt ttggtgttta ttgtattcct ctctgataaa taactagaga 1800
gatcaaacca gtaagagtgt taaagctata ttgttcacaa atcttgggct agagtcagag 1860
caagagagaag caaatacaag atgatgtaca cttagatgtt tctcatgagt ttctcctgtg 1920
catcatcttc atactcttaa tctcaaatac ttgcatttt tctccc

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(2) INFORMATION FOR SEQ ID NO:1995:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 576 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..576
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571523

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1995:

```

Lys His Lys His Ile Phe Tyr Gln Thr Pro Thr Ala Leu Phe Ser Thr
1          5          10          15
Ser Phe Leu Ile Ile Thr Lys Arg Glu Lys Lys Thr Met Glu Leu Thr
20          25          30
Leu Asn Ser Ser Ser Ser Leu Ile Lys Arg Lys Asp Ala Lys Ser Ser
35          40          45
Arg Asn Gln Glu Ser Ser Ser Asn Asn Met Thr Phe Ala Lys Met Lys
50          55          60
Pro Pro Thr Tyr Gln Phe Gln Ala Lys Asn Ser Val Lys Glu Met Lys
65          70          75          80
Phe Thr His Glu Lys Thr Phe Thr Pro Glu Gly Glu Thr Leu Glu Lys
85          90          95
Trp Glu Lys Leu His Val Leu Ser Tyr Pro His Ser Lys Asn Asp Ala
100         105         110
Ser Val Pro Val Phe Val Met Leu Pro Leu Asp Thr Val Thr Met Ser
115         120         125
Gly His Leu Asn Lys Pro Arg Ala Met Asn Ala Ser Leu Met Ala Leu
130         135         140

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Lys	Gly	Ala	Gly	Val	Glu	Gly	Val	Met	Val	Asp	Ala	Trp	Trp	Gly	Leu	
145					150					155					160	
Val	Glu	Lys	Asp	Gly	Pro	Met	Asn	Tyr	Asn	Trp	Glu	Gly	Tyr	Ala	Glu	
				165					170						175	
Leu	Ile	Gln	Met	Val	Gln	Lys	His	Gly	Leu	Lys	Leu	Gln	Val	Val	Met	
			180					185						190		
Ser	Phe	His	Gln	Cys	Gly	Gly	Asn	Val	Gly	Asp	Ser	Cys	Ser	Ile	Pro	
		195					200					205				
Leu	Pro	Pro	Trp	Val	Leu	Glu	Glu	Ile	Ser	Lys	Asn	Pro	Asp	Leu	Val	
		210				215					220					
Tyr	Thr	Asp	Lys	Ser	Gly	Arg	Arg	Asn	Pro	Glu	Tyr	Ile	Ser	Leu	Gly	
225				230						235					240	
Cys	Asp	Ser	Val	Pro	Val	Leu	Arg	Gly	Arg	Thr	Pro	Ile	Gln	Val	Tyr	
			245						250					255		
Ser	Asp	Phe	Met	Arg	Ser	Phe	Arg	Glu	Arg	Phe	Glu	Gly	Tyr	Ile	Gly	
			260					265					270			
Gly	Val	Ile	Ala	Glu	Ile	Gln	Val	Gly	Met	Gly	Pro	Cys	Gly	Glu	Leu	
		275					280					285				
Arg	Tyr	Pro	Ser	Tyr	Pro	Glu	Ser	Asn	Gly	Thr	Trp	Arg	Phe	Pro	Gly	
		290				295					300					
Ile	Gly	Glu	Phe	Gln	Cys	Tyr	Asp	Lys	Tyr	Met	Lys	Ser	Ser	Leu	Gln	
305				310						315					320	
Ala	Tyr	Ala	Glu	Ser	Ile	Gly	Lys	Thr	Asn	Trp	Gly	Thr	Ser	Gly	Pro	
			325						330					335		
His	Asp	Ala	Gly	Glu	Tyr	Lys	Asn	Leu	Pro	Glu	Asp	Thr	Glu	Phe	Phe	
		340					345						350			
Arg	Arg	Asp	Gly	Thr	Trp	Asn	Ser	Glu	Tyr	Gly	Lys	Phe	Phe	Met	Glu	
		355				360						365				
Trp	Tyr	Ser	Gly	Lys	Leu	Leu	Glu	His	Gly	Asp	Gln	Leu	Leu	Ser	Ser	
		370			375						380					
Ala	Lys	Gly	Ile	Phe	Gln	Gly	Ser	Gly	Ala	Lys	Leu	Ser	Gly	Lys	Val	
385					390				395						400	
Ala	Gly	Ile	His	Trp	His	Tyr	Asn	Thr	Arg	Ser	His	Ala	Ala	Glu	Leu	
			405						410					415		
Thr	Ala	Gly	Tyr	Tyr	Asn	Thr	Arg	Asn	His	Asp	Gly	Tyr	Leu	Pro	Ile	
		420				425							430			
Ala	Lys	Met	Phe	Asn	Lys	His	Gly	Val	Val	Leu	Asn	Phe	Thr	Cys	Met	
		435					440					445				
Glu	Met	Lys	Asp	Gly	Glu	Gln	Pro	Glu	His	Ala	Asn	Cys	Ser	Pro	Glu	
		450			455						460					
Gly	Leu	Val	Lys	Gln	Val	Gln	Asn	Ala	Thr	Arg	Gln	Ala	Gly	Thr	Glu	
465				470					475						480	
Leu	Ala	Gly	Glu	Asn	Ala	Leu	Glu	Arg	Tyr	Asp	Ser	Ser	Ala	Phe	Gly	
			485						490					495		
Gln	Val	Val	Ala	Thr	Asn	Arg	Ser	Asp	Ser	Gly	Asn	Gly	Leu	Thr	Ala	
		500				505							510			
Phe	Thr	Tyr	Leu	Arg	Met	Asn	Lys	Arg	Leu	Phe	Glu	Gly	Gln	Asn	Trp	
		515				520						525				
Gln	Gln	Leu	Val	Glu	Phe	Val	Lys	Asn	Met	Lys	Glu	Gly	Gly	His	Gly	
		530				535					540					
Arg	Arg	Leu	Ser	Lys	Glu	Asp	Thr	Thr	Gly	Ser	Asp	Leu	Tyr	Val	Gly	
545				550					555						560	
Phe	Val	Lys	Gly	Lys	Ile	Ala	Glu	Asn	Val	Glu	Glu	Ala	Ala	Leu	Val	
			565						570					575		

(2) INFORMATION FOR SEQ ID NO:1996:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 548 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

{D} TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..548
(D) OTHER INFORMATION: / Ceres Seq. ID 1571524
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1996:

Met	Glu	Leu	Thr	Leu	Asn	Ser	Ser	Ser	Ser	Leu	Ile	Lys	Arg	Lys	Asp
1				5						10				15	
Ala	Lys	Ser	Ser	Arg	Asn	Gln	Glu	Ser	Ser	Asn	Asn	Met	Thr	Phe	
			20					25				30			
Ala	Lys	Met	Lys	Pro	Pro	Thr	Tyr	Gln	Phe	Gln	Ala	Lys	Asn	Ser	Val
		35					40					45			
Lys	Glu	Met	Lys	Phe	Thr	His	Glu	Lys	Thr	Phe	Thr	Pro	Glu	Gly	Glu
	50					55					60				
Thr	Leu	Glu	Lys	Trp	Glu	Lys	Leu	His	Val	Leu	Ser	Tyr	Pro	His	Ser
65				70					75					80	
Lys	Asn	Asp	Ala	Ser	Val	Pro	Val	Phe	Val	Met	Leu	Pro	Leu	Asp	Thr
				85					90					95	
Val	Thr	Met	Ser	Gly	His	Leu	Asn	Lys	Pro	Arg	Ala	Met	Asn	Ala	Ser
				100				105					110		
Leu	Met	Ala	Leu	Lys	Gly	Ala	Gly	Val	Glu	Gly	Val	Met	Val	Asp	Ala
	115						120						125		
Trp	Trp	Gly	Leu	Val	Glu	Lys	Asp	Gly	Pro	Met	Asn	Tyr	Asn	Trp	Glu
	130					135					140				
Gly	Tyr	Ala	Glu	Leu	Ile	Gln	Met	Val	Gln	Lys	His	Gly	Leu	Lys	Leu
145					150					155				160	
Gln	Val	Val	Met	Ser	Phe	His	Gln	Cys	Gly	Gly	Asn	Val	Gly	Asp	Ser
				165					170					175	
Cys	Ser	Ile	Pro	Leu	Pro	Pro	Trp	Val	Leu	Glu	Glu	Ile	Ser	Lys	Asn
			180					185					190		
Pro	Asp	Leu	Val	Tyr	Thr	Asp	Lys	Ser	Gly	Arg	Arg	Asn	Pro	Glu	Tyr
	195						200					205			
Ile	Ser	Leu	Gly	Cys	Asp	Ser	Val	Pro	Val	Leu	Arg	Gly	Arg	Thr	Pro
	210					215						220			
Ile	Gln	Val	Tyr	Ser	Asp	Phe	Met	Arg	Ser	Phe	Arg	Glu	Arg	Phe	Glu
225					230					235				240	
Gly	Tyr	Ile	Gly	Gly	Val	Ile	Ala	Glu	Ile	Gln	Val	Gly	Met	Gly	Pro
				245					250					255	
Cys	Gly	Glu	Leu	Arg	Tyr	Pro	Ser	Tyr	Pro	Glu	Ser	Asn	Gly	Thr	Trp
		260						265					270		
Arg	Phe	Pro	Gly	Ile	Gly	Glu	Phe	Gln	Cys	Tyr	Asp	Lys	Tyr	Met	Lys
	275						280					285			
Ser	Ser	Leu	Gln	Ala	Tyr	Ala	Glu	Ser	Ile	Gly	Lys	Thr	Asn	Trp	Gly
	290					295					300				
Thr	Ser	Gly	Pro	His	Asp	Ala	Gly	Glu	Tyr	Lys	Asn	Leu	Pro	Glu	Asp
	305				310					315				320	
Thr	Glu	Phe	Phe	Arg	Arg	Asp	Gly	Thr	Trp	Asn	Ser	Glu	Tyr	Gly	Lys
				325					330					335	
Phe	Phe	Met	Glu	Trp	Tyr	Ser	Gly	Lys	Leu	Glu	His	Gly	Asp	Gln	
		340						345				350			
Leu	Leu	Ser	Ser	Ala	Lys	Gly	Ile	Phe	Gln	Gly	Ser	Gly	Ala	Lys	Leu
	355					360						365			
Ser	Gly	Lys	Val	Ala	Gly	Ile	His	Trp	His	Tyr	Asn	Thr	Arg	Ser	His
	370					375					380				
Ala	Ala	Glu	Leu	Thr	Ala	Gly	Tyr	Tyr	Asn	Thr	Arg	Asn	His	Asp	Gly
385					390					395				400	
Tyr	Leu	Pro	Ile	Ala	Lys	Met	Phe	Asn	Lys	His	Gly	Val	Val	Leu	Asn
				405					410					415	
Phe	Thr	Cys	Met	Glu	Met	Lys	Asp	Gly	Glu	Gln	Pro	Glu	His	Ala	Asn
			420					425						430	

Cys Ser Pro Glu Gly Leu Val Lys Gln Val Gln Asn Ala Thr Arg Gln
435 440 445
Ala Gly Thr Glu Leu Ala Gly Glu Asn Ala Leu Glu Arg Tyr Asp Ser
450 455 460
Ser Ala Phe Gly Gln Val Val Ala Thr Asn Arg Ser Asp Ser Gly Asn
465 470 475 480
Gly Leu Thr Ala Phe Thr Tyr Leu Arg Met Asn Lys Arg Leu Phe Glu
485 490 495
Gly Gln Asn Trp Gln Gln Leu Val Glu Phe Val Lys Asn Met Lys Glu
500 505 510
Gly Gly His Gly Arg Arg Leu Ser Lys Glu Asp Thr Thr Gly Ser Asp
515 520 525
Leu Tyr Val Gly Phe Val Lys Gly Lys Ile Ala Glu Asn Val Glu Glu
530 535 540
Ala Ala Leu Val
545

(2) INFORMATION FOR SEQ ID NO:1997:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 519 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..519

(D) OTHER INFORMATION: / Ceres Seq. ID 1571525

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1997:

Met Thr Phe Ala Lys Met Lys Pro Pro Thr Tyr Gln Phe Gln Ala Lys
1 5 10 15
Asn Ser Val Lys Glu Met Lys Phe Thr His Glu Lys Thr Phe Thr Pro
20 25 30
Glu Gly Glu Thr Leu Glu Lys Trp Glu Lys Leu His Val Leu Ser Tyr
35 40 45
Pro His Ser Lys Asn Asp Ala Ser Val Pro Val Phe Val Met Leu Pro
50 55 60
Leu Asp Thr Val Thr Met Ser Gly His Leu Asn Lys Pro Arg Ala Met
65 70 75 80
Asn Ala Ser Leu Met Ala Leu Lys Gly Ala Gly Val Glu Gly Val Met
85 90 95
Val Asp Ala Trp Trp Gly Leu Val Glu Lys Asp Gly Pro Met Asn Tyr
100 105 110
Asn Trp Glu Gly Tyr Ala Glu Leu Ile Gln Met Val Gln Lys His Gly
115 120 125
Leu Lys Leu Gln Val Val Met Ser Phe His Gln Cys Gly Gly Asn Val
130 135 140
Gly Asp Ser Cys Ser Ile Pro Leu Pro Pro Thr Val Leu Glu Glu Ile
145 150 155 160
Ser Lys Asn Pro Asp Leu Val Tyr Thr Asp Lys Ser Gly Arg Arg Asn
165 170 175
Pro Glu Tyr Ile Ser Leu Gly Cys Asp Ser Val Pro Val Leu Arg Gly
180 185 190
Arg Thr Pro Ile Gln Val Tyr Ser Asp Phe Met Arg Ser Phe Arg Glu
195 200 205
Arg Phe Glu Gly Tyr Ile Gly Gly Val Ile Ala Glu Ile Gln Val Gly
210 215 220
Met Gly Pro Cys Gly Glu Leu Arg Tyr Pro Ser Tyr Pro Glu Ser Asn
225 230 235 240
Gly Thr Trp Arg Phe Pro Gly Ile Gly Glu Phe Gln Cys Tyr Asp Lys
245 250 255
Tyr Met Lys Ser Ser Leu Gln Ala Tyr Ala Glu Ser Ile Gly Lys Thr

260 265 270
Asn Trp Gly Thr Ser Gly Pro His Asp Ala Gly Glu Tyr Lys Asn Leu
275 280
Pro Glu Asp Thr Glu Phe Phe Arg Arg Asp Gly Thr Trp Asn Ser Glu
290 295 300
Tyr Gly Lys Phe Phe Met Glu Trp Tyr Ser Gly Lys Leu Leu Glu His
305 310 315
Gly Asp Gln Leu Leu Ser Ser Ala Lys Gly Ile Phe Gln Gly Ser Gly
325 330 335
Ala Lys Leu Ser Gly Lys Val Ala Gly Ile His Trp His Tyr Asn Thr
340 345 350
Arg Ser His Ala Ala Glu Leu Thr Ala Gly Tyr Tyr Asn Thr Arg Asn
355 360 365
His Asp Gly Tyr Leu Pro Ile Ala Lys Met Phe Asn Lys His Gly Val
370 375 380
Val Leu Asn Phe Thr Cys Met Glu Met Lys Asp Gly Glu Gln Pro Glu
385 390 395
His Ala Asn Cys Ser Pro Glu Gly Leu Val Lys Gln Val Gln Asn Ala
405 410 415
Thr Arg Gln Ala Gly Thr Glu Leu Ala Gly Glu Asn Ala Leu Glu Arg
420 425 430
Tyr Asp Ser Ser Ala Phe Gly Gln Val Val Ala Thr Asn Arg Ser Asp
435 440 445
Ser Gly Asn Gly Leu Thr Ala Phe Thr Tyr Leu Arg Met Asn Lys Arg
450 455 460
Leu Phe Glu Gly Gln Asn Trp Gln Gln Leu Val Glu Phe Val Lys Asn
465 470 475
Met Lys Glu Gly Gly His Gly Arg Arg Leu Ser Lys Glu Asp Thr Thr
485 490 495
Gly Ser Asp Leu Tyr Val Gly Phe Val Lys Gly Lys Ile Ala Glu Asn
500 505 510
Val Glu Glu Ala Ala Leu Val
515

(2) INFORMATION FOR SEQ ID NO:1998:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1446 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1446
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571529

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1998:

gacacgatcc	atccaaagaa	acttcaattt	tggggttttc	cttcgtcttc	ttcttcttct	60
ttcttcttct	gatcgagagg	gacatgggtc	ttaccagccg	ccgttgacga	ctacgacgac	120
catctctctc	ctcttcatct	ttctctcttc	tgcttttctc	tatttctcat	ttcttccaaa	180
ttcaccattt	ccttccacca	ctcagagatc	ttcctttctt	attagctatg	ttcttcttca	240
acaagccatc	ttctagcgcc	gccgctgcgc	gatcgataga	ttcttccgcc	gcccgagaaa	300
attccaaagg	acccaagtat	tcgaaattta	ctcagcagga	gcttctctgt	tgcaaaccca	360
ttcttaccgc	tggttggttg	atttcaacgt	ttttgatcat	tagtgtttac	ttcatctccc	420
ttggtgttat	ttctctcttt	gtcttccagg	atgttgttga	gatcgttgat	cgttatgata	480
gtgcgatcat	acctctatat	gatagggtca	acaagggtgc	atacattcca	ggaaactggaa	540
ataaatcttg	taccggagcg	ctaatgtgct	ctaaagctat	gaagcagcct	attctatgat	600
attaccagct	tgagaaactc	taccagaatc	accgcaggta	tgtgaaaagc	cgaagtgtat	660
cgcaattgag	aagtgtgaaa	gatgagaatc	aaatagacgc	atgcaagcct	gaggatgatt	720
ttggttggtc	gccaatgtgt	ccatgtggtc	taattgcttg	gagttctctt	aatgacacat	780
acgttctcat	aagaaataac	cagggtttta	cggtaaacaa	gaaagggaat	gcattggaaga	840
gcgacaagga	acacaagtgt	gggaaaaatg	tgtttcccaa	gaactttcag	aagggcaatc	900
tcactggttg	tgccagctca	gatccaaata	aaccattgag	tgatcaagag	gatctgatcg	960

tgtggatgag	gactgctgcg	ttgccaacat	ttagaaaatt	atacggggaag	atagagagtg	1020
acttgagaa	gggtgagaac	atacaagtga	ctctgcagaa	caactacaac	acatacagtt	1080
tcagtgaggaa	gaagaagcct	gttctgtcaa	caacaagtgt	gcttggtgga	aagaacgact	1140
tcctcgccat	tgcttacctc	accgttgggg	gaatctgttt	cgctctggca	cttgcattta	1200
cgcctcatgta	tcttctgaaa	cccaggcgac	tcggtgatcc	tacctactgt	tcgtggaaac	1260
gaattccctgg	aggctcgtaa	acagatgact	gcacatctcg	cgtatataaa	tctacttata	1320
tctgtgtgta	atttgatcca	aaattgaaa	tgatgatctt	ttttttttta	atatagatgt	1380
gaaatgtatg	tatgatgtta	cagttggaat	atgctcatta	catagaatga	ttgatgcTtt	1440
cctatc						

(2) INFORMATION FOR SEQ ID NO:1999:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 350 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..350

(D) OTHER INFORMATION: / Ceres Seq. ID 1571530

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1999:

Met	Ser	Ser	Ser	Asn	Thr	Pro	Ser	Ser	Ser	Ala	Ala	Ala	Ala	Gly	Ser
1				5					10					15	
Ile	Asp	Ser	Ser	Ala	Ala	Arg	Arg	Asn	Ser	Lys	Arg	Pro	Lys	Tyr	Ser
			20					25					30		
Lys	Phe	Thr	Gln	Gln	Glu	Leu	Pro	Ala	Cys	Lys	Pro	Ile	Leu	Thr	Pro
			35				40					45			
Gly	Trp	Val	Ile	Ser	Thr	Phe	Leu	Ile	Ile	Ser	Val	Ile	Phe	Ile	Pro
			50				55				60				
Leu	Gly	Val	Ile	Ser	Leu	Phe	Ala	Ser	Gln	Asp	Val	Val	Glu	Ile	Val
			65				70			75				80	
Asp	Arg	Tyr	Asp	Ser	Ala	Cys	Ile	Pro	Leu	Ser	Asp	Arg	Ala	Asn	Lys
			85					90						95	
Val	Ala	Tyr	Ile	Gln	Gly	Thr	Gly	Asn	Lys	Ser	Cys	Thr	Arg	Thr	Leu
			100					105					110		
Ile	Val	Pro	Lys	Arg	Met	Lys	Gln	Pro	Ile	Tyr	Val	Tyr	Tyr	Gln	Leu
			115				120						125		
Glu	Asn	Phe	Tyr	Gln	Asn	His	Arg	Arg	Tyr	Val	Lys	Ser	Arg	Ser	Asp
			130				135					140			
Ser	Gln	Leu	Arg	Ser	Val	Lys	Asp	Glu	Asn	Gln	Ile	Asp	Ala	Cys	Lys
			145			150				155				160	
Pro	Glu	Asp	Asp	Phe	Gly	Gly	Gln	Pro	Ile	Val	Pro	Cys	Gly	Leu	Ile
			165					170						175	
Ala	Trp	Ser	Leu	Phe	Asn	Asp	Thr	Tyr	Val	Leu	Ser	Arg	Asn	Asn	Gln
			180					185					190		
Gly	Leu	Thr	Val	Asn	Lys	Lys	Gly	Ile	Ala	Trp	Lys	Ser	Asp	Lys	Glu
			195				200					205			
His	Lys	Phe	Gly	Lys	Asn	Val	Phe	Pro	Lys	Asn	Phe	Gln	Lys	Gly	Asn
			210				215				220				
Leu	Thr	Gly	Gly	Ala	Ser	Leu	Asp	Pro	Asn	Lys	Pro	Leu	Ser	Asp	Gln
			225			230				235				240	
Glu	Asp	Leu	Ile	Val	Trp	Met	Arg	Thr	Ala	Ala	Leu	Pro	Thr	Phe	Arg
			245					250					255		
Lys	Leu	Tyr	Gly	Lys	Ile	Glu	Ser	Asp	Leu	Glu	Lys	Gly	Glu	Asn	Ile
			260					265					270		
Gln	Val	Thr	Leu	Gln	Asn	Asn	Tyr	Asn	Thr	Tyr	Ser	Phe	Ser	Gly	Lys
			275				280						285		
Lys	Lys	Leu	Val	Leu	Ser	Thr	Thr	Ser	Trp	Leu	Gly	Gly	Lys	Asn	Asp
			290				295				300				
Phe	Leu	Gly	Ile	Ala	Tyr	Leu	Thr	Val	Gly	Gly	Ile	Cys	Phe	Val	Leu
			305			310				315				320	

Ala Leu Ala Phe Thr Val Met Tyr Leu Val Lys Pro Arg Arg Leu Gly
325 330 335
Asp Pro Thr Tyr Leu Ser Trp Asn Arg Ile Pro Gly Gly Arg
340 345 350

(2) INFORMATION FOR SEQ ID NO:2000:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 233 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..233

(D) OTHER INFORMATION: / Ceres Seq. ID 1571531

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2000:

Met Lys Gln Pro Ile Tyr Val Tyr Tyr Gln Leu Glu Asn Phe Tyr Gln
1 5 10 15
Asn His Arg Arg Tyr Val Lys Ser Arg Ser Asp Ser Gln Leu Arg Ser
20 25 30
Val Lys Asp Glu Asn Gln Ile Asp Ala Cys Lys Pro Glu Asp Asp Phe
35 40 45
Gly Gly Gln Pro Ile Val Pro Cys Gly Leu Ile Ala Trp Ser Leu Phe
50 55 60
Asn Asp Thr Tyr Val Leu Ser Arg Asn Asn Gln Gly Leu Thr Val Asn
65 70 75 80
Lys Lys Gly Ile Ala Trp Lys Ser Asp Lys Glu His Lys Phe Gly Lys
85 90 95
Asn Val Phe Pro Lys Asn Phe Gln Lys Gly Asn Leu Thr Gly Gly Ala
100 105 110
Ser Leu Asp Pro Asn Lys Pro Leu Ser Asp Gln Glu Asp Leu Ile Val
115 120 125
Trp Met Arg Thr Ala Ala Leu Pro Thr Phe Arg Lys Leu Tyr Gly Lys
130 135 140
Ile Glu Ser Asp Leu Glu Lys Gly Glu Asn Ile Gln Val Thr Leu Gln
145 150 155 160
Asn Asn Tyr Asn Thr Tyr Ser Phe Ser Gly Lys Lys Lys Leu Val Leu
165 170 175
Ser Thr Thr Ser Trp Leu Gly Gly Lys Asn Asp Phe Leu Gly Ile Ala
180 185 190
Tyr Leu Thr Val Gly Gly Ile Cys Phe Val Leu Ala Leu Ala Phe Thr
195 200 205
Val Met Tyr Leu Val Lys Pro Arg Arg Leu Gly Asp Pro Thr Tyr Leu
210 215 220
Ser Trp Asn Arg Ile Pro Gly Gly Arg
225 230

(2) INFORMATION FOR SEQ ID NO:2001:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1458 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1458

(D) OTHER INFORMATION: / Ceres Seq. ID 1571543

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2001:

aaaaattctcg aaatcggaaa atttacacag agaagcgcca tgacctaaaa atctcaaaac 60
ttcccaaca aaaatggcgc ttttactcaa cccatttcc tttacctacc ttgtacatta 120
ccctttttc caaatctcac tttccactg aaataacccc atggcgagaga atcagaactg 180

tgcgaggatg	acgagagcgg	cggcgaaacg	aaaagcgtcg	tccatggcgt	tagacgaaaa	240
cccagttagt	aagaagagag	ttgttctcgg	agagcttccg	aatatgtcca	atgtcgttgc	300
tgtaccocat	caagaagaag	agacccttaa	ggctaaaaa	agtgttaata	cotcgaagag	360
gcagatgaag	aaggctttga	tgattcctga	agctagcgta	ctaatacgat	cgagatctgt	420
tgatcctcag	atgtgtgagc	cttttgctag	tgatatattg	gcttatctcc	gtgaaatgga	480
gggggaagcg	aaacatagac	cactacctga	ttatatgaa	aaggttcaga	gtgattttaa	540
tcacacacat	agagcggttt	tgggtgattg	gttagtgagg	gttgctgagg	agtacaagct	600
tgtttcggat	acgctttatc	tcactatctc	ctatgttgat	agattcttgt	ctgtgaagcc	660
tattaacagg	cagaagcttc	agcttctggg	agtttctgca	atgcttattg	cgtcgaaaaa	720
tgaagagata	ggctctccta	aagttgaaga	tttttgttac	attacgggata	atacattttac	780
taaaacaagg	gtgggtgtcg	tggaggcgga	tatacttctt	gctctgcagt	ttgaattagg	840
aaqcccaaac	atcaaaacat	tactaagacg	gtttacacgg	gttgacacaag	aagattttcaa	900
agactaccaa	ttgcagatag	agttcctttg	ttgctatcta	tcagaattga	gtatgttaga	960
ttacacctgt	gtgaagtatt	tgccatctct	tttgtctgct	tcagctgtat	ttcttgcccg	1020
gttcacatc	cgtccaaaac	aacatccttg	gaatcaaatg	ctagaagaat	acacaaaagta	1080
caaaagcagt	gatctacaag	tgtgcgtggg	tatcatacat	gacttgtatc	taagcagaag	1140
aggaacacct	ctagaagctg	ttagaaataa	tacaaagcaa	cacaagtaca	agtgcggttc	1200
gaccatgcct	gtttcacocg	agctacacct	tgctttcttt	gaagatatta	ccattagagg	1260
aatggcgctg	aagaagcttg	aagctttatg	attgggaagt	ttagttacct	gaattttggg	1320
ttgtatatat	ctgttagaat	ggcagattag	tattgagtat	tatctctttt	acggtatggt	1380
caatgatttt	tGctwacac	tagttaAgaa	actttttttt	ttTgctTgac	cattttttca	1440
atggttttatt	agatttttt					

(2) INFORMATION FOR SEQ ID NO:2002:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 369 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..369

(D) OTHER INFORMATION: / Ceres Seq. ID 1571544

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2002:

Met	Ala	Glu	Asn	Gln	Asn	Cys	Ala	Arg	Met	Thr	Arg	Ala	Ala	Ala	Lys
1			5						10					15	
Arg	Lys	Ala	Ser	Ser	Met	Ala	Leu	Asp	Glu	Asn	Pro	Val	Ser	Lys	Lys
			20					25					30		
Arg	Val	Val	Leu	Gly	Glu	Leu	Pro	Asn	Met	Ser	Asn	Val	Val	Ala	Val
			35					40				45			
Pro	Asn	Gln	Glu	Arg	Glu	Thr	Leu	Lys	Ala	Lys	Thr	Ser	Val	Asn	Thr
			50				55				60				
Ser	Lys	Arg	Gln	Met	Lys	Lys	Ala	Leu	Met	Ile	Pro	Glu	Ala	Ser	Val
			65				70			75				80	
Leu	Ile	Glu	Ser	Arg	Ser	Val	Asp	Pro	Gln	Met	Cys	Glu	Pro	Phe	Ala
			85					90						95	
Ser	Asp	Ile	Cys	Ala	Tyr	Leu	Arg	Glu	Met	Glu	Gly	Lys	Pro	Lys	His
			100					105					110		
Arg	Pro	Leu	Pro	Asp	Tyr	Ile	Glu	Lys	Val	Gln	Ser	Asp	Leu	Thr	Pro
			115				120					125			
His	Met	Arg	Ala	Val	Leu	Val	Asp	Trp	Leu	Val	Glu	Val	Ala	Glu	Glu
			130				135					140			
Tyr	Lys	Leu	Val	Ser	Asp	Thr	Leu	Tyr	Leu	Thr	Ile	Ser	Tyr	Val	Asp
			145				150				155				160
Arg	Phe	Leu	Ser	Val	Lys	Pro	Ile	Asn	Arg	Gln	Lys	Leu	Gln	Leu	Val
			165					170						175	
Gly	Val	Ser	Ala	Met	Leu	Ile	Ala	Ser	Lys	Tyr	Glu	Glu	Ile	Gly	Pro
			180					185					190		
Pro	Lys	Val	Glu	Asp	Phe	Cys	Tyr	Ile	Thr	Asp	Asn	Thr	Phe	Thr	Lys
			195				200					205			
Gln	Glu	Val	Val	Ser	Met	Glu	Ala	Asp	Ile	Leu	Leu	Ala	Leu	Gln	Phe

210	215	220
Glu Leu Gly Ser Pro Thr Ile Lys Thr Phe Leu Arg Arg Phe Thr Arg		
225	230	235
Val Ala Gln Glu Asp Phe Lys Asp Ser Gln Leu Gln Ile Glu Phe Leu		
240	245	250
Cys Cys Tyr Leu Ser Glu Leu Ser Met Leu Asp Tyr Thr Cys Val Lys		
255	260	265
Tyr Leu Pro Ser Ser Leu Leu Ser Ala Ser Ala Val Phe Leu Ala Arg Phe		
270	275	280
Ile Ile Arg Pro Lys Gln His Pro Trp Asn Gln Met Leu Glu Glu Tyr		
285	290	300
Thr Lys Tyr Lys Ala Ala Asp Leu Gln Val Cys Val Gly Ile Ile His		
310	315	320
Asp Leu Tyr Leu Ser Arg Arg Gly Asn Thr Leu Glu Ala Val Arg Asn		
325	330	335
Lys Tyr Lys Gln His Lys Tyr Lys Cys Val Ala Thr Met Pro Val Ser		
340	345	350
Pro Glu Leu Pro Leu Ala Phe Phe Glu Asp Ile Thr Ile Arg Gly Met		
355	360	365

Ala

(2) INFORMATION FOR SEQ ID NO:2003:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 360 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..360
(D) OTHER INFORMATION: / Ceres Seq. ID 1571545

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2003:

Met Thr Arg Ala Ala Lys Arg Lys Ala Ser Ser Met Ala Leu Asp	
1	5
Glu Asn Pro Val Ser Lys Lys Arg Val Val Leu Gly Glu Leu Pro Asn	
20	25
Met Ser Asn Val Val Ala Val Pro Asn Gln Glu Arg Glu Thr Leu Lys	
35	40
Ala Lys Thr Ser Val Asn Thr Ser Lys Arg Gln Met Lys Lys Ala Leu	
50	55
Met Ile Pro Glu Ala Ser Val Leu Ile Glu Ser Arg Ser Val Asp Pro	
65	70
Gln Met Cys Glu Pro Phe Ala Ser Asp Ile Cys Ala Tyr Leu Arg Glu	
85	90
Met Glu Gly Lys Pro Lys His Arg Pro Leu Pro Asp Tyr Ile Glu Lys	
100	105
Val Gln Ser Asp Leu Thr Pro His Met Arg Ala Val Leu Val Asp Trp	
115	120
Leu Val Glu Val Ala Glu Glu Tyr Lys Leu Val Ser Asp Thr Leu Tyr	
130	135
Leu Thr Ile Ser Tyr Val Asp Arg Phe Leu Ser Val Lys Pro Ile Asn	
145	150
Arg Gln Lys Leu Gln Leu Val Gly Val Ser Ala Met Leu Ile Ala Ser	
165	170
Lys Tyr Glu Glu Ile Gly Pro Pro Lys Val Glu Asp Phe Cys Tyr Ile	
180	185
Thr Asp Asn Thr Phe Thr Lys Gln Glu Val Val Ser Met Glu Ala Asp	
195	200
Ile Leu Leu Ala Leu Gln Phe Glu Leu Gly Ser Pro Thr Ile Lys Thr	
210	215
	220

Phe Leu Arg Arg Phe Thr Arg Val Ala Gln Glu Asp Phe Lys Asp Ser
225 230 235 240
Gln Leu Gln Ile Glu Phe Leu Cys Cys Tyr Leu Ser Glu Leu Ser Met
245 250 255
Leu Asp Tyr Thr Cys Val Lys Tyr Leu Pro Ser Leu Leu Ser Ala Ser
260 265 270
Ala Val Phe Leu Ala Arg Phe Ile Ile Arg Pro Lys Gln His Pro Trp
275 280 285
Asn Gln Met Leu Glu Glu Tyr Thr Lys Tyr Lys Ala Ala Asp Leu Gln
290 295 300
Val Cys Val Gly Ile Ile His Asp Leu Tyr Leu Ser Arg Arg Gly Asn
305 310 315 320
Thr Leu Glu Ala Val Arg Asn Lys Tyr Lys Gln His Lys Tyr Cys
325 330 335
Val Ala Thr Met Pro Val Ser Pro Glu Leu Pro Leu Ala Phe Phe Glu
340 345 350
Asp Ile Thr Ile Arg Gly Met Ala
355 360

(2) INFORMATION FOR SEQ ID NO:2004:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 348 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..348

(D) OTHER INFORMATION: / Ceres Seq. ID 1571546

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2004:

Met Ala Leu Asp Glu Asn Pro Val Ser Lys Lys Arg Val Val Leu Gly
1 5 10 15
Glu Leu Pro Asn Met Ser Asn Val Val Ala Val Pro Asn Gln Glu Arg
20 25 30
Glu Thr Leu Lys Ala Lys Thr Ser Val Asn Thr Ser Lys Arg Gln Met
35 40 45
Lys Lys Ala Leu Met Ile Pro Glu Ala Ser Val Leu Ile Glu Ser Arg
50 55 60
Ser Val Asp Pro Gln Met Cys Glu Pro Phe Ala Ser Asp Ile Cys Ala
65 70 75 80
Tyr Leu Arg Glu Met Glu Gly Lys Pro Lys His Arg Pro Leu Pro Asp
85 90 95
Tyr Ile Glu Lys Val Gln Ser Asp Leu Thr Pro His Met Arg Ala Val
100 105 110
Leu Val Asp Trp Leu Val Glu Val Ala Glu Glu Tyr Lys Leu Val Ser
115 120 125
Asp Thr Leu Tyr Leu Thr Ile Ser Tyr Val Asp Arg Phe Leu Ser Val
130 135 140
Lys Pro Ile Asn Arg Gln Lys Leu Gln Leu Val Gly Val Ser Ala Met
145 150 155 160
Leu Ile Ala Ser Lys Tyr Glu Glu Ile Gly Pro Pro Lys Val Glu Asp
165 170 175
Phe Cys Tyr Ile Thr Asp Asn Thr Phe Thr Lys Gln Glu Val Val Ser
180 185 190
Met Glu Ala Asp Ile Leu Leu Ala Leu Gln Phe Glu Leu Gly Ser Pro
195 200 205
Thr Ile Lys Thr Phe Leu Arg Arg Phe Thr Arg Val Ala Gln Glu Asp
210 215 220
Phe Lys Asp Ser Gln Leu Gln Ile Glu Phe Leu Cys Cys Tyr Leu Ser
225 230 235 240
Glu Leu Ser Met Leu Asp Tyr Thr Cys Val Lys Tyr Leu Pro Ser Leu

	245		250		255										
Leu	Ser	Ala	Ser	Ala	Val	Phe	Leu	Ala	Arg	Phe	Ile	Ile	Arg	Pro	Lys
	260		265		270										
Gln	His	Pro	Trp	Asn	Gln	Met	Leu	Glu	Glu	Tyr	Thr	Lys	Tyr	Lys	Ala
	275		280		285										
Ala	Asp	Leu	Gln	Val	Cys	Val	Gly	Ile	Ile	His	Asp	Leu	Tyr	Leu	Ser
	290		295		300										
Arg	Arg	Gly	Asn	Thr	Leu	Glu	Ala	Val	Arg	Asn	Lys	Tyr	Lys	Gln	His
	305		310		315										
Lys	Tyr	Lys	Cys	Val	Ala	Thr	Met	Pro	Val	Ser	Pro	Glu	Leu	Pro	Leu
	325		330		335										
Ala	Phe	Phe	Glu	Asp	Ile	Thr	Ile	Arg	Gly	Met	Ala				
	340		345												

(2) INFORMATION FOR SEQ ID NO:2005:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1203 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1203
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571547

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2005:

acaaaagcat	cataagaaga	agaagaact	acaatagtta	atcaatcaaa	gagaagtaag	60
agaaatggca	gattctaact	gtggatgtgg	ctctctctgc	aaatgtgggtg	actctttcgg	120
tgtgataaatt	ggaaagcttg	tctttttcag	caagaatttg	ccttcaaaagt	atgaagattg	180
ggaggcaggt	acaaaagctt	tgctcgacaa	ggaaaatata	atcggcgatgg	gatcgattgg	240
atcagctctat	agagcatctt	tcgaaggagg	agttttccatt	gcagtgaaaga	agcttgagac	300
cttaggaaga	atcagaagaac	aagaagagtt	tgagcaagaa	attggacggc	ttggaggttt	360
gcaacatccg	aatctgtctt	ctttccaagg	ttaactattt	tcctcaacaa	tgcagttgat	420
ctctctctgag	tttgtcccta	atggtagcct	ctacgataat	ctacacctaa	gaattttccc	480
gggaaccacg	tcaagctatg	ggaatactga	tittgaattgg	cacagaagat	ttcagattgc	540
tttaggaact	gcaaaaagcgc	tctcttttct	tcacaatgac	tgtaaaaccgg	cgattcttca	600
tctcaatggt	aagtccacca	acattcttct	agacgaaagg	tacgagccaa	agctatcgga	660
ttatgggtta	gaaaagtttc	ttccggttat	ggacagcttt	ggtttgacta	agaagtcca	720
caacgcgggt	gggtacattg	ctccagagtt	agctcagcag	agtttgagag	cgagtgagaa	780
atgcatgtg	tatagttacg	gtgtggttct	tcttgagctg	gttacaggta	gaaaaccggt	840
ggagctccca	tcggaaaacc	aagtcttgat	cttgagagac	tatgtgaggg	attttgttga	900
gactggttca	gcttctgatt	gttttgacag	TYTaagACgt	tgagagagtt	tgaagagaat	960
gagctgattc	aagtcatgaa	tttaggactc	ctttgtacgt	ccgagaatcc	actgaagaga	1020
ccgagcagtg	ctgaggttgg	gcagggttct	gaatcaatca	gaaatggatt	tgatcaatga	1080
tgaagctttt	tccttttttt	tgagcaaaaga	ttgcatagga	aatgtgcaga	taagttttat	1140
ttttgggat	tttccagttt	tagatttacg	tttgtcaat	gaaattgtta	ctctggtttm	1200

cac

(2) INFORMATION FOR SEQ ID NO:2006:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 292 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..292
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571548

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2006:

Met	Ala	Asp	Ser	Asn	Cys	Gly	Cys	Gly	Ser	Ser	Cys	Lys	Cys	Gly	Asp
1					5			10				15			
Ser	Phe	Gly	Val	Ile	Ile	Gly	Lys	Leu	Val	Leu	Phe	Ser	Lys	Asn	Leu

(2) INFORMATION FOR SEQ ID NO:2007:

(A) LENGTH: 238 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..238

(D) OTHER INFORMATION: / Ceres Seq. ID 1571549

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2007:

Met	Gly	Ser	Ile	Gly	Ser	Val	Tyr	Arg	Ala	Ser	Phe	Glu	Gly	Gly	Val
1				5					10					15	
Ser	Ile	Ala	Val	Lys	Lys	Leu	Glu	Thr	Leu	Gly	Arg	Ile	Arg	Asn	Gln
		20						25					30		
Glu	Glu	Phe	Glu	Gln	Glu	Ile	Gly	Arg	Leu	Gly	Gly	Leu	Gln	His	Pro
		35					40					45			
Asn	Leu	Ser	Ser	Phe	Gln	Gly	Tyr	Tyr	Phe	Ser	Ser	Thr	Met	Gln	Leu
	50					55					60				
Ile	Leu	Ser	Glu	Phe	Val	Pro	Asn	Gly	Ser	Leu	Tyr	Asp	Asn	Leu	His
	65				70					75				80	
Leu	Arg	Ile	Phe	Pro	Gly	Thr	Ser	Ser	Ser	Tyr	Gly	Asn	Thr	Asp	Leu
				85					90					95	
Asn	Trp	His	Arg	Arg	Phe	Gln	Ile	Ala	Leu	Gly	Thr	Ala	Lys	Ala	Leu
			100					105					110		

Ser Phe Leu His Asn Asp Cys Lys Pro Ala Ile Leu His Leu Asn Val
115 120 125
Lys Ser Thr Asn Ile Leu Leu Asp Glu Arg Tyr Glu Ala Lys Leu Ser
130 135 140
Asp Tyr Gly Leu Glu Lys Phe Leu Pro Val Met Asp Ser Phe Gly Leu
145 150 155 160
Thr Lys Lys Phe His Asn Ala Val Gly Tyr Ile Ala Pro Glu Leu Ala
165 170 175
Gln Gln Ser Leu Arg Ala Ser Glu Lys Cys Asp Val Tyr Ser Tyr Gly
180 185 190
Val Val Leu Leu Glu Leu Val Thr Gly Arg Lys Pro Val Glu Ser Pro
195 200 205
Ser Glu Asn Gln Val Leu Ile Leu Arg Asp Tyr Val Arg Asp Leu Leu
210 215 220
Glu Thr Gly Ser Ala Ser Asp Cys Phe Asp Ser Xaa Arg Arg
225 230 235

(2) INFORMATION FOR SEQ ID NO:2008:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 177 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..177
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571550

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2008:

Met Gln Leu Ile Leu Ser Glu Phe Val Pro Asn Gly Ser Leu Tyr Asp
1 5 10 15
Asn Leu His Leu Arg Ile Phe Pro Gly Thr Ser Ser Ser Tyr Gly Asn
20 25 30
Thr Asp Leu Asn Trp His Arg Arg Phe Gln Ile Ala Leu Gly Thr Ala
35 40 45
Lys Ala Leu Ser Phe Leu His Asn Asp Cys Lys Pro Ala Ile Leu His
50 55 60
Leu Asn Val Lys Ser Thr Asn Ile Leu Leu Asp Glu Arg Tyr Glu Ala
65 70 75 80
Lys Leu Ser Asp Tyr Gly Leu Glu Lys Phe Leu Pro Val Met Asp Ser
85 90 95
Phe Gly Leu Thr Lys Lys Phe His Asn Ala Val Gly Tyr Ile Ala Pro
100 105 110
Glu Leu Ala Gln Gln Ser Leu Arg Ala Ser Glu Lys Cys Asp Val Tyr
115 120 125
Ser Tyr Gly Val Val Leu Leu Glu Leu Val Thr Gly Arg Lys Pro Val
130 135 140
Glu Ser Pro Ser Glu Asn Gln Val Leu Ile Leu Arg Asp Tyr Val Arg
145 150 155 160
Asp Leu Leu Glu Thr Gly Ser Ala Ser Asp Cys Phe Asp Ser Xaa Arg
165 170 175

Arg

(2) INFORMATION FOR SEQ ID NO:2009:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1154 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -

(B) LOCATION: 1..1154

(D) OTHER INFORMATION: / Ceres Seq. ID 1571559

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2009:

agccctcttc	ccaattatttg	atcaattttct	aaagaaaacc	ccttcctcta	ctagtcctcc	60
tcctatatat	acaaaatctt	aagaaatctc	tctacttgtt	tcctctgtta	tcataatctc	120
ttctctctat	ttctctcttc	ttctctcttt	acctctgttt	tttttttcat	tcacacagagc	180
ccaggttgat	tgatttttgt	attcagagat	atggggagag	gaaggattga	gattaaagag	240
attgagaata	tcaacagctg	tcaagtcact	ttctctaaga	gacgaaaagg	tttgatcaag	300
aagggtctaa	agcttttgat	ttctctgtac	gccgagggtg	ctcttatcat	cttctccagc	360
accggcaaga	tttacgatatt	ctccagcgct	tgatggagc	aaattctttc	tagatatgga	420
tacactactg	cgctccactga	gcataaacia	caagagagac	accaactctc	aatttgtgtc	480
tcacatggaa	atgaagctgt	gttgcgaaat	gatgattcta	tgaagggtga	acttgaaaga	540
ttacagcttg	caattgagag	acttaagggt	aaggagcttg	aaggtatgag	tttcccggtg	600
cttattttct	ttgaaaacca	gttgaacgag	agcttgcata	gtgtcaagga	tcaaaagaca	660
caaatccctg	tcaaccagat	tgagagatcc	aggatacagg	agaaaaaagc	attggaagaa	720
aaccaaatct	tgccgcaaca	ggttgagatg	ttggggagag	gttcaggacc	aaaagtgttg	780
aatgaaaggg	ctcaagattc	tagcccgaga	gccgatcccg	agagctcttc	actcagaagag	840
gatgagaatg	acaaacgagga	gcaccattcc	gacactctct	tgcagttggg	gttgctgctg	900
acggggtatt	gcacaaagag	aaagaagccg	aagatcgaa	tggtctcgca	taactctggg	960
agtcgaatgg	cttctgattg	atggaatcga	ttatttttct	aattctgggt	gtttaggggt	1020
ctctatgtgt	cttctgtgtt	ctggctgttc	ttttgcttta	tttcaactca	agttagcttt	1080
ttttaatgtt	taggtggaac	atttttccat	aatcaagaag	ggatttgatc	aatcaataac	1140
attagatttt	cytt					

(2) INFORMATION FOR SEQ ID NO:2010:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 256 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..256

(D) OTHER INFORMATION: / Ceres Seq. ID 1571560

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2010:

Met	Gly	Arg	Gly	Arg	Ile	Glu	Ile	Lys	Lys	Ile	Glu	Asn	Ile	Asn	Ser
1			5					10					15		
Arg	Gln	Val	Thr	Phe	Ser	Lys	Arg	Arg	Asn	Gly	Leu	Ile	Lys	Lys	Ala
			20					25					30		
Lys	Glu	Leu	Ser	Ile	Leu	Cys	Asp	Ala	Glu	Val	Ala	Leu	Ile	Ile	Phe
			35				40					45			
Ser	Ser	Thr	Gly	Lys	Ile	Tyr	Asp	Phe	Ser	Ser	Val	Cys	Met	Glu	Gln
			50				55				60				
Ile	Leu	Ser	Arg	Tyr	Gly	Tyr	Thr	Thr	Ala	Ser	Thr	Glu	His	Lys	Gln
			65				70				75				80
Gln	Arg	Glu	His	Gln	Leu	Leu	Ile	Cys	Ala	Ser	His	Gly	Asn	Glu	Ala
			85							90			95		
Val	Leu	Arg	Asn	Asp	Asp	Ser	Met	Lys	Val	Glu	Leu	Glu	Arg	Leu	Gln
			100					105					110		
Leu	Ala	Ile	Glu	Arg	Leu	Lys	Gly	Lys	Glu	Leu	Glu	Gly	Met	Ser	Phe
			115				120					125			
Pro	Asp	Leu	Ile	Ser	Phe	Glu	Asn	Gln	Leu	Asn	Glu	Ser	Leu	His	Ser
			130				135					140			
Val	Lys	Asp	Gln	Lys	Thr	Gln	Ile	Leu	Leu	Asn	Gln	Ile	Glu	Arg	Ser
			145				150				155				160
Arg	Ile	Gln	Glu	Lys	Lys	Ala	Leu	Glu	Glu	Asn	Gln	Ile	Leu	Arg	Lys
			165							170				175	
Gln	Val	Glu	Met	Leu	Gly	Arg	Gly	Ser	Gly	Pro	Lys	Val	Leu	Asn	Glu
			180				185					190			
Arg	Pro	Gln	Asp	Ser	Ser	Pro	Glu	Ala	Asp	Pro	Glu	Ser	Ser	Ser	Ser
			195				200					205			

Glu	Glu	Asp	Glu	Asn	Asp	Asn	Glu	Glu	His	His	Ser	Asp	Thr	Ser	Leu
210						215					220				
Gln	Leu	Gly	Leu	Ser	Ser	Thr	Gly	Tyr	Cys	Thr	Lys	Arg	Lys	Lys	Pro
225						230					235				240
Lys	Ile	Glu	Leu	Val	Cys	Asp	Asn	Ser	Gly	Ser	Gln	Val	Ala	Ser	Asp
				245					250					255	

(2) INFORMATION FOR SEQ ID NO:2011:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 195 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..195

(D) OTHER INFORMATION: / Ceres Seq. ID 1571561

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2011:

Met	Glu	Gln	Ile	Leu	Ser	Arg	Tyr	Gly	Tyr	Thr	Thr	Ala	Ser	Thr	Glu
1				5						10				15	
His	Lys	Gln	Gln	Arg	Glu	His	Gln	Leu	Ile	Cys	Ala	Ser	His	Gly	
			20					25				30			
Asn	Glu	Ala	Val	Leu	Arg	Asn	Asp	Asp	Ser	Met	Lys	Val	Glu	Leu	Glu
			35				40					45			
Arg	Leu	Gln	Leu	Ala	Ile	Glu	Arg	Leu	Lys	Gly	Lys	Glu	Leu	Glu	Gly
	50				55					60					
Met	Ser	Phe	Pro	Asp	Leu	Ile	Ser	Phe	Glu	Asn	Gln	Leu	Asn	Glu	Ser
65					70					75				80	
Leu	His	Ser	Val	Lys	Asp	Gln	Lys	Thr	Gln	Ile	Leu	Leu	Asn	Gln	Ile
				85					90					95	
Glu	Arg	Ser	Arg	Ile	Gln	Glu	Lys	Lys	Ala	Leu	Glu	Glu	Asn	Gln	Ile
			100					105					110		
Leu	Arg	Lys	Gln	Val	Glu	Met	Leu	Gly	Arg	Gly	Ser	Gly	Pro	Lys	Val
			115				120					125			
Leu	Asn	Glu	Arg	Pro	Gln	Asp	Ser	Ser	Pro	Glu	Ala	Asp	Pro	Glu	Ser
			130			135					140				
Ser	Ser	Ser	Glu	Glu	Asp	Glu	Asn	Asp	Asn	Glu	Glu	His	His	Ser	Asp
145				150						155				160	
Thr	Ser	Leu	Gln	Leu	Gly	Leu	Ser	Ser	Thr	Gly	Tyr	Cys	Thr	Lys	Arg
			165					170						175	
Lys	Lys	Pro	Lys	Ile	Glu	Leu	Val	Cys	Asp	Asn	Ser	Gly	Ser	Gln	Val
			180					185					190		

Ala Ser Asp

195

(2) INFORMATION FOR SEQ ID NO:2012:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 153 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..153

(D) OTHER INFORMATION: / Ceres Seq. ID 1571562

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2012:

Met	Lys	Val	Glu	Leu	Glu	Arg	Leu	Gln	Leu	Ala	Ile	Glu	Arg	Leu	Lys
1			5					10						15	
Gly	Lys	Glu	Leu	Glu	Gly	Met	Ser	Phe	Pro	Asp	Leu	Ile	Ser	Phe	Glu

Met Ala Val Ser Cys Asn His Ser Ala Ile Leu Phe Ser Pro Ser Ser

1	5	10	15
Thr Ala Gly Ser Ser Ser Val Thr Ser Ser Ser Ser Leu Ile Gly Phe			
20		25	30
Pro Arg Phe Gln Thr Leu Arg Phe Lys Ser Arg Ser Val Tyr Ser Lys			
35	40	45	
Ser Arg Ala Ser Ser Pro Val Ser Ala Leu Pro Ser Arg Ser Leu Glu			
50	55	60	
Ala Leu Ile Phe Asp Cys Asp Gly Val Ile Leu Glu Ser Glu Asn Leu			
65	70	75	80
His Arg Gln Ala Tyr Asn Asp Ala Phe Ser His Phe Asp Val Arg Cys			
85	90	95	
Pro Pro Ser Ser Ser Ala Ser Leu Asp Trp Ser Leu Glu Phe Tyr Asp			
100	105	110	
Lys Phe Gln Asn Leu Val Gly Gly Lys Pro Lys Met Arg Trp Tyr			
115	120	125	
Phe Lys Glu Asn Gly Trp Pro Thr Ser Thr Ile Phe Asp Ser Pro Pro			
130	135	140	
Gln Asn Asp Asp Asp Arg Ala Lys Leu Ile Asp Thr Leu Gln Asp Trp			
145	150	155	160
Lys Thr Asp Arg Tyr Lys Glu Ile Ile Lys Ser Gly Ser Val Glu Pro			
165	170	175	
Arg Pro Gly Val Ile Arg Leu Met Asp Glu Ala Lys Ala Ala Gly Lys			
180	185	190	
Lys Leu Ala Val Cys Ser Ala Ala Thr Lys Ser Ser Val Ile Leu Cys			
195	200	205	
Leu Glu Asn Leu Leu Asp Ile Glu Arg Phe Gln Gly Leu Asp Cys Phe			
210	215	220	
Leu Ala Gly Asp Asp Val Lys Glu Lys Lys Pro Asp Pro Ser Ile Tyr			
225	230	235	240
Ile Thr Ala Ala Glu Lys Leu Gly Val Ser Val Lys Asp Cys Leu Val			
245	250	255	
Val Gly Asp Ser Val Ile Gly Leu Gln Ala Ala Thr Lys Ala Gly Met			
260	265	270	
Ser Cys Val Ile Thr Tyr Thr Ser Thr Ser Asp Gln Asp Phe Asn			
275	280	285	
Asp Ala Ile Ala Val Tyr Pro Asp Leu Ser Asn Val Lys Leu Thr Asp			
290	295	300	
Leu Glu Thr Leu Leu Glu Thr Ile Val Thr Ala Ala			
305	310	315	

(2) INFORMATION FOR SEQ ID NO:2015:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 192 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..192

(D) OTHER INFORMATION: / Ceres Seq. ID 1571569

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2015:

Met Arg Trp Tyr Phe Lys Glu Asn Gly Trp Pro Thr Ser Thr Ile Phe			
1	5	10	15
Asp Ser Pro Pro Gln Asn Asp Asp Asp Arg Ala Lys Leu Ile Asp Thr			
20	25	30	
Leu Gln Asp Trp Lys Thr Asp Arg Tyr Lys Glu Ile Ile Lys Ser Gly			
35	40	45	
Ser Val Glu Pro Arg Pro Gly Val Ile Arg Leu Met Asp Glu Ala Lys			
50	55	60	
Ala Ala Gly Lys Lys Leu Ala Val Cys Ser Ala Ala Thr Lys Ser Ser			
65	70	75	80

Val	Ile	Leu	Cys	Leu	Glu	Asn	Leu	Leu	Asp	Ile	Glu	Arg	Phe	Gln	Gly	
			85						90					95		
Leu	Asp	Cys	Phe	Leu	Ala	Gly	Asp	Asp	Val	Lys	Glu	Lys	Lys	Pro	Asp	
		100					105						110			
Pro	Ser	Ile	Tyr	Ile	Thr	Ala	Ala	Glu	Lys	Leu	Gly	Val	Ser	Val	Lys	
		115					120					125				
Asp	Cys	Leu	Val	Val	Gly	Asp	Ser	Val	Ile	Gly	Leu	Gln	Ala	Ala	Thr	
	130					135					140					
Lys	Ala	Gly	Met	Ser	Cys	Val	Ile	Thr	Tyr	Thr	Ser	Ser	Thr	Ser	Asp	
	145				150				155					160		
Gln	Asp	Phe	Asn	Asp	Ala	Ile	Ala	Val	Tyr	Pro	Asp	Leu	Ser	Asn	Val	
			165						170					175		
Lys	Leu	Thr	Asp	Leu	Glu	Thr	Leu	Leu	Gln	Thr	Ile	Val	Thr	Ala	Ala	
		180					185						190			

(2) INFORMATION FOR SEQ ID NO:2016:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1714 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1714
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571570

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2016:

aatatataaaa	aatggatgga	tcaacgKgc	gcgatcatcc	ttaccctcat	cgtaacctac	60
attatatgggt	ttgtttctttt	acgtogttcg	tataaaggct	cacgtgtgtcg	gcccttagtg	120
ggcagttcttc	cagcactcat	aacaaatgct	caccgcgatgc	acgactctcat	cgccgataac	180
ctcccgatgt	ggcgccgtac	gtaccaaaacg	tgcatattcc	cgatcccgtt	cttggtctaa	240
aaacaaggtc	acgtgactgt	cacgtgtgac	ccaaagaatc	tggagcatat	cttgaagacc	300
cggttcgata	attaccocaa	gggtctctagc	tggcaatcag	tcttccacga	tctgttagga	360
gatgggatct	ttaattcaga	tgggtgacaca	tggcgggttc	aacgtaagac	cgctgcattg	420
gagttgcacta	cacgtaccct	tgcgcaagcc	atggctcggt	gggttgatcg	agccatcaag	480
aaccgtctcg	tggcgattct	tgaatcagct	aggagtcgag	ccgagccgat	tgatcttcaa	540
gatgttctttt	tacggctcac	tttcgataac	atttcggcgt	taacatttgg	taaatgacca	600
cggacactct	cgccggagtt	tcttgagaac	ggattcgcgg	tggcttttga	tggagccacc	660
gaagccactc	ttcaacgggt	tatcatgcct	gagtttattt	ggaagatcag	aaaaatggctt	720
cggtctcggtt	tggaaagatga	tatgacgga	agcatcagcc	acgtggataa	ttacttatca	780
gagatcataa	atacacgtaa	gctcgaattg	ctaggtcagc	aacaagatgg	atcccgcact	840
gatgatctat	tgtcacgggt	catgaagaaa	aaagaatcct	actcggataa	atatcttaaa	900
tacgtggcgt	taaattttcat	cctagctgga	cgtaaacagc	catcgggttc	tatgagttgg	960
ttcttctctgt	tgggttagtct	taacccacga	gtcgaagaaa	aaatcataaa	cgagatctcg	1020
accattctga	tcaagacacg	tgacaccaat	gtgtcgaaat	ggaccgaaga	gcggttgact	1080
ttcgatgaaa	ttgacagatt	gggtctactta	aaagcggcat	tgtccgaaac	attgaggctga	1140
ttatcatcgct	taccagaaga	ttctaaaattt	gttggttgcca	acgatatttt	acctgacggg	1200
acattttgtc	catcgggcat	aaacgtttaca	tattcgatat	attcgggttg	gcgatgaaa	1260
ttcattttgg	gtgaaagatga	tctcagattt	aaacccgaaa	gatggttaga	ggaagccggg	1320
gacgaaaaat	gtaaaccaata	caaattctgta	gcgttcaatg	ccggtccacg	gattttgtcta	1380
ggcaaaagct	tggcttattt	cgagatgaaa	tcaattactg	cttcgatattt	gcctccggcat	1440
cggtctacgg	tggctccggg	acatcgagtg	gagcagaaga	tgtcatttag	gtgtgtcatg	1500
aaagtgtgtc	ttaaaaatgga	tgtgcataaa	agggatttga	cgttgcgggt	ggagaaagtg	1560
gttaatgaga	tgaggaaaaa	gtgagattat	tgggaactaat	gatggttaac	atgatgaagt	1620
taaatgtgtc	accggtttgg	cataagcatt	aatgtggagc	atggtaattt	agaaattgtg	1680
ttgtgtgaag	caaaaataaat	ttaaaacata	cttt			

(2) INFORMATION FOR SEQ ID NO:2017:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 527 amino acids
- (B) TYPE: amino acid

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(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..527
(D) OTHER INFORMATION: / Ceres Seq. ID 1571571
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2017:

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[illegible]

Met	Asp	Gln	Xaa	Ala	Ala	Ile	Ile	Leu	Thr	Leu	Ile	Val	Thr	Tyr	Ile
1			5					25	10					15	
Ile	Trp	Phe	Val	Ser	Leu	Arg	Arg	Ser	Tyr	Lys	Gly	Pro	Arg	Val	Trp
			20					25					30		
Pro	Leu	Val	Gly	Ser	Leu	Pro	Ala	Leu	Ile	Thr	Asn	Ala	His	Arg	Met
		35					40					45			
His	Asp	Phe	Ile	Ala	Asp	Asn	Leu	Arg	Met	Cys	Gly	Gly	Thr	Tyr	Gln
	50					55				60					
Thr	Cys	Ile	Phe	Pro	Ile	Pro	Phe	Leu	Ala	Lys	Lys	Gln	Gly	His	Val
65					70					75				80	
Thr	Val	Thr	Cys	Asp	Pro	Lys	Asn	Leu	Glu	His	Ile	Leu	Lys	Thr	Arg
				85					90					95	
Phe	Asp	Asn	Tyr	Trp	Lys	Gly	Pro	Ser	Trp	Gln	Ser	Val	Phe	His	Asp
			100					105					110		
Leu	Leu	Gly	Asp	Gly	Ile	Phe	Asn	Ser	Asp	Gly	Asp	Thr	Trp	Arg	Phe
		115					120					125			
Gln	Arg	Lys	Thr	Ala	Ala	Leu	Glu	Phe	Thr	Thr	Arg	Thr	Leu	Arg	Gln
	130					135					140				
Ala	Met	Ala	Arg	Trp	Val	Asp	Arg	Ala	Ile	Lys	Asn	Arg	Leu	Val	Pro
145					150					155				160	
Ile	Leu	Glu	Ser	Ala	Arg	Ser	Arg	Ala	Glu	Pro	Ile	Asp	Leu	Gln	Asp
				165					170					175	
Val	Leu	Leu	Arg	Leu	Thr	Phe	Asp	Asn	Ile	Cys	Gly	Leu	Thr	Phe	Gly
			180					185					190		
Lys	Asp	Pro	Arg	Thr	Leu	Ser	Pro	Glu	Phe	Pro	Glu	Asn	Gly	Phe	Ala
		195					200					205			
Val	Ala	Phe	Asp	Gly	Ala	Thr	Glu	Ala	Thr	Leu	Gln	Arg	Phe	Ile	Met
	210					215					220				
Pro	Glu	Phe	Ile	Trp	Lys	Ile	Arg	Lys	Trp	Leu	Arg	Leu	Gly	Leu	Glu
225					230					235				240	
Asp	Asp	Met	Ser	Arg	Ser	Ile	Ser	His	Val	Asp	Asn	Tyr	Leu	Ser	Glu
				245					250					255	
Ile	Ile	Asn	Thr	Arg	Lys	Leu	Glu	Leu	Leu	Gly	Gln	Gln	Gln	Asp	Gly
		260						265					270		
Ser	Arg	His	Asp	Asp	Leu	Leu	Ser	Arg	Phe	Met	Lys	Lys	Lys	Glu	Ser
		275					280					285			

Tyr Ser Asp Lys Tyr Leu Lys Tyr Val Ala Leu Asn Phe Ile Leu Ala
290 295 300
Gly Arg Asn Thr Ser Ser Val Ala Met Ser Trp Phe Phe Trp Leu Val
305 310 315 320
Ser Leu Asn Pro Arg Val Glu Glu Lys Ile Ile Asn Glu Ile Cys Thr
325 330 335
Ile Leu Ile Lys Thr Arg Asp Thr Asn Val Ser Lys Trp Thr Asp Glu
340 345 350
Pro Leu Thr Phe Asp Glu Ile Asp Gln Leu Val Tyr Leu Lys Ala Ala
355 360 365
Leu Ser Glu Thr Leu Arg Leu Tyr Pro Ser Val Pro Glu Asp Ser Lys
370 375 380
Phe Val Val Ala Asn Asp Val Leu Pro Asp Gly Thr Phe Val Pro Ser
385 390 395 400
Gly Ser Asn Val Thr Tyr Ser Ile Tyr Ser Val Gly Arg Met Lys Phe
405 410 415
Ile Trp Gly Glu Asp Cys Leu Glu Phe Lys Pro Glu Arg Trp Leu Glu
420 425 430
Glu Ser Arg Asp Glu Lys Cys Asn Gln Tyr Lys Phe Val Ala Phe Asn
435 440 445
Ala Gly Pro Arg Ile Cys Leu Gly Lys Asp Leu Ala Tyr Leu Gln Met
450 455 460
Lys Ser Ile Thr Ala Ser Ile Leu Leu Arg His Arg Leu Thr Val Ala
465 470 475 480
Pro Gly His Arg Val Glu Gln Lys Met Ser Leu Thr Leu Phe Met Lys
485 490 495
Phe Gly Leu Lys Met Asp Val His Lys Arg Asp Leu Thr Leu Pro Val
500 505 510
Glu Lys Val Val Asn Glu Met Arg Lys Lys
515 520

(2) INFORMATION FOR SEQ ID NO:2019:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 475 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..475
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571573

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2019:

Met His Asp Phe Ile Ala Asp Asn Leu Arg Met Cys Gly Thr Tyr
1 5 10 15
Gln Thr Cys Ile Phe Pro Ile Pro Phe Leu Ala Lys Lys Gln Gly His
20 25 30
Val Thr Val Thr Cys Asp Pro Lys Asn Leu Glu His Ile Leu Lys Thr
35 40 45
Arg Phe Asp Asn Tyr Pro Lys Gly Pro Ser Trp Gln Ser Val Phe His
50 55 60
Asp Leu Leu Gly Asp Gly Ile Phe Asn Ser Asp Gly Asp Thr Trp Arg
65 70 75 80
Phe Gln Arg Lys Thr Ala Ala Leu Glu Phe Thr Thr Arg Thr Arg
85 90 95
Gln Ala Met Ala Arg Trp Val Asp Arg Ala Ile Lys Asn Arg Leu Val
100 105 110
Pro Ile Leu Glu Ser Ala Arg Ser Arg Ala Glu Pro Ile Asp Leu Gln
115 120 125
Asp Val Leu Leu Arg Leu Thr Phe Asp Asn Ile Cys Gly Leu Thr Phe
130 135 140
Gly Lys Asp Pro Arg Thr Leu Ser Pro Glu Phe Pro Glu Asn Gly Phe

145 150 155 160
Ala Val Ala Phe Asp Gly Ala Thr Glu Ala Thr Leu Gln Arg Phe Ile
165 170 175
Met Pro Glu Phe Ile Trp Lys Ile Arg Lys Trp Leu Arg Leu Gly Leu
180 185 190
Glu Asp Asp Met Ser Arg Ser Ile Ser His Val Asp Asn Tyr Leu Ser
195 200 205
Glu Ile Ile Asn Thr Arg Lys Leu Glu Leu Gly Gln Gln Gln Asp
210 215 220
Gly Ser Arg His Asp Asp Leu Leu Ser Arg Phe Met Lys Lys Lys Glu
225 230 235 240
Ser Tyr Ser Asp Lys Tyr Leu Lys Tyr Val Ala Leu Asn Phe Ile Leu
245 250 255
Ala Gly Arg Asn Thr Ser Ser Val Ala Met Ser Trp Phe Phe Trp Leu
260 265 270
Val Ser Leu Asn Pro Arg Val Glu Glu Lys Ile Ile Asn Glu Ile Cys
275 280 285
Thr Ile Leu Ile Lys Thr Arg Asp Thr Asn Val Ser Lys Trp Thr Asp
290 295 300
Glu Pro Leu Thr Phe Asp Glu Ile Asp Gln Leu Val Tyr Leu Lys Ala
305 310 315 320
Ala Leu Ser Glu Thr Leu Arg Leu Tyr Pro Ser Val Pro Glu Asp Ser
325 330 335
Lys Phe Val Val Ala Asn Asp Val Leu Pro Asp Gly Thr Phe Val Pro
340 345 350
Ser Gly Ser Asn Val Thr Tyr Ser Ile Tyr Ser Val Gly Arg Met Lys
355 360 365
Phe Ile Trp Gly Glu Asp Cys Leu Glu Phe Lys Pro Glu Arg Trp Leu
370 375 380
Glu Glu Ser Arg Asp Glu Lys Cys Asn Gln Tyr Lys Phe Val Ala Phe
385 390 395 400
Asn Ala Gly Pro Arg Ile Cys Leu Gly Lys Asp Leu Ala Tyr Leu Gln
405 410 415
Met Lys Ser Ile Thr Ala Ser Ile Leu Leu Arg His Arg Leu Thr Val
420 425 430
Ala Pro Gly His Arg Val Glu Gln Lys Met Ser Leu Thr Leu Phe Met
435 440 445
Lys Phe Gly Leu Lys Met Asp Val His Lys Arg Asp Leu Thr Leu Pro
450 455 460
Val Glu Lys Val Val Asn Glu Met Arg Lys Lys
465 470 475

(2) INFORMATION FOR SEQ ID NO:2020:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1276 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1276

(D) OTHER INFORMATION: / Ceres Seq. ID 1571582

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2020:

aaaWgaagtt	cctcattcaa	aaaagatttc	tcagccatca	aaattctctt	tctcttcac	60
caacaaaaaa	aaagcatacc	tctttttctt	ccatatagat	aagttaatta	agaaaaagaa	120
ttatcaggtt	ttgtttcgcc	tgatctgagg	aagttcatct	atggatcagg	ctcagtgcc	180
acaggagatt	gtagtgaagc	ccttggaaga	aatagtaaca	aacacatgcc	caaaagccaca	240
accgcaaccc	cttcaaacgc	acgacccacc	gtcgggtggg	ggagagagga	aggcaagacc	300
agaaaagat	caagctgtaa	actgtccgag	atgtaactca	accaacacaa	agttttgtta	360
ctacaacaat	tatagtttga	cgcagccaag	atacttctgc	aaaggttgta	gaaggtattg	420
gaccgaaGgc	ggttcgotta	ggaacattcc	tgttggcggt	ggctcaagaa	agaacaagag	480

atctcactct	ttttctctctg	atattagtaa	caatcactcg	gattctacac	aaccagctac	540
aaagaagcat	ctctctgac	atcaccacca	cctcatgagc	atgtctcaac	aaggtttgac	600
cggtcaaaac	ctcaaatcc	ttgagacgac	ccacaagat	ctcaatttag	gtttttcacc	660
acatgggatg	attaggacca	acttcactga	cctcatccac	aacattggca	acaacaccaa	720
caagagcaac	aacaataaca	atccattgat	tgttttctca	tgttctacca	tggtcacttc	780
ttctctggat	ctcataagaa	acaatagtaa	caatgggaat	tctcaaaatt	cttccttcat	840
gggatttcca	gttcataatg	aagatccagc	atcaggaggg	ttttcaatgc	aagatcatta	900
caagccttgc	aacacaaaca	ccacactgct	agggttttca	ttagatcatc	atcataataa	960
tggatttcat	ggaggggttc	aagaggagga	agaaggtgga	gaaggtgggt	atgatgtgaa	1020
tggaaggcac	ttgtttcctt	ttgaggattt	gaaattgcca	gtttcttctt	catcagcaac	1080
aattaatgtc	gacattaatg	aaacatcagaa	gcgaggaagc	ggtagtgtgc	cagctgctac	1140
gtctgtgtgg	tattggactg	ggatgttgag	tggaggatca	tggtgtcata	taatttctcg	1200
gtttgggtga	tgaagatagt	actattagtg	gttaattatt	gctatttatt	taattaatca	1260
atatgttctt	aatttc					

(2) INFORMATION FOR SEQ ID NO:2021:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 342 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..342
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571583

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2021:

Met	Asp	Thr	Ala	Gln	Trp	Pro	Gln	Glu	Ile	Val	Val	Lys	Pro	Leu	Glu
1		5						10						15	
Glu	Ile	Val	Thr	Asn	Thr	Cys	Pro	Lys	Pro	Gln	Pro	Gln	Pro	Leu	Gln
		20						25					30		
Thr	Gln	Gln	Pro	Pro	Ser	Val	Gly	Gly	Glu	Arg	Lys	Ala	Arg	Pro	Glu
		35					40					45			
Lys	Asp	Gln	Ala	Val	Asn	Cys	Pro	Arg	Cys	Asn	Ser	Thr	Asn	Thr	Lys
	50					55					60				
Phe	Cys	Tyr	Tyr	Asn	Asn	Tyr	Ser	Leu	Thr	Gln	Pro	Arg	Tyr	Phe	Cys
	65			70						75				80	
Lys	Gly	Cys	Arg	Arg	Tyr	Trp	Thr	Glu	Gly	Gly	Ser	Leu	Arg	Asn	Ile
			85					90					95		
Pro	Val	Gly	Gly	Gly	Ser	Arg	Lys	Asn	Lys	Arg	Ser	His	Ser	Phe	Ser
		100					105						110		
Ser	Asp	Ile	Ser	Asn	Asn	His	Ser	Asp	Ser	Thr	Gln	Pro	Ala	Thr	Lys
	115					120					125				
Lys	His	Leu	Ser	Asp	His	His	His	Leu	Met	Ser	Met	Ser	Gln	Gln	
	130				135					140					
Gly	Leu	Thr	Gly	Gln	Asn	Pro	Lys	Phe	Leu	Glu	Thr	Thr	Gln	Gln	Asp
	145			150					155						160
Leu	Asn	Leu	Gly	Phe	Ser	Pro	His	Gly	Met	Ile	Arg	Thr	Asn	Phe	Thr
			165					170						175	
Asp	Leu	Ile	His	Asn	Ile	Gly	Asn	Asn	Thr	Asn	Lys	Ser	Asn	Asn	Asn
		180					185						190		
Asn	Asn	Pro	Leu	Ile	Val	Ser	Ser	Cys	Ser	Thr	Met	Ala	Thr	Ser	Ser
		195					200					205			
Leu	Asp	Leu	Ile	Arg	Asn	Asn	Ser	Asn	Asn	Gly	Asn	Ser	Ser	Asn	Ser
	210					215					220				
Ser	Phe	Met	Gly	Phe	Pro	Val	His	Asn	Glu	Asp	Pro	Ala	Ser	Gly	Gly
	225			230					235						240
Phe	Ser	Met	Gln	Asp	His	Tyr	Lys	Pro	Cys	Asn	Thr	Asn	Thr	Thr	Leu
			245						250					255	
Leu	Gly	Phe	Ser	Leu	Asp	His	His	His	Asn	Asn	Gly	Phe	His	Gly	Gly
		260					265						270		
Phe	Gln	Gly	Gly	Glu	Glu	Gly	Gly	Gly	Gly	Asp	Asp	Val	Asn	Gly	

(2) INFORMATION FOR SEO ID NO:2022:

(A) LENGTH: 204 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(A) NAME/KEY: peptide

(B) LOCATION: 1..204

(D) OTHER INFORMATION: / Ceres Seq. ID 1571584

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2022:

(2) INFORMATION FOR SEQ ID NO:2023:

(A) LENGTH: 202 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(A) NAME/KEY: peptide

(B) LOCATION: 1..202

(D) OTHER INFORMATION: / Ceres Seq. ID 1571585

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2023:

Met Ser Gln Gln Gly Leu Thr Gly Gln Asn Pro Lys Phe Leu Glu Thr
1 5 10 15

```

Thr Gln Gln Asp Leu Asn Leu Gly Phe Ser Pro His Gly Met Ile Arg
      20      25      30
Thr Asn Phe Thr Asp Leu Ile His Asn Ile Gly Asn Asn Thr Asn Lys
      35      40      45
Ser Asn Asn Asn Asn Asn Pro Leu Ile Val Ser Ser Cys Ser Thr Met
      50      55      60
Ala Thr Ser Ser Leu Asp Leu Ile Arg Asn Asn Ser Asn Asn Gly Asn
      65      70      75      80
Ser Ser Asn Ser Ser Phe Met Gly Phe Pro Val His Asn Glu Asp Pro
      85      90      95
Ala Ser Gly Gly Phe Ser Met Gln Asp His Tyr Lys Pro Cys Asn Thr
      100      105      110
Asn Thr Thr Leu Leu Gly Phe Ser Leu Asp His His His Asn Asn Gly
      115      120      125
Phe His Gly Gly Phe Gln Gly Gly Glu Glu Gly Gly Glu Gly Asp
      130      135      140
Asp Val Asn Gly Arg His Leu Phe Pro Phe Glu Asp Leu Lys Leu Pro
      145      150      155      160
Val Ser Ser Ser Ser Ala Thr Ile Asn Val Asp Ile Asn Glu His Gln
      165      170      175
Lys Arg Gly Ser Gly Ser Asp Ala Ala Ala Thr Ser Gly Gly Tyr Trp
      180      185      190
Thr Gly Met Leu Ser Gly Gly Ser Trp Cys
      195      200

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(2) INFORMATION FOR SEQ ID NO:2024:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1709 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1709
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571586

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2024:

```

attttgtgca tttttctcaa gctgcgcgcg tttctcactc ttttttatct ctcaaatgtg 60
accttctctcg ttgttctttc gcacgcgctca ggagcagaag cttcaatctt tgataaatgc 120
gaggaaacaag gggttggtcg agcaagatct taaaaaattg gatgtaactg gtctacatcc 180
tctgtctctcc gaggtcattt ctcgccaggc cactattaat ataggaacca ttggtcatgt 240
cgctcatcga aagtcacactg ttgtttaaagc tatttctggt gtccagactg tccgttttaa 300
aaatgaattg gagcgttaaca ttaccattaa gcttggtatg gcaaacgcga agatttaca 360
atgtgaggat gagaattgcc ctagaccaat gtgctacaag gcctacggaa gtggaagaag 420
agacactccc aattgtgatg tccccggatt tgaaaactcc aagatgaaac tattgaggag 480
gtgtctcattc gttgattgcc ogggtcacga tattctcatg gcMacaatgc ttaatggagc 540
agccatcatg gatgggtgcac tacttttaac cgctgcacaa gaaacttgct cacaaccaca 600
aacgtctgaa catcttgctg ccgttgagat tatgcaactt aagcatatca tcatccttca 660
gaacaagatt gatcttattc aagagaatgt tgccattaat cagcacgagg caattcagaa 720
atttataatg aaactgtgtg ctgatgctgc tccgatcgtc cctgtctcag cacaactgaa 780
atacaacatt gatgtggtgt gcgagtacat tgtcaagaag atccaatcc ctgagagaaa 840
ttttgtgtca cccccaaata tgatagtgat tcggtctttt gatgtcaaca aacctgggta 900
tgaggttgat gagatcaaa gttggagtgc aggttgaaat atctacggg gtgttttag 960
agtcacaacca ttaatcgaaa tccgacctgt tatcgttacc aaagacgagc gtggcaactc 1020
aaaatgcact ccaatttact ctgcctcatc ttcaacttac cggaagcaga acgagcttca 1080
gtttgtgtgt cctgaaggtc taataggagt tggaaacaaca atggacccaa ctctcaactc 1140
tcgacatcga ttagtgtgtc aagtcctgtg tgaaatcggt tcaacttctg atgtattatg 1200
tgaactcgag gtgaacttct ttctctcagc acgtttgttg ggaagtggaa caaagggatc 1260
agagaaacaa gggaaagtgt caaagctaac gaaagagagc attctgatgc tcaactatgg 1320
ttcgatgtcc actggagcca agtttgtagg agtttaaagt gatctgccta acgtccaact 1380
gactgcgcct gtttgtacca gcaaaaggaga gaaagtggtc ctaagcagac gtgtggaaaa 1440
gcattggcgt ttgattgtgt ggggtcagat tcaagctgga accaccatcg aagtgcctcc 1500

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ttcacctttc taagctatgt gttatttttg tcttttttgt ttgtgtttct gaaaaaaga 1560
ttgttaaacc cctcaaaaag ataataaac tctttttctc gttggggagt ttggagagt 1620
tcgtctttgc ggattaaaca tcttcaaca gtacctgatt tgttattgtt actagtttgc 1680
tctttgttat tgtaactagt ttgctcttt

(2) INFORMATION FOR SEQ ID NO:2025:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 465 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..465

(D) OTHER INFORMATION: / Ceres Seq. ID 1571587

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2025:

Met	Ser	Arg	Asn	Lys	Gly	Leu	Ala	Glu	Gln	Asp	Leu	Lys	Lys	Leu	Asp
1				5					10					15	
Val	Thr	Val	Leu	His	Pro	Leu	Ser	Pro	Glu	Val	Ile	Ser	Arg	Gln	Ala
			20					25					30		
Thr	Ile	Asn	Ile	Gly	Thr	Ile	Gly	His	Val	Ala	His	Gly	Lys	Ser	Thr
		35					40					45			
Val	Val	Lys	Ala	Ile	Ser	Gly	Val	Gln	Thr	Val	Arg	Phe	Lys	Asn	Glu
		50				55					60				
Leu	Glu	Arg	Asn	Ile	Thr	Ile	Lys	Leu	Gly	Tyr	Ala	Asn	Ala	Lys	Ile
		65				70				75				80	
Tyr	Lys	Cys	Glu	Asp	Glu	Lys	Cys	Pro	Arg	Pro	Met	Cys	Tyr	Lys	Ala
				85					90				95		
Tyr	Gly	Ser	Gly	Lys	Glu	Asp	Thr	Pro	Asn	Cys	Asp	Val	Pro	Gly	Phe
			100					105					110		
Glu	Asn	Ser	Lys	Met	Lys	Leu	Leu	Arg	His	Val	Ser	Phe	Val	Asp	Cys
			115				120					125			
Pro	Gly	His	Asp	Ile	Leu	Met	Xaa	Thr	Met	Leu	Asn	Gly	Ala	Ala	Ile
			130			135						140			
Met	Asp	Gly	Ala	Leu	Leu	Leu	Ile	Ala	Ala	Asn	Glu	Thr	Cys	Pro	Gln
			145			150				155				160	
Pro	Gln	Thr	Ser	Glu	His	Leu	Ala	Ala	Val	Glu	Ile	Met	Gln	Leu	Lys
				165					170					175	
His	Ile	Ile	Ile	Leu	Gln	Asn	Lys	Ile	Asp	Leu	Ile	Gln	Glu	Asn	Val
			180				185						190		
Ala	Ile	Asn	Gln	His	Glu	Ala	Ile	Gln	Lys	Phe	Ile	Met	Asn	Thr	Val
			195				200					205			
Ala	Asp	Ala	Ala	Pro	Ile	Val	Pro	Val	Ser	Ala	Gln	Leu	Lys	Tyr	Asn
			210				215					220			
Ile	Asp	Val	Val	Cys	Glu	Tyr	Ile	Val	Lys	Lys	Ile	Pro	Ile	Pro	Glu
			225			230				235				240	
Arg	Asn	Phe	Val	Ser	Pro	Pro	Asn	Met	Ile	Val	Ile	Arg	Ser	Phe	Asp
				245					250					255	
Val	Asn	Lys	Pro	Gly	Tyr	Glu	Val	Asp	Glu	Ile	Lys	Gly	Gly	Val	Ala
			260					265					270		
Gly	Gly	Ser	Ile	Leu	Arg	Gly	Val	Leu	Arg	Val	Asn	Gln	Leu	Ile	Glu
			275				280					285			
Ile	Arg	Pro	Gly	Ile	Val	Thr	Lys	Asp	Glu	Arg	Gly	Asn	Ser	Lys	Cys
			290				295				300				
Thr	Pro	Ile	Tyr	Ser	Arg	Ile	Ile	Ser	Leu	Tyr	Ala	Glu	Gln	Asn	Glu
				310						315				320	
Leu	Gln	Phe	Ala	Val	Pro	Glu	Gly	Leu	Ile	Gly	Val	Gly	Thr	Thr	Met
			325						330					335	
Asp	Pro	Thr	Leu	Thr	Arg	Ala	Asp	Arg	Leu	Val	Gly	Gln	Val	Leu	Gly
			340					345					350		
Glu	Ile	Gly	Ser	Leu	Pro	Asp	Val	Phe	Val	Glu	Leu	Glu	Val	Asn	Phe

355	360	365
Phe Leu Leu Arg Arg Leu Leu Gly Val Arg Thr Lys Gly Ser Glu Lys		
370	375	380
Gln Gly Lys Val Ser Lys Leu Thr Lys Gly Glu Ile Leu Met Leu Asn		
385	390	395
Ile Gly Ser Met Ser Thr Gly Ala Lys Val Val Gly Val Lys Val Asp		
405	410	415
Leu Ala Lys Leu Gln Leu Thr Ala Pro Val Cys Thr Ser Lys Gly Glu		
420	425	430
Lys Val Ala Leu Ser Arg Arg Val Glu Lys His Trp Arg Leu Ile Gly		
435	440	445
Trp Gly Gln Ile Gln Ala Gly Thr Thr Ile Glu Val Pro Pro Ser Pro		
450	455	460

Phe
465

(2) INFORMATION FOR SEQ ID NO:2026:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 374 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..374

(D) OTHER INFORMATION: / Ceres Seq. ID 1571588

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2026:

Met Cys Tyr Lys Ala Tyr Gly Ser Gly Lys Glu Asp Thr Pro Asn Cys	
1	15
Asp Val Pro Gly Phe Glu Asn Ser Lys Met Lys Leu Leu Arg His Val	
20	30
Ser Phe Val Asp Cys Pro Gly His Asp Ile Leu Met Xaa Thr Met Leu	
35	45
Asn Gly Ala Ala Ile Met Asp Gly Ala Leu Leu Leu Ile Ala Ala Asn	
50	60
Glu Thr Cys Pro Gln Pro Gln Thr Ser Glu His Leu Ala Ala Val Glu	
65	75
Ile Met Gln Leu Lys His Ile Ile Ile Leu Gln Asn Lys Ile Asp Leu	
85	95
Ile Gln Glu Asn Val Ala Ile Asn Gln His Glu Ala Ile Gln Lys Phe	
100	110
Ile Met Asn Thr Val Ala Asp Ala Ala Pro Ile Val Pro Val Ser Ala	
115	125
Gln Leu Lys Tyr Asn Ile Asp Val Val Cys Glu Tyr Ile Val Lys Lys	
130	140
Ile Pro Ile Pro Glu Arg Asn Phe Val Ser Pro Pro Asn Met Ile Val	
145	155
Ile Arg Ser Phe Asp Val Asn Lys Pro Gly Tyr Glu Val Asp Glu Ile	
165	175
Lys Gly Gly Val Ala Gly Gly Ser Ile Leu Arg Gly Val Leu Arg Val	
180	190
Asn Gln Leu Ile Glu Ile Arg Pro Gly Ile Val Thr Lys Asp Glu Arg	
195	205
Gly Asn Ser Lys Cys Thr Pro Ile Tyr Ser Arg Ile Ser Leu Tyr	
210	220
Ala Glu Gln Asn Glu Leu Gln Phe Ala Val Pro Glu Gly Leu Ile Gly	
225	235
Val Gly Thr Thr Met Asp Pro Thr Leu Thr Arg Ala Asp Arg Leu Val	
245	255
Gly Gln Val Leu Gly Glu Ile Gly Ser Leu Pro Asp Val Phe Val Glu	
260	270

Leu Glu Val Asn Phe Phe Leu Leu Arg Arg Leu Leu Gly Val Arg Thr
275 280 285
Lys Gly Ser Glu Lys Gln Gly Lys Val Ser Lys Leu Thr Lys Gly Glu
290 295 300
Ile Leu Met Leu Asn Ile Gly Ser Met Ser Thr Gly Ala Lys Val Val
305 310 315 320
Gly Val Lys Val Asp Leu Ala Lys Leu Gln Leu Thr Ala Pro Val Cys
325 330 335
Thr Ser Lys Gly Glu Lys Val Ala Leu Ser Arg Arg Val Glu Lys His
340 345 350
Trp Arg Leu Ile Gly Trp Gly Gln Ile Gln Ala Gly Thr Thr Ile Glu
355 360 365
Val Pro Pro Ser Pro Phe
370

(2) INFORMATION FOR SEQ ID NO:2027:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 349 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..349
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571589

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2027:

Met Lys Leu Leu Arg His Val Ser Phe Val Asp Cys Pro Gly His Asp
1 5 10 15
Ile Leu Met Xaa Thr Met Leu Asn Gly Ala Ala Ile Met Asp Gly Ala
20 25 30
Leu Leu Leu Ile Ala Ala Asn Glu Thr Cys Pro Gln Pro Gln Thr Ser
35 40 45
Glu His Leu Ala Ala Val Glu Ile Met Gln Leu Lys His Ile Ile Ile
50 55 60
Leu Gln Asn Lys Ile Asp Leu Ile Gln Glu Asn Val Ala Ile Asn Gln
65 70 75 80
His Glu Ala Ile Gln Lys Phe Ile Met Asn Thr Val Ala Asp Ala Ala
85 90 95
Pro Ile Val Pro Val Ser Ala Gln Leu Lys Tyr Asn Ile Asp Val Val
100 105 110
Cys Glu Tyr Ile Val Lys Lys Ile Pro Ile Pro Glu Arg Asn Phe Val
115 120 125
Ser Pro Pro Asn Met Ile Val Ile Arg Ser Phe Asp Val Asn Lys Pro
130 135 140
Gly Tyr Glu Val Asp Glu Ile Lys Gly Gly Val Ala Gly Gly Ser Ile
145 150 155 160
Leu Arg Gly Val Leu Arg Val Asn Gln Leu Ile Glu Ile Arg Pro Gly
165 170 175
Ile Val Thr Lys Asp Glu Arg Gly Asn Ser Lys Cys Thr Pro Ile Tyr
180 185 190
Ser Arg Ile Ile Ser Leu Tyr Ala Glu Gln Asn Glu Leu Gln Phe Ala
195 200 205
Val Pro Glu Gly Leu Ile Gly Val Gly Thr Thr Met Asp Pro Thr Leu
210 215 220
Thr Arg Ala Asp Arg Glu Val Gly Gln Val Leu Gly Glu Ile Gly Ser
225 230 235 240
Leu Pro Asp Val Phe Val Glu Leu Glu Val Asn Phe Phe Leu Leu Arg
245 250 255
Arg Leu Leu Gly Val Arg Thr Lys Gly Ser Glu Lys Gln Gly Lys Val
260 265 270
Ser Lys Leu Thr Lys Gly Glu Ile Leu Met Leu Asn Ile Gly Ser Met

	275					280										285
Ser	Thr	Gly	Ala	Lys	Val	Val	Gly	Val	Lys	Val	Asp	Leu	Ala	Lys	Leu	
	290						295				300					
Gln	Leu	Thr	Ala	Pro	Val	Cys	Thr	Ser	Lys	Gly	Glu	Lys	Val	Ala	Leu	
	305					310				315					320	
Ser	Arg	Arg	Val	Glu	Lys	His	Trp	Arg	Leu	Ile	Gly	Trp	Gly	Gln	Ile	
				325					330						335	
Gln	Ala	Gly	Thr	Thr	Ile	Glu	Val	Pro	Pro	Ser	Pro	Phe				
				340					345							

(2) INFORMATION FOR SEQ ID NO:2028:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1468 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1468
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571612

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2028:

atctttacaa	aaccgattac	ttttgtcgga	atctgacgtc	agcatacctg	ctaccacttc	60
cagagttccaa	tcgatctctcg	cctcggttgaa	acgtttttccc	tcttcgattaa	tcacacagtg	120
ctccactcgt	atcatcacccg	cctccaacta	attttgccat	ctctctcgtt	gttccaaattt	180
gattctacta	gtgagctcccg	atttaattta	gggttttgaa	agatgtcagc	tttggaaaaat	240
tacggcttga	tctccattga	tctgccttc	cattttccctc	gatccaaatca	attgcagagc	300
tataagagga	atgcaaaatg	ggctctctcca	atagcagctg	ttgtacctaa	cttccatctt	360
cctatgcgca	gtctcgagga	taaaaacagg	acaaacacag	acgacataag	gtcccttaga	420
gtgatcacag	ccattaagac	acggtattta	cctgatggaa	gattcgacct	ccaagcatcac	480
gatgacttag	tcaacaacga	catagaaaaac	gggtctgaag	gtgtgattgt	tggtgggtaca	540
actggtgaag	gccaatgtat	gagctgggat	gagcacataa	tgcttatcgg	ccatactgta	600
aattgttttg	ggggaaggat	caaaagtcat	ggaaaacact	gaagtaactc	gactagggaa	660
gctattcatg	ccaactgagca	aggattcgcc	atgggaatgc	acggggcact	gcacattaac	720
ccttactatg	gaaaaacatc	cattgaaggc	atgaatgcgc	attttcaaac	cgttcttcat	780
atgggaccca	ctattatata	caacgtgcc	gggtcgaaagt	gtcaggatat	acctccccag	840
gttatcttta	aactctctca	gaacccta	atggctgggg	ttaaggaaatg	cgttggtaat	900
aaccgagttg	aagagtatac	tgagaaggga	attgtcggtt	ggagtggaaa	tgatgatcag	960
tgccatgatt	ctagatggga	tcacgggtgc	actggagtga	tatcggttac	tagcaattta	1020
gttcggggtt	tgatgaggaa	gttgatgtt	gaaggtagaa	actcagcggt	gaacgcgaag	1080
ctctctctct	taattggattg	gctattccaa	gaaccgaatc	ccattgggtg	aaacactgct	1140
ttggctcagt	taggagttgc	gagggcgggt	tttcgggtac	cttatgtgcc	attgcctctg	1200
tcacaaaagg	ttgagttcgt	taaaactggg	aaggaaatcg	gaaggagcga	tttttagaga	1260
gacagagagt	ttcaggtagt	tgatgatgat	gacttcatct	taatcggctg	atattagagt	1320
ctctccctg	aagattggtt	gtgtttatac	tttcttctgt	cagttggttag	tatttagact	1380
gatgagaaac	tcacagatgt	atcaagactt	ctacttggtg	taattgtttg	tctgttactt	1440
ttgtgtgatga	atctaatggc	tttgtctg				

(2) INFORMATION FOR SEQ ID NO:2029:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 364 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..364
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571613

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2029:

Met	Ser	Ala	Leu	Lys	Asn	Tyr	Gly	Leu	Ile	Asp	Ser	Ala	Leu	
1				5				10				15		
His	Phe	Pro	Arg	Ser	Asn	Gln	Leu	Gln	Ser	Tyr	Lys	Arg	Asn	Ala

Met Arg Ser Leu Glu Asp Lys Asn Arg Thr Asn Thr Asp Asp Ile Arg
1 5 10 15
Ser Leu Arg Val Ile Thr Ala Ile Lys Thr Pro Tyr Leu Pro Asp Gly
20 25 30
Arg Phe Asp Leu Gln Ala Tyr Asp Asp Leu Val Asn Thr Gln Ile Glu
35 40 45

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Asn Gly Ala Glu Gly Val Ile Val Gly Gly Thr Thr Gly Glu Gly Gln
50 55 60
Leu Met Ser Trp Asp Glu His Ile Met Leu Ile Gly His Thr Val Asn
65 70 75 80
Cys Phe Gly Gly Arg Ile Lys Val Ile Gly Asn Thr Gly Ser Asn Ser
85 90 95
Thr Arg Glu Ala Ile His Ala Thr Glu Gln Gly Phe Ala Met Gly Met
100 105 110
His Gly Ala Leu His Ile Asn Pro Tyr Tyr Gly Lys Thr Ser Ile Glu
115 120 125
Gly Met Asn Ala His Phe Gln Thr Val Leu His Met Gly Pro Thr Ile
130 135 140
Ile Tyr Asn Val Pro Gly Arg Thr Cys Gln Asp Ile Pro Pro Gln Val
145 150 155 160
Ile Phe Lys Leu Ser Gln Asn Pro Asn Met Ala Gly Val Lys Glu Cys
165 170 175
Val Gly Asn Asn Arg Val Glu Glu Tyr Thr Glu Lys Gly Ile Val Val
180 185 190
Trp Ser Gly Asn Asp Asp Gln Cys His Asp Ser Arg Trp Asp His Gly
195 200 205
Ala Thr Gly Val Ile Ser Val Thr Ser Asn Leu Val Pro Gly Leu Met
210 215 220
Arg Lys Leu Met Phe Glu Gly Arg Asn Ser Ala Leu Asn Ala Lys Leu
225 230 235 240
Leu Pro Leu Met Asp Trp Leu Phe Gln Glu Pro Asn Pro Ile Gly Val
245 250 255
Asn Thr Ala Leu Ala Gln Leu Gly Val Ala Arg Pro Val Phe Arg Leu
260 265 270
Pro Tyr Val Pro Leu Pro Leu Ser Lys Arg Ile Glu Phe Val Lys Leu
275 280 285
Val Lys Glu Ile Gly Arg Glu His Phe Val Gly Asp Arg Asp Val Gln
290 295 300
Val Leu Asp Asp Asp Asp Phe Ile Leu Ile Gly Arg Tyr
305 310 315

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(2) INFORMATION FOR SEQ ID NO:2031:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 252 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..252

(D) OTHER INFORMATION: / Ceres Seq. ID 1571615

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2031:

```

Met Ser Trp Asp Glu His Ile Met Leu Ile Gly His Thr Val Asn Cys
1 5 10 15
Phe Gly Gly Arg Ile Lys Val Ile Gly Asn Thr Gly Ser Asn Ser Thr
20 25 30
Arg Glu Ala Ile His Ala Thr Glu Gln Gly Phe Ala Met Gly Met His
35 40 45
Gly Ala Leu His Ile Asn Pro Tyr Tyr Gly Lys Thr Ser Ile Glu Gly
50 55 60
Met Asn Ala His Phe Gln Thr Val Leu His Met Gly Pro Thr Ile Ile
65 70 75 80
Tyr Asn Val Pro Gly Arg Thr Cys Gln Asp Ile Pro Pro Gln Val Ile
85 90 95
Phe Lys Leu Ser Gln Asn Pro Asn Met Ala Gly Val Lys Glu Cys Val
100 105 110
Gly Asn Asn Arg Val Glu Glu Tyr Thr Glu Lys Gly Ile Val Val Trp

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115	120	125
Ser Gly Asn Asp Asp Gln Cys His Asp Ser Arg Trp Asp His Gly Ala		
130	135	140
Thr Gly Val Ile Ser Val Thr Ser Asn Leu Val Pro Gly Leu Met Arg		
145	150	155
Lys Leu Met Phe Glu Gly Arg Asn Ser Ala Leu Asn Ala Lys Leu Leu		
165	170	175
Pro Leu Met Asp Trp Leu Phe Gln Glu Pro Asn Pro Ile Gly Val Asn		
180	185	190
Thr Ala Leu Ala Gln Leu Gly Val Ala Arg Pro Val Phe Arg Leu Pro		
195	200	205
Tyr Val Pro Leu Pro Leu Ser Lys Arg Ile Glu Phe Val Lys Leu Val		
210	215	220
Lys Glu Ile Gly Arg Glu His Phe Val Gly Asp Arg Asp Val Gln Val		
225	230	235
Leu Asp Asp Asp Asp Phe Ile Leu Ile Gly Arg Tyr		
245	250	

(2) INFORMATION FOR SEQ ID NO:2032:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1786 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1786

(D) OTHER INFORMATION: / Ceres Seq. ID 1571616

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2032:

acattcaactg	tcactactct	ctctctctct	ctaattctct	60
aggaacacag	taaaagactt	tggtcagct	ctctcctcct	120
atggccttita	gcaatgatgt	gtttactctt	ctctcctcga	180
cgacaacatc	tcttctctcc	ctagatccga	cgaaaccgaa	240
cgaatccaga	tgaagttagc	gacgAagttc	tcgctctgac	300
ataccgagag	gaggaaaacta	ggttacttta	cttgccggaac	360
gtttggcgat	tgacccccat	tgccacaaga	accgtaaaacg	420
gatttggaag	aaacgcgatc	gggtggtcgt	atggacgatt	480
gagacgacaa	tcgggttaac	cctagaccgg	ggactttacg	540
ccgaccacta	tggaatcgtt	tcaaacgtga	catgttgatt	600
cggttaacgt	tcaaaaacga	tcgatggacg	tgccgcaaac	660
tgcatcaacg	attcagtttg	tgacgaatgt	gatcgttcac	720
taaacccaat	ggtaacgcta	tggtgagaag	ctcagagacg	780
ggcagatggt	gacgcgatgt	gcactcttgg	atcgagtcac	840
gtttgtcccat	tgccgtgatg	ggcttgttga	cgcagtcacg	900
ctctaaacac	cacttaactc	accataacga	ggttatgttg	960
catgagggag	aaagctatgc	aagtgtaacc	tgcttacaat	1020
ctaaagaatg	ccgaggtgtg	gacacgggta	cttccatggt	1080
ctgggaaatg	tacgcaatag	tggttagcgc	aaacccgaca	1140
ctatgcgcgc	ccaaaaaaccc	cttttgctaa	agaggtgacg	1200
tagtcatttg	aaaggtatga	attggagatc	ggaaggagat	1260
cttcaactct	tcagagcgcg	ccgcgtctcg	cagCtagcga	1320
gaaatctctg	tcatttgctg	gacacattac	ttccgacgtc	1380
aggaactcga	gtttctctat	agttactacc	ccaccaccac	1440
tatatctaga	caaaaagtga	aattttacac	catttgtcat	1500
ttttttttgc	ttttcggtgt	gtgtgtttgt	gtcgtatttt	1560
cttcaaccgc	aagtttaaac	aagaaaaggg	aaaaaagaca	1620
aatcccgcaa	gtgtgtgtgt	ttgtttgggt	ctatctgata	1680
gtgctcctgt	ttctataccg	agaaaacaag	atattatctc	1740
aatttttgag	gtttataaat	taatataggg	ttataataat	

(2) INFORMATION FOR SEQ ID NO:2033:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 276 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..276
(D) OTHER INFORMATION: / Ceres Seq. ID 1571617
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2033:

Met	Val	Ile	Gln	Leu	Lys	Gln	Glu	Leu	Ile	Val	Asn	Ser	Phe	Lys	Thr
1			5					10						15	
Ile	Asp	Gly	Arg	Gly	Ala	Asn	Val	His	Ile	Ala	Asn	Gly	Gly	Cys	Ile
			20					25						30	
Thr	Ile	Gln	Phe	Val	Thr	Asn	Val	Ile	Val	His	Gly	Leu	His	Ile	His
			35					40						45	
Asp	Cys	Lys	Pro	Thr	Gly	Asn	Ala	Met	Val	Arg	Ser	Ser	Glu	Thr	His
			50					55						60	
Phe	Gly	Trp	Arg	Thr	Met	Ala	Asp	Gly	Asp	Ala	Ile	Ser	Ile	Phe	Gly
			65					70						75	
Ser	Ser	His	Val	Trp	Ile	Asp	His	Asn	Ser	Leu	Ser	His	Cys	Ala	Asp
			85					90						95	
Gly	Leu	Val	Asp	Ala	Val	Met	Gly	Ser	Thr	Ala	Ile	Thr	Ile	Ser	Asn
			100					105						110	
Asn	His	Leu	Thr	His	His	Asn	Glu	Val	Met	Leu	Leu	Gly	His	Ser	Asp
			115					120						125	
Ser	Tyr	Met	Arg	Asp	Lys	Ala	Met	Gln	Val	Thr	Ile	Ala	Tyr	Asn	His
			130					135						140	
Phe	Gly	Val	Gly	Leu	Ile	Gln	Arg	Met	Pro	Arg	Cys	Arg	His	Gly	Tyr
			145					150						155	
Phe	His	Val	Val	Asn	Asn	Asp	Tyr	Thr	His	Trp	Glu	Met	Tyr	Ala	Ile
			165					170						175	
Gly	Gly	Ser	Ala	Asn	Pro	Thr	Ile	Asn	Ser	Gln	Gly	Asn	Arg	Tyr	Ala
			180					185						190	
Ala	Pro	Lys	Asn	Pro	Phe	Ala	Lys	Glu	Val	Thr	Lys	Arg	Val	Asp	Thr
			195					200						205	
Pro	Ala	Ser	His	Trp	Lys	Gly	Trp	Asn	Trp	Arg	Ser	Glu	Gly	Asp	Leu
			210					215						220	
Leu	Gln	Asn	Gly	Ala	Tyr	Phe	Thr	Ser	Ser	Gly	Ala	Ala	Ala	Ser	Gly
			225					230						235	
Ser	Tyr	Ala	Arg	Ala	Ser	Ser	Leu	Ser	Ala	Lys	Ser	Ser	Ser	Leu	Val
			245					250						255	
Gly	His	Ile	Thr	Ser	Asp	Ala	Gly	Ala	Leu	Pro	Cys	Arg	Arg	Gly	Arg
			260					265						270	
Gln	Cys	Ser	Ser												
			275												

(2) INFORMATION FOR SEQ ID NO:2034:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 220 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..220
(D) OTHER INFORMATION: / Ceres Seq. ID 1571618

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2034:
Met Val Arg Ser Ser Glu Thr His Phe Gly Trp Arg Thr Met Ala Asp
1 5 10 15
Gly Asp Ala Ile Ser Ile Phe Gly Ser Ser His Val Trp Ile Asp His

20 25 30
Asn Ser Leu Ser His Cys Ala Asp Gly Leu Val Asp Ala Val Met Gly
35 40 45
Ser Thr Ala Ile Thr Ile Ser Asn Asn His Leu Thr His His Asn Glu
50 55 60
Val Met Leu Leu Gly His Ser Asp Ser Tyr Met Arg Asp Lys Ala Met
65 70 75 80
Gln Val Thr Ile Ala Tyr Asn His Phe Gly Val Gly Leu Ile Gln Arg
85 90 95
Met Pro Arg Cys Arg His Gly Tyr Phe His Val Val Asn Asn Asp Tyr
100 105 110
Thr His Trp Glu Met Tyr Ala Ile Gly Gly Ser Ala Asn Pro Thr Ile
115 120 125
Asn Ser Gln Gly Asn Arg Tyr Ala Ala Pro Lys Asn Pro Phe Ala Lys
130 135 140
Glu Val Thr Lys Arg Val Asp Thr Pro Ala Ser His Trp Lys Gly Trp
145 150 155 160
Asn Trp Arg Ser Glu Gly Asp Leu Leu Gln Asn Gly Ala Tyr Phe Thr
165 170 175
Ser Ser Gly Ala Ala Ala Ser Gly Ser Tyr Ala Arg Ala Ser Ser Leu
180 185 190
Ser Ala Lys Ser Ser Ser Leu Val Gly His Ile Thr Ser Asp Ala Gly
195 200 205
Ala Leu Pro Cys Arg Arg Gly Arg Gln Cys Ser Ser
210 215 220

(2) INFORMATION FOR SEQ ID NO:2035:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 207 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..207

(D) OTHER INFORMATION: / Ceres Seq. ID 1571619

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2035:

Met Ala Asp Gly Asp Ala Ile Ser Ile Phe Gly Ser Ser His Val Trp
1 5 10 15
Ile Asp His Asn Ser Leu Ser His Cys Ala Asp Gly Leu Val Asp Ala
20 25 30
Val Met Gly Ser Thr Ala Ile Thr Ile Ser Asn Asn His Leu Thr His
35 40 45
His Asn Glu Val Met Leu Leu Gly His Ser Asp Ser Tyr Met Arg Asp
50 55 60
Lys Ala Met Gln Val Thr Ile Ala Tyr Asn His Phe Gly Val Gly Leu
65 70 75 80
Ile Gln Arg Met Pro Arg Cys Arg His Gly Tyr Phe His Val Val Asn
85 90 95
Asn Asp Tyr Thr His Trp Glu Met Tyr Ala Ile Gly Gly Ser Ala Asn
100 105 110
Pro Thr Ile Asn Ser Gln Gly Asn Arg Tyr Ala Ala Pro Lys Asn Pro
115 120 125
Phe Ala Lys Glu Val Thr Lys Arg Val Asp Thr Pro Ala Ser His Trp
130 135 140
Lys Gly Trp Asn Trp Arg Ser Glu Gly Asp Leu Leu Gln Asn Gly Ala
145 150 155 160
Tyr Phe Thr Ser Ser Gly Ala Ala Ala Ser Gly Ser Tyr Ala Ala
165 170 175
Ser Ser Leu Ser Ala Lys Ser Ser Ser Leu Val Gly His Ile Thr Ser
180 185 190

Asp Ala Gly Ala Leu Pro Cys Arg Arg Gly Arg Gln Cys Ser Ser
195 200 205

(2) INFORMATION FOR SEQ ID NO:2036:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1176 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1176
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571628

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2036:

atactgtogt	ctccctggat	tctatcttct	cgatttttgt	gattcgaaca	cgattttacc	60
tatccttgag	cgatctcgat	cccaactttt	tgagttgatt	ttatttcagg	agttttccaa	120
aaatctgttg	ttaagtgggt	aatcggaaaa	tgtcgcagtc	ttccgtcgat	ataccgcaaa	180
aagggtgggtt	tagcttcgat	ctgtgcacaaa	ggaatgatat	gctgacacag	aagggtctta	240
aagcgccgtc	gtttctcaag	actgggaacga	ctatcgttgg	attgatattt	aaggatgggtg	300
taatacttgg	ggctgataca	cgggcaactg	aaggggcctat	tgtggctgat	aagaactgtg	360
agaagattca	ctacatggca	ccaaacattt	actgttggtg	tgcaaggaacc	gctgctgaca	420
ctgaagcagt	aactgatgat	gtcagctcac	agctgcgggt	gcatagatac	cgagctggcc	480
gagattctcg	agtcgttaact	gcattgaccc	ttctcaaaaa	acHtcttttc	agctaccaag	540
gccatgtctc	agctgtctct	gtgcttgggt	gagttgatat	taccggggcct	catcttccaa	600
cgatataccc	acacgggtct	actgacactc	taccatttgc	tacaatgggt	ctggtgtccc	660
ttgctgcocat	gtcagttgtt	gaagcaaaat	ataaagaagg	tctaaactaga	gatgaaggaa	720
tcaagtgtgt	tgctgaagcc	atatgtctct	gtatattcaa	cgaccttggt	agtggtagca	780
atgtgggat	ctgtgtgatc	actaaagggc	acaaggaata	cttgaggaat	tacatgggaac	840
caaaccccaa	aacctatgtt	agcagcaaa	gctattcatt	caccaagaaa	accagaggttc	900
tactaccacaa	aattaccacca	ttattggagc	gagtcgaaat	tgtagaagtg	gctggtgaag	960
ctatggagga	atgaatcttg	tgtagagagc	agatactaa	agtgaaacca	ttgtctatcc	1020
tcacatgaca	gtcatgttta	cgttttctac	ttgttccaat	atgaacgact	aaaatcgaa	1080
cgtagttgcc	tcatttttgt	ctttaaattt	ggcttgaact	tggtattaat	gagtatggat	1140
attgtgggtt	tgaaatttag	ctctccacata	attttc			

(2) INFORMATION FOR SEQ ID NO:2037:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 274 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..274
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571629

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2037:

Met	Ser	Gln	Ser	Ser	Val	Asp	Ile	Pro	Pro	Lys	Gly	Gly	Phe	Ser	Phe
1				5					10				15		
Asp	Leu	Cys	Lys	Arg	Asn	Asp	Met	Leu	Thr	Gln	Lys	Gly	Leu	Lys	Ala
			20					25					30		
Pro	Ser	Phe	Leu	Lys	Thr	Gly	Thr	Thr	Ile	Val	Gly	Leu	Ile	Phe	Lys
		35					40					45			
Asp	Gly	Val	Ile	Leu	Gly	Ala	Asp	Thr	Arg	Ala	Thr	Glu	Gly	Pro	Ile
	50					55					60				
Val	Ala	Asp	Lys	Asn	Cys	Glu	Lys	Ile	His	Tyr	Met	Ala	Pro	Asn	Ile
	65				70					75				80	
Tyr	Cys	Cys	Gly	Ala	Gly	Thr	Ala	Ala	Asp	Thr	Glu	Ala	Val	Thr	Asp
				85				90					95		
Met	Val	Ser	Ser	Gln	Leu	Arg	Leu	His	Arg	Tyr	Gln	Thr	Gly	Arg	Asp
			100				105						110		
Ser	Arg	Val	Val	Thr	Ala	Leu	Thr	Leu	Lys	Lys	Xaa	Leu	Phe	Ser	

(2) INFORMATION FOR SEQ ID NO:2038:

(A) LENGTH: 251 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ix) FEATURE:

(B) LOCATION: 1..251

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2038:

Met	Leu	Thr	Gln	Lys	Gly	Leu	Lys	Ala	Pro	Ser	Phe	Leu	Lys	Thr	Gly
1			5						10					15	
Thr	Thr	Ile	Val	Gly	Leu	Ile	Phe	Lys	Asp	Gly	Val	Ile	Leu	Gly	Ala
		20						25					30		
Asp	Thr	Arg	Ala	Thr	Glu	Gly	Pro	Ile	Val	Ala	Asp	Lys	Asn	Cys	Glu
		35					40					45			
Lys	Ile	His	Tyr	Met	Ala	Pro	Asn	Ile	Tyr	Cys	Cys	Gly	Ala	Gly	Thr
	50					55					60				
Ala	Ala	Asp	Thr	Glu	Ala	Val	Thr	Asp	Met	Val	Ser	Ser	Gln	Leu	Arg
65					70					75				80	
Leu	His	Arg	Tyr	Gln	Thr	Gly	Arg	Asp	Ser	Arg	Val	Val	Thr	Ala	Leu
				85				90						95	
Thr	Leu	Leu	Lys	Lys	Xaa	Leu	Phe	Ser	Tyr	Gln	Gly	His	Val	Ser	Ala
		100						105				110			
Ala	Leu	Val	Leu	Gly	Gly	Val	Asp	Ile	Thr	Gly	Pro	His	Leu	His	Thr
		115						120				125			
Ile	Tyr	Pro	His	Gly	Ser	Thr	Asp	Thr	Leu	Pro	Phe	Ala	Thr	Met	Gly
		130					135				140				
Ser	Gly	Ser	Leu	Ala	Ala	Met	Ser	Val	Phe	Glu	Ala	Lys	Tyr	Lys	Glu
145					150					155				160	
Gly	Leu	Thr	Arg	Asp	Glu	Gly	Ile	Lys	Leu	Val	Ala	Glu	Ala	Ile	Cys
				165					170					175	
Ser	Gly	Ile	Phe	Asn	Asp	Leu	Gly	Ser	Gly	Ser	Asn	Val	Asp	Ile	Cys
			180					185					190		
Val	Ile	Thr	Lys	Gly	His	Lys	Glu	Tyr	Leu	Arg	Asn	Tyr	Met	Glu	Pro
		195					200					205			
Asn	Pro	Arg	Thr	Tyr	Val	Ser	Ser	Lys	Gly	Tyr	Ser	Phe	Thr	Lys	Lys
	210					215						220			

Thr Glu Val Leu Leu Thr Lys Ile Thr Pro Leu Leu Glu Arg Val Glu
225 230 235 240
Ile Val Glu Val Ala Gly Glu Ala Met Glu Glu
245 250

(2) INFORMATION FOR SEQ ID NO:2039:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 199 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..199
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571631

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2039:

Met Ala Pro Asn Ile Tyr Cys Cys Gly Ala Gly Thr Ala Ala Asp Thr
1 5 10 15
Glu Ala Val Thr Asp Met Val Ser Ser Gln Leu Arg Leu His Arg Tyr
20 25 30
Gln Thr Gly Arg Asp Ser Arg Val Val Thr Ala Leu Thr Leu Leu Lys
35 40 45
Lys Xaa Leu Phe Ser Tyr Gln Gly His Val Ser Ala Ala Leu Val Leu
50 55 60
Gly Gly Val Asp Ile Thr Gly Pro His Leu His Thr Ile Tyr Pro His
65 70 75 80
Gly Ser Thr Asp Thr Leu Pro Phe Ala Thr Met Gly Ser Gly Ser Leu
85 90 95
Ala Ala Met Ser Val Phe Glu Ala Lys Tyr Lys Glu Gly Leu Thr Arg
100 105 110
Asp Glu Gly Ile Lys Leu Val Ala Glu Ala Ile Cys Ser Gly Ile Phe
115 120 125
Asn Asp Leu Gly Ser Gly Ser Asn Val Asp Ile Cys Val Ile Thr Lys
130 135 140
Gly His Lys Glu Tyr Leu Arg Asn Tyr Met Glu Pro Asn Pro Arg Thr
145 150 155 160
Tyr Val Ser Ser Lys Gly Tyr Ser Phe Thr Lys Lys Thr Glu Val Leu
165 170 175
Leu Thr Lys Ile Thr Pro Leu Leu Glu Arg Val Glu Ile Val Glu Val
180 185 190
Ala Gly Glu Ala Met Glu Glu
195

(2) INFORMATION FOR SEQ ID NO:2040:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1437 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1437
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571642

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2040:

aaaaacttca aattaaaagc ttctgtgtctt cataaaacc taatctcgcg acttcgtctc 60
tatccccaaa aacccttttc tctcttccct ctgtgtgtg accgagaaaa aaagatgact 120
aagaacagta accacgacga gaatgagttc acgacttttg aaccaaatac gaacacgaag 180
atacgtcttg aaagatgtga tgaagacgaa gttgtctga ggtctgtgtg tgcggcgag 240
gaaactcccc aaagatgagtc catgtttcgc gccggagaga gcgccgacac cgctgaagta 300
actgatgata ccaccagatgc cgattactac ttcgattctt actctcactt tggaaatcat 360
gaagagatgt tgaaggatgt tgtgagaaca aagacttata agaattgtat ttatcagaac 420

aagtttctta	tcaaggacaa	aattgttctt	gatgttggag	ctggaaccgg	aattttgtct	480
ctgttctgtg	ccaaggcagg	agctgctcat	gtctacgctg	ttgagtgttc	tcaaatggct	540
gacatggtca	aggagattgt	taaagctaat	ggaattttctg	atgttattac	ggatttgaaa	600
gggaagattg	aggagataga	gcttcccatc	cctaaagtgg	atgtgattat	atcggaatgg	660
atgggttact	ttttgttgtt	tgaataatgt	ttggacagtg	tcttgtatgc	tcgtgataaa	720
tggtctgttg	aagtgaggat	tgtgtaccac	gacaaagcct	ctctgcactc	tacagccata	780
gaggattcag	agtacaaaag	agacaaaatc	gaattttgga	acagtggtga	tggttttgac	840
atgtcatgta	ttaagaaaaa	agctatgatg	gaaccacttg	ttgacacagt	cgaccacaaac	900
caaatctgtc	ccgatagtag	gcttctaaag	acgatggata	tctcaaatgt	gtcctctggg	960
gatgtctctc	tcaacagctcc	ctttaagctt	gttgacacac	gcaatgacta	catccaagcc	1020
ctttagtccct	actttgatgt	atcgtttacc	atgtgccaca	agctgctggg	cttctcaaca	1080
ggaccgaaat	cccagctcac	acactggaaa	caaacagttc	tgtatctaga	agatgtgtta	1140
accatatgtg	agggtgagac	aatacctgga	actatgtccg	tttctctcaa	caagaagaat	1200
cctcgagaca	ttgacataaa	gctaagctat	tctttgaatg	gccagcattg	caagatctca	1260
aggaccacaac	actacaaaat	gcgttaaagt	tctctcataa	gaagcagaac	ttcagaagat	1320
acaattctca	tattgtgatt	tagtttttat	atctctcttt	tctccagatt	acaactttcc	1380
atattgttca	cattgcacaa	tttgcttcat	ctcaagttaa	attaatgatt	ttgtctcc	

(2) INFORMATION FOR SEQ ID NO:2041:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 390 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..390
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571643

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2041:

Met	Thr	Lys	Asn	Ser	Asn	His	Asp	Glu	Asn	Glu	Phe	Ile	Ser	Phe	Glu
1			5					10						15	
Pro	Asn	Gln	Asn	Thr	Lys	Ile	Arg	Phe	Glu	Asp	Ala	Asp	Glu	Asp	Glu
			20				25						30		
Val	Ala	Glu	Gly	Ser	Gly	Val	Ala	Gly	Glu	Glu	Thr	Pro	Gln	Asp	Glu
		35					40					45			
Ser	Met	Phe	Asp	Ala	Gly	Glu	Ser	Ala	Asp	Thr	Ala	Glu	Val	Thr	Asp
	50					55				60					
Asp	Thr	Thr	Ser	Ala	Asp	Tyr	Tyr	Phe	Asp	Ser	Tyr	Ser	His	Phe	Gly
	65				70				75					80	
Ile	His	Glu	Glu	Met	Leu	Lys	Asp	Val	Val	Arg	Thr	Lys	Thr	Tyr	Gln
				85				90						95	
Asn	Val	Ile	Tyr	Gln	Asn	Lys	Phe	Leu	Ile	Lys	Asp	Lys	Ile	Val	Leu
			100					105					110		
Asp	Val	Gly	Ala	Gly	Thr	Gly	Ile	Leu	Ser	Leu	Phe	Cys	Ala	Lys	Ala
		115				120						125			
Gly	Ala	Ala	His	Val	Tyr	Ala	Val	Glu	Cys	Ser	Gln	Met	Ala	Asp	Met
		130				135						140			
Ala	Lys	Glu	Ile	Val	Lys	Ala	Asn	Gly	Phe	Ser	Asp	Val	Ile	Thr	Val
	145				150				155					160	
Leu	Lys	Gly	Lys	Ile	Glu	Glu	Ile	Glu	Leu	Pro	Thr	Pro	Lys	Val	Asp
			165					170						175	
Val	Ile	Ile	Ser	Glu	Trp	Met	Gly	Tyr	Phe	Leu	Leu	Phe	Glu	Asn	Met
			180				185					190			
Leu	Asp	Ser	Val	Leu	Tyr	Ala	Arg	Asp	Lys	Trp	Leu	Val	Glu	Gly	Gly
		195				200						205			
Val	Val	Leu	Pro	Asp	Lys	Ala	Ser	Leu	His	Leu	Thr	Ala	Ile	Glu	Asp
		210				215					220				
Ser	Glu	Tyr	Lys	Glu	Asp	Lys	Ile	Glu	Phe	Trp	Asn	Ser	Val	Tyr	Gly
	225				230				235					240	
Phe	Asp	Met	Ser	Cys	Ile	Lys	Lys	Lys	Ala	Met	Met	Glu	Pro	Leu	Val
			245					250						255	

Asp	Thr	Val	Asp	Gln	Asn	Gln	Ile	Val	Thr	Asp	Ser	Arg	Leu	Leu	Lys
		260						265					270		
Thr	Met	Asp	Ile	Ser	Lys	Met	Ser	Ser	Gly	Asp	Ala	Ser	Phe	Thr	Ala
		275						280					285		
Pro	Phe	Lys	Leu	Val	Ala	Gln	Arg	Asn	Asp	Tyr	Ile	His	Ala	Leu	Val
		290						295					300		
Ala	Tyr	Phe	Asp	Val	Ser	Phe	Thr	Met	Cys	His	Lys	Leu	Leu	Gly	Phe
		305						310					315		320
Ser	Thr	Gly	Pro	Lys	Ser	Arg	Ala	Thr	His	Trp	Lys	Gln	Thr	Val	Leu
				325						330				335	
Tyr	Leu	Glu	Asp	Val	Leu	Thr	Ile	Cys	Glu	Gly	Glu	Thr	Ile	Thr	Gly
			340						345				350		
Thr	Met	Ser	Val	Ser	Pro	Asn	Lys	Lys	Asn	Pro	Arg	Asp	Ile	Asp	Ile
			355					360					365		
Lys	Leu	Ser	Tyr	Ser	Leu	Asn	Gly	Gln	His	Cys	Lys	Ile	Ser	Arg	Thr
			370				375					380			
Gln	His	Tyr	Lys	Met	Arg										
		385			390										

(2) INFORMATION FOR SEQ ID NO:2042:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 341 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..341

(D) OTHER INFORMATION: / Ceres Seq. ID 1571644

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2042:

Met	Phe	Asp	Ala	Gly	Glu	Ser	Ala	Asp	Thr	Ala	Glu	Val	Thr	Asp	Asp
1			5						10					15	
Thr	Thr	Ser	Ala	Asp	Tyr	Tyr	Phe	Asp	Ser	Tyr	Ser	His	Phe	Gly	Ile
			20					25						30	
His	Glu	Glu	Met	Leu	Lys	Asp	Val	Val	Arg	Thr	Lys	Thr	Tyr	Gln	Asn
			35				40					45			
Val	Ile	Tyr	Gln	Asn	Lys	Phe	Leu	Ile	Lys	Asp	Lys	Ile	Val	Leu	Asp
			50			55				60					
Val	Gly	Ala	Gly	Thr	Gly	Ile	Leu	Ser	Leu	Phe	Cys	Ala	Lys	Ala	Gly
			65		70				75					80	
Ala	Ala	His	Val	Tyr	Ala	Val	Glu	Cys	Ser	Gln	Met	Ala	Asp	Met	Ala
			85					90					95		
Lys	Glu	Ile	Val	Lys	Ala	Asn	Gly	Phe	Ser	Asp	Val	Ile	Thr	Val	Leu
			100				105					110			
Lys	Gly	Lys	Ile	Glu	Glu	Ile	Glu	Leu	Pro	Thr	Pro	Lys	Val	Asp	Val
			115				120					125			
Ile	Ile	Ser	Glu	Trp	Met	Gly	Tyr	Phe	Leu	Leu	Phe	Glu	Asn	Met	Leu
			130			135					140				
Asp	Ser	Val	Leu	Tyr	Ala	Arg	Asp	Lys	Trp	Leu	Val	Glu	Gly	Gly	Val
			145		150				155					160	
Val	Leu	Pro	Asp	Lys	Ala	Ser	Leu	His	Leu	Thr	Ala	Ile	Glu	Asp	Ser
			165						170				175		
Glu	Tyr	Lys	Glu	Asp	Lys	Ile	Glu	Phe	Trp	Asn	Ser	Val	Tyr	Gly	Phe
			180				185					190			
Asp	Met	Ser	Cys	Ile	Lys	Lys	Lys	Ala	Met	Met	Glu	Pro	Leu	Val	Asp
			195				200					205			
Thr	Val	Asp	Gln	Asn	Gln	Ile	Val	Thr	Asp	Ser	Arg	Leu	Leu	Lys	Thr
			210			215					220				
Met	Asp	Ile	Ser	Lys	Met	Ser	Ser	Gly	Asp	Ala	Ser	Phe	Thr	Ala	Pro
			225			230			235					240	
Phe	Lys	Leu	Val	Ala	Gln	Arg	Asn	Asp	Tyr	Ile	His	Ala	Leu	Val	Ala

(2) INFORMATION FOR SEO ID NO:2043:

(A) LENGTH: 306 amino acids

(C) STRANDEDNESS:

(D) TOPOLOGY: lin

MOLECULE TYPE: peptid

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..306

(D) OTHER INFORMATION: / Ceres Seq. ID 1571645

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2043:

Met	Leu	Lys	Asp	Val	Val	Arg	Thr	Lys	Thr	Tyr	Gln	Asn	Val	Ile	Tyr
1	Gln	Asn	Lys	Phe	Leu	Ile	Lys	Asp	Lys	Ile	Val	Leu	Asp	Val	Gly
				20				25					30		Ala
Gly	Thr	Gly	Ile	Leu	Ser	Leu	Phe	Cys	Ala	Lys	Ala	Gly	Ala	Ala	His
		35					40					45			
Val	Tyr	Ala	Val	Glu	Cys	Ser	Gln	Met	Ala	Asp	Met	Ala	Lys	Glu	Ile
	50					55					60				
Val	Lys	Ala	Asn	Gly	Phe	Ser	Asp	Val	Ile	Thr	Val	Leu	Lys	Gly	Lys
65				70						75				80	
Ile	Glu	Glu	Ile	Glu	Leu	Pro	Thr	Pro	Lys	Val	Asp	Val	Ile	Ile	Ser
				85					90					95	
Glu	Trp	Met	Gly	Tyr	Phe	Leu	Leu	Phe	Glu	Asn	Met	Leu	Asp	Ser	Val
		100						105				110			
Leu	Tyr	Ala	Arg	Asp	Lys	Trp	Leu	Val	Glu	Gly	Gly	Val	Val	Leu	Pro
		115					120					125			
Asp	Lys	Ala	Ser	Leu	His	Leu	Thr	Ala	Ile	Glu	Asp	Ser	Glu	Tyr	Lys
	130					135					140				
Glu	Asp	Lys	Ile	Glu	Phe	Trp	Asn	Ser	Val	Tyr	Gly	Phe	Asp	Met	Ser
145				150						155				160	
Cys	Ile	Lys	Lys	Lys	Ala	Met	Met	Glu	Pro	Leu	Val	Asp	Thr	Val	Asp
				165					170					175	
Gln	Asn	Gln	Ile	Val	Thr	Asp	Ser	Arg	Leu	Leu	Lys	Thr	Met	Asp	Ile
			180					185					190		
Ser	Lys	Met	Ser	Ser	Gly	Asp	Ala	Ser	Phe	Thr	Ala	Pro	Phe	Lys	Leu
		195					200					205			
Val	Ala	Gln	Arg	Asn	Asp	Tyr	Ile	His	Ala	Leu	Val	Ala	Tyr	Phe	Asp
	210					215					220				
Val	Ser	Phe	Thr	Met	Cys	His	Lys	Leu	Leu	Gly	Phe	Ser	Thr	Gly	Pro
225				230						235				240	
Lys	Ser	Arg	Ala	Thr	His	Trp	Lys	Gln	Thr	Val	Leu	Tyr	Leu	Glu	Asp
				245					250					255	
Val	Leu	Thr	Ile	Cys	Glu	Gly	Glu	Thr	Ile	Thr	Gly	Thr	Met	Ser	Val
		260						265					270		
Ser	Pro	Asn	Lys	Lys	Asn	Pro	Arg	Asp	Ile	Asp	Ile	Lys	Leu	Ser	Tyr
		275					280					285			

Ser Leu Asn Gly Gln His Cys Lys Ile Ser Arg Thr Gln His Tyr Lys
290 295 300
Met Arg
305

(2) INFORMATION FOR SEQ ID NO:2044:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 723 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..723
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571669

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2044:

agtcgtctag	ggtttgtttt	tgtttttttc	tccgattgtt	cagaggaatt	gcgaattaag	60
ataaagatga	ggccagtggt	cgtcggcaat	tccgagtatg	aaactcgcca	gtcggatctg	120
gaacgggtgt	tcgacaagta	tgggagagtc	gaccgagtgg	acatgaaatc	tggatagtct	180
tttgtgtact	ttgaggatga	acgtgatgct	gaagacgcta	ttcgcaaaat	cgacaatttt	240
cttttttgat	atgagaaaacg	caggttatca	gttgaatggg	caaagggtga	acgtggcagg	300
cctcgtgtgt	acgcgaaagc	cccttcaaat	ctgaagccta	caaagacact	gtttgtcatt	360
aactttgacc	ccattagatc	aaaagagcac	gacattgaaa	aacactttga	gccctatggt	420
aaggtcacca	aggtcggtat	cagacgcaac	ttctcatttg	ttcagtttga	aacacaagag	480
gatgctacaa	aagcccttga	agctactcaa	agaagcaaaa	tattggatag	gggtgtttcc	540
gtggagtatg	cgttgaaaga	gacgatgata	agagatgata	gaaatggtgg	tcgtagccCg	600
agaaggtctc	ttagtcCtgt	gtatcgtagG	cgctcatgtaa	tgatgtactg	tcgttatttt	660
aaagaaaatt	tggcaccttt	tgtataaaca	gaatttccta	tacctcgacg	tttgtgttta	720
cgt						

(2) INFORMATION FOR SEQ ID NO:2045:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 228 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..228
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571670

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2045:

Ser	Arg	Leu	Gly	Phe	Val	Phe	Arg	Phe	Phe	Ser	Asp	Cys	Ser	Glu	Glu
1		5						10					15		
Leu	Arg	Ile	Lys	Ile	Lys	Met	Arg	Pro	Val	Phe	Val	Gly	Asn	Phe	Glu
		20						25					30		
Tyr	Glu	Thr	Arg	Gln	Ser	Asp	Leu	Glu	Arg	Leu	Phe	Asp	Lys	Tyr	Gly
		35					40					45			
Arg	Val	Asp	Arg	Val	Asp	Met	Lys	Ser	Gly	Tyr	Ala	Phe	Val	Tyr	Phe
		50				55					60				
Glu	Asp	Glu	Arg	Asp	Ala	Glu	Asp	Ala	Ile	Arg	Lys	Leu	Asp	Asn	Phe
		65			70				75					80	
Pro	Phe	Gly	Tyr	Glu	Lys	Arg	Arg	Leu	Ser	Val	Glu	Trp	Ala	Lys	Gly
		85						90					95		
Glu	Arg	Gly	Arg	Pro	Arg	Gly	Asp	Ala	Lys	Ala	Pro	Ser	Asn	Leu	Lys
		100					105						110		
Pro	Thr	Lys	Thr	Leu	Phe	Val	Ile	Asn	Phe	Asp	Pro	Ile	Arg	Thr	Lys
		115					120					125			
Glu	His	Asp	Ile	Glu	Lys	His	Phe	Glu	Pro	Tyr	Gly	Lys	Val	Thr	Asn
		130				135					140				
Val	Arg	Ile	Arg	Arg	Asn	Phe	Ser	Phe	Val	Gln	Phe	Glu	Thr	Gln	Glu
145				150					155					160	

Asp Ala Thr Lys Ala Leu Glu Ala Thr Gln Arg Ser Lys Ile Leu Asp
165 170 175
Arg Val Val Ser Val Glu Tyr Ala Leu Lys Asp Asp Asp Glu Arg Asp
180 185 190
Asp Arg Asn Gly Gly Arg Ser Pro Arg Arg Ser Leu Ser Pro Val Tyr
195 200 205
Arg Arg Arg His Val Met Met Tyr Cys Arg Tyr Phe Lys Glu Asn Leu
210 215 220
Ala Pro Phe Val
225

(2) INFORMATION FOR SEQ ID NO:2046:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 206 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..206

(D) OTHER INFORMATION: / Ceres Seq. ID 1571671

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2046:

Met Arg Pro Val Phe Val Gly Asn Phe Glu Tyr Glu Thr Arg Gln Ser
1 5 10 15
Asp Leu Glu Arg Leu Phe Asp Lys Tyr Gly Arg Val Asp Arg Val Asp
20 25 30
Met Lys Ser Gly Tyr Ala Phe Val Tyr Phe Glu Asp Glu Arg Asp Ala
35 40 45
Glu Asp Ala Ile Arg Lys Leu Asp Asn Phe Pro Phe Gly Tyr Glu Lys
50 55 60
Arg Arg Leu Ser Val Glu Trp Ala Lys Gly Glu Arg Gly Arg Pro Arg
65 70 75 80
Gly Asp Ala Lys Ala Pro Ser Asn Leu Lys Pro Thr Lys Thr Leu Phe
85 90 95
Val Ile Asn Phe Asp Pro Ile Arg Thr Lys Glu His Asp Ile Glu Lys
100 105 110
His Phe Glu Pro Tyr Gly Lys Val Thr Asn Val Arg Ile Arg Arg Asn
115 120 125
Phe Ser Phe Val Gln Phe Glu Thr Gln Glu Asp Ala Thr Lys Ala Leu
130 135 140
Glu Ala Thr Gln Arg Ser Lys Ile Leu Asp Arg Val Val Ser Val Glu
145 150 155 160
Tyr Ala Leu Lys Asp Asp Asp Glu Arg Asp Arg Asn Gly Gly Arg
165 170 175
Ser Pro Arg Arg Ser Leu Ser Pro Val Tyr Arg Arg Arg His Val Met
180 185 190
Met Tyr Cys Arg Tyr Phe Lys Glu Asn Leu Ala Pro Phe Val
195 200 205

(2) INFORMATION FOR SEQ ID NO:2047:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 174 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..174

(D) OTHER INFORMATION: / Ceres Seq. ID 1571672

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2047:

Met Lys Ser Gly Tyr Ala Phe Val Tyr Phe Glu Asp Glu Arg Asp Ala

1	5	10	15
Glu Asp Ala	Ile Arg Lys Leu Asp Asn Phe Pro Phe Gly Tyr Glu Lys		
	20	25	30
Arg Arg Leu	Ser Val Glu Trp Ala Lys Gly Glu Arg Gly Arg Pro Arg		
	35	40	45
Gly Asp Ala	Lys Ala Pro Ser Asn Leu Lys Pro Thr Lys Thr Leu Phe		
	50	55	60
Val Ile Asn	Phe Asp Pro Ile Arg Thr Lys Glu His Asp Ile Glu Lys		
	65	70	75
His Phe Glu	Pro Tyr Gly Lys Val Thr Asn Val Arg Ile Arg Arg Asn		
	85	90	95
Phe Ser Phe	Val Gln Phe Glu Thr Gln Glu Asp Ala Thr Lys Ala Leu		
	100	105	110
Glu Ala Thr	Gln Arg Ser Lys Ile Leu Asp Arg Val Val Ser Val Glu		
	115	120	125
Tyr Ala Leu	Lys Asp Asp Asp Glu Arg Asp Asp Arg Asn Gly Gly Arg		
	130	135	140
Ser Pro Arg	Arg Ser Leu Ser Pro Val Tyr Arg Arg Arg His Val Met		
	145	150	155
Met Tyr Cys	Arg Tyr Phe Lys Glu Asn Leu Ala Pro Phe Val		
	165	170	

(2) INFORMATION FOR SEQ ID NO:2048:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 967 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..967

(D) OTHER INFORMATION: / Ceres Seq. ID 1571677

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2048:

actcatttta	ctgttaagca	aacacaagat	aagaagaasac	aaacaatggc	gattctcttc	60
attttagatat	tttcctgat	tcttagcttc	tggatttttg	tgaaggatt	tgaaatggcg	120
gtgtcgcttt	tatcgaaatt	acgggtgtata	acagtagatg	ttactgttac	acttataagct	180
tacaaaggag	agcttgggtga	ttactattgt	atggctgcta	aagccattgg	tttgccttgt	240
ctgtattata	aacgagttca	tgaaggtttt	aaactagctt	atacagatat	ggcacaaaaa	300
tatccttggtt	tcggtttcca	tgccaaaatg	ccaaacattg	tttgggtgaa	aacttgtgtg	360
agagattcat	ttgtcaaggc	aggatatgag	tatgatgagg	agacatttga	gaagatattt	420
aggagaatct	attcgacgtt	tggttctgct	gcaccttact	ctgbgtttca	agattctcaa	480
cggtttttaa	gatggggcacg	caggaaaagt	cttatagctg	gacttgttag	caatgccgaa	540
taccgatatc	aagaagtatt	ttacacctCc	ttcgggtttga	gcaaggcaga	gtgggatttt	600
gggtgtattct	ctggaattga	agggatagag	aaaccagatc	cgaggatttt	tacGctgcgcg	660
ctagagagag	ccgggaataa	tattgcgcct	gaagagggtt	tgcataattg	agacagcatg	720
cgcaagattt	atgttccagc	aaagagtatt	gggatgcag	ctttgttggg	tgaagggttt	780
aagacggaag	ctgtctaaga	ctgtagataa	gctggagcca	ttgtgcttcc	agattttggtt	840
gctgttcaac	aacttttggg	gtctgataag	ttgaaatgtt	agaaaacaga	cctctcttaa	900
gtatgaaatc	taattgtatt	tagtattgca	catttgagta	aaataagttt	caacgcgttc	960
tttggtt						

(2) INFORMATION FOR SEQ ID NO:2049:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 255 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..255

(D) OTHER INFORMATION: / Ceres Seq. ID 1571678

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2049:

Met	Ala	Val	Ser	Leu	Leu	Ser	Lys	Leu	Arg	Cys	Ile	Thr	Val	Asp	Val
1			5					10						15	
Thr	Gly	Thr	Leu	Ile	Ala	Tyr	Lys	Gly	Glu	Leu	Gly	Asp	Tyr	Tyr	Cys
			20					25					30		
Met	Ala	Ala	Lys	Ala	Ile	Gly	Leu	Pro	Cys	Pro	Asp	Tyr	Lys	Arg	Val
			35				40					45			
His	Glu	Gly	Phe	Lys	Leu	Ala	Tyr	Thr	Asp	Met	Ala	Gln	Lys	Tyr	Pro
			50			55					60				
Cys	Phe	Gly	Phe	His	Ala	Lys	Met	Pro	Asn	Ile	Val	Trp	Trp	Lys	Thr
65				70					75					80	
Cys	Val	Arg	Asp	Ser	Phe	Val	Lys	Ala	Gly	Tyr	Glu	Tyr	Asp	Glu	Glu
			85					90					95		
Thr	Phe	Glu	Lys	Ile	Phe	Arg	Arg	Ile	Tyr	Ser	Thr	Phe	Gly	Ser	Ala
			100					105					110		
Ala	Pro	Tyr	Ser	Xaa	Phe	Gln	Asp	Ser	Gln	Pro	Phe	Leu	Arg	Trp	Ala
			115				120					125			
Arg	Arg	Lys	Gly	Leu	Ile	Val	Gly	Leu	Val	Ser	Asn	Ala	Glu	Tyr	Arg
			130			135					140				
Tyr	Gln	Glu	Val	Ile	Leu	Pro	Ser	Phe	Gly	Leu	Ser	Lys	Ala	Glu	Trp
145				150					155					160	
Asp	Phe	Gly	Val	Phe	Ser	Gly	Ile	Glu	Gly	Ile	Glu	Lys	Pro	Asp	Pro
				165				170						175	
Arg	Ile	Phe	Thr	Leu	Ala	Leu	Glu	Arg	Ala	Gly	Asn	Asn	Ile	Ala	Pro
			180					185					190		
Glu	Glu	Val	Leu	His	Ile	Gly	Asp	Ser	Met	Arg	Lys	Asp	Tyr	Val	Pro
			195				200					205			
Ala	Lys	Ser	Ile	Gly	Met	His	Ala	Leu	Leu	Val	Asp	Arg	Phe	Lys	Thr
			210			215					220				
Glu	Ala	Ala	Lys	Asp	Trp	Ile	Glu	Ala	Gly	Ala	Ile	Val	Leu	Pro	Asp
225				230					235					240	
Leu	Val	Ala	Val	Gln	Gln	Leu	Leu	Glu	Ser	Asp	Lys	Leu	Lys	Cys	
			245					250					255		

(2) INFORMATION FOR SEQ ID NO:2050:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 223 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..223

(D) OTHER INFORMATION: / Ceres Seq. ID 1571679

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2050:

Met	Ala	Ala	Lys	Ala	Ile	Gly	Leu	Pro	Cys	Pro	Asp	Tyr	Lys	Arg	Val
1			5					10						15	
His	Glu	Gly	Phe	Lys	Leu	Ala	Tyr	Thr	Asp	Met	Ala	Gln	Lys	Tyr	Pro
			20					25					30		
Cys	Phe	Gly	Phe	His	Ala	Lys	Met	Pro	Asn	Ile	Val	Trp	Trp	Lys	Thr
			35				40					45			
Cys	Val	Arg	Asp	Ser	Phe	Val	Lys	Ala	Gly	Tyr	Glu	Tyr	Asp	Glu	Glu
			50			55					60				
Thr	Phe	Glu	Lys	Ile	Phe	Arg	Arg	Ile	Tyr	Ser	Thr	Phe	Gly	Ser	Ala
65				70					75					80	
Ala	Pro	Tyr	Ser	Xaa	Phe	Gln	Asp	Ser	Gln	Pro	Phe	Leu	Arg	Trp	Ala
			85					90					95		
Arg	Arg	Lys	Gly	Leu	Ile	Val	Gly	Leu	Val	Ser	Asn	Ala	Glu	Tyr	Arg
			100				105						110		
Tyr	Gln	Glu	Val	Ile	Leu	Pro	Ser	Phe	Gly	Leu	Ser	Lys	Ala	Glu	Trp
			115				120						125		

Asp Phe Gly Val Phe Ser Gly Ile Glu Gly Ile Glu Lys Pro Asp Pro
130 135 140
Arg Ile Phe Thr Leu Ala Leu Glu Arg Ala Gly Asn Asn Ile Ala Pro
145 150 155 160
Glu Glu Val Leu His Ile Gly Asp Ser Met Arg Lys Asp Tyr Val Pro
165 170 175
Ala Lys Ser Ile Gly Met His Ala Leu Leu Val Asp Arg Phe Lys Thr
180 185 190
Glu Ala Ala Lys Asp Trp Ile Glu Ala Gly Ala Ile Val Leu Pro Asp
195 200 205
Leu Val Ala Val Gln Gln Leu Glu Ser Asp Lys Leu Lys Cys
210 215 220

(2) INFORMATION FOR SEQ ID NO:2051:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 197 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..197
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571680

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2051:

Met Ala Gln Lys Tyr Pro Cys Phe Gly Phe His Ala Lys Met Pro Asn
1 5 10 15
Ile Val Trp Trp Lys Thr Cys Val Arg Asp Ser Phe Val Lys Ala Gly
20 25 30
Tyr Glu Tyr Asp Glu Glu Thr Phe Glu Lys Ile Phe Arg Arg Ile Tyr
35 40 45
Ser Thr Phe Gly Ser Ala Ala Pro Tyr Ser Xaa Phe Gln Asp Ser Gln
50 55 60
Pro Phe Leu Arg Trp Ala Arg Arg Lys Gly Leu Ile Val Gly Leu Val
65 70 75 80
Ser Asn Ala Glu Tyr Arg Tyr Gln Glu Val Ile Leu Pro Ser Phe Gly
85 90 95
Leu Ser Lys Ala Glu Trp Asp Phe Gly Val Phe Ser Gly Ile Glu Gly
100 105 110
Ile Glu Lys Pro Asp Pro Arg Ile Phe Thr Leu Ala Leu Glu Arg Ala
115 120 125
Gly Asn Asn Ile Ala Pro Glu Glu Val Leu His Ile Gly Asp Ser Met
130 135 140
Arg Lys Asp Tyr Val Pro Ala Lys Ser Ile Gly Met His Ala Leu Leu
145 150 155 160
Val Asp Arg Phe Lys Thr Glu Ala Ala Lys Asp Trp Ile Glu Ala Gly
165 170 175
Ala Ile Val Leu Pro Asp Leu Val Ala Val Gln Gln Leu Leu Glu Ser
180 185 190
Asp Lys Leu Lys Cys
195

(2) INFORMATION FOR SEQ ID NO:2052:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1604 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1604
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571687

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2052:

atttttagatc	cgatattatt	agaaagcaac	caaaactccgg	ctccggttac	tcggggagttc	60
aagtttttggg	ttttgtatggg	tactgtctcga	actcgtaccg	gtatcatctc	cgctcgtttt	120
aaattcttcca	ggtctctgtt	ccctcgccat	caccgtacta	acagcatgaa	gataaaaaaca	180
ggaaacgtttt	tgggggtttt	gatatcatgt	attcttataa	acttagctgc	gatcatggaa	240
cgtgcagacg	agaatctcatt	gccttcgggt	tataaagaag	tgagtgaaag	atttaacgca	300
ggaccatcag	atttaggtcta	cttaacattc	gttagaaaact	ttgttcaagg	acttgcacata	360
ccattagcag	gagttcttgt	cattacotat	gatcgtccca	ttgttcttgc	aataggtaact	420
gtctgttggg	ctttatacaac	tgctgcagtt	ggagccagca	gctacttcac	tcaggttgct	480
ttatggagag	cagtgaaatgg	ttttggaatt	gcaattgtta	taccgcgct	tcaactcgtt	540
attgcagata	gttataaagga	tggtgcgaga	ggagctggtt	tcggaattgt	gaacctcatt	600
ggtaacaatcg	gtggtatagg	aggaggtgtt	gtagcaactg	ttatggctgg	tcacagattt	660
tggggcctac	cgggatggcg	ttgtgctttt	ataatgatgg	cagcgctcag	cgcagtgatc	720
ggattactgt	tctttctctt	cgtgtgtgac	ccgagaaaga	acattgaacg	agagggaacta	780
ttggctcata	agatgaattc	gaactcgggt	tggaaatgatt	cattagcagc	tgcaaaatct	840
ctgcgtcaaa	taagtacctt	tcagataaat	gtcgcgcaag	gaatcattgg	ttcgtttccg	900
tggaccgcga	tggttttctt	tacaatgtgg	tttgagctta	ttggcttcga	tcataaccag	960
actgcagctt	tgcttggggg	atttgtcata	ggaggagcga	taggaacatt	aatgggaggg	1020
ataatagcgg	ataaaatgtc	gcggatatat	ccgaattcgg	gtagagtgat	gtgtgcgcag	1080
ttcagtgcat	tcattgggaat	cccattctct	attattcttc	tgaagatgat	cccaacaaag	1140
acaacagcgt	actcaatctt	ctcgataaact	ctcttctctga	tgggtctttac	cataactttg	1200
tcgggatcag	cggtttaatgc	accgatgttt	gcagaagtgg	ttctctccag	gcacgcgtata	1260
atgatctacg	cgtttgaccg	tgccttcgaa	gggtcattct	catctttttg	tcgcgctttt	1320
gtgggaattt	tgtctgagaa	aattgtttgg	tatgactcaa	gaggtattga	tcctttgaaa	1380
ggttctctct	ttcgtgaggg	tgatgcctct	tcaaaagggg	ttctgtcaat	gatggctggt	1440
ccgttttggc	ctgtttgtct	ctgtttacat	ccgtttgcat	ttgttttttc	gaagatcgca	1500
gaaaaacgcga	aaatcgcgag	ctctaaagaa	actgaaatga	tcagagagac	ttgtctcatgt	1560
agtcacgttt	tgtattcttt	tataccacaa	acgattttta	aacc		

(2) INFORMATION FOR SEQ ID NO:2053:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 514 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..514

(D) OTHER INFORMATION: / Ceres Seq. ID 1571688

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2053:

Ile	Leu	Asp	Pro	Ile	Phe	Ile	Glu	Ser	Asn	Gln	Thr	Pro	Ala	Pro	Val
1			5						10					15	
Thr	Arg	Glu	Phe	Lys	Phe	Trp	Ile	Leu	Met	Gly	His	Ala	Arg	Thr	Arg
			20						25				30		
Thr	Gly	Ile	Ile	Ser	Val	Ala	Phe	Lys	Phe	Phe	Arg	Ser	Leu	Phe	Pro
			35						40				45		
Arg	His	His	Arg	Thr	Asn	Ser	Met	Lys	Ile	Lys	Thr	Gly	Thr	Phe	Leu
			50				55					60			
Gly	Val	Ser	Ile	Ser	Leu	Ile	Leu	Ile	Asn	Leu	Ala	Ala	Ile	Met	Glu
65					70				75					80	
Arg	Ala	Asp	Glu	Asn	Leu	Leu	Pro	Ser	Val	Tyr	Lys	Glu	Val	Ser	Glu
					85				90				95		
Ala	Phe	Asn	Ala	Gly	Pro	Ser	Asp	Leu	Gly	Tyr	Leu	Thr	Phe	Val	Arg
			100						105				110		
Asn	Phe	Val	Gln	Gly	Leu	Ala	Ser	Pro	Leu	Ala	Gly	Val	Leu	Val	Ile
			115				120					125			
Thr	Tyr	Asp	Arg	Pro	Ile	Val	Leu	Ala	Ile	Gly	Thr	Val	Cys	Trp	Ala
			130				135					140			
Leu	Ser	Thr	Ala	Ala	Val	Gly	Ala	Ser	Ser	Tyr	Phe	Ile	Gln	Val	Ala
			145				150			155				160	
Leu	Trp	Arg	Ala	Val	Asn	Gly	Phe	Gly	Leu	Ala	Ile	Val	Ile	Pro	Ala

COLETTI

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 489 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
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(A) NAME/KEY: peptide
(B) LOCATION: 1..489
(D) OTHER INFORMATION: / Ceres Seq. ID 1571689

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2054:

Met Gly His Ala Arg Thr Arg Thr Gly Ile Ile Ser Val Ala Phe Lys
1 5 10 15
Phe Phe Arg Ser Leu Phe Pro Arg His His Arg Thr Asn Ser Met Lys
20 25 30

Ile Lys Thr Gly Thr Phe Leu Gly Val Ser Ile Ser Leu Ile Leu Ile
35 40 45
Asn Leu Ala Ala Ile Met Glu Arg Ala Asp Glu Asn Leu Leu Pro Ser
50 55 60
Val Tyr Lys Glu Val Ser Glu Ala Phe Asn Ala Gly Pro Ser Asp Leu
65 70 75 80
Gly Tyr Leu Thr Phe Val Arg Asn Phe Val Gln Gly Leu Ala Ser Pro
85 90 95
Leu Ala Gly Val Leu Val Ile Thr Tyr Asp Arg Pro Ile Val Leu Ala
100 105 110
Ile Gly Thr Val Cys Trp Ala Leu Ser Thr Ala Ala Val Gly Ala Ser
115 120 125
Ser Tyr Phe Ile Gln Val Ala Leu Trp Arg Ala Val Asn Gly Phe Gly
130 135 140
Leu Ala Ile Val Ile Pro Ala Leu Gln Ser Phe Ile Ala Asp Ser Tyr
145 150 155 160
Lys Asp Gly Ala Arg Gly Ala Gly Phe Gly Met Leu Asn Leu Ile Gly
165 170 175
Thr Ile Gly Gly Ile Gly Gly Gly Val Val Ala Thr Val Met Ala Gly
180 185 190
Ser Glu Phe Trp Gly Ile Pro Gly Trp Arg Cys Ala Phe Ile Met Met
195 200 205
Ala Ala Leu Ser Ala Val Ile Gly Leu Leu Val Phe Leu Phe Val Val
210 215 220
Asp Pro Arg Lys Asn Ile Glu Arg Glu Glu Met Ala His Lys Met
225 230 235 240
Asn Ser Asn Ser Val Trp Asn Asp Ser Leu Ala Ala Lys Ser Val
245 250 255
Val Lys Val Ser Thr Phe Gln Ile Ile Val Ala Gln Gly Ile Ile Gly
260 265 270
Ser Phe Pro Trp Thr Ala Met Val Phe Phe Thr Met Trp Phe Glu Leu
275 280 285
Ile Gly Phe Asp His Asn Gln Thr Ala Ala Leu Leu Gly Val Phe Ala
290 295 300
Thr Gly Gly Ala Ile Gly Thr Leu Met Gly Gly Ile Ile Ala Asp Lys
305 310 315 320
Met Ser Arg Ile Tyr Pro Asn Ser Gly Arg Val Met Cys Ala Gln Phe
325 330 335
Ser Ala Phe Met Gly Ile Pro Phe Ser Ile Ile Leu Leu Lys Val Ile
340 345 350
Pro Gln Ser Thr Ser Ser Tyr Ser Ile Phe Ser Ile Thr Leu Phe Leu
355 360 365
Met Gly Leu Thr Ile Thr Trp Cys Gly Ser Ala Val Asn Ala Pro Met
370 375 380
Phe Ala Glu Val Val Pro Pro Arg His Arg Thr Met Ile Tyr Ala Phe
385 390 395 400
Asp Arg Ala Phe Glu Gly Ser Phe Ser Ser Phe Ala Ala Pro Leu Val
405 410 415
Gly Ile Leu Ser Glu Lys Met Phe Gly Tyr Asp Ser Arg Gly Ile Asp
420 425 430
Pro Leu Lys Gly Ser Ser Val Arg Glu Ala Asp Ala Leu Ser Lys Gly
435 440 445
Leu Leu Ser Met Met Ala Val Pro Phe Gly Leu Cys Cys Leu Cys Tyr
450 455 460
Thr Pro Leu His Phe Val Phe Gln Lys Asp Arg Glu Asn Ala Lys Ile
465 470 475 480
Ala Ser Ser Lys Glu Thr Glu Met Ile
485

(2) INFORMATION FOR SEQ ID NO:2055:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 459 amino acids

(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..459
(D) OTHER INFORMATION: / Ceres Seq. ID 1571690
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2055:

Met	Lys	Ile	Lys	Thr	Gly	Thr	Phe	Leu	Gly	Val	Ser	Ile	Ser	Leu	Ile
1			5						10					15	
Leu	Ile	Asn	Leu	Ala	Ala	Ile	Met	Glu	Arg	Ala	Asp	Glu	Asn	Leu	Leu
			20					25				30			
Pro	Ser	Val	Tyr	Lys	Glu	Val	Ser	Glu	Ala	Phe	Asn	Ala	Gly	Pro	Ser
			35				40					45			
Asp	Leu	Gly	Tyr	Leu	Thr	Phe	Val	Arg	Asn	Phe	Val	Gln	Gly	Leu	Ala
	50				55					60					
Ser	Pro	Leu	Ala	Gly	Val	Leu	Val	Ile	Thr	Tyr	Asp	Arg	Pro	Ile	Val
65					70				75					80	
Leu	Ala	Ile	Gly	Thr	Val	Cys	Trp	Ala	Leu	Ser	Thr	Ala	Ala	Val	Gly
			85						90					95	
Ala	Ser	Ser	Tyr	Phe	Ile	Gln	Val	Ala	Leu	Trp	Arg	Ala	Val	Asn	Gly
			100					105					110		
Phe	Gly	Leu	Ala	Ile	Val	Ile	Pro	Ala	Leu	Gln	Ser	Phe	Ile	Ala	Asp
			115				120					125			
Ser	Tyr	Lys	Asp	Gly	Ala	Arg	Gly	Ala	Gly	Phe	Gly	Met	Leu	Asn	Leu
	130				135					140					
Ile	Gly	Thr	Ile	Gly	Gly	Ile	Gly	Gly	Gly	Val	Val	Ala	Thr	Val	Met
145				150					155					160	
Ala	Gly	Ser	Glu	Phe	Trp	Gly	Ile	Pro	Gly	Trp	Arg	Cys	Ala	Phe	Ile
			165						170					175	
Met	Met	Ala	Ala	Leu	Ser	Ala	Val	Ile	Gly	Leu	Leu	Val	Phe	Leu	Phe
			180				185						190		
Val	Val	Asp	Pro	Arg	Lys	Asn	Ile	Glu	Arg	Glu	Glu	Leu	Met	Ala	His
		195					200					205			
Lys	Met	Asn	Ser	Asn	Ser	Val	Trp	Asn	Asp	Ser	Leu	Ala	Ala	Ala	Lys
	210					215					220				
Ser	Val	Val	Lys	Val	Ser	Thr	Phe	Gln	Ile	Ile	Val	Ala	Gln	Gly	Ile
225					230					235					240
Ile	Gly	Ser	Phe	Pro	Trp	Thr	Ala	Met	Val	Phe	Phe	Thr	Met	Trp	Phe
			245						250					255	
Glu	Leu	Ile	Gly	Phe	Asp	His	Asn	Gln	Thr	Ala	Ala	Leu	Leu	Gly	Val
			260					265					270		
Phe	Ala	Thr	Gly	Gly	Ala	Ile	Gly	Thr	Leu	Met	Gly	Gly	Ile	Ile	Ala
			275				280					285			
Asp	Lys	Met	Ser	Arg	Ile	Tyr	Pro	Asn	Ser	Gly	Arg	Val	Met	Cys	Ala
	290				295						300				
Gln	Phe	Ser	Ala	Phe	Met	Gly	Ile	Pro	Phe	Ser	Ile	Ile	Leu	Leu	Lys
			310						315					320	
Val	Ile	Pro	Gln	Ser	Thr	Ser	Ser	Tyr	Ser	Ile	Phe	Ser	Ile	Thr	Leu
			325					330					335		
Phe	Leu	Met	Gly	Leu	Thr	Ile	Thr	Trp	Cys	Gly	Ser	Ala	Val	Asn	Ala
		340					345						350		
Pro	Met	Phe	Ala	Glu	Val	Val	Pro	Pro	Arg	His	Arg	Thr	Met	Ile	Tyr
		355					360					365			
Ala	Phe	Asp	Arg	Ala	Phe	Glu	Gly	Ser	Phe	Ser	Ser	Phe	Ala	Ala	Pro
		370				375					380				
Leu	Val	Gly	Ile	Leu	Ser	Glu	Lys	Met	Phe	Gly	Tyr	Asp	Ser	Arg	Gly
385					390					395					400
Ile	Asp	Pro	Leu	Lys	Gly	Ser	Ser	Val	Arg	Glu	Ala	Asp	Ala	Leu	Ser
			405						410					415	

Lys Gly Leu Leu Ser Met Met Ala Val Pro Phe Gly Leu Cys Cys Leu
420 425 430
Cys Tyr Thr Pro Leu His Phe Val Phe Gln Lys Asp Arg Glu Asn Ala
435 440 445
Lys Ile Ala Ser Ser Lys Glu Thr Glu Met Ile
450 455

(2) INFORMATION FOR SEQ ID NO:2056:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1305 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1305

(D) OTHER INFORMATION: / Ceres Seq. ID 1571691

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2056:

aatggaatca cactatacaca atcataacca caaaaacaaa cactatggga cacctcaaaa 60
gtctctttac tattcttttc ctaatagcta tgtcgtcaac cgtaaacatt gccggtaaaa 120
taccgcgat catcgtgttt ggcgactctt ccgttgatgc cggaacaac aactatatcc 180
caactgttgc tagaagaac tttgagccat atggacggga ctttgttgtt ggaagccga 240
cgggacggtt ttgtaacgga aagattgcga cggattttat gtccgaagcc ttagggctta 300
aaccaatcat tcgggcatac ttggatcctt cttataacat ttacagactt gcaacagggt 360
ttacctttgc ttctgtctgc actggctatg acaacgccac ttctgatgtt ctgtcggcat 420
tacctctatg gaacacaact gaataactaca aagaatacca acaaaaactt aaagcatacc 480
aaggaagaag cagacgcaca gagactatag aaagctctct ctacctcata agcataggga 540
ccaacgattt cctcgagaat tactttgtct ttccggggcg ttcttcgcaa tattccgtca 600
gtctttacca agattttcta gccggaatcg cgaaagaatt tgtgaagaag ttgcatggac 660
ttggtgtcag aaagatctca ctagggtggg tactctcaat gggatgcatt cctttagaga 720
gagccaccaa caattggcact ggaggtgagt cgcgtaggac gtacaacgac atagccgttc 780
agttcaacag caagcttgat aagattggtt agaagctgaa caaagagctt cctgttctca 840
acctogtttt ctcaaaatcca tatgagccat ttatgcggat catcaagaac cctctctctt 900
ttgggttcga ggtggtggga gccgcatgCt gcgcgacagg gatgtctcag atgggatgatg 960
gttgtcaaaag gaataaccca ttacatgta caaacgcaga caagtatgtg ttttgggact 1020
catttcaccc aacacagaag actaatcaca tcatggccaa tgctctcatg aacagcacat 1080
tccttcactt cctctaaatg atttttatgt ttgtgtgtgg aaactaaata gatataaag 1140
taatattatt attagggatt gcttttgata tgcactctgt atgtatttat atttaagtag 1200
attttgctct tgtgttagtt agcgaaacct acgtttcttt tctagattat ggtgtgccta 1260
tttatgtagc ttattttatc ctctttagtt attctcaata tatcc

(2) INFORMATION FOR SEQ ID NO:2057:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 364 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..364

(D) OTHER INFORMATION: / Ceres Seq. ID 1571692

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2057:

Trp Asn His Thr Ile Thr Ile Ile Thr Thr Lys Thr Asn Thr Met Gly
1 5 10
His Leu Lys Ser Leu Phe Thr Ile Leu Phe Leu Ile Ala Met Ser Ser
20 25 30
Thr Val Thr Phe Ala Gly Lys Ile Pro Ala Ile Ile Val Phe Gly Asp
35 40 45
Ser Ser Val Asp Ala Gly Asn Asn Asn Tyr Ile Pro Thr Val Ala Arg
50 55 60
Ser Asn Phe Glu Pro Tyr Gly Arg Asp Phe Val Gly Gly Lys Pro Thr

65					70					75					80
Gly	Arg	Phe	Cys	Asn	Gly	Lys	Ile	Ala	Thr	Asp	Phe	Met	Ser	Glu	Ala
				85					90					95	
Leu	Gly	Leu	Lys	Pro	Ile	Ile	Pro	Ala	Tyr	Leu	Asp	Pro	Ser	Tyr	Asn
			100					105					110		
Ile	Ser	Asp	Phe	Ala	Thr	Gly	Val	Thr	Phe	Ala	Ser	Ala	Ala	Thr	Gly
		115					120				125				
Tyr	Asp	Asn	Ala	Thr	Ser	Asp	Val	Leu	Ser	Val	Leu	Pro	Leu	Trp	Lys
	130					135					140				
Gln	Leu	Glu	Tyr	Tyr	Lys	Glu	Tyr	Gln	Thr	Lys	Leu	Lys	Ala	Tyr	Gln
145					150					155				160	
Gly	Lys	Asp	Arg	Ala	Thr	Glu	Thr	Ile	Glu	Ser	Ser	Leu	Tyr	Leu	Ile
			165						170					175	
Ser	Ile	Gly	Thr	Asn	Asp	Phe	Leu	Glu	Asn	Tyr	Phe	Val	Phe	Pro	Gly
		180						185					190		
Arg	Ser	Ser	Gln	Tyr	Ser	Val	Ser	Leu	Tyr	Gln	Asp	Phe	Leu	Ala	Gly
		195					200					205			
Ile	Ala	Lys	Glu	Phe	Val	Lys	Lys	Leu	His	Gly	Leu	Gly	Ala	Arg	Lys
	210					215					220				
Ile	Ser	Leu	Gly	Gly	Leu	Pro	Pro	Met	Gly	Cys	Met	Pro	Leu	Glu	Arg
225					230					235					240
Ala	Thr	Asn	Ile	Gly	Thr	Gly	Gly	Glu	Cys	Val	Gly	Arg	Tyr	Asn	Asp
				245					250					255	
Ile	Ala	Val	Gln	Phe	Asn	Ser	Lys	Leu	Asp	Lys	Met	Val	Glu	Lys	Leu
		260						265					270		
Asn	Lys	Glu	Leu	Pro	Gly	Ser	Asn	Leu	Val	Phe	Ser	Asn	Pro	Tyr	Glu
		275					280						285		
Pro	Phe	Met	Arg	Ile	Ile	Lys	Asn	Pro	Ser	Ser	Phe	Gly	Phe	Glu	Val
		290				295					300				
Val	Gly	Ala	Ala	Cys	Cys	Ala	Thr	Gly	Met	Phe	Glu	Met	Gly	Tyr	Gly
305					310					315					320
Cys	Gln	Arg	Asn	Asn	Pro	Phe	Thr	Cys	Thr	Asn	Ala	Asp	Lys	Tyr	Val
			325					330						335	
Phe	Trp	Asp	Ser	Phe	His	Pro	Thr	Gln	Lys	Thr	Asn	His	Ile	Met	Ala
			340					345					350		
Asn	Ala	Leu	Met	Asn	Ser	Thr	Phe	Pro	His	Phe	Leu				
		355				360									

(2) INFORMATION FOR SEQ ID NO:2058:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 350 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..350

(D) OTHER INFORMATION: / Ceres Seq. ID 1571693

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2058:

Met	Gly	His	Leu	Lys	Ser	Leu	Phe	Thr	Ile	Leu	Phe	Leu	Ile	Ala	Met
1			5					10					15		
Ser	Ser	Thr	Val	Thr	Phe	Ala	Gly	Lys	Ile	Pro	Ala	Ile	Ile	Val	Phe
			20					25				30			
Gly	Asp	Ser	Ser	Val	Asp	Ala	Gly	Asn	Asn	Asn	Tyr	Ile	Pro	Thr	Val
	35						40					45			
Ala	Arg	Ser	Asn	Phe	Glu	Pro	Tyr	Gly	Arg	Asp	Phe	Val	Gly	Gly	Lys
	50				55						60				
Pro	Thr	Gly	Arg	Phe	Cys	Asn	Gly	Lys	Ile	Ala	Thr	Asp	Phe	Met	Ser
65					70				75					80	
Glu	Ala	Leu	Gly	Leu	Lys	Pro	Ile	Ile	Pro	Ala	Tyr	Leu	Asp	Pro	Ser
			85					90					95		

Tyr Asn Ile Ser Asp Phe Ala Thr Gly Val Thr Phe Ala Ser Ala Ala
100 105 110
Thr Gly Tyr Asp Asn Ala Thr Ser Asp Val Leu Ser Val Leu Pro Leu
115 120 125
Trp Lys Gln Leu Glu Tyr Tyr Lys Glu Tyr Gln Thr Lys Leu Lys Ala
130 135 140
Tyr Gln Gly Lys Asp Arg Ala Thr Glu Thr Ile Glu Ser Ser Leu Tyr
145 150 155 160
Leu Ile Ser Ile Gly Thr Asn Asp Phe Leu Glu Asn Tyr Phe Val Phe
165 170 175
Pro Gly Arg Ser Ser Gln Tyr Ser Val Ser Leu Tyr Gln Asp Phe Leu
180 185 190
Ala Gly Ile Ala Lys Glu Phe Val Lys Lys Leu His Gly Leu Gly Ala
195 200 205
Arg Lys Ile Ser Leu Gly Gly Leu Pro Pro Met Gly Cys Met Pro Leu
210 215 220
Glu Arg Ala Thr Asn Ile Gly Thr Gly Gly Glu Cys Val Gly Arg Tyr
225 230 235 240
Asn Asp Ile Ala Val Gln Phe Asn Ser Lys Leu Asp Lys Met Val Glu
245 250 255
Lys Leu Asn Lys Glu Leu Pro Gly Ser Asn Leu Val Phe Ser Asn Pro
260 265 270
Tyr Glu Pro Phe Met Arg Ile Ile Lys Asn Pro Ser Ser Phe Gly Phe
275 280 285
Glu Val Val Gly Ala Ala Cys Cys Ala Thr Gly Met Phe Glu Met Gly
290 295 300
Tyr Gly Cys Gln Arg Asn Asn Pro Phe Thr Cys Thr Asn Ala Asp Lys
305 310 315 320
Tyr Val Phe Trp Asp Ser Phe His Pro Thr Gln Lys Thr Asn His Ile
325 330 335
Met Ala Asn Ala Leu Met Asn Ser Thr Phe Pro His Phe Leu
340 345 350

(2) INFORMATION FOR SEQ ID NO:2059:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 335 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..335

(D) OTHER INFORMATION: / Ceres Seq. ID 1571694

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2059:

Met Ser Ser Thr Val Thr Phe Ala Gly Lys Ile Pro Ala Ile Val
1 5 10 15
Phe Gly Asp Ser Ser Val Asp Ala Gly Asn Asn Asn Tyr Ile Pro Thr
20 25 30
Val Ala Arg Ser Asn Phe Glu Pro Tyr Gly Arg Asp Phe Val Gly Gly
35 40 45
Lys Pro Thr Gly Arg Phe Cys Asn Gly Lys Ile Ala Thr Asp Phe Met
50 55 60
Ser Glu Ala Leu Gly Leu Lys Pro Ile Ile Pro Ala Tyr Leu Asp Pro
65 70 75 80
Ser Tyr Asn Ile Ser Asp Phe Ala Thr Gly Val Thr Phe Ala Ser Ala
85 90 95
Ala Thr Gly Tyr Asp Asn Ala Thr Ser Asp Val Leu Ser Val Leu Pro
100 105 110
Leu Trp Lys Gln Leu Glu Tyr Tyr Lys Glu Tyr Gln Thr Lys Leu Lys
115 120 125
Ala Tyr Gln Gly Lys Asp Arg Ala Thr Glu Thr Ile Glu Ser Ser Leu

130	135	140
Tyr Leu Ile Ser Ile Gly Thr Asn Asp Phe Leu Glu Asn Tyr Phe Val		
145	150	155
Phe Pro Gly Arg Ser Ser Gln Tyr Ser Val Ser Leu Tyr Gln Asp Phe		
	165	170
Leu Ala Gly Ile Ala Lys Glu Phe Val Lys Lys Leu His Gly Leu Gly		
	180	185
Ala Arg Lys Ile Ser Leu Gly Gly Leu Pro Pro Met Gly Cys Met Pro		
	195	200
Leu Glu Arg Ala Thr Asn Ile Gly Thr Gly Gly Glu Cys Val Gly Arg		
	210	215
Tyr Asn Asp Ile Ala Val Gln Phe Asn Ser Lys Leu Asp Lys Met Val		
	225	230
Glu Lys Leu Asn Lys Glu Leu Pro Gly Ser Asn Leu Val Phe Ser Asn		
	245	250
Pro Tyr Glu Pro Phe Met Arg Ile Ile Lys Asn Pro Ser Ser Phe Gly		
	260	265
Phe Glu Val Val Gly Ala Ala Cys Cys Ala Thr Gly Met Phe Glu Met		
	275	280
Gly Tyr Gly Cys Gln Arg Asn Asn Pro Phe Thr Cys Thr Asn Ala Asp		
	290	295
Lys Tyr Val Phe Trp Asp Ser Phe His Pro Thr Gln Lys Thr Asn His		
	305	310
Ile Met Ala Asn Ala Leu Met Asn Ser Thr Phe Pro His Phe Leu		
	325	330
		335

(2) INFORMATION FOR SEQ ID NO:2060:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1213 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1213
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571703

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2060:

atagattacg	taagagtctc	tctctctctc	tctctggaag	agggccttgg	gattgttttc	60
tctctctctc	tcagcttcta	atcgaattcg	ttatcgaaat	gaaagtctcg	acccttcgtc	120
gttgctccctc	aatacgcctc	attcttttga	ttagcatccc	taaaactaaa	atcgcagaga	180
gaatttctcc	gtttggaatc	ctaccaaatt	ggggcgcttt	tggaataaat	gccaccgttt	240
atgtccggtc	tcagagctgt	atcttctcta	ctttcatgtc	gaaacgcgat	tagcaggaaa	300
ctcgttagtc	gttctgggag	ctctcgaggg	agttttgtat	cagatcaaat	taggagattt	360
ggttctcttt	coggcgctga	gagatgttct	tctaatttgt	tgatgtccaa	tgatgacgct	420
agagctctct	tcgggagatt	gcctggcctc	gtgagcctac	ttcagagacg	gcattttctg	480
gggtgcggag	atggggaaaga	aggtggttgt	gagttatcaa	agatctatga	agagagacgt	540
gtcttagggt	atactccgga	gcacaattgt	aacgtagtgt	cagctgtaga	cttgtagcat	600
ggatttgttc	cttggtgtca	gcgctctgag	gttcttaaa	aataccctga	tggttcattt	660
gatgctgaat	tggagattgg	tttcaagtgt	ctcgttgaga	gttacatttc	ccatgtcgaa	720
tcggagaggg	cgaaatggat	taagaactaca	gcgagggaca	ctggcctgtt	tgaccatttg	780
ataaacctct	ggcaatttaa	gccaggggccc	attcctggaa	cctgcgacct	tcacttccat	840
gtagatttca	aattcaattc	accctctcat	cgccagggtg	cgtaattgtt	cttcaaggag	900
gtagcatcaa	gacttgtggg	ggcattcagt	gatcgatgcc	gactagtgtg	tggtccagaa	960
gtcccgagtag	atgaaaaacg	atatgagcaa	agagccttga	acatatctat	atataatat	1020
catggaagta	acaacacatc	agtttagttt	tcacttgttt	ttctagagag	cgattgcgca	1080
tagcatgttt	tgttttctta	aatatatagt	aatgctgttt	cataagaaga	tgaacacatt	1140
agatgtttgt	ttaaatgtta	agcagaaaaa	ataaacacat	ccatttctct	gttggagtta	1200
ttttttcac	tc					

(2) INFORMATION FOR SEQ ID NO:2061:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 256 amino acids

(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..256
 (D) OTHER INFORMATION: / Ceres Seq. ID 1571704
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2061:
Met Pro Pro Phe Met Ser Gly Leu Arg Ala Val Ser Ser Leu Leu Ser
1 5 10 15
Cys Arg Asn Ala Ile Ser Arg Lys Leu Val Ser Arg Ser Gly Ile Ser
 20 25 30
Arg Gly Ser Phe Val Ser Asp Gln Ile Arg Arg Phe Gly Ser Leu Ser
 35 40 45
Gly Val Glu Arg Cys Ser Ser Asn Trp Leu Met Ser Asn Asp Asp Ala
50 55 60
Arg Val Ser Phe Arg Arg Leu Pro Gly Ser Val Ser Leu Leu Gln Arg
65 70 75 80
Arg His Phe Leu Gly Cys Gly Asp Gly Glu Glu Gly Gly Gly Glu Leu
 85 90 95
Ser Lys Ile Tyr Glu Glu Arg Arg Val Leu Gly Tyr Thr Pro Glu Gln
 100 105 110
Met Phe Asn Val Val Ala Ala Val Asp Leu Tyr His Gly Phe Val Pro
 115 120 125
Trp Cys Gln Arg Ser Glu Val Leu Lys Glu Tyr Pro Asp Gly Ser Phe
130 135 140
Asp Ala Glu Leu Glu Ile Gly Phe Lys Phe Leu Val Glu Ser Tyr Ile
145 150 155 160
Ser His Val Glu Ser Glu Arg Pro Lys Trp Ile Lys Thr Thr Ala Arg
 165 170 175
Asp Thr Gly Leu Phe Asp His Leu Ile Asn Leu Trp Gln Phe Lys Pro
 180 185 190
Gly Pro Ile Pro Gly Thr Cys Asp Leu His Phe His Val Asp Phe Lys
 195 200 205
Phe Asn Ser Pro Leu Tyr Arg Gln Val Ala Ser Met Phe Phe Lys Glu
210 215 220
Val Ala Ser Arg Leu Val Gly Ala Phe Ser Asp Arg Cys Arg Leu Val
225 230 235 240
Tyr Gly Pro Gly Val Arg Val Asp Glu Asn Ala Tyr Glu Gln Arg Ala
 245 250 255

(2) INFORMATION FOR SEQ ID NO:2062:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 252 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
 (B) LOCATION: 1..252
 (D) OTHER INFORMATION: / Ceres Seq. ID 1571705

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2062:

Met Ser Gly Leu Arg Ala Val Ser Ser Leu Leu Ser Cys Arg Asn Ala
1 5 10 15
Ile Ser Arg Lys Leu Val Ser Arg Ser Gly Ile Ser Arg Gly Ser Phe
 20 25 30
Val Ser Asp Gln Ile Arg Arg Phe Gly Ser Leu Ser Gly Val Glu Arg
35 40 45

Cys	Ser	Ser	Asn	Trp	Leu	Met	Ser	Asn	Asp	Asp	Ala	Arg	Val	Ser	Phe		
50						55					60						
Arg	Arg	Leu	Pro	Gly	Ser	Val	Ser	Leu	Leu	Gln	Arg	Arg	His	Phe	Leu		
65						70				75					80		
Gly	Cys	Gly	Asp	Gly	Glu	Glu	Gly	Gly	Gly	Glu	Leu	Ser	Lys	Ile	Tyr		
				85						90				95			
Glu	Glu	Arg	Arg	Val	Leu	Gly	Tyr	Thr	Pro	Glu	Gln	Met	Phe	Asn	Val		
				100					105					110			
Val	Ala	Ala	Val	Asp	Leu	Tyr	His	Gly	Phe	Val	Pro	Trp	Cys	Gln	Arg		
				115					120					125			
Ser	Glu	Val	Leu	Lys	Glu	Tyr	Pro	Asp	Gly	Ser	Phe	Asp	Ala	Glu	Leu		
								135					140				
Glu	Ile	Gly	Phe	Lys	Phe	Leu	Val	Glu	Ser	Tyr	Ile	Ser	His	Val	Glu		
								150					155		160		
Ser	Glu	Arg	Pro	Lys	Trp	Ile	Lys	Thr	Thr	Ala	Arg	Asp	Thr	Gly	Leu		
									170					175			
Phe	Asp	His	Leu	Ile	Asn	Leu	Trp	Gln	Phe	Lys	Pro	Gly	Pro	Ile	Pro		
									185					190			
Gly	Thr	Cys	Asp	Leu	His	Phe	His	Val	Asp	Phe	Lys	Phe	Asn	Ser	Pro		
								200					205				
Leu	Tyr	Arg	Gln	Val	Ala	Ser	Met	Phe	Phe	Lys	Glu	Val	Ala	Ser	Arg		
								215					220				
Leu	Val	Gly	Ala	Phe	Ser	Asp	Arg	Cys	Arg	Leu	Val	Tyr	Gly	Pro	Gly		
								230					235		240		
Val	Arg	Val	Asp	Glu	Asn	Ala	Tyr	Glu	Gln	Arg	Ala						
								245			250						

(2) INFORMATION FOR SEQ ID NO:2063:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 198 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..198

(D) OTHER INFORMATION: / Ceres Seq. ID 1571706

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2063:

Met	Ser	Asn	Asp	Asp	Ala	Arg	Val	Ser	Phe	Arg	Arg	Leu	Pro	Gly	Ser		
1					5				10				15				
Val	Ser	Leu	Leu	Gln	Arg	Arg	His	Phe	Leu	Gly	Cys	Gly	Asp	Gly	Glu		
				20				25					30				
Glu	Gly	Gly	Gly	Glu	Leu	Ser	Lys	Ile	Tyr	Glu	Glu	Arg	Arg	Val	Leu		
				35				40					45				
Gly	Tyr	Thr	Pro	Glu	Gln	Met	Phe	Asn	Val	Val	Ala	Ala	Val	Asp	Leu		
				50				55					60				
Tyr	His	Gly	Phe	Val	Pro	Trp	Cys	Gln	Arg	Ser	Glu	Val	Leu	Lys	Glu		
				65				70					75		80		
Tyr	Pro	Asp	Gly	Ser	Phe	Asp	Ala	Glu	Leu	Glu	Ile	Gly	Phe	Lys	Phe		
				85					90					95			
Leu	Val	Glu	Ser	Tyr	Ile	Ser	His	Val	Glu	Ser	Glu	Arg	Pro	Lys	Trp		
				100				105					110				
Ile	Lys	Thr	Thr	Ala	Arg	Asp	Thr	Gly	Leu	Phe	Asp	His	Leu	Ile	Asn		
				115				120					125				
Leu	Trp	Gln	Phe	Lys	Pro	Gly	Pro	Ile	Pro	Gly	Thr	Cys	Asp	Leu	His		
				130				135					140				
Phe	His	Val	Asp	Phe	Lys	Phe	Asn	Ser	Pro	Leu	Tyr	Arg	Gln	Val	Ala		
				145					155					160			
Ser	Met	Phe	Phe	Lys	Glu	Val	Ala	Ser	Arg	Leu	Val	Gly	Ala	Phe	Ser		
				165					170					175			
Asp	Arg	Cys	Arg	Leu	Val	Tyr	Gly	Pro	Gly	Val	Arg	Val	Asp	Glu	Asn		

180
Ala Tyr Glu Gln Arg Ala
195

185

190

(2) INFORMATION FOR SEQ ID NO:2064:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1592 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1592

(D) OTHER INFORMATION: / Ceres Seq. ID 1571707

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2064:

```
gatttcgcat ttactatcct gggtatgtct caattcttct tcatcttctt ccttcagttc
gtgtctctgt tctgattgat tactctcaca aaactcatct ttctaatgtc taaagggtcta
atcttttagt atactcaaaa atctgtttct aagttctgac aagtttctga aacgaaattc
aagttttttt atacatatgt tcatcttctca gaacagggtt taattaaaca agagatgtca
attttggcga tggttttcgt aacataaaca tgagatttga ttgttctgtg cagatctcat
agtttaactg gtttgagtct agaaatttgc agtgatgcag ctgcacgcc attgttacc
actgagaaga tagataccat ggctcaagat ttcaacctga actcaagaac ttcttcttca
agaaaaagaa gattgcgtcg ctctagaagt gtcctctctg gtgattgtat gtacaatgat
gatgtcaaaa tgcagcaaac acctctcat ccagagtaaaa tcccaatgtt cagtgtcta
aaccgcgaat tcaaggcagat gatcatgttc ttggctttat atcttaccat tggatctctc
tgtttctacc tctgtgagaga ccagatctcc gggtcataaaa ccagtgggtg ggtagatgct
ctctattctt gtatagtaac gatgacaaat gttggatacg gtgacctgtg ccttaagtgt
tcgcctcaca ggctacttgc ttgtgccttc gtcttctcgg gaatggctct cgttggctac
ctcttaagtc gaggcgccga tttatctagt gagaaaacag aggcctttct cgttggggct
ttcattttgc gtcaaaagctt tgggtccaca gacattctca aggagttgca tctaacaag
ttgagatata aatgctatgc tacatgcctt gtctctgtat tctcttctat tgttggcagc
taatttcctg taatgggtga gaaaatgcgc gttatctcag ctcttctact gctctgctcc
acgggttaca cattgggtta tggagataag agttttaact cggaaagccg acgcctttt
gctgtgtttt ggcattgtac gaggaccata tggtttTggc tcagtttttc ctctatgtaA
gctgagctaa atacagaaaa caaacagagg cggttgggtga aatgggtttt aacgcgaaga
atcacaacaa atgatctcga agcagctgat ctcatggaag atggmgtgtg tggagctgca
gagttttat tgtataaact gaaagaaatg ggtaagattg atgagaaga taattctggg
ataatggaat agttcgaaga acttgattac gatgaatcag gaactctcac gactctcagc
atcgtttttg ctacagaccac gtctcagatt caaaggtaag cctcattatc atcatcatca
tcatcttgcc aagacgaatc agaattcttg ttagttata ccttcacaca acaaaaagcc
aaagagatgt aacagttttt tggaaatttt gttgtttttt cctgtttgtg ttgtgaagt
aatgccacag tctaactctt tgcattgttc tc
```

(2) INFORMATION FOR SEQ ID NO:2065:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 253 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..253

(D) OTHER INFORMATION: / Ceres Seq. ID 1571708

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2065:

```
Met Ala Gln Asp Phe Asn Leu Asn Ser Arg Thr Ser Ser Ser Arg Lys
1 5 10 15
Arg Arg Leu Arg Arg Ser Arg Ser Ala Pro Arg Gly Asp Cys Met Tyr
20 25 30
Asn Asp Asp Val Lys Ile Asn Glu Pro Pro Pro His Pro Ser Lys Ile
35 40 45
Pro Met Phe Ser Asp Leu Asn Pro Asn Leu Arg Arg Val Ile Met Phe
```

50	55	60
Leu Ala Leu Tyr Leu Thr Ile Gly Thr Leu Cys Phe Tyr Leu Val Arg		
65	70	75
Asp Gln Ile Ser Gly His Lys Thr Ser Gly Val Val Asp Ala Leu Tyr		80
	85	90
Phe Cys Ile Val Thr Met Thr Thr Val Gly Tyr Gly Asp Leu Val Pro		95
	100	105
Asn Ser Ser Ala Ser Arg Leu Leu Ala Cys Ala Phe Val Phe Ser Gly		110
	115	120
Met Val Leu Val Gly His Leu Leu Ser Arg Ala Ala Asp Tyr Leu Val		125
	130	135
Glu Lys Gln Glu Ala Leu Leu Val Arg Ala Phe His Leu Arg Gln Ser		140
	145	150
Phe Gly Pro Thr Asp Ile Leu Lys Glu Leu His Thr Asn Lys Leu Arg		155
	160	165
Tyr Lys Cys Tyr Ala Thr Cys Leu Val Leu Val Val Leu Phe Ile Val		170
	175	180
Gly Thr Ile Phe Leu Val Met Val Glu Lys Met Pro Val Ile Ser Ala		185
	190	195
Phe Tyr Cys Val Cys Ser Thr Val Thr Thr Leu Gly Tyr Gly Asp Lys		200
	205	210
Ser Phe Asn Ser Glu Ala Gly Arg Leu Phe Ala Val Phe Trp Ile Leu		215
	220	225
Thr Ser Thr Ile Cys Phe Trp Leu Ser Phe Ser Ser Met		230
	235	240
	245	250

(2) INFORMATION FOR SEQ ID NO:2066:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 223 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..223

(D) OTHER INFORMATION: / Ceres Seq. ID 1571709

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2066:

Met Tyr Asn Asp Asp Val Lys Ile Asp Glu Pro Pro Pro His Pro Ser	
1	5
Lys Ile Pro Met Phe Ser Asp Leu Asn Pro Asn Leu Arg Arg Val Ile	10
	15
Met Phe Leu Ala Leu Tyr Leu Thr Ile Gly Thr Leu Cys Phe Tyr Leu	20
	25
Val Arg Asp Gln Ile Ser Gly His Lys Thr Ser Gly Val Val Asp Ala	30
	35
Leu Tyr Phe Cys Ile Val Thr Met Thr Thr Val Gly Tyr Gly Asp Leu	40
	45
Val Pro Asn Ser Ser Ala Ser Arg Leu Leu Ala Cys Ala Phe Val Phe	50
	55
Ser Gly Met Val Leu Val Gly His Leu Leu Ser Arg Ala Ala Asp Tyr	60
	65
Leu Val Glu Lys Gln Glu Ala Leu Leu Val Arg Ala Phe His Leu Arg	70
	75
Gln Ser Phe Gly Pro Thr Asp Ile Leu Lys Glu Leu His Thr Asn Lys	80
	85
Leu Arg Tyr Lys Cys Tyr Ala Thr Cys Leu Val Val Leu Phe	90
	95
Ile Val Gly Thr Ile Phe Leu Val Met Val Glu Lys Met Pro Val Ile	100
	105
Ser Ala Phe Tyr Cys Val Cys Ser Thr Val Thr Thr Leu Gly Tyr Gly	110
	115
	120
	125
	130
	135
	140
	145
	150
	155
	160
	165
	170
	175
	180
	185
	190

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Asp Lys Ser Phe Asn Ser Glu Ala Gly Arg Leu Phe Ala Val Phe Trp
195 200 205
Ile Leu Thr Ser Thr Ile Cys Phe Trp Leu Ser Phe Ser Ser Met
210 215 220

(2) INFORMATION FOR SEQ ID NO:2067:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 204 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..204
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571710

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2067:

Met	Phe	Ser	Asp	Leu	Asn	Pro	Asn	Leu	Arg	Val	Ile	Met	Phe	Leu
1			5					10				15		
Ala	Leu	Tyr	Leu	Thr	Ile	Gly	Thr	Leu	Cys	Phe	Tyr	Leu	Val	Arg
	20						25					30		
Gln	Ile	Ser	Gly	His	Lys	Thr	Ser	Gly	Val	Val	Asp	Ala	Leu	Tyr
	35					40					45			
Cys	Ile	Val	Thr	Met	Thr	Thr	Val	Gly	Tyr	Gly	Asp	Leu	Val	Pro
	50				55					60				
Ser	Ser	Ala	Ser	Arg	Leu	Ala	Cys	Ala	Phe	Val	Phe	Ser	Gly	Met
	65			70				75				80		
Val	Leu	Val	Gly	His	Leu	Leu	Ser	Arg	Ala	Ala	Asp	Tyr	Leu	Val
			85					90				95		
Lys	Gln	Glu	Ala	Leu	Leu	Val	Arg	Ala	Phe	His	Leu	Arg	Gln	Ser
	100						105					110		
Gly	Pro	Thr	Asp	Ile	Leu	Lys	Glu	Leu	His	Thr	Asn	Lys	Leu	Arg
	115				120						125			
Lys	Cys	Tyr	Ala	Thr	Cys	Leu	Val	Leu	Val	Val	Leu	Phe	Ile	Val
	130				135						140			
Thr	Ile	Phe	Leu	Val	Met	Val	Glu	Lys	Met	Pro	Val	Ile	Ser	Ala
	145				150				155				160	
Tyr	Cys	Val	Cys	Ser	Thr	Val	Thr	Thr	Leu	Gly	Tyr	Gly	Asp	Lys
			165					170				175		
Phe	Asn	Ser	Glu	Ala	Gly	Arg	Leu	Phe	Ala	Val	Phe	Trp	Ile	Leu
			180				185					190		
Ser	Thr	Ile	Cys	Phe	Trp	Leu	Ser	Phe	Ser	Ser	Met			
	195					200								

(2) INFORMATION FOR SEQ ID NO:2068:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1324 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1324
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571734

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2068:

ctatcgaaac	tctctctgac	ttgtttgtgt	tctctcaaat	cctctgataa	gaatcaatgg	60
cgaaggaatt	agcagagaaa	gctaaagaag	ctYttctaga	tgatgacttc	gatgttgctg	120
ttgacttata	ctccaaagcc	attgacttgg	atcccaattg	gcgccctctc	ttcgccgcatc	180
gtgctcaggc	caacatcaaa	atcgataact	tcactgaagc	tgttgtagat	gcgaacaaag	240
ccattgagtt	ggagccaaag	ggtgcaaaag	cctatctcag	aaagggcact	gcttgtagta	300
agctagaaga	atatagtagt	gctaaagcag	ccttggaata	gggagctctt	gttgcaacga	360
atgaacacaa	gttttaagaag	atgatatagat	aatgcgatct	tcgtattgca	gaagaagaga	420

aagatttgggt	tcagccgatg	ccaccgagtt	tgccttcaag	ctctacaaca	ccactagcaa	480
cggaagctga	tgtctctcct	gttccaatto	ctgcagcacc	tgccaaaccg	atgttcaggc	540
acgagttcta	ccagaaacca	gaagaagcgg	tggtgacaat	tttcgccaaa	aaagtaccta	600
agggaacgt	aactgtcgag	tttggtgagc	agattctgag	tgttgtcatt	gatgttgctg	660
gagaggaagc	ttatcatctc	cagccgagat	tgttcgggaa	gataatacca	gagaagtgcg	720
gatttgaagt	attgtcgacc	aaagttgaga	tccgtcttgc	gaaagcagag	ataatcacct	780
gggcctccct	tgaatatggt	aaagggcaca	gtgttttgcc	caaaccacca	gtctcatcag	840
cgctgtcgca	gagaccagtg	taccatcttt	ctaagccagc	aaaagactgg	gacaagttgg	900
aagctggaat	gaagaacacg	gagaagggat	agaagcttga	tggagatgca	gctatgaaca	960
aatttttccg	cgacatatac	tcgagtgca	atgaagacat	gagcggggca	atgaacaaat	1020
catttgcaga	gtcgaatggg	acggtaactg	cgacaaactg	gaaagaagtt	gggactaaga	1080
aagtggagag	cactccacca	gatggcatgg	agctcaagaa	gtgggagtat	tgatctctct	1140
aaaaaccctt	tttctggttt	ttgttataaa	aaagtctgac	aaatcttttg	aacttttaag	1200
gtgttttttt	ttttggtttc	tgctcgaaat	tgctctctct	cattcttgcg	ttgtgtgtct	1260
aaagaaacgt	ctgatacttt	gattttgtat	tagaaaaacta	aaactcgcaa	gtctgtttgt	1320

(2) INFORMATION FOR SEQ ID NO:2069:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 358 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..358

(D) OTHER INFORMATION: / Ceres Seq. ID 1571735

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2069:

Met	Ala	Lys	Glu	Leu	Ala	Glu	Lys	Ala	Lys	Glu	Ala	Xaa	Leu	Asp	Asp
1			5						10				15		
Asp	Phe	Asp	Val	Ala	Val	Asp	Leu	Tyr	Ser	Lys	Ala	Ile	Asp	Leu	Asp
			20					25				30			
Pro	Asn	Cys	Ala	Ala	Phe	Phe	Ala	Asp	Arg	Ala	Gln	Ala	Asn	Ile	Lys
			35				40					45			
Ile	Asp	Asn	Phe	Thr	Glu	Ala	Val	Val	Asp	Ala	Asn	Lys	Ala	Ile	Glu
			50			55					60				
Leu	Glu	Pro	Thr	Leu	Ala	Lys	Ala	Tyr	Leu	Arg	Lys	Gly	Thr	Ala	Cys
			65			70			75			80			
Met	Lys	Leu	Glu	Glu	Tyr	Ser	Thr	Ala	Lys	Ala	Ala	Leu	Glu	Lys	Gly
			85					90				95			
Ala	Ser	Val	Ala	Pro	Asn	Glu	Pro	Lys	Phe	Lys	Lys	Met	Ile	Asp	Glu
			100				105					110			
Cys	Asp	Leu	Arg	Ile	Ala	Glu	Glu	Lys	Asp	Leu	Val	Gln	Pro	Met	
			115				120				125				
Pro	Pro	Ser	Leu	Pro	Ser	Ser	Ser	Thr	Thr	Pro	Leu	Ala	Thr	Glu	Ala
			130				135				140				
Asp	Ala	Pro	Pro	Val	Pro	Ile	Pro	Ala	Ala	Pro	Ala	Lys	Pro	Met	Phe
			145			150				155				160	
Arg	His	Glu	Phe	Tyr	Gln	Lys	Pro	Glu	Glu	Ala	Val	Val	Thr	Ile	Phe
			165					170					175		
Ala	Lys	Lys	Val	Pro	Lys	Glu	Asn	Val	Thr	Val	Glu	Phe	Gly	Glu	Gln
			180				185					190			
Ile	Leu	Ser	Val	Val	Ile	Asp	Val	Ala	Gly	Glu	Glu	Ala	Tyr	His	Leu
			195				200					205			
Gln	Pro	Arg	Leu	Phe	Gly	Lys	Ile	Ile	Pro	Glu	Lys	Cys	Arg	Phe	Glu
			210			215				220					
Val	Leu	Ser	Thr	Lys	Val	Glu	Ile	Arg	Leu	Ala	Lys	Ala	Glu	Ile	Ile
			225			230				235				240	
Thr	Trp	Ala	Ser	Leu	Glu	Tyr	Gly	Lys	Gly	Gln	Ser	Val	Leu	Pro	Lys
			245				250					255			
Pro	Asn	Val	Ser	Ser	Ala	Leu	Ser	Gln	Arg	Pro	Val	Tyr	Pro	Ser	Ser

[illegible]

(2) INFORMATION FOR SEQ ID NO:2071:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 250 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..250
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571737

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2071:

Met Ile Asp Glu Cys Asp Leu Arg Ile Ala Glu Glu Glu Lys Asp Leu
1 5 10 15
Val Gln Pro Met Pro Pro Ser Leu Pro Ser Ser Ser Thr Thr Pro Leu
20 25 30
Ala Thr Glu Ala Asp Ala Pro Pro Val Pro Ile Pro Ala Ala Pro Ala
35 40 45
Lys Pro Met Phe Arg His Glu Phe Tyr Gln Lys Pro Glu Glu Ala Val
50 55 60
Val Thr Ile Phe Ala Lys Lys Val Pro Lys Glu Asn Val Thr Val Glu
65 70 75 80
Phe Gly Glu Gln Ile Leu Ser Val Val Ile Asp Val Ala Gly Glu Glu
85 90 95
Ala Tyr His Leu Gln Pro Arg Leu Phe Gly Lys Ile Ile Pro Glu Lys
100 105 110
Cys Arg Phe Glu Val Leu Ser Thr Lys Val Glu Ile Arg Leu Ala Lys
115 120 125
Ala Glu Ile Ile Thr Trp Ala Ser Leu Glu Tyr Gly Lys Gly Gln Ser
130 135 140
Val Leu Pro Lys Pro Asn Val Ser Ser Ala Leu Ser Gln Arg Pro Val
145 150 155 160
Tyr Pro Ser Ser Lys Pro Ala Lys Asp Trp Asp Lys Leu Glu Ala Glu
165 170 175
Val Lys Lys Gln Glu Lys Asp Glu Lys Leu Asp Gly Asp Ala Ala Met
180 185 190
Asn Lys Phe Phe Ser Asp Ile Tyr Ser Ser Ala Asp Glu Asp Met Arg
195 200 205
Arg Ala Met Asn Lys Ser Phe Ala Glu Ser Asn Gly Thr Val Leu Ser
210 215 220
Thr Asn Trp Lys Glu Val Gly Thr Lys Lys Val Glu Ser Thr Pro Pro
225 230 235 240
Asp Gly Met Glu Leu Lys Lys Trp Glu Tyr
245 250

(2) INFORMATION FOR SEQ ID NO:2072:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 767 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..767
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571750

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2072:

atcatcacaa ctactatcac accaaactca aaaaacacaa accacaagag gatcatattca 60
ttttttattg ttctgtttta atcatcatca tcagaagaaa aatggtttgcg atatcggaga 120
tcaagtcgac ggtggatgac acggcggcga attgtttgat gctttatctc agagtgggac 180
aagaaaaacgt tgacgggtggc gatcaaaaaa gcgttttcac atgtaaaacg tgtttgaagc 240
agtttcattc gttccaagcc ttaggaggtc accgtgcgag tcacaagaag cctaacaacg 300

acgcgtttgtc gtctagattg atgaagaagg tgaaaaacgct gtcgcacatc tgtcccatat 360
gtggagtggg gtttccgatg ggacaagcgt tgggaggaga catgaggaga cacaggaacg 420
agagtggNgg ctgctgtgtg cgcgtttggt acacgcgctt tgttgccgga gccacgggtg 480
actacgttga agaaatctav cagtgggaag agagtggctt gtttgatct gagtctaggg 540
atgtgtgaca atttgaatct caagttggag cttggaagaa cagtttattg attttattta 600
ttttccttaa attttcga tatatattgt tctctcatc ttggaatttt tcttaatttt 660
ctagattata catacatccg cagatttagg aaactttcat agagtgtaat cttttctttc 720
tgtaaaaata tattttactt gtacgattgg agatttgta tgagatc

(2) INFORMATION FOR SEQ ID NO:2073:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 217 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..217

(D) OTHER INFORMATION: / Ceres Seq. ID 1571751

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2073:

His His Asn Tyr Tyr His Thr Lys Leu Lys Lys His Lys Pro Gln Glu
1 5 10 15
Asp His Phe Ile Phe Tyr Cys Phe Val Leu Ile Ile Ile Arg Arg
20 25 30
Lys Met Val Ala Ile Ser Glu Ile Lys Ser Thr Val Asp Val Thr Ala
35 40 45
Ala Asn Cys Leu Met Leu Leu Ser Arg Val Gly Gln Glu Asn Val Asp
50 55 60
Gly Gly Asp Gln Lys Arg Val Phe Thr Cys Lys Thr Cys Leu Lys Gln
65 70 75 80
Phe His Ser Phe Gln Ala Leu Gly Gly His Arg Ala Ser His Lys Lys
85 90 95
Pro Asn Asn Asp Ala Leu Ser Ser Arg Leu Met Lys Lys Val Lys Thr
100 105 110
Ser Ser His Pro Cys Pro Ile Cys Gly Val Glu Phe Pro Met Gly Gln
115 120 125
Ala Leu Gly Gly His Met Arg Arg His Arg Asn Glu Ser Xaa Gly Cys
130 135 140
Trp Trp Arg Val Gly Tyr Thr Arg Phe Val Ala Gly Ala His Gly Asp
145 150 155 160
Tyr Val Glu Glu Ile Xaa Gln Trp Glu Glu Ser Gly Leu Phe Gly Ser
165 170 175
Glu Ser Arg Asp Gly Gly Gln Phe Glu Ser Gln Val Gly Ala Trp Lys
180 185 190
Asn Ser Leu Ile Leu Phe Ile Phe Leu Lys Phe Ser Glu Tyr Ile
195 200 205
Cys Phe Ser His Ser Leu Asn Phe Ser
210 215

(2) INFORMATION FOR SEQ ID NO:2074:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 184 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..184

(D) OTHER INFORMATION: / Ceres Seq. ID 1571752

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2074:

Met Val Ala Ile Ser Glu Ile Lys Ser Thr Val Asp Val Thr Ala Ala

1	5	10	15
Asn Cys Leu Met	Leu Leu Ser Arg Val	Gly Gln Glu Asn Val	Asp Gly
20	25	30	
Gly Asp Gln Lys	Arg Val Phe Thr Cys	Lys Thr Cys Leu Lys	Gln Phe
35	40	45	
His Ser Phe Gln	Ala Leu Gly Gly	His Arg Ala Ser	His Lys Lys Pro
50	55	60	
Asn Asn Asp Ala	Leu Ser Ser Arg	Leu Met Lys Lys	Val Lys Thr Ser
65	70	75	80
Ser His Pro Cys	Pro Ile Cys Gly	Val Glu Phe Pro	Met Gly Gln Ala
85	90	95	
Leu Gly Gly His	Met Arg Arg His	Arg Asn Glu Ser	Xaa Gly Cys Trp
100	105	110	
Trp Arg Val Gly	Tyr Thr Arg Phe	Val Ala Gly Ala	His Gly Asp Tyr
115	120	125	
Val Glu Glu Ile	Xaa Gln Trp Glu	Glu Ser Gly Leu	Phe Gly Ser Glu
130	135	140	
Ser Arg Asp Gly	Gly Gln Phe Glu	Ser Gln Val Gly	Ala Trp Lys Asn
145	150	155	160
Ser Leu Leu Ile	Leu Phe Ile Phe	Leu Lys Phe Ser	Glu Tyr Ile Cys
165	170	175	
Phe Ser His Ser	Leu Asn Phe Ser		
180			

(2) INFORMATION FOR SEQ ID NO:2075:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 165 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..165

(D) OTHER INFORMATION: / Ceres Seq. ID 1571753

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2075:

Met Leu Leu Ser	Arg Val Gly Gln Glu	Asn Val Asp Gly	Gly Asp Gln
1	5	10	15
Lys Arg Val Phe	Thr Cys Lys Thr Cys	Leu Lys Gln Phe	His Ser Phe
20	25	30	
Gln Ala Leu Gly	Gly His Arg Ala Ser	His Lys Lys Pro	Asn Asn Asp
35	40	45	
Ala Leu Ser Ser	Arg Leu Met Lys Lys	Val Lys Thr Ser	Ser His Pro
50	55	60	
Cys Pro Ile Cys	Gly Val Glu Phe Pro	Met Gly Gln Ala	Leu Gly Gly
65	70	75	80
His Met Arg Arg	His Arg Asn Glu Ser	Xaa Gly Cys Trp	Trp Arg Val
85	90	95	
Gly Tyr Thr Arg	Phe Val Ala Gly Ala	His Gly Asp Tyr	Val Glu Glu
100	105	110	
Ile Xaa Gln Trp	Glu Glu Ser Gly Leu	Phe Gly Ser Glu	Ser Arg Asp
115	120	125	
Gly Gly Gln Phe	Glu Ser Gln Val Gly	Ala Trp Lys Asn	Ser Leu Leu
130	135	140	
Ile Leu Phe Ile	Phe Leu Lys Phe	Ser Glu Tyr Ile	Cys Phe Ser His
145	150	155	160
Ser Leu Asn Phe	Ser		
165			

(2) INFORMATION FOR SEQ ID NO:2076:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 949 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
 (A) NAME/KEY: -
 (B) LOCATION: 1..949
 (D) OTHER INFORMATION: / Ceres Seq. ID 1571770
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2076:

ctccacgatt	ctgacaaaaa	aaaggagaag	gaataagaga	aaagtgaagt	tgtgtttgt	60
atcgatcaga	aaatggcgac	gtcgatgata	cagaggatgt	tcaagcaagg	gacgaaaatc	120
gtctgcgtcg	gcgctaacta	cgccgctcac	gccaaaagaac	taggcacacg	cgtccccaag	180
gaaccagtta	tattcttgaa	gccaaacatca	tcatacttag	aaaatggagg	aacaattgag	240
atcccacatc	ctttggattc	acttcaccaa	gaagtagaac	tcgctttagt	gattggacag	300
aaagctagag	atgtacctga	atcaatagcc	atggattaca	ttggaggaga	tgccggtgtc	360
cttgatatga	ctgctaggga	actccaaagt	tcgtctaagg	catctgggtc	cccatggacg	420
gttgcgaaag	gacaagatac	cttcactcct	atcagctctg	ttctgcacaa	ggcgatgggt	480
cgtgatcccg	ataatctaga	actttggctc	aaggttgatg	gtgaacaacg	acagaagggt	540
ttgacaaaag	atatgatatt	caagggtccc	tacctcatta	gctacataag	ttctataatg	600
accctttacg	aaggagatgt	catcttgaca	ggcacaccag	aaggtgttgg	acctgtaaag	660
ataggtcaga	agataacggc	cggaatcacc	ggtctatctg	aagttcaatt	cgatgtggag	720
aggcggtgta	agcccttgag	ctaataagtg	gttttattta	tctttcatac	aaaaatgtca	780
attttataaa	agcatctcta	aaattttcat	cacttactgt	gtttccctaag	gaaggaggaa	840
ataaaacctg	ttactcaatt	tatttgtaat	ctctataaca	atggctctaa	gaccggttta	900
aattgtttat	atgggagagt	atttgtaaag	ttgtgatatt	tactgttgc		

(2) INFORMATION FOR SEQ ID NO:2077:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 223 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..223
 (D) OTHER INFORMATION: / Ceres Seq. ID 1571771
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2077:

Met	Ala	Thr	Ser	Met	Ile	Gln	Arg	Met	Phe	Lys	Gln	Gly	Thr	Lys	Ile	
1				5					10					15		
Val	Cys	Val	Gly	Arg	Asn	Tyr	Ala	Ala	His	Ala	Lys	Glu	Leu	Gly	Asn	
			20				25				30					
Ala	Val	Pro	Lys	Glu	Pro	Val	Ile	Phe	Leu	Lys	Pro	Thr	Ser	Ser	Tyr	
			35				40				45					
Leu	Glu	Asn	Gly	Gly	Thr	Ile	Glu	Ile	Pro	His	Pro	Leu	Asp	Ser	Leu	
			50				55				60					
His	His	Glu	Val	Glu	Leu	Ala	Leu	Val	Ile	Gly	Gln	Lys	Ala	Arg	Asp	
			65				70				75			80		
Val	Pro	Glu	Ser	Ile	Ala	Met	Asp	Tyr	Ile	Gly	Gly	Tyr	Ala	Val	Ala	
			85				90				95					
Leu	Asp	Met	Thr	Ala	Arg	Glu	Leu	Gln	Ala	Ser	Ala	Lys	Ala	Ser	Gly	
			100				105				110					
Leu	Pro	Trp	Thr	Val	Ala	Lys	Gly	Gln	Asp	Thr	Phe	Thr	Pro	Ile	Ser	
			115				120				125					
Ser	Val	Leu	Pro	Lys	Ala	Met	Val	Arg	Asp	Pro	Asp	Asn	Leu	Glu	Leu	
			130				135				140					
Trp	Leu	Lys	Val	Asp	Gly	Glu	Thr	Arg	Gln	Lys	Gly	Leu	Thr	Lys	Asp	
			145				150				155			160		
Met	Ile	Phe	Lys	Val	Pro	Tyr	Leu	Ile	Ser	Tyr	Ile	Ser	Ser	Ile	Met	
			165				170				175					
Thr	Leu	Tyr	Glu	Gly	Asp	Val	Ile	Leu	Thr	Gly	Thr	Pro	Glu	Gly	Val	
			180				185				190					
Gly	Pro	Val	Lys	Ile	Gly	Gln	Lys	Ile	Thr	Ala	Gly	Ile	Thr	Gly	Leu	

195 200 205
Ser Glu Val Gln Phe Asp Val Glu Arg Arg Val Lys Pro Leu Ser
210 215 220

(2) INFORMATION FOR SEQ ID NO:2078:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 219 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..219

(D) OTHER INFORMATION: / Ceres Seq. ID 1571772

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2078:

Met Ile Gln Arg Met Phe Lys Gln Gly Thr Lys Ile Val Cys Val Gly
1 5 10 15
Arg Asn Tyr Ala Ala His Ala Lys Glu Leu Gly Asn Ala Val Pro Lys
20 25 30
Glu Pro Val Ile Phe Leu Lys Pro Thr Ser Ser Tyr Leu Glu Asn Gly
35 40 45
Gly Thr Ile Glu Ile Pro His Pro Leu Asp Ser Leu His His Glu Val
50 55 60
Glu Leu Ala Leu Val Ile Gly Gln Lys Ala Arg Asp Val Pro Glu Ser
65 70 75 80
Ile Ala Met Asp Tyr Ile Gly Gly Tyr Ala Val Ala Leu Asp Met Thr
85 90 95
Ala Arg Glu Leu Gln Ala Ser Ala Lys Ala Ser Gly Leu Pro Trp Thr
100 105 110
Val Ala Lys Gly Gln Asp Thr Phe Thr Pro Ile Ser Ser Val Leu Pro
115 120 125
Lys Ala Met Val Arg Asp Pro Asp Asn Leu Glu Leu Trp Leu Lys Val
130 135 140
Asp Gly Glu Thr Arg Gln Lys Gly Leu Thr Lys Asp Met Ile Phe Lys
145 150 155 160
Val Pro Tyr Leu Ile Ser Tyr Ile Ser Ser Ile Met Thr Leu Tyr Glu
165 170 175
Gly Asp Val Ile Leu Thr Gly Thr Pro Glu Gly Val Gly Pro Val Lys
180 185 190
Ile Gly Gln Lys Ile Thr Ala Gly Ile Thr Gly Leu Ser Glu Val Gln
195 200 205
Phe Asp Val Glu Arg Arg Val Lys Pro Leu Ser
210 215

(2) INFORMATION FOR SEQ ID NO:2079:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 215 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..215

(D) OTHER INFORMATION: / Ceres Seq. ID 1571773

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2079:

Met Phe Lys Gln Gly Thr Lys Ile Val Cys Val Gly Arg Asn Tyr Ala
1 5 10 15
Ala His Ala Lys Glu Leu Gly Asn Ala Val Pro Lys Glu Pro Val Ile
20 25 30
Phe Leu Lys Pro Thr Ser Ser Tyr Leu Glu Asn Gly Gly Thr Ile Glu
35 40 45

```

Ile Pro His Pro Leu Asp Ser Leu His His Glu Val Glu Leu Ala Leu
  50          55          60
Val Ile Gly Gln Lys Ala Arg Asp Val Pro Glu Ser Ile Ala Met Asp
  65          70          75          80
Tyr Ile Gly Gly Tyr Ala Val Ala Leu Asp Met Thr Ala Arg Glu Leu
          85          90          95
Gln Ala Ser Ala Lys Ala Ser Gly Leu Pro Trp Thr Val Ala Lys Gly
  100          105          110
Gln Asp Thr Phe Thr Pro Ile Ser Ser Val Leu Pro Lys Ala Met Val
  115          120          125
Arg Asp Pro Asp Asn Leu Glu Leu Trp Leu Lys Val Asp Gly Glu Thr
  130          135          140
Arg Gln Lys Gly Leu Thr Lys Asp Met Ile Phe Lys Val Pro Tyr Leu
  145          150          155          160
Ile Ser Tyr Ile Ser Ser Ile Met Thr Leu Tyr Glu Gly Asp Val Ile
          165          170          175
Leu Thr Gly Thr Pro Glu Gly Val Gly Pro Val Lys Ile Gly Gln Lys
  180          185          190
Ile Thr Ala Gly Ile Thr Gly Leu Ser Glu Val Gln Phe Asp Val Glu
  195          200          205
Arg Arg Val Lys Pro Leu Ser
  210          215

```

(2) INFORMATION FOR SEQ ID NO:2080:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1323 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1323
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571788

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2080:

```

gtttctaatt gctttcgacg acaatcgatc gtagagaagt ctacctcgta gacatctctc      60
tcacaaatcc aattcaatta coattgtttg ttattatctg atgtcggaata tgcaattctc      120
tcgtgtgttt aatccctttg ttatcttctt ctgtctcgcc gtggttgac caattatctc      180
ggctgatgtc gctatcttga gaacggacta ttaccaaata acatgtcctg atttcacaa      240
aattgtgcgt gaagcgttta caaccaaca agtccaaca ccaacaactg cggcggggac      300
ctctcgcttc tttttccatg attgtttcct tgaaggttgt gatgcatctg tcttgatgcg      360
gaccaactcg ttcaacaaag cggaacgvgA tgatgatctc aatgattccc tcccgggaga      420
tgcttttgac atcgtcaccg gcatcaagac agctctcgag ttgtcttgtc ctggtgtgat      480
atctgcgcgc gatattctag cgcaggctac acgtgacctt gtcaaatgg taggaggacc      540
ttactttgac gtaaagcttg gtcgtaaaag cggattcgaa tccaagctc ataaagtacg      600
aggaatgtc ccaatggcaa accagactgt tcttgacatc caccgggat tcaagaaaaa      660
cggttttagt ctctcgagag ttgtagcatt aagcggggct cacacacttg gattctctca      720
ctgcaaaagg ttttccgaga ggctctacgg atcccgctgt gataaagaaa tcaaccgcgc      780
attcgcagcc gctctcaaa gctcttgcaa aaaccacacc gtggatgata caatcgccgc      840
gtttaacgac gtgatgatc caggaaagtt cgacaacatg tacttcaaga acctaaagcg      900
aggcgtaggg ctttttagctg ctgaccacat ccttattaaa gacaacagca ccaagccgtt      960
tgtgtgatca tacgcaacta acgagacgac attctttgag gatitcgctc gtgcgatgga      1020
gaaacttgcc acggtcggcg tcaaggcgca taaagatgga gaagtgaagc taaggtgcga      1080
ccaacttcaa aatctcaacg tttaaagaag aaaaagaaac acaaaaccat ataaatataa      1140
tattatttct gttttatttg cggaggagtt gaggagaaga aaggttttgt ttggtatata      1200
gtttaataac tactattat aagcaagatc ttgtaacaac tcaagttggg atgttttaatt      1260
tttccatgaa aattcaaac gttgtattga aagtatatag ataaaaaac atattatata      1320
tcg

```

(2) INFORMATION FOR SEQ ID NO:2081:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 334 amino acids
- (B) TYPE: amino acid

- (C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..334
(D) OTHER INFORMATION: / Ceres Seq. ID 1571789
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2081:

Met Ser Asn Met Gln Phe Ser Arg Gly Phe Asn Pro Phe Val Ile Phe
1 5 10 15
Phe Cys Leu Ala Val Val Ala Pro Ile Ile Ser Ala Asp Val Ala Ile
20 25 30
Leu Arg Thr Asp Tyr Tyr Gln Lys Thr Cys Pro Asp Phe His Lys Ile
35 40 45
Val Arg Glu Ala Val Thr Thr Lys Gln Val Gln Gln Pro Thr Thr Ala
50 55 60
Ala Gly Thr Leu Arg Leu Phe Phe His Asp Cys Phe Leu Glu Gly Cys
65 70 75 80
Asp Ala Ser Val Leu Ile Ala Thr Asn Ser Phe Asn Lys Ala Glu Xaa
85 90 95
Asp Asp Asp Leu Asn Asp Ser Leu Pro Gly Asp Ala Phe Asp Ile Val
100 105 110
Thr Arg Ile Lys Thr Ala Leu Glu Leu Ser Cys Pro Gly Val Val Ser
115 120 125
Cys Ala Asp Ile Leu Ala Gln Ala Thr Arg Asp Leu Val Thr Met Val
130 135 140
Gly Gly Pro Tyr Phe Asp Val Lys Leu Gly Arg Lys Asp Gly Phe Glu
145 150 155 160
Ser Lys Ala His Lys Val Arg Gly Asn Val Pro Met Ala Asn Gln Thr
165 170 175
Val Pro Asp Ile His Gly Ile Phe Lys Lys Asn Gly Phe Ser Leu Arg
180 185 190
Glu Met Val Ala Leu Ser Gly Ala His Thr Ile Gly Phe Ser His Cys
195 200 205
Lys Glu Phe Ser Asp Arg Leu Tyr Gly Ser Arg Ala Asp Lys Glu Ile
210 215 220
Asn Pro Arg Phe Ala Ala Ala Leu Lys Asp Leu Cys Lys Asn His Thr
225 230 235 240
Val Asp Asp Thr Ile Ala Ala Phe Asn Asp Val Met Thr Pro Gly Lys
245 250 255
Phe Asp Asn Met Tyr Phe Lys Asn Leu Lys Arg Gly Leu Gly Leu Leu
260 265 270
Ala Ser Asp His Ile Leu Ile Lys Asp Asn Ser Thr Lys Pro Phe Val
275 280 285
Asp Leu Tyr Ala Thr Asn Glu Thr Ala Phe Phe Glu Asp Phe Ala Arg
290 295 300
Ala Met Glu Lys Leu Gly Thr Val Gly Val Lys Gly Asp Lys Asp Gly
305 310 315 320
Glu Val Arg Arg Arg Cys Asp His Phe Asn Asn Leu Asn Val
325 330

- (2) INFORMATION FOR SEQ ID NO:2082:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 331 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..331
(D) OTHER INFORMATION: / Ceres Seq. ID 1571790

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2082:

Met	Gln	Phe	Ser	Arg	Gly	Phe	Asn	Pro	Phe	Val	Ile	Phe	Phe	Cys	Leu
1			5						10					15	
Ala	Val	Val	Ala	Pro	Ile	Ile	Ser	Ala	Asp	Val	Ala	Ile	Leu	Arg	Thr
			20					25					30		
Asp	Tyr	Tyr	Gln	Lys	Thr	Cys	Pro	Asp	Phe	His	Lys	Ile	Val	Arg	Glu
			35					40				45			
Ala	Val	Thr	Thr	Lys	Gln	Val	Gln	Gln	Pro	Thr	Thr	Ala	Ala	Gly	Thr
			50			55					60				
Leu	Arg	Leu	Phe	Phe	His	Asp	Cys	Phe	Leu	Glu	Gly	Cys	Asp	Ala	Ser
65					70					75				80	
Val	Leu	Ile	Ala	Thr	Asn	Ser	Phe	Asn	Lys	Ala	Glu	Xaa	Asp	Asp	Asp
			85					90					95		
Leu	Asn	Asp	Ser	Leu	Pro	Gly	Asp	Ala	Phe	Asp	Ile	Val	Thr	Arg	Ile
			100					105					110		
Lys	Thr	Ala	Leu	Glu	Leu	Ser	Cys	Pro	Gly	Val	Val	Ser	Cys	Ala	Asp
			115					120				125			
Ile	Leu	Ala	Gln	Ala	Thr	Arg	Asp	Leu	Val	Thr	Met	Val	Gly	Gly	Pro
			130			135					140				
Tyr	Phe	Asp	Val	Lys	Leu	Gly	Arg	Lys	Asp	Gly	Phe	Glu	Ser	Lys	Ala
145					150					155					160
His	Lys	Val	Arg	Gly	Asn	Val	Pro	Met	Ala	Asn	Gln	Thr	Val	Pro	Asp
			165						170					175	
Ile	His	Gly	Ile	Phe	Lys	Lys	Asn	Gly	Phe	Ser	Leu	Arg	Glu	Met	Val
			180					185					190		
Ala	Leu	Ser	Gly	Ala	His	Thr	Ile	Gly	Phe	Ser	His	Cys	Lys	Glu	Phe
			195					200				205			
Ser	Asp	Arg	Leu	Tyr	Gly	Ser	Arg	Ala	Asp	Lys	Glu	Ile	Asn	Pro	Arg
			210			215					220				
Phe	Ala	Ala	Ala	Leu	Lys	Asp	Leu	Cys	Lys	Asn	His	Thr	Val	Asp	Asp
225					230					235				240	
Thr	Ile	Ala	Ala	Phe	Asn	Asp	Val	Met	Thr	Pro	Gly	Lys	Phe	Asp	Asn
			245						250				255		
Met	Tyr	Phe	Lys	Asn	Leu	Lys	Arg	Gly	Leu	Gly	Leu	Leu	Ala	Ser	Asp
			260					265					270		
His	Ile	Leu	Ile	Lys	Asp	Asn	Ser	Thr	Lys	Pro	Phe	Val	Asp	Leu	Tyr
			275					280				285			
Ala	Thr	Asn	Glu	Thr	Ala	Phe	Phe	Glu	Asp	Phe	Ala	Arg	Ala	Met	Glu
			290			295					300				
Lys	Leu	Gly	Thr	Val	Gly	Val	Lys	Gly	Asp	Lys	Asp	Gly	Glu	Val	Arg
305					310					315				320	
Arg	Arg	Cys	Asp	His	Phe	Asn	Asn	Leu	Asn	Val					
			325						330						

(2) INFORMATION FOR SEQ ID NO:2083:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 192 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..192

(D) OTHER INFORMATION: / Ceres Seq. ID 1571791

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2083:

Met	Val	Gly	Gly	Pro	Tyr	Phe	Asp	Val	Lys	Leu	Gly	Arg	Lys	Asp	Gly
1			5					10					15		
Phe	Glu	Ser	Lys	Ala	His	Lys	Val	Arg	Gly	Asn	Val	Pro	Met	Ala	Asn
			20					25					30		
Gln	Thr	Val	Pro	Asp	Ile	His	Gly	Ile	Phe	Lys	Lys	Asn	Gly	Phe	Ser
			35				40					45			

Leu	Arg	Glu	Met	Val	Ala	Leu	Ser	Gly	Ala	His	Thr	Ile	Gly	Phe	Ser
50						55					60				
His	Cys	Lys	Glu	Phe	Ser	Asp	Arg	Leu	Tyr	Gly	Ser	Arg	Ala	Asp	Lys
65						70				75					80
Glu	Ile	Asn	Pro	Arg	Phe	Ala	Ala	Ala	Leu	Lys	Asp	Leu	Cys	Lys	Asn
					85				90					95	
His	Thr	Val	Asp	Asp	Thr	Ile	Ala	Ala	Phe	Asn	Asp	Val	Met	Thr	Pro
					100				105					110	
Gly	Lys	Phe	Asp	Asn	Met	Tyr	Phe	Lys	Asn	Leu	Lys	Arg	Gly	Leu	Gly
					115				120					125	
Leu	Leu	Ala	Ser	Asp	His	Ile	Leu	Ile	Lys	Asp	Asn	Ser	Thr	Lys	Pro
					130				135					140	
Phe	Val	Asp	Leu	Tyr	Ala	Thr	Asn	Glu	Thr	Ala	Phe	Phe	Glu	Asp	Phe
					145					155				160	
Ala	Arg	Ala	Met	Glu	Lys	Leu	Gly	Thr	Val	Gly	Val	Lys	Gly	Asp	Lys
					165				170					175	
Asp	Gly	Glu	Val	Arg	Arg	Arg	Cys	Asp	His	Phe	Asn	Asn	Leu	Asn	Val
					180				185					190	

(2) INFORMATION FOR SEQ ID NO:2084:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1125 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1125

(D) OTHER INFORMATION: / Ceres Seq. ID 1571792

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2084:

acattgcaac	actttctaca	aaaacaagat	gaagattgca	aagttttctg	ttctactctt	60
gcttttattt	attttccccc	tgccattagc	gcagCtgaaa	tttaagtttt	acagtgaatc	120
gtgcccta	gcagagacta	tcgtagaaaa	cctggttcgc	cagcagtttg	ctcgtgaccc	180
ttcaatcacg	gcgcctttga	ctcgtatgca	ttttcacgac	tgttttctgc	agggctgcga	240
cgcttctctc	ctcatagacc	caacgacgtc	tcaactatcg	gaaaaaaacg	ccggcccaaa	300
ctttagcgtg	agagggttgc	agctgatgca	cgagatcaag	acggcaactcg	aagctcaatg	360
tcctctacg	gtctcgtgtg	cagatatagt	cacgctcgcc	acacgtgacg	ccgtgtttct	420
aggtggagga	ccaagctacg	tggtcccccac	cggaactcgc	gatggcttgg	tgtcgaatcc	480
tgaagacgcc	aatgagatcc	tcctccacc	attcatatcc	gtcgaaggca	tgtaagtgt	540
tttcggcaac	aaaaggaatga	atgtttttga	ttcgtatgct	cttttggggg	cgacacacgt	600
tgggatcgcg	tcttgttgga	attttgtgga	ccgggtcacg	aactttcaag	gaaccggagt	660
gcccgaccca	tcctatggacc	ccactttggc	tgccagggtta	aggaacacat	gtgcggttcc	720
agggcgcttc	gcggcactgg	accagtcgat	gccagtaaac	ccggtctcat	tcgacaactt	780
gttcttttgt	cagatcacag	agaggaaaag	aattttgtct	attgaccaac	tgatcgcaag	840
gcaccggcgc	acttctgggt	ttgtacttca	gtatgcgtcc	aacaacgaac	tattcaaacg	900
tcagttcgca	atcgcaatgg	tgaagatggg	agccgtttgac	gtgcttaccg	gttcagctcg	960
tgagatcagg	acgaattgta	gagcattcaa	ctaaagcttt	ataacaagtt	tctatatctg	1020
attattgatt	gtttttccct	taatttccgc	ttctgatgat	gaattgtgaa	tggtgatgtg	1080
ttgcctatat	atgtatgtac	gtatatcttt	aaaataaggt	ttggc		

(2) INFORMATION FOR SEQ ID NO:2085:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 330 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..330

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2085:

(2) INFORMATION FOR SEQ ID NO:2086:

(A) LENGTH: 321 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..321

(D) OTHER INFORMATION: / Ceres Seq. ID 1571794

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2086:

Met	Lys	Ile	Ala	Lys	Phe	Ser	Val	Leu	Leu	Leu	Leu	Leu	Phe	Ile	Phe
1				5					10					15	
Pro	Val	Ala	Leu	Ala	Gln	Leu	Lys	Phe	Lys	Phe	Tyr	Ser	Glu	Ser	Cys
			20					25					30		
Pro	Asn	Ala	Glu	Thr	Ile	Val	Glu	Asn	Leu	Val	Arg	Gln	Gln	Phe	Ala

35	40	45
Arg Asp Pro Ser Ile Thr	Ala Leu Thr Arg Met His Phe His Asp	
50	55	60
Cys Phe Val Gln Gly Cys Asp Ala Ser Leu Leu Ile Asp Pro Thr Thr		
65	70	75
Ser Gln Leu Ser Glu Lys Asn Ala Gly Pro Asn Phe Ser Val Arg Gly		
85	90	95
Phe Glu Leu Ile Asp Glu Ile Lys Thr Ala Leu Glu Ala Gln Cys Pro		
100	105	110
Ser Thr Val Ser Cys Ser Asp Ile Val Thr Leu Ala Thr Arg Asp Ala		
115	120	125
Val Phe Leu Gly Gly Gly Pro Ser Tyr Val Val Pro Thr Gly Arg Arg		
130	135	140
Asp Gly Phe Val Ser Asn Pro Glu Asp Ala Asn Glu Ile Leu Pro Pro		
145	150	155
Pro Phe Ile Ser Val Glu Gly Met Leu Ser Phe Phe Gly Asn Lys Gly		
165	170	175
Met Asn Val Phe Asp Ser Val Ala Leu Leu Gly Ala His Thr Val Gly		
180	185	190
Ile Ala Ser Cys Gly Asn Phe Val Asp Arg Val Thr Asn Phe Gln Gly		
195	200	205
Thr Gly Leu Pro Asp Pro Ser Met Asp Pro Thr Leu Ala Gly Arg Leu		
210	215	220
Arg Asn Thr Cys Ala Val Pro Gly Gly Phe Ala Ala Leu Asp Gln Ser		
225	230	235
Met Pro Val Thr Pro Val Ser Phe Asp Asn Leu Phe Phe Gly Gln Ile		
245	250	255
Arg Glu Arg Lys Gly Ile Leu Leu Ile Asp Gln Leu Ile Ala Ser Asp		
260	265	270
Pro Ala Thr Ser Gly Val Val Leu Gln Tyr Ala Ser Asn Asn Glu Leu		
275	280	285
Phe Lys Arg Gln Phe Ala Ile Ala Met Val Lys Met Gly Ala Val Asp		
290	295	300
Val Leu Thr Gly Ser Ala Gly Glu Ile Arg Thr Asn Cys Arg Ala Phe		
305	310	315
Asn		320

(2) INFORMATION FOR SEQ ID NO:2087:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 262 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..262

(D) OTHER INFORMATION: / Ceres Seq. ID 1571795

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2087:

Met His Phe His Asp Cys Phe Val Gln Gly Cys Asp Ala Ser Leu Leu	
1	15
Ile Asp Pro Thr Thr Ser Gln Leu Ser Glu Lys Asn Ala Gly Pro Asn	
20	30
Phe Ser Val Arg Gly Phe Glu Leu Ile Asp Glu Ile Lys Thr Ala Leu	
35	45
Glu Ala Gln Cys Pro Ser Thr Val Ser Cys Ser Asp Ile Val Thr Leu	
50	60
Ala Thr Arg Asp Ala Val Phe Leu Gly Gly Gly Pro Ser Tyr Val Val	
65	80
Pro Thr Gly Arg Arg Asp Gly Phe Val Ser Asn Pro Glu Asp Ala Asn	
85	95

Glu Ile Leu Pro Pro Pro Phe Ile Ser Val Glu Gly Met Leu Ser Phe
100 105 110
Phe Gly Asn Lys Gly Met Asn Val Phe Asp Ser Val Ala Leu Leu Gly
115 120 125
Ala His Thr Val Gly Ile Ala Ser Cys Gly Asn Phe Val Asp Arg Val
130 135 140
Thr Asn Phe Gln Gly Thr Gly Leu Pro Asp Pro Ser Met Asp Pro Thr
145 150 155 160
Leu Ala Gly Arg Leu Arg Asn Thr Cys Ala Val Pro Gly Gly Phe Ala
165 170 175
Ala Leu Asp Gln Ser Met Pro Val Thr Pro Val Ser Phe Asp Asn Leu
180 185 190
Phe Phe Gly Gln Ile Arg Glu Arg Lys Gly Ile Leu Leu Ile Asp Gln
195 200 205
Leu Ile Ala Ser Asp Pro Ala Thr Ser Gly Val Val Leu Gln Tyr Ala
210 215 220
Ser Asn Asn Glu Leu Phe Lys Arg Gln Phe Ala Ile Ala Met Val Lys
225 230 235 240
Met Gly Ala Val Asp Val Leu Thr Gly Ser Ala Gly Glu Ile Arg Thr
245 250 255
Asn Cys Arg Ala Phe Asn
260

(2) INFORMATION FOR SEQ ID NO:2088:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1173 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1173
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571796

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2088:

gttgcttatt	tcttctggat	aagagcttct	tgatgggttg	aaacctctga	gtgaagaaga	60
agcgccatgg	ctgggattac	cagcagcacc	gttggtattca	acgcgcctct	caccggaata	120
acocaaacag	tatcatcaca	tctactcttc	tctgttgatt	ccaaactctg	tagtcttcgt	180
ctctccaaa	ccgaactgtc	tttactaat	ctcactcctt	ctcctgcctg	tgctttcgcc	240
gtcacttgcc	gcttcggcgg	tggtgggtga	ggttatcgat	tctctggaga	caatagaaga	300
ggtagggcga	aagaagctga	aattgatgaa	gctcttgata	tctcctcaat	taggtcagct	360
actgttaagg	ttatcgatgg	gcaacaaaaa	atgcttggtt	tagtgtctaa	agacgaagcc	420
gttcgaatgg	ctgatgatgc	tgaacttgat	ctgggKatac	tatcgccctga	tgccagatcct	480
ccggttggtta	aaattgatga	ctacagataa	tacagatacg	acacgcacaaa	gaggaacaaa	540
gatcagcaaa	agaaaaaac	tcgcattggat	ttaaaggagc	ttaaaatggg	ttataatatt	600
gatcagcatg	attattccgt	tcgtctaaagg	gctgcacaaa	agttcttgca	agatgggtgac	660
aaggtttaagg	tgattgtgag	catgaagaag	cgagaaaaag	agttcagaaa	tatcgctatt	720
gaactctctca	gacgtttttc	aaccgaataa	ggggagcttg	caactgaaga	gagcaaaaaac	780
ttcagggagca	gaaatatggt	cattatcttg	gtcccaaaaa	agaaaatgat	tcggaacaca	840
caagaaccac	ccacaagaaa	gaagaaaaaa	acagcggaaa	acgaagcttc	agcttcagct	900
cgacaaaataa	cagctgagcc	tgagccctgag	ctggaacctg	agcctgagcc	tgagcctgag	960
cctgagcctg	agcctgagcc	agagcctctca	cagatcgatt	cttgagtgtta	aaatctttgtg	1020
gtagagtttt	cagagctaaa	gtaaaagttt	gtatatattc	ttttctacca	tgctcaaga	1080
gagccaaagag	ctgtataaca	aatagagttta	gtcctatttg	aatgatgttc	ttcgtttgtga	1140
gatcttttct	ctaactctatt	ttttgtttta	act			

(2) INFORMATION FOR SEQ ID NO:2089:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 312 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..312

(D) OTHER INFORMATION: / Ceres Seq. ID 1571797

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2089:

Met	Ala	Gly	Ile	Thr	Ser	Ser	Thr	Val	Gly	Phe	Asn	Ala	Val	Phe	Thr
1					5				10					15	
Gly	Ile	Thr	Lys	Thr	Val	Ser	Ser	His	Ser	Leu	Phe	Ser	Val	Asp	Ser
			20					25					30		
Lys	Leu	Cys	Ser	Leu	Arg	Leu	Ser	Lys	Thr	Glu	Leu	Ser	Phe	Thr	Asn
		35					40					45			
Leu	Thr	Pro	Ser	Pro	Arg	Arg	Ala	Phe	Ala	Val	Thr	Cys	Arg	Phe	Gly
		50				55					60				
Gly	Gly	Gly	Gly	Gly	Tyr	Arg	Phe	Ser	Gly	Asp	Asn	Arg	Arg	Gly	Arg
65					70				75					80	
Pro	Lys	Glu	Ala	Glu	Ile	Asp	Glu	Ala	Leu	Asp	Ile	Ser	Ser	Ile	Arg
				85					90					95	
Ser	Ala	Thr	Val	Arg	Leu	Ile	Asp	Gly	Gln	Gln	Asn	Met	Leu	Gly	Leu
			100					105					110		
Val	Ser	Lys	Asp	Glu	Ala	Val	Arg	Met	Ala	Asp	Asp	Ala	Glu	Leu	Asp
		115					120					125			
Leu	Xaa	Ile	Leu	Ser	Pro	Asp	Ala	Asp	Pro	Pro	Val	Val	Lys	Met	Met
		130				135					140				
Asp	Tyr	Ser	Lys	Tyr	Arg	Tyr	Glu	Gln	Gln	Lys	Arg	Lys	Lys	Asp	Gln
145					150					155				160	
Gln	Lys	Lys	Thr	Thr	Arg	Met	Asp	Leu	Lys	Glu	Leu	Lys	Met	Gly	Tyr
			165					170						175	
Asn	Ile	Asp	Gln	His	Asp	Tyr	Ser	Val	Arg	Leu	Arg	Ala	Ala	Gln	Lys
			180				185					190			
Phe	Leu	Gln	Asp	Gly	Asp	Lys	Val	Lys	Val	Ile	Val	Ser	Met	Lys	Gly
		195				200					205				
Arg	Glu	Asn	Glu	Phe	Arg	Asn	Ile	Ala	Ile	Glu	Leu	Leu	Arg	Arg	Phe
		210				215					220				
Gln	Thr	Glu	Ile	Gly	Glu	Leu	Ala	Thr	Glu	Glu	Ser	Lys	Asn	Phe	Arg
225					230				235					240	
Asp	Arg	Asn	Met	Phe	Ile	Ile	Leu	Val	Pro	Asn	Lys	Glu	Met	Ile	Arg
			245						250					255	
Lys	Pro	Gln	Glu	Pro	Pro	Thr	Arg	Lys	Lys	Lys	Thr	Ala	Glu	Asn	
			260					265				270			
Glu	Ala	Ser	Ala	Ser	Ala	Ala	Glu	Ile	Thr	Ala	Glu	Pro	Glu	Pro	Glu
		275									285				
Pro	Glu	Pro	Glu	Pro	Glu	Pro	Glu	Pro	Glu	Pro	Glu	Pro	Glu	Pro	Glu
		290				295					300				
Pro	Glu	Pro	Leu	Gln	Ile	Asp	Ser								
305					310										

(2) INFORMATION FOR SEQ ID NO:2090:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 204 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..204

(D) OTHER INFORMATION: / Ceres Seq. ID 1571798

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2090:

Met	Leu	Gly	Leu	Val	Ser	Lys	Asp	Glu	Ala	Val	Arg	Met	Ala	Asp	Asp
1					5				10				15		
Ala	Glu	Leu	Asp	Leu	Xaa	Ile	Leu	Ser	Pro	Asp	Ala	Asp	Pro	Pro	Val
			20					25					30		

Val	Lys	Met	Met	Asp	Tyr	Ser	Lys	Tyr	Arg	Tyr	Glu	Gln	Gln	Lys	Arg	
	35						40					45				
Lys	Lys	Asp	Gln	Gln	Lys	Lys	Thr	Thr	Arg	Met	Asp	Leu	Lys	Glu	Leu	
	50					55					60					
Lys	Met	Gly	Tyr	Asn	Ile	Asp	Gln	His	Asp	Tyr	Ser	Val	Arg	Leu	Arg	
	65				70				75					80		
Ala	Ala	Gln	Lys	Phe	Leu	Gln	Asp	Gly	Asp	Lys	Val	Lys	Val	Ile	Val	
				85					90					95		
Ser	Met	Lys	Gly	Arg	Glu	Asn	Glu	Phe	Arg	Asn	Ile	Ala	Ile	Glu	Leu	
			100					105					110			
Leu	Arg	Arg	Phe	Gln	Thr	Glu	Ile	Gly	Glu	Leu	Ala	Thr	Glu	Glu	Ser	
			115				120					125				
Lys	Asn	Phe	Arg	Asp	Arg	Asn	Met	Phe	Ile	Ile	Leu	Val	Pro	Asn	Lys	
	130					135					140					
Glu	Met	Ile	Arg	Lys	Pro	Gln	Glu	Pro	Pro	Thr	Arg	Lys	Lys	Lys	Lys	
	145				150					155				160		
Thr	Ala	Glu	Asn	Glu	Ala	Ser	Ala	Ser	Ala	Ala	Glu	Ile	Thr	Ala	Glu	
			165					170						175		
Pro	Glu	Pro	Glu	Pro	Glu	Pro	Glu	Pro	Glu	Pro	Glu	Pro	Glu	Pro	Glu	
			180				185						190			
Pro	Glu	Pro	Glu	Pro	Glu	Pro	Leu	Gln	Ile	Asp	Ser					
			195			200										

(2) INFORMATION FOR SEQ ID NO:2091:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 192 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..192

(D) OTHER INFORMATION: / Ceres Seq. ID 1571799

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2091:

Met	Ala	Asp	Asp	Ala	Glu	Leu	Asp	Leu	Xaa	Ile	Leu	Ser	Pro	Asp	Ala	
1				5					10					15		
Asp	Pro	Pro	Val	Val	Lys	Met	Met	Asp	Tyr	Ser	Lys	Tyr	Arg	Tyr	Glu	
			20					25					30			
Gln	Gln	Lys	Arg	Lys	Lys	Asp	Gln	Gln	Lys	Lys	Thr	Thr	Arg	Met	Asp	
		35				40					45					
Leu	Lys	Glu	Leu	Lys	Met	Gly	Tyr	Asn	Ile	Asp	Gln	His	Asp	Tyr	Ser	
	50				55					60						
Val	Arg	Leu	Arg	Ala	Ala	Gln	Lys	Phe	Leu	Gln	Asp	Gly	Asp	Lys	Val	
	65			70				75						80		
Lys	Val	Ile	Val	Ser	Met	Lys	Gly	Arg	Glu	Asn	Glu	Phe	Arg	Asn	Ile	
			85					90					95			
Ala	Ile	Glu	Leu	Leu	Arg	Arg	Phe	Gln	Thr	Glu	Ile	Gly	Glu	Leu	Ala	
			100				105						110			
Thr	Glu	Glu	Ser	Lys	Asn	Phe	Arg	Asp	Arg	Asn	Met	Phe	Ile	Ile	Leu	
		115				120						125				
Val	Pro	Asn	Lys	Glu	Met	Ile	Arg	Lys	Pro	Gln	Glu	Pro	Pro	Thr	Arg	
	130				135						140					
Lys	Lys	Lys	Lys	Thr	Ala	Glu	Asn	Glu	Ala	Ser	Ala	Ser	Ala	Ala	Glu	
	145			150					155					160		
Ile	Thr	Ala	Glu	Pro	Glu	Pro	Glu	Pro	Glu	Pro	Glu	Pro	Glu	Pro	Glu	
		165					170						175			
Pro	Glu	Pro	Glu	Pro	Glu	Pro	Glu	Pro	Leu	Gln	Ile	Asp	Ser			
		180				185						190				

(2) INFORMATION FOR SEQ ID NO:2092:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1185 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..1185
(D) OTHER INFORMATION: / Ceres Seq. ID 1571800
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2092:

gacgatgacg	atgatgatga	tgatgatgaa	gttgatggag	atgataatga	gaaggagaaa	60
attgggttat	acgaggtcaa	gaagggaat	ctaactgtca	aattcacaaa	ttgggggtgct	120
tcaatcatat	ctctccattt	cccagacaaa	aatggtaaaa	tggacgatat	tgttcttgge	180
tatgatagcg	tcaaaaacct	caagaccgac	aagggtttat	tcggagcaac	cgttggccga	240
gtagcaaat	gaataggaaa	gggcaaatc	aagttgaatg	gtaaaagata	caagacaagt	300
gtcaacgaNt	ggaaaaaaca	cactccatgg	tggcaagaaa	gggtttgggg	atgttgtgtg	360
ggcagttgca	aaacaccagt	acgatggcaa	gaaaccacac	attgtcttca	ctcacacaag	420
tcctgacggc	gatcaagggt	ttccgggaga	actcaagtgc	acggtgacat	ataaacttgt	480
caaaagacaat	gaattgagtg	tggtgatgga	ggcaaaagCct	aaggataaag	caactccggg	540
gaacttagct	catcatagtt	attggaatct	tggttggtcat	aattccggag	atattttgtc	600
tgaagaaaatt	caaatccctcg	gctcgggtta	tacccccgtc	gacggtgagc	tcattccacc	660
cggggaataat	aatccggtga	aaggaacagc	atacgaattt	ctccaactcc	gtccattaaa	720
agataaatatg	aaggatctta	aaacaggata	tgatataaat	tattgcttag	atggtaaaagg	780
aaaaaaagatg	agaaaaaatg	ttgaactcgt	agataagaaa	tcaggggagg	aaatggagtt	840
atccccgaac	caagcgggtt	tgcaattcta	taccggaggg	atgttaaaag	atgtccaaagg	900
gaagaattggg	gcagtttacc	aagctttcgg	gggattatgt	ttagaacac	aaagttaact	960
agacgcatgt	aacctccca	aatttccttc	acagattgtc	gagccaggga	aaaaatacaa	1020
acacacttgt	ctcttcaagt	tttctattgt	ttcatagatt	gttttagatg	ttgttaaatg	1080
aacacccttg	gaaccatgtc	caatgttcat	gaacaagaaa	ctaaatacat	tgtaatattt	1140
tgtaacaagt	cttaaatatt	caaattatat	aaacctaacg	tgaac		

(2) INFORMATION FOR Ceres Seq ID NO:2093:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 141 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..141
(D) OTHER INFORMATION: / Ceres Seq. ID 1571801
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2093:

Asp	Asp	Asp	Asp	Asp	Asp	Asp	Asp	Asp	Asp	Glu	Val	Asp	Gly	Asp	Asp	Asn
1										5		10			15	
Glu	Lys	Glu	Lys	Ile	Gly	Leu	Tyr	Glu	Leu	Lys	Lys	Gly	Asn	Leu	Thr	
										20		25		30		
Val	Lys	Phe	Thr	Asn	Trp	Gly	Ala	Ser	Ile	Ile	Ser	Leu	His	Phe	Pro	
										35		40		45		
Asp	Lys	Asn	Gly	Lys	Met	Asp	Asp	Ile	Val	Leu	Gly	Tyr	Asp	Ser	Val	
										50		55		60		
Lys	Thr	Tyr	Lys	Thr	Asp	Lys	Val	Tyr	Phe	Gly	Ala	Thr	Val	Gly	Arg	
										65		70		75		
Val	Ala	Asn	Arg	Ile	Gly	Lys	Gly	Lys	Phe	Lys	Leu	Asn	Gly	Lys	Glu	
										85		90		95		
Tyr	Lys	Thr	Ser	Val	Asn	Xaa	Trp	Lys	Lys	His	Thr	Pro	Trp	Trp	Gln	
										100		105		110		
Glu	Arg	Val	Trp	Gly	Cys	Cys	Val	Gly	Ser	Cys	Lys	Thr	Pro	Val	Arg	
										115		120		125		
Trp	Gln	Glu	Thr	Thr	His	Cys	Leu	His	Ser	His	Lys	Ser				
										130		135		140		

(2) INFORMATION FOR SEQ ID NO:2094:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 259 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..259
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571802

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2094:

Met Val Lys Ser Thr Arg Gln Val Ser Thr Xaa Gly Lys Asn Thr Leu
1 5 10 15
His Gly Gly Lys Lys Gly Phe Gly Asp Val Val Trp Ala Val Ala Lys
20 25 30
His Gln Tyr Asp Gly Lys Lys Pro His Ile Val Phe Thr His Thr Ser
35 40 45
Pro Asp Gly Asp Gln Gly Phe Pro Gly Glu Leu Ser Val Thr Val Thr
50 55 60
Tyr Lys Leu Val Lys Asp Asn Glu Leu Ser Val Val Met Glu Ala Lys
65 70 75 80
Pro Lys Asp Lys Ala Thr Pro Val Asn Leu Ala His His Ser Tyr Trp
85 90 95
Asn Leu Gly Gly His Asn Ser Gly Asp Ile Leu Ser Glu Glu Ile Gln
100 105 110
Ile Leu Gly Ser Gly Tyr Thr Pro Val Asp Gly Glu Leu Ile Pro Thr
115 120 125
Gly Lys Ile Asn Pro Val Lys Gly Thr Ala Tyr Asp Phe Leu Gln Leu
130 135 140
Arg Pro Ile Lys Asp Asn Met Lys Asp Leu Lys Thr Gly Tyr Asp Ile
145 150 155 160
Asn Tyr Cys Leu Asp Gly Lys Ala Lys Lys Met Arg Lys Ile Val Glu
165 170 175
Leu Val Asp Lys Lys Ser Gly Arg Lys Met Glu Leu Ser Gly Asn Gln
180 185 190
Ala Gly Leu Gln Phe Tyr Thr Gly Gly Met Leu Lys Asp Val Lys Gly
195 200 205
Lys Asn Gly Ala Val Tyr Gln Ala Phe Gly Gly Leu Cys Leu Glu Thr
210 215 220
Gln Ser Tyr Pro Asp Ala Leu Asn His Pro Lys Phe Pro Ser Gln Ile
225 230 235 240
Val Glu Pro Gly Lys Lys Tyr Lys His Thr Met Leu Phe Lys Phe Ser
245 250 255
Ile Val Ser

(2) INFORMATION FOR SEQ ID NO:2095:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 183 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..183
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571803

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2095:

Met Glu Ala Lys Pro Lys Asp Lys Ala Thr Pro Val Asn Leu Ala His
1 5 10 15
His Ser Tyr Trp Asn Leu Gly Gly His Asn Ser Gly Asp Ile Leu Ser

20										25					30				
Glu	Glu	Ile	Gln	Ile	Leu	Gly	Ser	Gly	Tyr	Thr	Pro	Val	Asp	Gly	Glu				
35							40	45											
Leu	Ile	Pro	Thr	Gly	Lys	Ile	Asn	Pro	Val	Lys	Gly	Thr	Ala	Tyr	Asp				
50							55	60											
Phe	Leu	Gln	Leu	Arg	Pro	Ile	Lys	Asp	Asn	Met	Lys	Asp	Leu	Lys	Thr				
65					70	75					80								
Gly	Tyr	Asp	Ile	Asn	Tyr	Cys	Leu	Asp	Gly	Lys	Ala	Lys	Lys	Met	Arg				
85				90				95				100							
Lys	Ile	Val	Glu	Leu	Val	Asp	Lys	Lys	Ser	Gly	Arg	Lys	Met	Glu	Leu				
105			110			115			120			125							
Ser	Gly	Asn	Gln	Ala	Gly	Leu	Gln	Phe	Tyr	Thr	Gly	Gly	Met	Leu	Lys				
130		135		140		145		150		155		160		165					
Asp	Val	Lys	Gly	Lys	Asn	Gly	Ala	Val	Tyr	Gln	Ala	Phe	Gly	Gly	Leu				
170		175		180		185		190		195		200		205					
Cys	Leu	Glu	Thr	Gln	Ser	Tyr	Pro	Asp	Ala	Leu	Asn	His	Pro	Lys	Phe				
145			150			155			160			165			170				
Pro	Ser	Gln	Ile	Val	Glu	Pro	Gly	Lys	Lys	Tyr	Lys	His	Thr	Met	Leu				
165				170				175				180							
Phe	Lys	Phe	Ser	Ile	Val	Ser													
180		185		190		195		200		205		210		215					

(2) INFORMATION FOR SEO ID NO:2096:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 554 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: DNA (genomic)
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(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..554
(D) OTHER INFORMATION: / Ceres Seq. ID 1571812

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2096:

actctatcagat	gaaacctcttgg	aggttatgggt	ctatcaccaa	aagtcctagat	gataacaagg	60
aagatgagccaa	atgcagcatc	tgcgaagaaat	aatatcacgt	tggagatgaa	gtgtggagac	120
acacgtctgta	gcacacatcac	catgtgaagt	gttgccaaga	gtgtgtgcg	ataaagaagt	180
tgtgcccaatg	ctgcaaaagcc	cacagocggc	ctcctctcaa	tacaacgtct	tctcttctct	240
ccctgcttctg	tgttatagtt	ctctctatca	aagcctctga	acaaacaatg	aacctctcgta	300
aaaagaagctg	caccaatttcc	tttgtgtaca	taccaattca	cacccgctgt	tgtctctctc	360
cccttttctgc	taatgacaaa	gcatactcgt	gtttctcttg	tcatttcttc	tcttttaactg	420
tgtgacttcg	taatgtaaa	tgggaagaa	ggaaacgatt	tctttgtaac	tttgaagact	480
cagtaaacat	tgactKttta	attcttaaaa	tggacaatt	tgttgaaaag	caacaaaag	540
ctcggtctct	tgat					

(2) INFORMATION FOR SEQ ID NO:2097:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 73 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..73
(D) OTHER INFORMATION: / Ceres Seq. ID 1571813

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2097:

Tyr	Gln	Met	Lys	Pro	Leu	Ser	Tyr	Gly	Ser	Ile	Thr	Lys	Ser	Pro	Ser
1				5					10					15	
Asp	Asn	Lys	Glu	Asp	Ala	Lys	Cys	Ser	Ile	Cys	Gln	Glu	Glu	Tyr	Thr
			20					25					30		
Ile	Gly	Asp	Glu	Val	Gly	Arg	Leu	His	Cys	Glu	His	Thr	Tyr	His	Val
		35					40					45			

Lys Cys Val Gln Glu Trp Leu Arg Met Lys Ser Trp Cys Pro Ile Cys
50 55 60

Lys Ala Thr Ala Glu Thr Ser Ser Lys
65 70

(2) INFORMATION FOR SEQ ID NO:2098:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 71 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..71

(D) OTHER INFORMATION: / Ceres Seq. ID 1571814

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2098:

Met Lys Pro Leu Ser Tyr Gly Ser Ile Thr Lys Ser Pro Ser Asp Asn
1 5 10 15

Lys Glu Asp Ala Lys Cys Ser Ile Cys Gln Glu Glu Tyr Thr Ile Gly
20 25 30

Asp Glu Val Gly Arg Leu His Cys Glu His Thr Tyr His Val Lys Cys
35 40 45

Val Gln Glu Trp Leu Arg Met Lys Ser Trp Cys Pro Ile Cys Lys Ala
50 55 60

Thr Ala Glu Thr Ser Ser Lys
65 70

(2) INFORMATION FOR SEQ ID NO:2099:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 40 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..40

(D) OTHER INFORMATION: / Ceres Seq. ID 1571815

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2099:

Met Gly Leu Ser Pro Lys Val Leu Val Ile Thr Arg Lys Met Pro Asn
1 5 10 15

Ala Ala Ser Ala Arg Lys Asn Ile Arg Leu Glu Met Lys Leu Gly Gly
20 25 30

Tyr Thr Val Ser Thr His Thr Met
35 40

(2) INFORMATION FOR SEQ ID NO:2100:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1617 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1617

(D) OTHER INFORMATION: / Ceres Seq. ID 1571820

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2100:

cccgacagta	gaaagcaaaa	attcttcato	gactcaaat	caaaaaactca	tctctctcta	60
tctctatttc	tctgtgtcca	tagctcaccg	tcgcatcgca	gatctactcc	ttccgcaata	120
aattttaccg	gcggagggtat	cagatctcgc	cgatctgttg	tagcagctac	tgatttttgg	180
gcttctcatt	tgatatgtgg	gaaacgagga	gtagaggacg	atggaaaatc	tgatctctct	240
ggttaacaag	atacacagag	cttgcaaggc	tttaggagac	catggagact	ccagcgcttt	300

acctactctt	tgggattcc	tgccgtcgat	cgccgtcggt	ggtggtcaga	gtcaggagaa	360
gtcttcagtc	ctgggagaga	tgtgtgggaaa	ggacttttta	ccccgtggat	ctggcattgt	420
tactcgaag	ccoccttgtct	tacagttgca	aaagatcgat	gatggaaCcc	ggagatattgc	480
agagtttctt	cacctcccca	ggaaaaagtt	tactgatttt	gctgctgtga	ggaaggagat	540
ctaaagttag	actgacagag	agactggagc	cagcaaggct	atttctagtgt	ttcccaattca	600
ccttagcata	tactctccca	atgttgtcaa	cttgacaactg	atagatcttc	cagggtcttac	660
aaaaagttgt	gttgatggac	aatctgatag	tatagtgaag	gacattgaaa	acatggttgc	720
gtctctacat	gaaaagoccc	actgcacatc	tttggcaatc	tcacctgcaa	accaagatct	780
tgctacccca	gatgcaatta	aaatttcccg	tgaggttgat	ccactcgggg	acagaaactt	840
tggtgtcttg	acaaagattg	atcttatgga	caaggggacg	gatgcagttg	aaattcttga	900
agggagatct	tttaaacctta	aatatccgtg	ggttggtgtc	gtcaaccgtt	cccaagcaga	960
tattaaacaag	aatgtcgaca	tgattgcgcg	tcggaaaaaga	gagaggaggt	acttttccaa	1020
tactactgag	tataggcacc	ttgctaataa	aatgggttcc	gagcattttg	caaagatgct	1080
ctccaaagcat	ctagaacgtg	tgatcaagtc	gagaatttcc	ggcattcagt	cactttattaa	1140
caaaaacagta	ttagagctgg	aaactgaact	aagtgcgcct	ggaaaagcta	ttgcagctga	1200
tgacgggggg	aagttgtact	caataatgga	gatattgtcg	ctttttgatc	aaattattcaa	1260
agagcatctt	gatggagtgc	gtgctgtgtg	tgaaaaagtg	tacaacgtgt	ttgataacca	1320
ctctctcgcg	gctctgaaga	gactccaat	tgacaagcag	ctagcagatg	acaacatccg	1380
gaagctgttc	actgaggtcg	atggttacc	gcctcacttg	attgtctctg	acgaaggtta	1440
cgctgtcttc	attgagctct	ctattgtctc	catcagaggc	ccctgtgaag	catctgttga	1500
caaccgtatg	actctttact	ttcatctcta	aaaagatgta	tcaaaaacct	acataaacct	1560
aataagcttc	tctctcgtt	ttttttttt	ttctatggtt	aaatattagg	ttcatgc	

(2) INFORMATION FOR SEQ ID NO:2101:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 429 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..429

(D) OTHER INFORMATION: / Ceres Seq. ID 1571821

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2101:

Met	Glu	Asn	Leu	Ile	Ser	Leu	Val	Asn	Lys	Ile	Gln	Arg	Ala	Cys	Thr
1				5						10				15	
Ala	Leu	Gly	Asp	His	Gly	Asp	Ser	Ser	Ala	Leu	Pro	Thr	Leu	Trp	Asp
			20					25					30		
Ser	Leu	Pro	Ala	Ile	Ala	Val	Val	Gly	Gln	Ser	Ser	Gly	Lys	Ser	
			35				40					45			
Ser	Val	Leu	Glu	Ser	Ile	Val	Gly	Lys	Asp	Phe	Leu	Pro	Arg	Gly	Ser
			50			55				60					
Gly	Ile	Val	Thr	Arg	Arg	Pro	Leu	Val	Leu	Gln	Lys	Ile	Asp		
			65			70			75				80		
Asp	Gly	Thr	Arg	Glu	Tyr	Ala	Glu	Phe	Leu	His	Leu	Pro	Arg	Lys	Lys
			85					90					95		
Phe	Thr	Asp	Phe	Ala	Ala	Val	Arg	Lys	Glu	Ile	Gln	Asp	Glu	Thr	Asp
			100					105					110		
Arg	Glu	Thr	Gly	Arg	Ser	Lys	Ala	Ile	Ser	Ser	Val	Pro	Ile	His	Leu
			115				120					125			
Ser	Ile	Tyr	Ser	Pro	Asn	Val	Val	Asn	Leu	Thr	Leu	Ile	Asp	Leu	Pro
			130			135					140				
Gly	Leu	Thr	Lys	Val	Ala	Val	Asp	Gly	Gln	Ser	Asp	Ser	Ile	Val	Lys
			145			150				155				160	
Asp	Ile	Glu	Asn	Met	Val	Arg	Ser	Tyr	Ile	Glu	Lys	Pro	Asn	Cys	Ile
			165					170					175		
Ile	Leu	Ala	Ile	Ser	Pro	Ala	Asn	Gln	Asp	Leu	Ala	Thr	Ser	Asp	Ala
			180				185					190			
Ile	Lys	Ile	Ser	Arg	Glu	Val	Asp	Pro	Ser	Gly	Asp	Arg	Thr	Phe	Gly
			195			200					205				
Val	Leu	Thr	Lys	Ile	Asp	Leu	Met	Asp	Lys	Gly	Thr	Asp	Ala	Val	Glu

210	215	220
Ile Leu Glu Gly Arg Ser Phe Lys Leu Lys Tyr Pro Trp Val Gly Val		
225	230	235
Val Asn Arg Ser Gln Ala Asp Ile Asn Lys Asn Val Asp Met Ile Ala		
	245	250
Ala Arg Lys Arg Glu Arg Glu Tyr Phe Ser Asn Thr Thr Glu Tyr Arg		
	260	265
His Leu Ala Asn Lys Met Gly Ser Glu His Leu Ala Lys Met Leu Ser		
	275	280
Lys His Leu Glu Arg Val Ile Lys Ser Arg Ile Pro Gly Ile Gln Ser		
	290	295
Leu Ile Asn Lys Thr Val Leu Glu Leu Glu Thr Glu Leu Ser Arg Leu		
305	310	315
Gly Lys Pro Ile Ala Ala Asp Ala Gly Gly Lys Leu Tyr Ser Ile Met		
	325	330
Glu Ile Cys Arg Leu Phe Asp Gln Ile Phe Lys Glu His Leu Asp Gly		
	340	345
Val Arg Ala Gly Gly Glu Lys Val Tyr Asn Val Phe Asp Asn His Leu		
	355	360
Pro Ala Ala Leu Lys Arg Leu Gln Phe Asp Lys Gln Leu Ala Met Asp		
	370	375
Asn Ile Arg Lys Leu Val Thr Glu Ala Asp Gly Tyr Gln Pro His Leu		
385	390	395
Ile Ala Pro Glu Gln Gly Tyr Arg Arg Leu Ile Glu Ser Ser Ile Val		
	405	410
Ser Ile Arg Gly Pro Ala Glu Ala Ser Val Asp Thr Val		
	420	425

(2) INFORMATION FOR SEQ ID NO:2102:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 265 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..265

(D) OTHER INFORMATION: / Ceres Seq. ID 1571822

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2102:

Met Val Arg Ser Tyr Ile Glu Lys Pro Asn Cys Ile Ile Leu Ala Ile	
1	5
Ser Pro Ala Asn Gln Asp Leu Ala Thr Ser Asp Ala Ile Lys Ile Ser	
	10
Arg Glu Val Asp Pro Ser Gly Asp Arg Thr Phe Gly Val Leu Thr Lys	
	15
Ile Asp Leu Met Asp Lys Gly Thr Asp Ala Val Glu Ile Leu Glu Gly	
	20
Arg Ser Phe Lys Leu Lys Tyr Pro Trp Val Gly Val Val Asn Arg Ser	
	25
Gln Ala Asp Ile Asn Lys Asn Val Asp Met Ile Ala Ala Arg Lys Arg	
	30
Glu Arg Glu Tyr Phe Ser Asn Thr Thr Glu Tyr Arg His Leu Ala Asn	
	35
Lys Met Gly Ser Glu His Leu Ala Lys Met Leu Ser Lys His Leu Glu	
	40
Arg Val Ile Lys Ser Arg Ile Pro Gly Ile Gln Ser Leu Ile Asn Lys	
	45
Thr Val Leu Glu Leu Glu Thr Glu Leu Ser Arg Leu Gly Lys Pro Ile	
	50
Ala Ala Asp Ala Gly Gly Lys Leu Tyr Ser Ile Met Glu Ile Cys Arg	
	55
	60
	65
	70
	75
	80
	85
	90
	95
	100
	105
	110
	115
	120
	125
	130
	135
	140
	145
	150
	155
	160
	165
	170
	175

Leu Phe Asp Gln Ile Phe Lys Glu His Leu Asp Gly Val Arg Ala Gly
180 185 190
Gly Glu Lys Val Tyr Asn Val Phe Asp Asn His Leu Pro Ala Ala Leu
195 200 205
Lys Arg Leu Gln Phe Asp Lys Gln Leu Ala Met Asp Asn Ile Arg Lys
210 215 220
Leu Val Thr Glu Ala Asp Gly Tyr Gln Pro His Leu Ile Ala Pro Glu
225 230 235 240
Gln Gly Tyr Arg Arg Leu Ile Glu Ser Ser Ile Val Ser Ile Arg Gly
245 250 255
Pro Ala Glu Ala Ser Val Asp Thr Val
260 265

(2) INFORMATION FOR SEQ ID NO:2103:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 214 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..214

(D) OTHER INFORMATION: / Ceres Seq. ID 1571823

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2103:

Met Asp Lys Gly Thr Asp Ala Val Glu Ile Leu Glu Gly Arg Ser Phe
1 5 10 15
Lys Leu Lys Tyr Pro Trp Val Gly Val Val Asn Arg Ser Gln Ala Asp
20 25 30
Ile Asn Lys Asn Val Asp Met Ile Ala Ala Arg Lys Arg Glu Arg Glu
35 40 45
Tyr Phe Ser Asn Thr Thr Gly Tyr Arg His Leu Ala Asn Lys Met Gly
50 55 60
Ser Glu His Leu Ala Lys Met Leu Ser Lys His Leu Glu Arg Val Ile
65 70 75 80
Lys Ser Arg Ile Pro Gly Ile Gln Ser Leu Ile Asn Lys Thr Val Leu
85 90 95
Glu Leu Glu Thr Glu Leu Ser Arg Leu Gly Lys Pro Ile Ala Ala Asp
100 105 110
Ala Gly Gly Lys Leu Tyr Ser Ile Met Glu Ile Cys Arg Leu Phe Asp
115 120 125
Gln Ile Phe Lys Glu His Leu Asp Gly Val Arg Ala Gly Gly Glu Lys
130 135 140
Val Tyr Asn Val Phe Asp Asn His Leu Pro Ala Ala Leu Lys Arg Leu
145 150 155 160
Gln Phe Asp Lys Gln Leu Ala Met Asp Asn Ile Arg Lys Leu Val Thr
165 170 175
Glu Ala Asp Gly Tyr Gln Pro His Leu Ile Ala Pro Glu Gln Gly Tyr
180 185 190
Arg Arg Leu Ile Glu Ser Ser Ile Val Ser Ile Arg Gly Pro Ala Glu
195 200 205
Ala Ser Val Asp Thr Val
210

(2) INFORMATION FOR SEQ ID NO:2104:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1476 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -

(B) LOCATION: 1..1476

(D) OTHER INFORMATION: / Ceres Seq. ID 1571824

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2104:

aaaaagtgtgc	gaaGctctct	cattgagtaa	actaacggct	atatctctc	tgatattcaa	60
aatttgctcg	aagaaacgac	gatggcagcc	gaaacgaagg	ttcagggtttc	agatccagag	120
gcagagtttc	ttaattcgaa	gcaggagact	ggatcacgag	gggagctttt	caaggagaaac	180
gtccggccat	tgaaagagagg	tgcgaatgtt	ggattctcta	accacgctct	caaattctcac	240
tctgaccacc	aattgagaaa	gaattctcat	gagaaaacga	ggaatttgat	tgaagccatt	300
gatgagtagt	aaggagatga	ccttttatct	ccatggatag	agtgtataaa	atgggtacaa	360
gaggcttttc	caccagagg	acaagtgtca	ggactgttag	tgatatatga	gcaattgtgtt	420
cgtaaatttt	ggcactctga	acgtttacaag	gatgatcttc	gttatcttaa	agtcctgtgtg	480
gaatatcggg	agcattgcgc	tgtgcggaa	gtgatttaca	agtttttggg	ggtcaatgaq	540
attggaaga	cacatgctgt	ctactatata	gcttatgctt	tgacacatga	gtttaagaat	600
aaggtcaaaa	ctgctaata	gatcttcaat	cttggaaatc	ctagggatgc	aaagccagt	660
gaaaagtgtg	atgacgcgta	caagaagttt	atggtgagaa	cgatgagaag	gtccaacaca	720
gctgatgaag	aaccaaaagg	gaataatgac	ttaccgtcaa	gaagcttttg	cactttattg	780
tccaggggag	ataataatgc	aagaaggcag	gcgttaggaa	gttctaacc	acaagccaaa	840
aagctaaagc	caaatcaatc	atccaagaca	ccttttgcta	tctacgcaga	tcagttttca	900
gacaccacat	cagggaaatc	accagagtca	gacaagtcaa	gaccagagtt	tggtagttgg	960
ctcatgcttg	gaggcagagc	agagaggaa	aaagaaaaca	attctttacc	tagaaaatgt	1020
gcatacttca	aggttctctc	gaaccatt	gtgagaactg	ttgcagcagc	atctgctttc	1080
acccttgagg	ttttgtctga	tgaagaagaa	tgtaacagaa	aggaagaaga	aaagaagaag	1140
aatgatgaaa	ctatctcatc	atcatcaaac	gttctgccc	ttaatggcgc	cogtgagata	1200
aaaaaagaaa	cagagctgct	acgcagaga	cctttaagac	atttcccacc	caacagcttc	1260
ctacgatgat	gatattggac	ttctctctc	acacgatctt	atgggtttgag	atttgagctt	1320
ttgtctataa	agctccttgt	gtgttttttg	ctatttggat	ttgtttttgt	gatgtactgt	1380
gatatactat	cctactatgt	accatgatgt	gcctttcatg	ttttgaaatt	aatgtgactt	1440

(2) INFORMATION FOR SEQ ID NO:2105:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 395 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..395

(D) OTHER INFORMATION: / Ceres Seq. ID 1571825

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2105:

Met	Ala	Ala	Glu	Thr	Lys	Val	Gln	Val	Ser	Asp	Pro	Glu	Ala	Glu	Phe
1			5					10					15		
Leu	Asn	Ser	Lys	Gln	Glu	Thr	Gly	Tyr	Glu	Trp	Glu	Leu	Phe	Lys	Glu
			20					25					30		
Asn	Val	Arg	Pro	Leu	Lys	Arg	Gly	Arg	Asn	Val	Gly	Ile	Leu	Asn	His
			35					40					45		
Ala	Leu	Lys	Ser	His	Ser	Asp	His	Gln	Leu	Arg	Lys	Asn	Leu	Ile	Glu
			50				55					60			
Lys	Arg	Arg	Asn	Leu	Ile	Glu	Ala	Ile	Asp	Gly	Tyr	Glu	Gly	Asp	Asp
65				70					75					80	
Pro	Leu	Ser	Pro	Trp	Ile	Glu	Cys	Ile	Lys	Trp	Val	Gln	Glu	Ala	Phe
				85					90					95	
Pro	Pro	Gly	Gly	Glu	Cys	Ser	Gly	Leu	Leu	Val	Ile	Tyr	Glu	Gln	Cys
			100					105					110		
Val	Arg	Lys	Phe	Trp	His	Ser	Glu	Arg	Tyr	Lys	Asp	Asp	Leu	Arg	Tyr
			115				120					125			
Leu	Lys	Val	Trp	Leu	Glu	Tyr	Ala	Glu	His	Cys	Ala	Asp	Ala	Glu	Val
			130				135					140			
Ile	Tyr	Lys	Phe	Leu	Glu	Val	Asn	Glu	Ile	Gly	Lys	Thr	His	Ala	Val
145				150					155					160	
Tyr	Tyr	Ile	Ala	Tyr	Ala	Leu	His	Ile	Glu	Phe	Lys	Asn	Lys	Val	Lys

	165		170		175										
Thr	Ala	Asn	Glu	Ile	Phe	Asn	Leu	Gly	Ile	Ser	Arg	Asp	Ala	Lys	Pro
	180		185		190		195		200		205		210		215
Val	Glu	Lys	Leu	Asn	Asp	Ala	Tyr	Lys	Lys	Phe	Met	Val	Arg	Thr	Met
	220		225		230		235		240		245		250		255
Arg	Arg	Ser	Asn	Thr	Ala	Asp	Glu	Glu	Pro	Lys	Glu	Asn	Asn	Asp	Leu
	260		265		270		275		280		285		290		295
Pro	Ser	Arg	Ser	Phe	Gly	Thr	Leu	Leu	Ser	Arg	Gly	Asp	Asn	Asn	Ala
	300		305		310		315		320		325		330		335
Arg	Arg	Gln	Ala	Leu	Gly	Ser	Ser	Asn	Pro	Glu	Ala	Lys	Lys	Leu	Lys
	340		345		350		355		360		365		370		375
Pro	Asn	Gln	Ser	Ser	Lys	Thr	Pro	Phe	Ala	Ile	Tyr	Ala	Asp	Ala	Val
	380		385		390		395		400		405		410		415
Ser	Asp	Thr	Thr	Ser	Gly	Asn	Gln	Pro	Glu	Ser	Asp	Lys	Ser	Arg	Pro
	420		425		430		435		440		445		450		455
Glu	Phe	Gly	Ser	Trp	Leu	Met	Leu	Gly	Gly	Arg	Ala	Glu	Arg	Asn	Lys
	460		465		470		475		480		485		490		495
Glu	Asn	Asn	Ser	Leu	Pro	Arg	Lys	Trp	Ala	Ser	Phe	Lys	Val	Pro	Gln
	500		505		510		515		520		525		530		535
Lys	Pro	Ile	Val	Arg	Thr	Val	Ala	Ala	Ala	Ser	Ala	Phe	Thr	Phe	Glu
	540		545		550		555		560		565		570		575
Val	Phe	Val	Asp	Glu	Glu	Glu	Cys	Thr	Glu	Glu	Glu	Glu	Glu	Lys	Lys
	580		585		590		595		600		605		610		615
Lys	Asn	Asp	Glu	Thr	Ile	Ser	Ser	Ser	Ser	Asn	Val	Leu	Pro	Leu	Asn
	620		625		630		635		640		645		650		655
Gly	Gly	Arg	Glu	Ile	Lys	Lys	Glu	Thr	Glu	Leu	Leu	Arg	Gln	Asn	Pro
	660		665		670		675		680		685		690		695
Leu	Arg	His	Phe	Pro	Pro	Asn	Ser	Phe	Leu	Arg					
	700		705		710		715		720		725		730		735

(2) INFORMATION FOR SEQ ID NO:2106:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1641 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1641
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571826

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2106:

ataaagattcca	cacatcacgct	tactcttttg	gctattttcca	acccccctta	tgtttatttct	60
ttccttttcca	ggcattttgga	cagccttgga	actgtttgtgg	gcatacaaac	accaggaggt	120
taagaaaccca	tataaggata	ctctgatcaa	tgtaaagag	cttgatttct	caaaaccaga	180
aggtctcttcg	ggatcatctc	tagatctgg	tgaaagacca	cccggtctca	acgactttgg	240
aatgggtggcc	tggtgcctag	atatgtcgac	cccagagttt	ccatgggggc	gaaaactctt	300
ctggtattg	aatgatgtca	ccctcaaagc	tggttctttt	ggctctagag	aggacgcggt	360
tttctctgtct	gttactgaac	tgcgtttgtc	caagaagctt	cccttgattt	acttggcagc	420
aaattctctgt	gcccgacttg	gggttgctga	agaagtcaaa	gcctgtctca	aaattgggatg	480
gtcggatgaa	atttccctcg	agaatgggtt	tcagtataata	tacotaagcc	ctgaagacca	540
cgaagagatt	ggatcatctg	tcattgcccc	tgaagtaag	ctccctagat	gggaaactag	600
gtgggtgatt	gatacagtcg	ttggcaaaaga	agatgggtatt	gggtgagaga	acttaacagg	660
aagtggggccc	atagcgggtg	cttactcaaa	ggcatacaat	gaaactttta	ctttaacctt	720
tggtagtggg	agaacgggtg	gaattgtgtc	ttatcttggc	gcctcaggta	tgcggtgcat	780
acagagactt	gatcagccga	tcactcttgac	tggtcttctc	acactcaaca	agttactctg	840
gcgtgagctg	tatatgcttc	acatgcaact	gggtggccgc	aaaatcatgg	gcacaaatgg	900
tggttttcat	cttacagctc	cagatgatct	tgaaggcgta	tcagcaattc	tcaactggct	960
cagctacatt	ctctgttaag	tggtgtgttc	tcttctgtgt	cttgccctct	tagatccacc	1020
ggagagaatt	gtggagtatg	tcccagagaa	ctcttgcgac	ccacagcggc	cttactcgtg	1080
ggcctaaagac	aataccggta	aatggcttgg	aggtatcttt	gataaaaata	gtttcatatga	1140
gactcttgaa	ggctggggcaa	ggacggtagt	gactggtaga	gccaaagctc	ggggaataacc	1200

cggtggagtt	gttgcagttg	agacacagac	tgatcatgcag	atcatcccgag	cagatcctgg	1260
acagottgac	tctcatgaaa	gagtggttcc	gcaagcaggg	caagtctggt	ttcctgattc	1320
agcggccaag	actgctcaag	cacttatgga	tttcaaccgg	gaagagcttc	cattgtttat	1380
cctagcgaac	tgagaggggt	tttcaggtgg	gcagagagat	cttttcgaag	gaataactca	1440
ggcaggttca	actatagtag	aaaatctgag	aacctatcgt	cagccagtg	ttgtgtacat	1500
cccaatgatg	ggagaGctgc	gcggtggagc	gtgggttgg	gttgacagcc	agataaattc	1560
ggattatgtt	gaaatgtatg	ctgatgaac	agctcgtgga	aatgtgctgc	agccagaag	1620
gacaatagag	ataaaattta	g				

(2) INFORMATION FOR SEQ ID NO:2107:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 530 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..530

(D) OTHER INFORMATION: / Ceres Seq. ID 1571827

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2107:

Met	Leu	Phe	Leu	Ser	Phe	Ser	Gly	Ile	Trp	Thr	Ala	Leu	Glu	Leu	Leu
1			5						10				15		
Trp	Ala	Ser	Gln	His	Pro	Gly	Val	Lys	Lys	Pro	Tyr	Lys	Asp	Thr	Leu
			20					25					30		
Ile	Asn	Val	Lys	Glu	Leu	Val	Phe	Ser	Lys	Pro	Glu	Gly	Ser	Ser	Gly
			35				40					45			
Thr	Ser	Leu	Asp	Leu	Val	Glu	Arg	Pro	Pro	Gly	Leu	Asn	Asp	Phe	Gly
			50				55				60				
Met	Val	Ala	Trp	Cys	Leu	Asp	Met	Ser	Thr	Pro	Glu	Phe	Pro	Met	Gly
			65			70				75				80	
Arg	Lys	Leu	Leu	Val	Ile	Ala	Asn	Asp	Val	Thr	Phe	Lys	Ala	Gly	Ser
			85					90						95	
Phe	Gly	Pro	Arg	Glu	Asp	Ala	Phe	Phe	Leu	Ala	Val	Thr	Glu	Leu	Ala
			100				105						110		
Cys	Ala	Lys	Lys	Leu	Pro	Leu	Ile	Tyr	Leu	Ala	Ala	Asn	Ser	Gly	Ala
			115				120					125			
Arg	Leu	Gly	Val	Ala	Glu	Glu	Val	Lys	Ala	Cys	Phe	Lys	Val	Gly	Trp
			130				135				140				
Ser	Asp	Glu	Ile	Ser	Pro	Glu	Asn	Gly	Phe	Gln	Tyr	Ile	Tyr	Leu	Ser
			145			150			155					160	
Pro	Glu	Asp	His	Glu	Arg	Ile	Gly	Ser	Ser	Val	Ile	Ala	His	Glu	Val
			165					170						175	
Lys	Leu	Pro	Ser	Gly	Glu	Thr	Arg	Trp	Val	Ile	Asp	Thr	Ile	Val	Gly
			180				185						190		
Lys	Glu	Asp	Gly	Ile	Gly	Val	Glu	Asn	Leu	Thr	Gly	Ser	Gly	Ala	Ile
			195				200					205			
Ala	Gly	Ala	Tyr	Ser	Lys	Ala	Tyr	Asn	Glu	Thr	Phe	Thr	Leu	Thr	Phe
			210				215					220			
Val	Ser	Gly	Arg	Thr	Val	Gly	Ile	Gly	Ala	Tyr	Leu	Ala	Arg	Leu	Gly
			225			230			235					240	
Met	Arg	Cys	Ile	Gln	Arg	Leu	Asp	Gln	Pro	Ile	Ile	Leu	Thr	Gly	Phe
			245					250						255	
Ser	Thr	Leu	Asn	Lys	Leu	Leu	Gly	Arg	Glu	Val	Tyr	Ser	Ser	His	Met
			260				265						270		
Gln	Leu	Gly	Gly	Pro	Lys	Ile	Met	Gly	Thr	Asn	Gly	Val	Val	His	Leu
			275				280					285			
Thr	Val	Ser	Asp	Asp	Leu	Glu	Gly	Val	Ser	Ala	Ile	Leu	Asn	Trp	Leu
			290				295				300				
Ser	Tyr	Ile	Pro	Ala	Tyr	Val	Gly	Gly	Pro	Leu	Pro	Val	Leu	Ala	Pro
			305			310			315					320	
Leu	Asp	Pro	Pro	Glu	Arg	Ile	Val	Glu	Tyr	Val	Pro	Glu	Asn	Ser	Cys

				325						330									335
Asp	Pro	Arg	Ala	Ile	Ala	Gly	Val	Lys	Asp	Asn	Thr	Gly	Lys	Trp					
			340				345					350							
Leu	Gly	Gly	Ile	Phe	Asp	Lys	Asn	Ser	Phe	Ile	Glu	Thr	Leu	Glu	Gly				
		355					360						365						
Trp	Ala	Arg	Thr	Val	Val	Thr	Gly	Arg	Ala	Lys	Leu	Gly	Gly	Ile	Pro				
		370				375						380							
Val	Gly	Val	Val	Ala	Val	Glu	Thr	Gln	Thr	Val	Met	Gln	Ile	Ile	Pro				
		385				390					395				400				
Ala	Asp	Pro	Gly	Gln	Leu	Asp	Ser	His	Glu	Arg	Val	Val	Pro	Gln	Ala				
			405						410					415					
Gly	Gln	Val	Trp	Phe	Pro	Asp	Ser	Ala	Ala	Lys	Thr	Ala	Gln	Ala	Leu				
		420				425							430						
Met	Asp	Phe	Asn	Arg	Glu	Glu	Leu	Pro	Leu	Phe	Ile	Leu	Ala	Asn	Trp				
		435				440						445							
Arg	Gly	Phe	Ser	Gly	Gly	Gln	Arg	Asp	Leu	Phe	Glu	Gly	Ile	Leu	Gln				
		450				455					460								
Ala	Gly	Ser	Thr	Ile	Val	Glu	Asn	Leu	Arg	Thr	Tyr	Arg	Gln	Pro	Val				
		465				470					475				480				
Phe	Val	Tyr	Ile	Pro	Met	Met	Gly	Glu	Leu	Arg	Gly	Gly	Ala	Trp	Val				
			485						490					495					
Val	Val	Asp	Ser	Gln	Ile	Asn	Ser	Asp	Tyr	Val	Glu	Met	Tyr	Ala	Asp				
		500						505					510						
Glu	Thr	Ala	Arg	Gly	Asn	Val	Leu	Glu	Pro	Glu	Gly	Thr	Ile	Glu	Ile				
		515				520							525						

Lys Phe
530

(2) INFORMATION FOR SEQ ID NO:2108:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 466 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..466

(D) OTHER INFORMATION: / Ceres Seq. ID 1571828

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2108:

Met	Val	Ala	Trp	Cys	Leu	Asp	Met	Ser	Thr	Pro	Glu	Phe	Pro	Met	Gly				
1			5						10				15						
Arg	Lys	Leu	Leu	Val	Ile	Ala	Asn	Asp	Val	Thr	Phe	Lys	Ala	Gly	Ser				
			20					25					30						
Phe	Gly	Pro	Arg	Glu	Asp	Ala	Phe	Phe	Leu	Ala	Val	Thr	Glu	Leu	Ala				
		35					40					45							
Cys	Ala	Lys	Lys	Leu	Pro	Leu	Ile	Tyr	Leu	Ala	Ala	Asn	Ser	Gly	Ala				
		50				55					60								
Arg	Leu	Gly	Val	Ala	Glu	Glu	Val	Lys	Ala	Cys	Phe	Lys	Val	Gly	Trp				
		65			70				75			80							
Ser	Asp	Glu	Ile	Ser	Pro	Glu	Asn	Gly	Phe	Gln	Tyr	Ile	Tyr	Leu	Ser				
			85					90				95							
Pro	Glu	Asp	His	Glu	Arg	Ile	Gly	Ser	Ser	Val	Ile	Ala	His	Glu	Val				
		100					105					110							
Lys	Leu	Pro	Ser	Gly	Glu	Thr	Arg	Trp	Val	Ile	Asp	Thr	Ile	Val	Gly				
		115				120					125								
Lys	Glu	Asp	Gly	Ile	Gly	Val	Glu	Asn	Leu	Thr	Gly	Ser	Gly	Ala	Ile				
		130				135					140								
Ala	Gly	Ala	Tyr	Ser	Lys	Ala	Tyr	Asn	Glu	Thr	Phe	Thr	Leu	Thr	Phe				
		145			150				155					160					
Val	Ser	Gly	Arg	Thr	Val	Gly	Ile	Gly	Ala	Tyr	Leu	Ala	Arg	Glu	Gly				
			165					170					175						

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Met Arg Cys Ile Gln Arg Leu Asp Gln Pro Ile Ile Leu Thr Gly Phe
      180      185      190
Ser Thr Leu Asn Lys Leu Leu Gly Arg Glu Val Tyr Ser Ser His Met
      195      200      205
Gln Leu Gly Gly Pro Lys Ile Met Gly Thr Asn Gly Val Val His Leu
      210      215      220
Thr Val Ser Asp Asp Leu Glu Gly Val Ser Ala Ile Leu Asn Trp Leu
      225      230      235      240
Ser Tyr Ile Pro Ala Tyr Val Gly Gly Pro Leu Pro Val Leu Ala Pro
      245      250      255
Leu Asp Pro Pro Glu Arg Ile Val Glu Tyr Val Pro Glu Asn Ser Cys
      260      265      270
Asp Pro Arg Ala Ala Ile Ala Gly Val Lys Asp Asn Thr Gly Lys Trp
      275      280      285
Leu Gly Gly Ile Phe Asp Lys Asn Ser Phe Ile Glu Thr Leu Glu Gly
      290      295      300
Trp Ala Arg Thr Val Val Thr Gly Arg Ala Lys Leu Gly Gly Ile Pro
      305      310      315      320
Val Gly Val Val Ala Val Glu Thr Gln Thr Val Met Gln Ile Ile Pro
      325      330      335
Ala Asp Pro Gly Gln Leu Asp Ser His Glu Arg Val Val Pro Gln Ala
      340      345      350
Gly Gln Val Trp Phe Pro Asp Ser Ala Ala Lys Thr Ala Gln Ala Leu
      355      360      365
Met Asp Phe Asn Arg Glu Glu Leu Pro Leu Phe Ile Leu Ala Asn Trp
      370      375      380
Arg Gly Phe Ser Gly Gly Gln Arg Asp Leu Phe Glu Gly Ile Leu Gln
      385      390      395      400
Ala Gly Ser Thr Ile Val Glu Asn Leu Arg Thr Tyr Arg Gln Pro Val
      405      410      415
Phe Val Tyr Ile Pro Met Met Gly Glu Leu Arg Gly Gly Ala Trp Val
      420      425      430
Val Val Asp Ser Gln Ile Asn Ser Asp Tyr Val Glu Met Tyr Ala Asp
      435      440      445
Glu Thr Ala Arg Gly Asn Val Leu Glu Pro Glu Gly Thr Ile Glu Ile
      450      455      460
Lys Phe
      465

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(2) INFORMATION FOR SEQ ID NO:2109:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 459 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..459

(D) OTHER INFORMATION: / Ceres Seq. ID 1571829

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2109:

```

Met Ser Thr Pro Glu Phe Pro Met Gly Arg Lys Leu Leu Val Ile Ala
1      5      10      15
Asn Asp Val Thr Phe Lys Ala Gly Ser Phe Gly Pro Arg Glu Asp Ala
      20      25      30
Phe Phe Leu Ala Val Thr Glu Leu Ala Cys Ala Lys Lys Leu Pro Leu
      35      40      45
Ile Tyr Leu Ala Ala Asn Ser Gly Ala Arg Leu Gly Val Ala Glu Glu
      50      55      60
Val Lys Ala Cys Phe Lys Val Gly Trp Ser Asp Glu Ile Ser Pro Glu
      65      70      75      80
Asn Gly Phe Gln Tyr Ile Tyr Leu Ser Pro Glu Asp His Glu Arg Ile

```

120

tccggccaag actgtaaaaa ctccgggtggt gatggcgggtg gcggttccgt taccocgact 180
agcattctcc cggaggttcc ttctccttat tctacgtcg agattctcca agcgtttaag 240
ttgatagaca gagacaacga cggagcgtgtc tctagacacg atcttgagtc gttacttagc 300
cggttaggtc ctgactcttt gaaggaggag gagatcaacg ttatgcttaa agaggtggac 360
tgcgacggcg acggtacgat cgtcttgaa gagcttgca gtcgtgtagt ctctttagat 420
ccggctcgtg actcgactga gctgaaggag actttcgagt tctttgacgc ggatcgtaac 480
ggtttgatct cggctgatga gcttctacga gttttctcga ccattggaga tgaRcggtgc 540
acgttagatg attgtaagcg tatgatgca gatgttgatg aggacgggtg t

(2) INFORMATION FOR SEQ ID NO:2111:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 197 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..197

(D) OTHER INFORMATION: / Ceres Seq. ID 1571831

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2111:

Lys Ile His Thr Met Lys Leu Ala Lys Leu Ile Pro Lys Arg Phe Phe
1 5 10 15
Ile Arg Ser Lys Asp Arg Ser Thr Val Ser Lys Ser Pro Thr Ala Phe
20 25 30
Ser Phe Gly Ser Ala Ser Ser Ser Gly Gln Asp Cys Lys Asn Ser
35 40 45
Gly Gly Asp Gly Gly Gly Gly Ser Val Thr Pro Thr Ser Ile Leu Pro
50 55 60
Glu Val Pro Ser Pro Tyr Ser Tyr Val Glu Ile Leu Gln Ala Phe Lys
65 70 75 80
Leu Ile Asp Arg Asp Asn Asp Gly Ala Val Ser Arg His Asp Leu Glu
85 90 95
Ser Leu Leu Ser Arg Leu Gly Pro Asp Pro Leu Thr Glu Glu Glu Ile
100 105 110
Asn Val Met Leu Lys Glu Val Asp Cys Asp Gly Asp Gly Thr Ile Arg
115 120 125
Leu Glu Glu Leu Ala Ser Arg Val Val Ser Leu Asp Pro Ala Arg Asp
130 135 140
Ser Thr Glu Leu Lys Glu Thr Phe Glu Phe Phe Asp Ala Asp Arg Asn
145 150 155 160
Gly Leu Ile Ser Ala Asp Glu Leu Leu Arg Val Phe Ser Thr Ile Gly
165 170 175
Asp Xaa Arg Cys Thr Leu Asp Asp Cys Lys Arg Met Ile Ala Asp Val
180 185 190
Asp Glu Asp Gly Asp
195

(2) INFORMATION FOR SEQ ID NO:2112:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 193 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..193

(D) OTHER INFORMATION: / Ceres Seq. ID 1571832

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2112:

Met Lys Leu Ala Lys Leu Ile Pro Lys Arg Phe Phe Ile Arg Ser Lys
1 5 10 15
Asp Arg Ser Thr Val Ser Lys Ser Pro Thr Ala Phe Ser Phe Gly Ser

gtataaaaa	taagaattct	gaatgctctt	catatttttg	ttttttgtca	ctcttttttt	60
gcctatgctt	acaaacacct	aactctcttg	attatcagtt	tttaagctct	cttcaagctg	120
cagggtacat	caatccaatg	cttcagatct	tagcaagctc	tccaacatgt	cagatgagag	180
tgctataaca	ctcatcagtc	gttcgcatct	accccaagtt	atgggagctct	gttggtttga	240
acacagaaga	gcagagcaac	acaaaagtca	gaggctttag	atgtcttgtc	ctccaactgt	300
ataacagtc	tgtcgaataga	gttgagactc	tctccaattt	agacacacaa	octtactctg	360
acaggatata	tgtcgaatag	attttgagtg	gaggatctgg	atttgacctc	agaagaagaat	420
caaggactat	cgaaaaagct	gttgaggatc	ctcttgagct	acctaaagtct	acctaatgatg	480
cttgagatag	cgtgaacgca	cgtgtgaag	atagtgaagt	gtactctac	cgcacagtca	540
tcttcacaga	tccttttcgt	gaggccaata	actctcttgt	tatctgtgat	acttggaac	600
cagctgggtga	gccattcca	acaaaacaac	gtgctaaagc	ctgtgagatc	tctagttaaca	660
agaagagctc	tgggcaggtt	ccatgtgttg	tgcatgaaca	agagatcaact	ttaactcagc	720
aaaacgtcaa	attgctctta	gtgtggcttg	ggtagcgctt	octctgtctc	cagggtctct	780
actaactgtg	atgtggagct	gacaagaatt	ggggcgctga	catcttaagt	gtcattataa	840
aagcttgttt	agtcctgtga	attaacatta	gtgtactaaa	tggtgaagtt	atgcctggac	900
agtTgagctt	ccaagtgtgc	ccagcgttag	gaattgatgc	aggttgatct	gtttgtgttg	960
cttagatagc	tcttgagaga	ctcacagaga	aagctgtgtg	tgctctaaac	cttgatacca	1020
aaccgataga	gggtgactgg	aacggtgtct	gttgccacac	caattacagt	accaagagca	1080
tgagagagga	agaggagatt	gaagtgatca	agaagcgctat	cttgaacctc	tgcCttgctc	1140
acaaagagga	catcagtgCc	tacggttgac	gaaacgagag	aaggtgtgac	ggaaagcagc	1200
agacagctag	tattgaccag	gttcctatgg	gcgtgcttga	cgctggatgc	tctattctgt	1260
tgggacgtga	caacagagcg	aaagaaagaa	gttactctaa	agatgcgcgt	ccagcatctg	1320
acatggagccc	atacatgttg	acctcaattt	ttggcagagac	cacactctct	tgggagccaa	1380
ctcttggagc	tgaagccttt	cgagctcaaa	ctctctcttt	gaattgttaa	attatgtgtca	1440
accttctcat	actctgatga	acaacagctg	ctatgtgttc	ctccaagttt	tttaaacatt	1500
cgaattaaag	caattgtttg	tgtcttttca	tttcatcttt	taaaaactcag	aatgttatgg	1560

acaatgttca tccttttata ttggttcttt tgactgtt

(2) INFORMATION FOR SEQ ID NO:2114:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 430 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..430

(D) OTHER INFORMATION: / Ceres Seq. ID 1571838

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2114:

Met	Ala	Gln	Ile	Leu	Ala	Ala	Ser	Pro	Thr	Cys	Gln	Met	Arg	Val	Pro
1				5					10					15	
Lys	His	Ser	Ser	Val	Ile	Ala	Ser	Ser	Ser	Lys	Leu	Trp	Ser	Ser	Val
				20				25					30		
Val	Leu	Lys	Gln	Lys	Lys	Gln	Ser	Asn	Asn	Lys	Val	Arg	Gly	Phe	Arg
				35				40				45			
Val	Leu	Ala	Leu	Gln	Ser	Asp	Asn	Ser	Thr	Val	Asn	Arg	Val	Glu	Thr
				50			55				60				
Leu	Leu	Asn	Leu	Asp	Thr	Lys	Pro	Tyr	Ser	Asp	Arg	Ile	Ile	Ala	Glu
65					70				75						80
Tyr	Ile	Trp	Ile	Gly	Gly	Ser	Gly	Ile	Asp	Leu	Arg	Ser	Lys	Ser	Arg
				85					90					95	
Thr	Ile	Glu	Lys	Pro	Val	Glu	Asp	Pro	Ser	Glu	Leu	Pro	Lys	Trp	Asn
				100				105					110		
Tyr	Asp	Gly	Ser	Ser	Thr	Gly	Gln	Ala	Pro	Gly	Glu	Asp	Ser	Glu	Val
				115				120				125			
Ile	Leu	Tyr	Pro	Gln	Ala	Ile	Phe	Arg	Asp	Pro	Phe	Arg	Gly	Gly	Asn
				130			135				140				
Asn	Ile	Leu	Val	Ile	Cys	Asp	Thr	Trp	Thr	Pro	Ala	Gly	Glu	Pro	Ile
145					150					155					160
Pro	Thr	Asn	Lys	Arg	Ala	Lys	Ala	Ala	Glu	Ile	Phe	Ser	Asn	Lys	Lys
				165					170					175	
Val	Ser	Gly	Glu	Val	Pro	Trp	Phe	Gly	Ile	Glu	Gln	Glu	Tyr	Thr	Leu
				180				185					190		
Leu	Gln	Gln	Asn	Val	Lys	Trp	Pro	Leu	Gly	Trp	Pro	Val	Gly	Ala	Phe
				195			200					205			
Pro	Gly	Pro	Gln	Gly	Pro	Tyr	Tyr	Cys	Gly	Val	Gly	Ala	Asp	Lys	Ile
				210			215					220			
Trp	Gly	Arg	Asp	Ile	Ser	Asp	Ala	His	Tyr	Lys	Ala	Cys	Leu	Tyr	Ala
225					230					235					240
Gly	Ile	Asn	Ile	Ser	Gly	Thr	Asn	Gly	Glu	Val	Met	Pro	Gly	Gln	Trp
				245					250					255	
Glu	Phe	Gln	Val	Gly	Pro	Ser	Val	Gly	Ile	Asp	Ala	Gly	Asp	His	Val
				260				265					270		
Trp	Cys	Ala	Arg	Tyr	Leu	Leu	Glu	Arg	Ile	Thr	Glu	Gln	Ala	Gly	Val
				275				280				285			
Val	Leu	Thr	Leu	Asp	Pro	Lys	Pro	Ile	Glu	Gly	Asp	Trp	Asn	Gly	Ala
				290			295				300				
Gly	Cys	His	Thr	Asn	Tyr	Ser	Thr	Lys	Ser	Met	Arg	Glu	Glu	Gly	Gly
305					310					315					320
Phe	Glu	Val	Ile	Lys	Lys	Ala	Ile	Leu	Asn	Leu	Ser	Leu	Arg	His	Lys
				325					330					335	
Glu	His	Ile	Ser	Ala	Tyr	Gly	Glu	Gly	Asn	Glu	Arg	Arg	Leu	Thr	Gly
				340				345					350		
Lys	His	Glu	Thr	Ala	Ser	Ile	Asp	Gln	Phe	Ser	Trp	Gly	Val	Ala	Asn
				355			360					365			
Arg	Gly	Cys	Ser	Ile	Arg	Val	Gly	Arg	Asp	Thr	Glu	Ala	Lys	Gly	Lys
				370			375					380			

Gly Tyr Leu Glu Asp Arg Arg Pro Ala Ser Asn Met Asp Pro Tyr Ile
385 390 395 400
Val Thr Ser Leu Leu Ala Glu Thr Thr Leu Leu Trp Glu Pro Thr Leu
405 410 415
Glu Ala Glu Ala Leu Ala Ala Gln Lys Leu Ser Leu Asn Val
420 425 430

(2) INFORMATION FOR SEQ ID NO:2115:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 418 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..418

(D) OTHER INFORMATION: / Ceres Seq. ID 1571839

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2115:

Met Arg Val Pro Lys His Ser Ser Val Ile Ala Ser Ser Ser Lys Leu
1 5 10 15
Trp Ser Ser Val Val Leu Lys Gln Lys Lys Gln Ser Asn Asn Lys Val
20 25 30
Arg Gly Phe Arg Val Leu Ala Leu Gln Ser Asp Asn Ser Thr Val Asn
35 40 45
Arg Val Glu Thr Leu Leu Asn Leu Asp Thr Lys Pro Tyr Ser Asp Arg
50 55 60
Ile Ile Ala Glu Tyr Ile Trp Ile Gly Gly Ser Gly Ile Asp Leu Arg
65 70 75 80
Ser Lys Ser Arg Thr Ile Glu Lys Pro Val Glu Asp Pro Ser Glu Leu
85 90 95
Pro Lys Trp Asn Tyr Asp Gly Ser Ser Thr Gly Gln Ala Pro Gly Glu
100 105 110
Asp Ser Glu Val Ile Leu Tyr Pro Gln Ala Ile Phe Arg Asp Pro Phe
115 120 125
Arg Gly Gly Asn Asn Ile Leu Val Ile Cys Asp Thr Trp Thr Pro Ala
130 135 140
Gly Glu Pro Ile Pro Thr Asn Lys Arg Ala Lys Ala Ala Glu Ile Phe
145 150 155 160
Ser Asn Lys Lys Val Ser Gly Glu Val Pro Trp Phe Gly Ile Glu Gln
165 170 175
Glu Tyr Thr Leu Leu Gln Gln Asn Val Lys Trp Pro Leu Gly Trp Pro
180 185 190
Val Gly Ala Phe Pro Gly Pro Gln Gly Pro Tyr Tyr Cys Gly Val Gly
195 200 205
Ala Asp Lys Ile Trp Gly Arg Asp Ile Ser Asp Ala His Tyr Lys Ala
210 215 220
Cys Leu Tyr Ala Gly Ile Asn Ile Ser Gly Thr Asn Gly Glu Val Met
225 230 235 240
Pro Gly Gln Trp Glu Phe Gln Val Gly Pro Ser Val Gly Ile Asp Ala
245 250 255
Gly Asp His Val Trp Cys Ala Arg Tyr Leu Leu Glu Arg Ile Thr Glu
260 265 270
Gln Ala Gly Val Val Leu Thr Leu Asp Pro Lys Pro Ile Glu Gly Asp
275 280 285
Trp Asn Gly Ala Gly Cys His Thr Asn Tyr Ser Thr Lys Ser Met Arg
290 295 300
Glu Glu Gly Gly Phe Glu Val Ile Lys Lys Ala Ile Leu Asn Leu Ser
305 310 315 320
Leu Arg His Lys Glu His Ile Ser Ala Tyr Gly Glu Gly Asn Glu Arg
325 330 335
Arg Leu Thr Gly Lys His Glu Thr Ala Ser Ile Asp Gln Phe Ser Trp

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340				345				350							
Gly	Val	Ala	Asn	Arg	Gly	Cys	Ser	Ile	Arg	Val	Gly	Arg	Asp	Thr	Glu
355				360				365							
Ala	Lys	Gly	Lys	Gly	Tyr	Leu	Glu	Asp	Arg	Arg	Pro	Ala	Ser	Asn	Met
370				375				380							
Asp	Pro	Tyr	Ile	Val	Thr	Ser	Leu	Leu	Ala	Glu	Thr	Thr	Leu	Leu	Trp
385				390				395				400			
Glu	Pro	Thr	Leu	Glu	Ala	Glu	Ala	Leu	Ala	Ala	Gln	Lys	Leu	Ser	Leu
				405				410				415			
Asn Val															

(2) INFORMATION FOR SEQ ID NO:2116:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1390 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1390
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571840

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2116:

aataataatt	agactttctg	actttctcac	gaacctctct	gtctcgctcca	ttacttaaaa	60
accaaattctt	tcattctctt	ccttcaccag	ttgactctct	ttcaatctat	ctctgaaatc	120
ctcaactctcc	taccgcaaaa	ccatgaactc	caacgaccag	gatccgattc	cggttcagacc	180
cgaagacaac	aacttctccg	gttccaaaac	ctacgccatg	agcgccaaaa	ctatgctaaag	240
tgcaatagta	atctctctct	tcgtcgctcat	tttaattggtc	ttctctccatc	tttaacgctcg	300
ttgggtatctc	ctccggtgctc	gtagacgtca	ttctcgtcgt	cgtagccgta	accgtcgccg	360
tacgattggtt	ttcttcaccg	ctgatccttc	caacgccgca	acttcgctcg	tcgcttcaag	420
tggaacttgat	ccaaaacgtta	ttaaattctct	ttctgttttc	actttctccg	acgagactca	480
taaaactccg	ccgaatgctg	cggtttggtt	atcggaattc	gaagagagcg	agacgggtcg	540
ggttttgcc	aattgtcaac	atacttttca	tgttgattgt	attgatattg	ggtttcaatc	600
tcattccact	tgctctctt	gtcgatctct	cgttgagcct	ctcgccggga	ttgaatcaac	660
ggcgccggcg	agggagaggg	aagttgtgat	tgcggttgat	tcgatccgg	ttttggtaat	720
tgaaccgagt	tctagctctg	gattgacgga	tgaaccacat	ggatctggat	cttctcaagt	780
gctgagggaa	gattccggga	gaaaaccggc	ggcgattgag	gttcggagga	ggaacttttag	840
cgagtttgaa	gatgagttga	ctcggagaga	ctcgccggcg	agtcagtcgt	ttaggtctctc	900
gatgagtcgg	atgttatctt	tcactcggat	gttgagttaga	gatagaagaa	gcgcttcgct	960
tcctatcgcc	ggaGctccgc	cgctatcgcc	gacgttaaag	tgccggatag	agatgaccga	1020
gtcacatata	gaacggggag	gagaaagag	taggtgactt	gtcacgtgtt	gggtctctgat	1080
tggtttaatg	ttaacccggg	gtaaaaaaag	gaattactac	aagtcaacag	gctttttctct	1140
aggtgttgat	tctggcgccc	aaggacaact	ggcgtaaaact	gagcttccag	gaatcaaatat	1200
tcacggtcta	ttatgattag	atagggttaga	tagatttgtg	taacgatgta	caaagtcatc	1260
tacaatatgt	aatctgtttc	catttatttt	atacatattc	ttttttttat	aattttcgaa	1320
gtctacacaa	actcttttat	taaaacacaa	tccaatggtc	ataattgtga	taaaagacttt	1380
gcksawwatt						

(2) INFORMATION FOR SEQ ID NO:2117:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 304 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..304
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571841

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2117:

Met	Asn	Ser	Asn	Asp	Gln	Asp	Pro	Ile	Pro	Phe	Arg	Pro	Glu	Asp	Asn
1			5					10					15		

```

Asn Phe Ser Gly Ser Lys Thr Tyr Ala Met Ser Gly Lys Ile Met Leu
      20      25      30
Ser Ala Ile Val Ile Leu Phe Phe Val Val Ile Leu Met Val Phe Leu
      35      40      45
His Leu Tyr Ala Arg Trp Tyr Leu Leu Arg Ala Arg Arg His Leu
      50      55      60
Arg Arg Arg Ser Arg Asn Arg Arg Ala Thr Met Val Phe Phe Thr Ala
      65      70      75      80
Asp Pro Ser Thr Ala Ala Thr Ser Val Val Ala Ser Arg Gly Leu Asp
      85      90      95
Pro Asn Val Ile Lys Ser Leu Pro Val Phe Thr Phe Ser Asp Glu Thr
      100      105      110
His Lys Asp Pro Ile Glu Cys Ala Val Cys Leu Ser Glu Phe Glu Glu
      115      120      125
Ser Glu Thr Gly Arg Val Leu Pro Asn Cys Gln His Thr Phe His Val
      130      135      140
Asp Cys Ile Asp Met Trp Phe His Ser His Ser Thr Cys Pro Leu Cys
      145      150      155      160
Arg Ser Leu Val Glu Pro Leu Ala Gly Ile Glu Ser Thr Ala Ala Ala
      165      170      175
Arg Glu Arg Glu Val Val Ile Ala Val Asp Ser Asp Pro Val Leu Val
      180      185      190
Ile Glu Pro Ser Ser Ser Ser Gly Leu Thr Asp Glu Pro His Gly Ser
      195      200      205
Gly Ser Ser Gln Met Leu Arg Glu Asp Ser Gly Arg Lys Pro Ala Ala
      210      215      220
Ile Glu Val Pro Arg Arg Thr Phe Ser Glu Phe Glu Asp Glu Leu Thr
      225      230      235      240
Arg Arg Asp Ser Pro Ala Ser Gln Ser Phe Arg Ser Pro Met Ser Arg
      245      250      255
Met Leu Ser Phe Thr Arg Met Leu Ser Arg Asp Arg Arg Ser Ala Ser
      260      265      270
Ser Pro Ile Ala Gly Ala Pro Pro Leu Ser Pro Thr Leu Ser Cys Arg
      275      280      285
Ile Gln Met Thr Glu Ser Asp Ile Glu Arg Gly Gly Glu Glu Ser Arg
      290      295      300

```

(2) INFORMATION FOR SEQ ID NO:2118:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 279 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..279
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571842

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2118:

```

Met Ser Gly Lys Ile Met Leu Ser Ala Ile Val Ile Leu Phe Phe Val
1      5      10      15
Val Ile Leu Met Val Phe Leu His Leu Tyr Ala Arg Trp Tyr Leu Leu
      20      25      30
Arg Ala Arg Arg Arg His Leu Arg Arg Arg Ser Arg Asn Arg Arg Ala
      35      40      45
Thr Met Val Phe Phe Thr Ala Asp Pro Ser Thr Ala Ala Thr Ser Val
      50      55      60
Val Ala Ser Arg Gly Leu Asp Pro Asn Val Ile Lys Ser Leu Pro Val
      65      70      75      80
Phe Thr Phe Ser Asp Glu Thr His Lys Asp Pro Ile Glu Cys Ala Val

```

(2) INFORMATION FOR SEQ ID NO:2119:

(A) LENGTH: 274 amino acids

(C) STRANDEDNESS:

(D) TOPOLOGY: \lim

(D) TOPOLOGY: linear
MOLECULE TYPE: peptide

FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..274

(D) OTHER INFORMATION: / Ceres Seq. ID 1571843

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2119:

Met	Leu	Ser	Ala	Ile	Val	Ile	Leu	Phe	Phe	Val	Val	Ile	Leu	Met	Val
			5						10					15	
Phe	Leu	His	Leu	Tyr	Ala	Arg	Trp	Tyr	Leu	Leu	Arg	Ala	Arg	Arg	Arg
			20					25					30		
His	Leu	Arg	Arg	Arg	Ser	Arg	Asn	Arg	Arg	Ala	Thr	Met	Val	Phe	Phe
		35					40					45			
Thr	Ala	Asp	Pro	Ser	Thr	Ala	Ala	Thr	Ser	Val	Val	Ala	Ser	Arg	Gly
		50					55				60				
Leu	Asp	Pro	Asn	Val	Ile	Lys	Ser	Leu	Pro	Val	Phe	Thr	Phe	Ser	Asp
		65			70					75				80	
Glu	Thr	His	Lys	Asp	Pro	Ile	Glu	Cys	Ala	Val	Cys	Leu	Ser	Glu	Phe
			85						90					95	
Glu	Glu	Ser	Glu	Thr	Gly	Arg	Val	Leu	Pro	Asn	Cys	Gln	His	Thr	Phe
			100					105					110		
His	Val	Asp	Cys	Ile	Asp	Met	Trp	Phe	His	Ser	His	Ser	Thr	Cys	Pro
		115					120					125			
Leu	Cys	Arg	Ser	Leu	Val	Glu	Pro	Leu	Ala	Gly	Ile	Glu	Ser	Thr	Ala
		130				135					140				
Ala	Ala	Arg	Glu	Arg	Glu	Val	Val	Ile	Ala	Val	Asp	Ser	Asp	Pro	Val
		145			150					155				160	
Leu	Val	Ile	Glu	Pro	Ser	Ser	Ser	Ser	Gly	Leu	Thr	Asp	Glu	Pro	His
			165						170					175	
Gly	Ser	Gly	Ser	Ser	Gln	Met	Leu	Arg	Glu	Asp	Ser	Gly	Arg	Lys	Pro
			180					185					190		

Ala Ala Ile Glu Val Pro Arg Arg Thr Phe Ser Glu Phe Glu Asp Glu
195 200 205
Leu Thr Arg Arg Asp Ser Pro Ala Ser Gln Ser Phe Arg Ser Pro Met
210 215 220
Ser Arg Met Leu Ser Phe Thr Arg Met Leu Ser Arg Asp Arg Arg Ser
225 230 235 240
Ala Ser Ser Pro Ile Ala Gly Ala Pro Pro Leu Ser Pro Thr Leu Ser
245 250 255
Cys Arg Ile Gln Met Thr Glu Ser Asp Ile Glu Arg Gly Gly Glu Glu
260 265 270
Ser Arg

(2) INFORMATION FOR SEQ ID NO:2120:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1405 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1405
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571844

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2120:

aaaaaatttta ttagccattc gagaaacaag gcatctctat ttttttgctt cttctaataag 60
actttcttcgt cactgatctc ccacgacgat ctcccaaaact cattttctcta cgttcatcga 120
tctctctcttt tctcgttttgc tctacgaaaa tcagccatgg atgaagagta cgagggtatt 180
gttctcggcga ccggtctcaa ggagtgtatc ctacgcggtc tcctttccgt cgatgggtgc 240
aagggtgcttc acatggacag gaatgactac tatggtggag aatcaaatctc tcttaatctc 300
aatcagctttt ggaagaagtt caggggagaa gagaaggctc ctgagcattt aggtgctagc 360
cgggattaca atgttgacat gatgcctaag tttatgatgg gaaatggcaa gcttgttcgt 420
acccttatct atacagatgt tacaagaagt ttgtccttca aagctgttga tggaaagctat 480
gttttcgtca aaggaaaggt tcaaaagggt ccagctactc ctatggaggc cctgaaatct 540
tctctcatgg gcataattga gaaacgtcga gccgcgaagt ttttcagttt tgttcaggaa 600
tacgatgaga aggacccaaa aacacacgat ggaatggatt tgaccagagt tacaacaaag 660
gaactgattg cgaaatatgg tcttgatggc aacactattg actttattgg tcacgcagtg 720
gcactTcaca cgaatgacca acatctcgat caaccgcctt ttgatactgt aatgagaatg 780
aagctctatg cggaatctct tgcacgtttc caaggaaacat ctccatatat ttatcctctc 840
tatgggttgg gagaactacc ccaggcattt gcacgactta gtgctgtcta tggttggcaca 900
tatatgttga acaaacctga gtgcaaggta gagtttgacg agggaggtaa ggttattggt 960
gtaaacatcg agggagagac tgcataaatgc aaaaagattg tgtgtgacc tcatacactg 1020
ccgaacaagg ttaggaaagt tggcagggtt gctcgggcca tcgccattat gagccaccgc 1080
attccaaaac ccaatgatgc tcaactcagt caggctatca taccccagaa acagtgtggc 1140
cgcaaatcgg atatgtatgt cttctgttgt tcgtactccc acaacgttgc tcccaaggga 1200
aaattcattg cattttgtgc tacagatgca gagactgata accctcaaac cgaactaaa 1260
cctggaactg atctctttggg tctctgttat gagatatct tcgacatgta tgaatagatc 1320
gagcctgtca acgagccaga gttggacaac tgctttatat caacgagcta tgatgctaca 1380
acacactttg agacaactgt tgcgg

(2) INFORMATION FOR SEQ ID NO:2121:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 416 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..416
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571845

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2121:

Met Asp Glu Glu Tyr Glu Val Ile Val Leu Gly Thr Gly Leu Lys Glu

1				5					10					15
Cys	Ile	Leu	Ser	Gly	Leu	Leu	Ser	Val	Asp	Gly	Val	Lys	Val	Leu
			20					25					30	His
Met	Asp	Arg	Asn	Asp	Tyr	Tyr	Gly	Gly	Glu	Ser	Thr	Ser	Leu	Asn
			35				40					45		Leu
Asn	Gln	Leu	Trp	Lys	Lys	Phe	Arg	Gly	Glu	Glu	Lys	Ala	Pro	Glu
			50			55					60			His
Leu	Gly	Ala	Ser	Arg	Asp	Tyr	Asn	Val	Asp	Met	Met	Pro	Lys	Phe
			65		70				75					80
Met	Gly	Asn	Gly	Lys	Leu	Val	Arg	Thr	Leu	Ile	His	Thr	Asp	Val
			85					90					95	Thr
Lys	Tyr	Leu	Ser	Phe	Lys	Ala	Val	Asp	Gly	Ser	Tyr	Val	Phe	Val
			100				105						110	Lys
Gly	Lys	Val	Gln	Lys	Val	Pro	Ala	Thr	Pro	Met	Glu	Ala	Leu	Lys
			115				120					125		Ser
Ser	Leu	Met	Gly	Ile	Phe	Glu	Lys	Arg	Arg	Ala	Gly	Lys	Phe	Phe
			130			135					140			Ser
Phe	Val	Gln	Glu	Tyr	Asp	Glu	Lys	Asp	Pro	Lys	Thr	His	Asp	Gly
			145		150				155					Met
Asp	Leu	Thr	Arg	Val	Thr	Thr	Lys	Glu	Leu	Ile	Ala	Lys	Tyr	Gly
			165					170						Leu
Asp	Gly	Asn	Thr	Ile	Asp	Phe	Ile	Gly	His	Ala	Val	Ala	Leu	His
			180				185						190	Thr
Asn	Asp	Gln	His	Leu	Asp	Gln	Pro	Ala	Phe	Asp	Thr	Val	Met	Arg
			195				200					205		Met
Lys	Leu	Tyr	Ala	Glu	Ser	Leu	Ala	Arg	Phe	Gln	Gly	Thr	Ser	Pro
			210			215					220			Tyr
Ile	Tyr	Pro	Leu	Tyr	Gly	Leu	Gly	Glu	Leu	Pro	Gln	Ala	Phe	Ala
			225		230				235					Arg
Leu	Ser	Ala	Val	Tyr	Gly	Gly	Thr	Tyr	Met	Leu	Asn	Lys	Pro	Glu
			245					250					255	Cys
Lys	Val	Glu	Phe	Asp	Glu	Gly	Gly	Lys	Val	Ile	Gly	Val	Thr	Ser
			260				265						270	Glu
Gly	Glu	Thr	Ala	Lys	Cys	Lys	Lys	Ile	Val	Cys	Asp	Pro	Ser	Tyr
			275				280					285		Leu
Pro	Asn	Lys	Val	Arg	Lys	Ile	Gly	Arg	Val	Ala	Arg	Ala	Ile	Ala
			290			295					300			Ile
Met	Ser	His	Pro	Ile	Pro	Asn	Thr	Asn	Asp	Ser	His	Ser	Val	Gln
			305		310				315					Val
Ile	Ile	Pro	Gln	Lys	Gln	Leu	Ala	Arg	Lys	Ser	Asp	Met	Tyr	Val
			325						330				335	Phe
Cys	Cys	Ser	Tyr	Ser	His	Asn	Val	Ala	Pro	Lys	Gly	Lys	Phe	Ile
			340				345						350	Ala
Phe	Val	Ser	Thr	Asp	Ala	Glu	Thr	Asp	Asn	Pro	Gln	Thr	Glu	Leu
			355				360					365		Lys
Pro	Gly	Thr	Asp	Leu	Leu	Gly	Pro	Val	Asp	Glu	Ile	Phe	Phe	Asp
			370		375						380			Met
Tyr	Asp	Arg	Tyr	Glu	Pro	Val	Asn	Glu	Pro	Glu	Leu	Asp	Asn	Cys
			385		390				395					400
Ile	Ser	Thr	Ser	Tyr	Asp	Ala	Thr	Thr	His	Phe	Glu	Thr	Thr	Val
			405					410					415	Ala

- (2) INFORMATION FOR SEQ ID NO:2122:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 384 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1.1384

(D) OTHER INFORMATION: / Ceres Seq. ID 1571846

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2122:

Met	Asp	Arg	Asn	Asp	Tyr	Tyr	Gly	Gly	Glu	Ser	Thr	Ser	Leu	Asn	Leu
1			5						10				15		
Asn	Gln	Leu	Trp	Lys	Lys	Phe	Arg	Gly	Glu	Glu	Lys	Ala	Pro	Glu	His
			20					25					30		
Leu	Gly	Ala	Ser	Arg	Asp	Tyr	Asn	Val	Asp	Met	Met	Pro	Lys	Phe	Met
		35					40				45				
Met	Gly	Asn	Gly	Lys	Leu	Val	Arg	Thr	Leu	Ile	His	Thr	Asp	Val	Thr
		50					55				60				
Lys	Tyr	Leu	Ser	Phe	Lys	Ala	Val	Asp	Gly	Ser	Tyr	Val	Phe	Val	Lys
		65				70				75					80
Gly	Lys	Val	Gln	Lys	Val	Pro	Ala	Thr	Pro	Met	Glu	Ala	Leu	Lys	Ser
			85						90					95	
Ser	Leu	Met	Gly	Ile	Phe	Glu	Lys	Arg	Arg	Ala	Gly	Lys	Phe	Phe	Ser
			100					105					110		
Phe	Val	Gln	Glu	Tyr	Asp	Glu	Lys	Asp	Pro	Lys	Thr	His	Asp	Gly	Met
			115				120					125			
Asp	Leu	Thr	Arg	Val	Thr	Thr	Lys	Glu	Leu	Ile	Ala	Lys	Tyr	Gly	Leu
							135				140				
Asp	Gly	Asn	Thr	Ile	Asp	Phe	Ile	Gly	His	Ala	Val	Ala	Leu	His	Thr
					150				155					160	
Asn	Asp	Gln	His	Leu	Asp	Gln	Pro	Ala	Phe	Asp	Thr	Val	Met	Arg	Met
				165					170					175	
Lys	Leu	Tyr	Ala	Glu	Ser	Leu	Ala	Arg	Phe	Gln	Gly	Thr	Ser	Pro	Tyr
			180					185					190		
Ile	Tyr	Pro	Leu	Tyr	Gly	Leu	Gly	Glu	Leu	Pro	Gln	Ala	Phe	Ala	Arg
			195				200					205			
Leu	Ser	Ala	Val	Tyr	Gly	Gly	Thr	Tyr	Met	Leu	Asn	Lys	Pro	Glu	Cys
							215				220				
Lys	Val	Glu	Phe	Asp	Glu	Gly	Gly	Lys	Val	Ile	Gly	Val	Thr	Ser	Glu
					230					235					240
Gly	Glu	Thr	Ala	Lys	Cys	Lys	Lys	Ile	Val	Cys	Asp	Pro	Ser	Tyr	Leu
				245					250					255	
Pro	Asn	Lys	Val	Arg	Lys	Ile	Gly	Arg	Val	Ala	Arg	Ala	Ile	Ala	Ile
			260				265						270		
Met	Ser	His	Pro	Ile	Pro	Asn	Thr	Asn	Asp	Ser	His	Ser	Val	Gln	Val
							280					285			
Ile	Ile	Pro	Gln	Lys	Gln	Leu	Ala	Arg	Lys	Ser	Asp	Met	Tyr	Val	Phe
						295					300				
Cys	Cys	Ser	Tyr	Ser	His	Asn	Val	Ala	Pro	Lys	Gly	Lys	Phe	Ile	Ala
					310					315				320	
Phe	Val	Ser	Thr	Asp	Ala	Glu	Thr	Asp	Asn	Pro	Gln	Thr	Glu	Leu	Lys
				325					330					335	
Pro	Gly	Thr	Asp	Leu	Leu	Gly	Pro	Val	Asp	Glu	Ile	Phe	Phe	Asp	Met
				340				345					350		
Tyr	Asp	Arg	Tyr	Glu	Pro	Val	Asn	Glu	Pro	Glu	Leu	Asp	Asn	Cys	Phe
			355				360				365				
Ile	Ser	Thr	Ser	Tyr	Asp	Ala	Thr	Thr	His	Phe	Glu	Thr	Thr	Val	Ala
					375						380				

(2) INFORMATION FOR SEQ ID NO:2123:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 342 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..342

(D) OTHER INFORMATION: / Ceres Seq. ID 1571847

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2123:

Met	Met	Pro	Lys	Phe	Met	Met	Gly	Asn	Gly	Lys	Leu	Val	Arg	Thr	Leu	
1				5					10					15		
Ile	His	Thr	Asp	Val	Thr	Lys	Tyr	Leu	Ser	Phe	Lys	Ala	Val	Asp	Gly	
			20					25					30			
Ser	Tyr	Val	Phe	Val	Lys	Gly	Lys	Val	Gln	Lys	Val	Pro	Ala	Thr	Pro	
			35				40					45				
Met	Glu	Ala	Leu	Lys	Ser	Ser	Leu	Met	Gly	Ile	Phe	Glu	Lys	Arg	Arg	
			50				55				60					
Ala	Gly	Lys	Phe	Phe	Ser	Phe	Val	Gln	Glu	Tyr	Asp	Glu	Lys	Asp	Pro	
65					70				75					80		
Lys	Thr	His	Asp	Gly	Met	Asp	Leu	Thr	Arg	Val	Thr	Thr	Lys	Glu	Leu	
			85					90						95		
Ile	Ala	Lys	Tyr	Gly	Leu	Asp	Gly	Asn	Thr	Ile	Asp	Phe	Ile	Gly	His	
			100					105					110			
Ala	Val	Ala	Leu	His	Thr	Asn	Asp	Gln	His	Leu	Asp	Gln	Pro	Ala	Phe	
			115				120					125				
Asp	Thr	Val	Met	Arg	Met	Lys	Leu	Tyr	Ala	Glu	Ser	Leu	Ala	Arg	Phe	
			130				135					140				
Gln	Gly	Thr	Ser	Pro	Tyr	Ile	Tyr	Pro	Leu	Tyr	Gly	Leu	Gly	Glu	Leu	
145					150				155					160		
Pro	Gln	Ala	Phe	Ala	Arg	Leu	Ser	Ala	Val	Tyr	Gly	Gly	Thr	Tyr	Met	
					165				170					175		
Leu	Asn	Lys	Pro	Glu	Cys	Lys	Val	Glu	Phe	Asp	Glu	Gly	Gly	Lys	Val	
					180			185					190			
Ile	Gly	Val	Thr	Ser	Glu	Gly	Glu	Thr	Ala	Lys	Cys	Lys	Lys	Ile	Val	
					195			200					205			
Cys	Asp	Pro	Ser	Tyr	Leu	Pro	Asn	Lys	Val	Arg	Lys	Ile	Gly	Arg	Val	
					210		215					220				
Ala	Arg	Ala	Ile	Ala	Ile	Met	Ser	His	Pro	Ile	Pro	Asn	Thr	Asn	Asp	
225					230					235				240		
Ser	His	Ser	Val	Gln	Val	Ile	Ile	Pro	Gln	Lys	Gln	Leu	Ala	Arg	Lys	
					245				250					255		
Ser	Asp	Met	Tyr	Val	Phe	Cys	Cys	Ser	Tyr	Ser	His	Asn	Val	Ala	Pro	
					260			265					270			
Lys	Gly	Lys	Phe	Ile	Ala	Phe	Val	Ser	Thr	Asp	Ala	Glu	Thr	Asp	Asn	
			275					280				285				
Pro	Gln	Thr	Glu	Leu	Lys	Pro	Gly	Thr	Asp	Leu	Leu	Gly	Pro	Val	Asp	
					290			295				300				
Glu	Ile	Phe	Phe	Asp	Met	Tyr	Asp	Arg	Tyr	Glu	Pro	Val	Asn	Glu	Pro	
					310				315					320		
Glu	Leu	Asp	Asn	Cys	Phe	Ile	Ser	Thr	Ser	Tyr	Asp	Ala	Thr	Thr	His	
					325				330					335		
Phe	Glu	Thr	Thr	Val	Ala											
					340											

(2) INFORMATION FOR SEQ ID NO:2124:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 884 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..884

(D) OTHER INFORMATION: / Ceres Seq. ID 1571867

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2124:

```

acacaattca gattccaatt ttctcaaaat ctaaaatcaa tctctcaaat ctctcaaccg    60
tgatcaagat gcagatcttc gtttaagactc tcaccggaaa gactatcacc ctgcgaggtgg    120
aaagctctcg caccatcgac aacgttaagg ccaagatcca ggataaggaa ggtattctctc    180
cggatcagca gaggcttatt ttccgccgga agcagttgga ggatggccgc acgtttggcgg    240
attacaatat ccagaaggaa tccaccctcc acttggttct caggctccgt ggtgggtatgc    300
agattttcgt taaaaaccCta acgggaaga gaattactct tgaggtggag agctctgaca    360
ccattgacaa cgtaacaggcc aagatccaag ataaggaggg tattctctcg gaccagcaga    420
ggttgatctt cgccggaaag caacttgagg acggcagaaac ttggcggtat tacaacatcc    480
agaaggagtc tacgctttat ttggtcttgc gtctgcgtgg aggtatgcag atcttctgtaa    540
agacttttgc cggaaagacc atcaactctg aagttgagag ctccgacacc attgataacg    600
tgaaggctaa gatccaggac aaggaaggca ttctctcgga ccagcagcgt ctcatctctg    660
cggaagaaga ccttgaggat ggacgtactt tggccgacta caacatccag aaggagtcta    720
ctcttcactt ggtctctcgt ctccgtggtg gtttctaaac cttgtctctc tctcttatgg    780
ttactgaacc aagttcatgt atcgtttcat ctagtacttt ggtgggttat gttttggggc    840
catgtacagc ctctgataaa taattgatcg actatgttcc cgctc

```

(2) INFORMATION FOR SEQ ID NO:2125:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 251 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..251

(D) OTHER INFORMATION: / Ceres Seq. ID 1571868

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2125:

```

Thr Ile Gln Ile Pro Ile Phe Ser Asn Ser Lys Ile Asn Leu Ser Asn
1           5           10           15
Leu Ser Thr Val Ile Lys Met Gln Ile Phe Val Lys Thr Leu Thr Gly
20           25           30
Lys Thr Ile Thr Leu Glu Val Glu Ser Ser Asp Thr Ile Asp Asn Val
35           40           45
Lys Ala Lys Ile Gln Asp Lys Glu Gly Ile Pro Pro Asp Gln Gln Arg
50           55           60
Leu Ile Phe Ala Gly Lys Gln Leu Glu Asp Gly Arg Thr Leu Ala Asp
65           70           75           80
Tyr Asn Ile Gln Lys Glu Ser Thr Leu His Leu Val Leu Arg Leu Arg
85           90           95
Gly Gly Met Gln Ile Phe Val Lys Thr Leu Thr Gly Lys Thr Ile Thr
100          105          110
Leu Glu Val Glu Ser Ser Asp Thr Ile Asp Asn Val Lys Ala Lys Ile
115          120          125
Gln Asp Lys Glu Gly Ile Pro Pro Asp Gln Gln Arg Leu Ile Phe Ala
130          135          140
Gly Lys Gln Leu Glu Asp Gly Arg Thr Leu Ala Asp Tyr Asn Ile Gln
145          150          155          160
Lys Glu Ser Thr Leu His Leu Val Leu Arg Leu Arg Gly Gly Met Gln
165          170          175          180
Ile Phe Val Lys Thr Leu Thr Gly Lys Thr Ile Thr Leu Glu Val Glu
185          190          195
Ser Ser Asp Thr Ile Asp Asn Val Lys Ala Lys Ile Gln Asp Lys Glu
200          205          210
Gly Ile Pro Pro Asp Gln Gln Arg Leu Ile Phe Ala Gly Lys Gln Leu
215          220          225
Glu Asp Gly Arg Thr Leu Ala Asp Tyr Asn Ile Gln Lys Glu Ser Thr
230          235          240          245
Leu His Leu Val Leu Arg Leu Arg Gly Gly Phe
250

```

(2) INFORMATION FOR SEQ ID NO:2126:

(i) SEQUENCE CHARACTERISTICS:

2025 RELEASE UNDER E.O. 14176

- (A) LENGTH: 229 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..229
(D) OTHER INFORMATION: / Ceres Seq. ID 1571869

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2126:

Met Gln Ile Phe Val Lys Thr Leu Thr Gly Lys Thr Ile Thr Leu Glu
1 5 10 15
Val Glu Ser Ser Asp Thr Ile Asp Asn Val Lys Ala Lys Ile Gln Asp
20 25 30
Lys Glu Gly Ile Pro Pro Asp Gln Gln Arg Leu Ile Phe Ala Gly Lys
35 40 45
Gln Leu Glu Asp Gly Arg Thr Leu Ala Asp Tyr Asn Ile Gln Lys Glu
50 55 60
Ser Thr Leu His Leu Val Leu Arg Leu Arg Gly Gly Met Gln Ile Phe
65 70 75 80
Val Lys Thr Leu Thr Gly Lys Thr Ile Thr Leu Glu Val Glu Ser Ser
85 90 95
Asp Thr Ile Asp Asn Val Lys Ala Lys Ile Gln Asp Lys Glu Gly Ile
100 105 110
Pro Pro Asp Gln Gln Arg Leu Ile Phe Ala Gly Lys Gln Leu Glu Asp
115 120 125
Gly Arg Thr Leu Ala Asp Tyr Asn Ile Gln Lys Glu Ser Thr Leu His
130 135 140
Leu Val Leu Arg Leu Arg Gly Gly Met Gln Ile Phe Val Lys Thr Leu
145 150 155 160
Thr Gly Lys Thr Ile Thr Leu Glu Val Glu Ser Ser Asp Thr Ile Asp
165 170 175
Asn Val Lys Ala Lys Ile Gln Asp Lys Glu Gly Ile Pro Pro Asp Gln
180 185 190
Gln Arg Leu Ile Phe Ala Gly Lys Gln Leu Glu Asp Gly Arg Thr Leu
195 200 205
Ala Asp Tyr Asn Ile Gln Lys Glu Ser Thr Leu His Leu Val Leu Arg
210 215 220
Leu Arg Gly Gly Phe
225

(2) INFORMATION FOR SEQ ID NO:2127:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 153 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..153
(D) OTHER INFORMATION: / Ceres Seq. ID 1571870

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2127:

Met Gln Ile Phe Val Lys Thr Leu Thr Gly Lys Thr Ile Thr Leu Glu
1 5 10 15
Val Glu Ser Ser Asp Thr Ile Asp Asn Val Lys Ala Lys Ile Gln Asp
20 25 30
Lys Glu Gly Ile Pro Pro Asp Gln Gln Arg Leu Ile Phe Ala Gly Lys
35 40 45
Gln Leu Glu Asp Gly Arg Thr Leu Ala Asp Tyr Asn Ile Gln Lys Glu
50 55 60
Ser Thr Leu His Leu Val Leu Arg Leu Arg Gly Met Gln Ile Phe

65	70	75	80
Val Lys Thr Leu Thr Gly Lys Thr Ile Thr Leu Glu Val Glu Ser Ser			
	85	90	95
Asp Thr Ile Asp Asn Val Lys Ala Lys Ile Gln Asp Lys Glu Gly Ile			
	100	105	110
Pro Pro Asp Gln Gln Arg Leu Ile Phe Ala Gly Lys Gln Leu Glu Asp			
	115	120	125
Gly Arg Thr Leu Ala Asp Tyr Asn Ile Gln Lys Glu Ser Thr Leu His			
	130	135	140
Leu Val Leu Arg Leu Arg Gly Gly Phe			
145	150		

(2) INFORMATION FOR SEQ ID NO:2128:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 833 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..833
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571871

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2128:

caaaccgaagt	ttcttcttaa	gctgtatttg	aaatggtata	tatttcacac	accaaacaga	60
tcagaagcta	aaaggtaata	atataatggc	ggatttgagg	gacgaaaaag	gtaacccaat	120
ccatctaacc	gacacacagg	gaaacccaat	tgtcgacctg	actgatgagc	acggtaaccc	180
catgtaccta	accgggtgtg	ttagctccac	tcctcagcat	aaggagagta	ctaccagcga	240
cattgcagag	caccctaact	gcaccgtttg	agaaacacat	ccggcagctg	ctccaactgg	300
gtctggtgct	gccaccgctg	ccactgcgac	aggagtctct	gctggtactg	gagcaaccac	360
cacaggggcag	caacaccatg	ggtcgcttga	agagcatctt	cgctggtctg	gaagttcatc	420
tagctctagc	tcggaggatg	acggggcaag	agggaggagg	aagaagagca	taaaggagaa	480
aattaaagag	aagtttcagta	gcggcaaaac	caaggacgaa	caaacaccaa	ccaccgcac	540
aacaacagga	octgccacta	ccgaccaacc	tcacgagaag	aagggcattc	tcgagaagat	600
caaggacaag	cttccccggc	accataacca	caaccaccca	tgaacaccaa	tcatatgacg	660
tcctttgttac	atgaataaat	cgtttgcaag	aatttCatta	gggcttatga	agaatcaata	720
tatatgtcta	gtgaagttaa	ctaaatttta	gttgtgtttg	cttgcagttt	gtgaatgtga	780
ccatcgtggt	atcatgttct	tgtttattta	taaagaagga	actgtatttt	gct	

(2) INFORMATION FOR SEQ ID NO:2129:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 185 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..185
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571872

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2129:

Met Ala Asp Leu Arg Asp Glu Lys Gly Asn Pro Ile His Leu Thr Asp							
1	5	10	15				
Thr Gln Gly Asn Pro Ile Val Asp Leu Thr Asp Glu His Gly Asn Pro							
	20	25	30				
Met Tyr Leu Thr Gly Val Val Ser Thr Pro Gln His Lys Glu Ser							
	35	40	45				
Thr Thr Ser Asp Ile Ala Glu His Pro Thr Ser Thr Val Gly Glu Thr							
	50	55	60				
His Pro Ala Ala Ala Pro Thr Gly Ala Gly Ala Ala Thr Ala Ala Thr							
65	70	75	80				
Ala Thr Gly Val Ser Ala Gly Thr Gly Ala Thr Thr Thr Gly Gln Gln							
	85	90	95				

His His Gly Ser Leu Glu Glu His Leu Arg Arg Ser Gly Ser Ser Ser
100 105 110
Ser Ser Ser Ser Glu Asp Asp Gly Gln Gly Gly Arg Arg Lys Lys Ser
115 120 125
Ile Lys Glu Lys Ile Lys Glu Lys Phe Ser Ser Gly Lys His Lys Asp
130 135 140
Glu Gln Thr Pro Thr Thr Ala Thr Thr Thr Gly Pro Ala Thr Thr Asp
145 150 155 160
Gln Pro His Glu Lys Lys Gly Ile Leu Glu Lys Ile Lys Asp Lys Leu
165 170 175
Pro Gly His His Asn His Asn His Pro
180 185

(2) INFORMATION FOR SEQ ID NO:2130:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 153 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..153

(D) OTHER INFORMATION: / Ceres Seq. ID 1571873

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2130:

Met Tyr Leu Thr Gly Val Val Ser Ser Thr Pro Gln His Lys Glu Ser
1 5 10 15
Thr Thr Ser Asp Ile Ala Glu His Pro Thr Ser Thr Val Gly Glu Thr
20 25 30
His Pro Ala Ala Ala Pro Thr Gly Ala Gly Ala Ala Thr Ala Ala Thr
35 40 45
Ala Thr Gly Val Ser Ala Gly Thr Gly Ala Thr Thr Thr Gly Gln Gln
50 55 60
His His Gly Ser Leu Glu Glu His Leu Arg Arg Ser Gly Ser Ser Ser
65 70 75 80
Ser Ser Ser Ser Glu Asp Asp Gly Gln Gly Gly Arg Arg Lys Lys Ser
85 90 95
Ile Lys Glu Lys Ile Lys Glu Lys Phe Ser Ser Gly Lys His Lys Asp
100 105 110
Glu Gln Thr Pro Thr Thr Ala Thr Thr Thr Gly Pro Ala Thr Thr Asp
115 120 125
Gln Pro His Glu Lys Lys Gly Ile Leu Glu Lys Ile Lys Asp Lys Leu
130 135 140
Pro Gly His His Asn His Asn His Pro
145 150

(2) INFORMATION FOR SEQ ID NO:2131:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1091 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -

(B) LOCATION: 1..1091

(D) OTHER INFORMATION: / Ceres Seq. ID 1571874

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2131:

atcttatctt gctttaaagc ttttggcgag tttgcttggt tggtagtggt tggttatgga 60
gtctccgttc aaacctgatg tcgtcagagg tcaagtggct ctcataccg gtggtggatc 120
cggtatcggt tttgagatct cttctcagtt ttgcacaacat ggagctctcta tcgctatcat 180
gggacgacga aaacaagtcc tcgatcagcg cgtctctgct cttcgatctc ttggaatcca 240
ggctattgga ttggaaggtg atgttcgtaa gcaagaagat gcgagaagag ttgtggaagc 300

aacttatcag	catttttgga	aacttgatat	tcttggttaac	gccgctgctg	ggaattttct	360
ggctgctgct	gaggattttg	ctcctaattg	cttcagaaca	gtcttagaca	ttgatcgctg	420
aggaacatct	aacatgtgtc	acgcagctct	caagtatctt	aagaaaggag	cgctggaag	480
agactcatca	agcgggtggag	gttcgattat	taacattagc	gcgactttgc	actacacgpc	540
ttcttggtac	caaatatcatg	tctctgCagc	caaggctgca	gttgatgcta	ccacaagaaa	600
cttggcattg	gagtggggaa	ctgactatga	tattagagtg	aacgggattg	ctccaggtcc	660
tattggagtg	acacctggaa	tgagttaact	tgtacctgag	gagattgaaa	acaaaaccag	720
agagtacatg	cctctttata	aagttggaga	gaagtgggat	atcgctatgg	ctgcactcta	780
cctcagctgt	gattctggga	aatatgtgag	cggactaaca	atggtggtag	atggaggact	840
gtggcttagc	aaacctggcc	acttgcttaa	agaagcggtg	aagcaactct	ctcgtgcggt	900
ggagaagag	tctagggcca	agcctgtttg	tctcccaacc	agcaactgtg	agatcatttg	960
aatttcagat	atcaataaag	tgcaacttga	aaaaatgttt	tggtttattg	aattacattg	1020
gagactgaga	aaatggtatt	aagattatgt	agatcaaact	atcttatgca	caataaagta	1080
gctttctttg	c					

(2) INFORMATION FOR SEQ ID NO:2132:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 316 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..316
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571875

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2132:

Phe	Tyr	Phe	Val	Leu	Lys	Leu	Leu	Ala	Ser	Leu	Leu	Val	Cys	Glu	Cys
1			5						10					15	
Val	Val	Met	Glu	Ser	Pro	Phe	Lys	Pro	Asp	Val	Val	Arg	Gly	Gln	Val
			20					25					30		
Ala	Leu	Ile	Thr	Gly	Gly	Gly	Ser	Gly	Ile	Gly	Phe	Glu	Ile	Ser	Ser
		35					40					45			
Gln	Phe	Gly	Lys	His	Gly	Ala	Ser	Ile	Ala	Ile	Met	Gly	Arg	Arg	Lys
		50				55									
Gln	Val	Leu	Asp	Asp	Ala	Val	Ser	Ala	Leu	Arg	Ser	Leu	Gly	Ile	Gln
		65			70					75				80	
Ala	Ile	Gly	Leu	Glu	Gly	Asp	Val	Arg	Lys	Gln	Glu	Asp	Ala	Arg	Arg
		85						90					95		
Val	Val	Glu	Ala	Thr	Tyr	Gln	His	Phe	Gly	Lys	Leu	Asp	Ile	Leu	Val
		100						105					110		
Asn	Ala	Ala	Ala	Gly	Asn	Phe	Leu	Ala	Ala	Glu	Asp	Leu	Ser	Pro	
		115					120			125					
Asn	Gly	Phe	Arg	Thr	Val	Leu	Asp	Ile	Asp	Ala	Val	Gly	Thr	Phe	Asn
		130				135				140					
Met	Cys	His	Ala	Ala	Leu	Lys	Tyr	Leu	Lys	Lys	Gly	Ala	Pro	Gly	Arg
		145			150					155				160	
Asp	Ser	Ser	Ser	Gly	Gly	Gly	Ser	Ile	Ile	Asn	Ile	Ser	Ala	Thr	Leu
				165				170						175	
His	Tyr	Thr	Ala	Ser	Trp	Tyr	Gln	Ile	His	Val	Ser	Ala	Ala	Lys	Ala
			180					185						190	
Ala	Val	Asp	Ala	Thr	Thr	Arg	Asn	Leu	Ala	Leu	Glu	Trp	Gly	Thr	Asp
		195					200					205			
Tyr	Asp	Ile	Arg	Val	Asn	Gly	Ile	Ala	Pro	Gly	Pro	Ile	Gly	Gly	Thr
		210				215						220			
Pro	Gly	Met	Ser	Lys	Leu	Val	Pro	Glu	Glu	Ile	Glu	Asn	Lys	Thr	Arg
		225			230					235					240
Glu	Tyr	Met	Pro	Leu	Tyr	Lys	Val	Gly	Glu	Lys	Trp	Asp	Ile	Ala	Met
			245					250						255	
Ala	Ala	Leu	Tyr	Leu	Ser	Cys	Asp	Ser	Gly	Lys	Tyr	Val	Ser	Gly	Leu
		260						265					270		
Thr	Met	Val	Val	Asp	Gly	Gly	Leu	Trp	Leu	Ser	Lys	Pro	Arg	His	Leu

275 280 285
Pro Lys Glu Ala Val Lys Gln Leu Ser Arg Ala Val Glu Lys Arg Ser
290 295 300
Arg Ala Lys Pro Val Gly Leu Pro Thr Ser Lys Leu
305 310 315

(2) INFORMATION FOR SEQ ID NO:2133:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 298 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..298
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571876

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2133:

Met Glu Ser Pro Phe Lys Pro Asp Val Val Arg Gly Gln Val Ala Leu
1 5 10 15
Ile Thr Gly Gly Gly Ser Gly Ile Gly Phe Glu Ile Ser Ser Gln Phe
20 25 30
Gly Lys His Gly Ala Ser Ile Ala Ile Met Gly Arg Arg Lys Gln Val
35 40 45
Leu Asp Asp Ala Val Ser Ala Leu Arg Ser Leu Gly Ile Gln Ala Ile
50 55 60
Gly Leu Glu Gly Asp Val Arg Lys Gln Glu Asp Ala Arg Arg Val Val
65 70 75 80
Glu Ala Thr Tyr Gln His Phe Gly Lys Leu Asp Ile Leu Val Asn Ala
85 90 95
Ala Ala Gly Asn Phe Leu Ala Ala Ala Glu Asp Leu Ser Pro Asn Gly
100 105 110
Phe Arg Thr Val Leu Asp Ile Asp Ala Val Gly Thr Phe Asn Met Cys
115 120 125
His Ala Ala Leu Lys Tyr Leu Lys Lys Gly Ala Pro Gly Arg Asp Ser
130 135 140
Ser Ser Gly Gly Gly Ser Ile Ile Asn Ile Ser Ala Thr Leu His Tyr
145 150 155 160
Thr Ala Ser Trp Tyr Gln Ile His Val Ser Ala Ala Lys Ala Ala Val
165 170 175
Asp Ala Thr Thr Arg Asn Leu Ala Leu Glu Trp Gly Thr Asp Tyr Asp
180 185 190
Ile Arg Val Asn Gly Ile Ala Pro Gly Pro Ile Gly Gly Thr Pro Gly
195 200 205
Met Ser Lys Leu Val Pro Glu Glu Ile Glu Asn Lys Thr Arg Glu Tyr
210 215 220
Met Pro Leu Tyr Lys Val Gly Glu Lys Trp Asp Ile Ala Met Ala Ala
225 230 235 240
Leu Tyr Leu Ser Cys Asp Ser Gly Lys Tyr Val Ser Gly Leu Thr Met
245 250 255
Val Val Asp Gly Gly Leu Trp Leu Ser Lys Pro Arg His Leu Pro Lys
260 265 270
Glu Ala Val Lys Gln Leu Ser Arg Ala Val Glu Lys Arg Ser Arg Ala
275 280 285
Lys Pro Val Gly Leu Pro Thr Ser Lys Leu
290 295

(2) INFORMATION FOR SEQ ID NO:2134:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 257 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..257
(D) OTHER INFORMATION: / Ceres Seq. ID 1571877
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2134:

```
Met Gly Arg Arg Lys Gln Val Leu Asp Asp Ala Val Ser Ala Leu Arg
1      5      10      15
Ser Leu Gly Ile Gln Ala Ile Gly Leu Glu Gly Asp Val Arg Lys Gln
20      25      30
Glu Asp Ala Arg Arg Val Val Glu Ala Thr Tyr Gln His Phe Gly Lys
35      40      45
Leu Asp Ile Leu Val Asn Ala Ala Gly Asn Phe Leu Ala Ala Ala
50      55      60
Glu Asp Leu Ser Pro Asn Gly Phe Arg Thr Val Leu Asp Ile Asp Ala
65      70      75
Val Gly Thr Phe Asn Met Cys His Ala Ala Leu Lys Tyr Leu Lys Lys
85      90      95
Gly Ala Pro Gly Arg Asp Ser Ser Ser Gly Gly Ser Ile Ile Asn
100     105     110
Ile Ser Ala Thr Leu His Tyr Thr Ala Ser Trp Tyr Gln Ile His Val
115     120     125
Ser Ala Ala Lys Ala Ala Val Asp Ala Thr Thr Arg Asn Leu Ala Leu
130     135     140
Glu Trp Gly Thr Asp Tyr Asp Ile Arg Val Asn Gly Ile Ala Pro Gly
145     150     155
Pro Ile Gly Gly Thr Pro Gly Met Ser Lys Leu Val Pro Glu Glu Ile
165     170     175
Glu Asn Lys Thr Arg Glu Tyr Met Pro Leu Tyr Lys Val Gly Glu Lys
180     185     190
Trp Asp Ile Ala Met Ala Ala Leu Tyr Leu Ser Cys Asp Ser Gly Lys
195     200     205
Tyr Val Ser Gly Leu Thr Met Val Val Asp Gly Gly Leu Trp Leu Ser
210     215     220
Lys Pro Arg His Leu Pro Lys Glu Ala Val Lys Gln Leu Ser Arg Ala
225     230     235
Val Glu Lys Arg Ser Arg Ala Lys Pro Val Gly Leu Pro Thr Ser Lys
245     250     255
Leu
```

(2) INFORMATION FOR SEQ ID NO:2135:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1253 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..1253
(D) OTHER INFORMATION: / Ceres Seq. ID 1571884

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2135:

```
gaaacataat ttctaagtgc tcaattttct tttggtctct ccaaaactctc tccccggaac 60
gatgtgctta tacagaagag cattcgtttg ttttcaacca gcccttattt gacacttggc 120
actatgggtta agaaaaattt gccggccggc tgcaaaattg gagatgttct tttgtttgac 180
ccgaccaagg aagagatagt caccgtcccc gacaaaacaa ttcccgaaga gctcatggat 240
gaagaaatga tgggagcttc coattggatgg ggatttttct gtgaccggag tgatcgttcc 300
gtacgtatca gcgacatttt caatcctttg gcatccaaaa caaacctgtc catgatcttc 360
ctgcctaggc ttacgggtct gcccaactggc caaacccgaaa aagtttttaa cgtagaccatg 420
tccttctctt ctctctctgg tgagggaagac tgtgtagtgg ctatcaagtt ttccggatgc 480
cagctgagtc tgtgcagacc cggttgtgac cttgagtggg ctaacattgt aaccctttc 540
```

aactgttttg	acaactcaag	tctcatgtat	tccaaaagag	acccaaaatt	ttacttacct	600
gccccctggag	gcaactactat	gttctctat	gacctccact	tcaaatcaga	tgactccccct	660
gggctccatg	agttgttcta	tcgagaccat	ccagtggtgg	atcagtcaga	gtggagctt	720
ttgagttcat	gttcaggac	ggaataccct	gtggagtcac	cttcgtgtgg	tgaccgtttT	780
cctagtcaaa	tggtatgcgc	ttggtctttt	tttctgTcaa	attttaaaagg	aacttaccac	840
aaaacaaaga	ggttgatgg	ttttagagaa	gaggagacga	cggagagaaa	aattatgtgt	900
tacaccgagg	acattggaga	catgtgcatt	ttccttgcaa	gcaacgaggc	ttctgtatc	960
ccgcttagct	cctgcctcgg	cctcaagcct	aactgcgtct	attatatggg	acgtgggttt	1020
ggtttttacc	atctcactac	cggagaggca	catcattata	aagctcccaa	aggtgcacca	1080
agcgctctga	ccgccccotta	ctggcttctc	ccatttgcta	tctagtata	ctatttctgt	1140
ctttgtgtac	acttgaagtt	tctctctacc	ggtttaaatt	ggtaacacct	aaagattggt	1200
aatgttctaa	gttcaatttt	aagttaaaac	atccagacc	agaatcccg	ctt	

(2) INFORMATION FOR SEQ ID NO:2136:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 369 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..369

(D) OTHER INFORMATION: / Ceres Seq. ID 1571885

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2136:

Met	Ser	Gln	Phe	Leu	Phe	Gly	Leu	Ser	Lys	Leu	Ser	Pro	Arg	Asn	Asp
1				5					10					15	
Val	Leu	Ile	Gln	Lys	Ser	Ile	Arg	Leu	Phe	Ser	Thr	Ser	Pro	Tyr	Leu
			20					25					30		
Thr	Leu	Gly	Thr	Arg	Val	Lys	Lys	Ile	Leu	Pro	Ala	Gly	Cys	Lys	Ile
		35					40					45			
Gly	Asp	Val	Leu	Leu	Phe	Asp	Pro	Thr	Lys	Glu	Glu	Ile	Val	Thr	Val
	50					55					60				
Pro	Asp	Lys	Thr	Ile	Pro	Glu	Glu	Leu	Met	Asp	Glu	Glu	Met	Met	Gly
	65					70				75					80
Ala	Ser	His	Gly	Trp	Gly	Phe	Phe	Cys	Asp	Arg	Thr	Asp	Arg	Ser	Val
			85						90					95	
Arg	Ile	Ser	Asp	Ile	Phe	Asn	Pro	Leu	Ala	Ser	Lys	Thr	Asn	Pro	Val
			100					105					110		
Met	Ile	Pro	Leu	Pro	Arg	Leu	Thr	Ala	Leu	Pro	Thr	Gly	Gln	Thr	Glu
			115			120						125			
Lys	Val	Phe	Asn	Val	Ala	Met	Ser	Phe	Ser	Ser	Pro	Leu	Gly	Glu	Glu
	130					135					140				
Asp	Cys	Val	Val	Ala	Ile	Lys	Phe	Ser	Gly	Ile	Gln	Leu	Ser	Leu	Cys
	145				150					155					160
Arg	Pro	Gly	Cys	Asp	Leu	Glu	Trp	Thr	Asn	Ile	Val	Thr	Pro	Phe	Asn
			165						170					175	
Cys	Leu	Asp	Asn	Ser	Ser	Leu	Met	Tyr	Ser	Lys	Arg	Asp	Gln	Lys	Phe
			180					185					190		
Tyr	Leu	Pro	Ala	Pro	Gly	Gly	Asn	Tyr	Leu	Phe	Ser	Tyr	Asp	Leu	His
		195					200					205			
Phe	Lys	Ser	Asp	Asp	Ser	Pro	Gly	Leu	His	Glu	Leu	Phe	Tyr	Arg	Asp
	210					215						220			
His	Pro	Val	Leu	Asp	Gln	Ser	Glu	Trp	Glu	Leu	Leu	Ser	Ser	Cys	Ser
	225				230					235					240
Arg	Thr	Glu	Tyr	Leu	Val	Glu	Ser	Pro	Ser	Gly	Gly	Asp	Arg	Phe	Pro
			245						250					255	
Ser	Gln	Met	Val	Cys	Ala	Trp	Leu	Leu	Phe	Arg	Ser	Asn	Leu	Lys	Gly
			260					265					270		
Ile	Tyr	His	Lys	Thr	Lys	Arg	Leu	Met	Val	Phe	Arg	Glu	Glu	Glu	Thr
		275					280					285			
Thr	Glu	Gly	Lys	Ile	Met	Cys	Tyr	Thr	Glu	Asp	Ile	Gly	Asp	Met	Cys

290	295	300
Ile Phe Leu Ala Ser Asn Glu Ala Phe Cys Ile Pro Ala Ser Ser Cys		
305	310	315
Leu Gly Leu Lys Pro Asn Cys Val Tyr Tyr Met Gly Arg Gly Phe Gly		
	325	330
Phe Tyr Asp Leu Thr Thr Gly Glu Ala His His Tyr Lys Ala Pro Lys		
	340	345
Gly Ala Pro Ser Ala Leu Thr Ala Pro Tyr Trp Leu Pro Phe Ala		
	355	360
		365
Ile		

(2) INFORMATION FOR SEQ ID NO:2137:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 296 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..296

- (D) OTHER INFORMATION: / Ceres Seq. ID 1571886

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2137:

Met Asp Glu Glu Met Met Gly Ala Ser His Gly Trp Gly Phe Phe Cys	
1	5
Asp Arg Thr Asp Arg Ser Val Arg Ile Ser Asp Ile Phe Asn Pro Leu	
	20
Ala Ser Lys Thr Asn Pro Val Met Ile Pro Leu Pro Arg Leu Thr Ala	
	35
Leu Pro Thr Gly Gln Thr Glu Lys Val Phe Asn Val Ala Met Ser Phe	
	50
Ser Ser Pro Leu Gly Glu Asp Cys Val Val Ala Ile Lys Phe Ser	
	65
Gly Ile Gln Leu Ser Leu Cys Arg Pro Gly Cys Asp Leu Glu Trp Thr	
	85
Asn Ile Val Thr Pro Phe Asn Cys Leu Asp Asn Ser Ser Leu Met Tyr	
	100
Ser Lys Arg Asp Gln Lys Phe Tyr Leu Pro Ala Pro Gly Gly Asn Tyr	
	115
Leu Phe Ser Tyr Asp Leu His Phe Lys Ser Asp Asp Ser Pro Gly Leu	
	130
His Glu Leu Phe Tyr Arg Asp His Pro Val Leu Asp Gln Ser Glu Trp	
	145
Glu Leu Leu Ser Ser Cys Ser Arg Thr Glu Tyr Leu Val Glu Ser Pro	
	165
Ser Gly Gly Asp Arg Phe Pro Ser Gln Met Val Cys Ala Trp Leu Leu	
	180
Phe Arg Ser Asn Leu Lys Gly Ile Tyr His Lys Thr Lys Arg Leu Met	
	195
Val Phe Arg Glu Glu Glu Thr Thr Glu Gly Lys Ile Met Cys Tyr Thr	
	210
Glu Asp Ile Gly Asp Met Cys Ile Phe Leu Ala Ser Asn Glu Ala Phe	
	225
Cys Ile Pro Ala Ser Ser Cys Leu Gly Leu Lys Pro Asn Cys Val Tyr	
	245
Tyr Met Gly Arg Gly Phe Gly Phe Tyr Asp Leu Thr Thr Gly Glu Ala	
	260
His His Tyr Lys Ala Pro Lys Gly Ala Pro Ser Ala Leu Thr Ala Pro	
	275
Tyr Trp Leu Pro Pro Phe Ala Ile	
	290
	295

(2) INFORMATION FOR SEQ ID NO:2138:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 292 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..292

(D) OTHER INFORMATION: / Ceres Seq. ID 1571887

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2138:

Met Met Gly Ala Ser His Gly Trp Gly Phe Phe Cys Asp Arg Thr Asp
1 5 10 15
Arg Ser Val Arg Ile Ser Asp Ile Phe Asn Pro Leu Ala Ser Lys Thr
20 25 30
Asn Pro Val Met Ile Pro Leu Pro Arg Leu Thr Ala Leu Pro Thr Gly
35 40 45
Gln Thr Glu Lys Val Phe Asn Val Ala Met Ser Phe Ser Ser Pro Leu
50 55 60
Gly Glu Glu Asp Cys Val Val Ala Ile Lys Phe Ser Gly Ile Gln Leu
65 70 75 80
Ser Leu Cys Arg Pro Gly Cys Asp Leu Glu Trp Thr Asn Ile Val Thr
85 90 95
Pro Phe Asn Cys Leu Asp Asn Ser Ser Leu Met Tyr Ser Lys Arg Asp
100 105 110
Gln Lys Phe Tyr Leu Pro Ala Pro Gly Gly Asn Tyr Leu Phe Ser Tyr
115 120 125
Asp Leu His Phe Lys Ser Asp Asp Ser Pro Gly Leu His Glu Leu Phe
130 135 140
Tyr Arg Asp His Pro Val Leu Asp Gln Ser Glu Trp Glu Leu Leu Ser
145 150 155 160
Ser Cys Ser Arg Thr Glu Tyr Leu Val Glu Ser Pro Ser Gly Gly Asp
165 170 175
Arg Phe Pro Ser Gln Met Val Cys Ala Trp Leu Leu Phe Arg Ser Asn
180 185 190
Leu Lys Gly Ile Tyr His Lys Thr Lys Arg Leu Met Val Phe Arg Glu
195 200 205
Glu Glu Thr Thr Glu Gly Lys Ile Met Cys Tyr Thr Glu Asp Ile Gly
210 215 220
Asp Met Cys Ile Phe Leu Ala Ser Asn Glu Ala Phe Cys Ile Pro Ala
225 230 235 240
Ser Ser Cys Leu Gly Leu Lys Pro Asn Cys Val Tyr Tyr Met Gly Arg
245 250 255
Gly Phe Gly Phe Tyr Asp Leu Thr Thr Gly Glu Ala His His Tyr Lys
260 265 270
Ala Pro Lys Gly Ala Pro Ser Ala Leu Thr Ala Pro Tyr Trp Leu Pro
275 280 285
Pro Phe Ala Ile
290

(2) INFORMATION FOR SEQ ID NO:2139:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1312 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1312

(D) OTHER INFORMATION: / Ceres Seq. ID 1571888

(X1) SEQUENCE DESCRIPTION: SEQ ID:193						
acctataaaa	cacacactct	caggagagaa	gtgttataga	tctgtctctc	tttccctaaa	60
caacactggt	attttctctc	cagccgcgcc	atgtctctgc	tctcagatct	cgtaataacct	120
aacctcacgc	atgccacccg	gaagaatcac	ccgcgaatac	tatgcgtcgg	tatgcctcga	180
atggatatca	gaagacaagc	caggacaccta	ccagggccag	tgcactgatc	atcaaaagct	240
ccaagtgtga	actcacgacg	atccagcacta	ggtcagcgtc	ctggagaaag	cagtgaagtc	300
attctatacc	ctcgggaact	attcaaggat	cccttcagga	aggcccaaca	catctctTgt	360
gtgtgtgtgt	gottacaacac	cagctgggtga	tctctattca	accacaagaa	ggcacaacgc	420
tgataaagtc	tttcagccacc	ccagcgtttgc	caaggagagg	ccttggttat	ggattgagca	480
agaaataact	ttgtgcaaa	aggatgtgtga	ctggccaatt	gctgtgcctg	ttgtgtgcta	540
ccctgtgccct	cagggaactct	actacttgtgt	tgtgggaagt	gacaaaagca	ttgtgctgta	600
catgtgtggat	gctcactaca	aggcctctgt	ttacgcgggt	attgtgtatt	cttgtataca	660
tgagaaagtc	atgccaggcc	agtgggaagt	ccaagtccgc	ctctgtgagg	gtattagttc	720
ttgttgatcaa	ttgtgggttg	ctcgataact	tctcagagg	atactagaa	tctctgtgtg	780
aatttgtcagc	tttcgaccga	aacacagctc	gggtgtactg	aatggagctg	gagctcaact	840
caactcacgc	actaagacaa	tcagaaaacga	tggaggatata	gaagtgtatc	agaaagcgat	900
agggaagctt	Tcagctgaaa	cgaaaagaac	acattctgtc	tatccgtgaa	ggaaaaccgt	960
gtgctctcac	tggaagaacac	gtaaccccgac	acatacaaac	attctcttgg	ggagtcgcga	1020
accctgtgagc	ctcagttaga	gtggagcgtg	acacagagaa	ggaatctaaa	gggtactctg	1080
aagacagaag	gccagctctc	aacatggatc	cttacgttgt	caactccaat	atcgtcgtga	1140
cgccactact	cggttgtgat	acacatttcat	gatttgattt	ctctccaat	tggtttgttt	1200
tttttccctt	ctgtattgac	ttttcgataa	taaaaaataa	attcttatta	ttgcggtattg	1260
ttgtgcactt	ttgttatttg	tttcagataa	taaaaaagc	gcttcttaag	gt	

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 195 amino acids

(C) STRANDEDNESS:

MOLECULE TYPE: peptid

(A) NAME

(A) NAME/KEY: peptide

(B) LOCATION: 1..195

(D) OTHER INFORMATION: / Ceres Seq. ID 1571889

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2140:

[illegible]

(2) INFORMATION FOR SEQ ID NO:2141:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 151 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..151
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571890

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2141:

Met	Gln	Lys	Asp	Val	Asn	Trp	Pro	Ile	Gly	Trp	Pro	Val	Gly	Gly	Trp
1			5						10				15		
Pro	Gly	Pro	Gln	Gly	Pro	Tyr	Tyr	Cys	Gly	Val	Gly	Ala	Asp	Lys	Ala
			20					25				30			
Ile	Gly	Arg	Asp	Ile	Val	Asp	Ala	His	Tyr	Lys	Ala	Cys	Leu	Tyr	Ala
			35				40					45			
Gly	Ile	Gly	Ile	Ser	Gly	Ile	Asn	Gly	Glu	Val	Met	Pro	Gly	Gln	Trp
			50			55					60				
Glu	Phe	Gln	Val	Gly	Pro	Val	Glu	Gly	Ile	Ser	Ser	Gly	Asp	Gln	Val
65				70					75					80	
Trp	Val	Ala	Arg	Tyr	Leu	Leu	Glu	Arg	Ile	Thr	Glu	Ile	Ser	Gly	Val
			85					90					95		
Ile	Val	Ser	Phe	Asp	Pro	Lys	Pro	Val	Pro	Gly	Asp	Trp	Asn	Gly	Ala
			100				105						110		
Gly	Ala	His	Cys	Asn	Tyr	Ser	Thr	Lys	Thr	Met	Arg	Asn	Asp	Gly	Gly
			115				120					125			
Leu	Glu	Val	Ile	Lys	Lys	Ala	Ile	Gly	Lys	Leu	Ser	Ala	Glu	Thr	Gln
			130			135					140				
Arg	Thr	His	Cys	Cys	Leu	Arg									
145				150											

(2) INFORMATION FOR SEQ ID NO:2142:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 657 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..657
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571891

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2142:

ggtggggacca	aaggaggagg	ccatggggggc	cttgacattg	atgagctcat	gaaacacagc	60
aaaggaggag	gaggaggtaa	caaaggGcaat	cataatcata	gcgcctaaagg	gattgtgggt	120
ggcccaatgg	gtccaggcgg	tccgatgggt	ccaggcggctc	cgatgggtcca	agggtggctcg	180
atgggtatga	tgggtccagg	tgggtccgatg	agtatgatgg	gtccaggcgg	tcctatgggt	240
ccaatgggtg	gcccaaggcgg	ctcttaccoca	gcggttccaa	gcttggccaat	gagtgagggt	300
ggaggatatt	atccaggggcc	gcctcaggcca	agtcagcaaa	tgaaccaaca	acaatatatg	360
caaatgatga	tgaaccaaca	gcagcaacaa	caacaacaac	aacaagctgc	agctcatggt	420
ggctatggcg	gtggtcacgg	tggcgacatg	taccatccga	tgatgtacgc	tcggccttat	480
cctgcagtta	attatgtcca	cctccaccoca	atgcgcgctc	ctcactcgga	ttcttatact	540
catatgttca	gcgatgagaa	tccaggtagt	tgtagtatta	tgtgatcctc	ttttgtaatg	600
ttatttagaa	tatggacatg	tatgcttgct	ttagtcttat	gttttttttt	tttgggg	

(2) INFORMATION FOR SEQ ID NO:2143:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 194 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..194

(D) OTHER INFORMATION: / Ceres Seq. ID 1571892

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2143:

Gly Gly Thr Lys Gly Gly Gly His Gly Gly Leu Asp Ile Asp Glu Leu
1 5 10 15
Met Lys His Ser Lys Gly Gly Gly Gly Asn Lys Gly Asn His Asn
20 25 30
His Ser Ala Lys Gly Ile Gly Gly Gly Pro Met Gly Pro Gly Gly Pro
35 40 45
Met Gly Pro Gly Gly Pro Met Gly Gln Gly Gly Pro Met Gly Met Met
50 55 60
Gly Pro Gly Gly Pro Met Ser Met Met Gly Pro Gly Gly Pro Met Gly
65 70 75 80
Pro Met Gly Gly Gln Gly Gly Ser Tyr Pro Ala Val Gln Gly Leu Pro
85 90 95
Met Ser Gly Gly Gly Gly Tyr Tyr Pro Gly Pro Pro Gln Ala Ser Gln
100 105 110
Gln Met Asn Gln Gln Gln Tyr Met Gln Met Met Met Asn Gln Gln Gln
115 120 125
Gln Gln Gln Gln Gln Gln Ala Ala Ala His Gly Gly Tyr Gly Gly
130 135 140
Gly His Gly Gly Asp Met Tyr His Pro Met Met Tyr Ala Arg Pro Tyr
145 150 155 160
Pro Ala Val Asn Tyr Ala His Pro Pro Pro Met Pro Pro Pro His Ser
165 170 175
Asp Ser Tyr Thr His Met Phe Ser Asp Glu Asn Pro Gly Ser Cys Ser
180 185 190
Ile Met

(2) INFORMATION FOR SEQ ID NO:2144:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 178 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..178

(D) OTHER INFORMATION: / Ceres Seq. ID 1571893

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2144:

Met Lys His Ser Lys Gly Gly Gly Gly Gly Asn Lys Gly Asn His Asn
1 5 10 15
His Ser Ala Lys Gly Ile Gly Gly Gly Pro Met Gly Pro Gly Gly Pro
20 25 30
Met Gly Pro Gly Gly Pro Met Gly Gln Gly Gly Pro Met Gly Met Met
35 40 45
Gly Pro Gly Gly Pro Met Ser Met Met Gly Pro Gly Gly Pro Met Gly
50 55 60
Pro Met Gly Gly Gln Gly Gly Ser Tyr Pro Ala Val Gln Gly Leu Pro
65 70 75 80
Met Ser Gly Gly Gly Gly Tyr Tyr Pro Gly Pro Pro Gln Ala Ser Gln
85 90 95
Gln Met Asn Gln Gln Gln Tyr Met Gln Met Met Met Asn Gln Gln Gln
100 105 110
Gln Gln Gln Gln Gln Gln Ala Ala Ala His Gly Gly Tyr Gly Gly
115 120 125
Gly His Gly Gly Asp Met Tyr His Pro Met Met Tyr Ala Arg Pro Tyr

130 135 140
Pro Ala Val Asn Tyr Ala His Pro Pro Pro Met Pro Pro Pro His Ser
145 150 155 160
Asp Ser Tyr Thr His Met Phe Ser Asp Glu Asn Pro Gly Ser Cys Ser
165 170 175
Ile Met

(2) INFORMATION FOR SEQ ID NO:2145:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 152 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..152
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571894

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2145:

Met Gly Pro Gly Gly Pro Met Gly Pro Gly Gly Pro Met Gly Gln Gly
1 5 10 15
Gly Pro Met Gly Met Met Gly Pro Gly Gly Pro Met Ser Met Met Gly
20 25 30
Pro Gly Gly Pro Met Gly Pro Met Gly Gly Gln Gly Gly Ser Tyr Pro
35 40 45
Ala Val Gln Gly Leu Pro Met Ser Gly Gly Gly Gly Tyr Tyr Pro Gly
50 55 60
Pro Pro Gln Ala Ser Gln Gln Met Asn Gln Gln Gln Tyr Met Gln Met
65 70 75 80
Met Met Asn Gln Gln Gln Gln Gln Gln Gln Gln Ala Ala Ala
85 90 95
His Gly Gly Tyr Gly Gly Gly His Gly Gly Asp Met Tyr His Pro Met
100 105 110
Met Tyr Ala Arg Pro Tyr Pro Ala Val Asn Tyr Ala His Pro Pro Pro
115 120 125
Met Pro Pro Pro His Ser Asp Ser Tyr Thr His Met Phe Ser Asp Glu
130 135 140
Asn Pro Gly Ser Cys Ser Ile Met
145 150

(2) INFORMATION FOR SEQ ID NO:2146:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 982 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..982
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571898

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2146:

aaagcccaaa tgttgctcaa ggcctctccc gctctctctc tcttgagctc cggctccacc 60
ggcggtgGaa atctgtttcc tccgtcgaga aattcgtcga atcgtctggt ttctccgagt 120
ggatctaagt ttctgtttca ggcggcgaaa ggaacgaaca cgaagtctgt aaccggagtt 180
gtattcgaac cttttgagga agtgaagaaa gaactggacc tcgttcccac tacccctttt 240
gtttctctcg ctgcgccaca gtctctccgac gatgctgaat ctgcacatca cgaatcagatc 300
aacgtggagt acaacgtctc gtatgtctac catgccctgt atgcctactt tgacagagac 360
aatgtcggtc tgaagggttt cgcgaagttt ttttaacgatt cgagtcttga agaacgaggt 420
gattcgtaga tgtttatgga gtatcagaac aagcgtgggt ggagagtga gctcgaagtc 480
attttgatgc ccgtctctga gtttgatcac gaggagaagg gagatgcatt gcatgcgatg 540
gagcttgcac tgtcttttga gaaacttaca aatgaaaagc ttctgaagtt acaaaagtgt 600

gggtgtgaaga acaatgatgt tcagctgggt gattttgtag aatctgagtt tctaggcgag 660
caggtcgaaag ctatcaagaa aatctcagag tacgttgcac agctaagaag aataggaaaag 720
gggtcatggag tgtggcattt tgatcaaatg cttctcaatg atgagggttta aggaaggaga 780
gttcagcttc tgcagttgat gacaatcttc cttgtgctat atggcaccgt tctatctcta 840
taacgacgtc tctaagtttg gtccgagaaa agtgttcttg ctcgttcttt cttttctttg 900
tttttggtta accgaatgct tgtgagtggt tacttaataa tgttaactcgt agtctgataa 960
taaatgcaag tcccactgtt tc

(2) INFORMATION FOR SEQ ID NO:2147:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 256 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..256

(D) OTHER INFORMATION: / Ceres Seq. ID 1571899

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2147:

Lys Ala Gln Met Leu Leu Lys Ala Ser Pro Ala Leu Ser Leu Ser
1 5 10 15
Ser Gly Ser Thr Gly Gly Gly Asn Leu Phe Pro Pro Ser Arg Asn Ser
20 25 30
Ser Asn Arg Leu Phe Ser Pro Ser Gly Ser Lys Phe Ser Val Gln Ala
35 40 45
Ala Lys Gly Thr Asn Thr Lys Ser Leu Thr Gly Val Val Phe Glu Pro
50 55 60
Phe Glu Glu Val Lys Lys Glu Leu Asp Leu Val Pro Thr Thr Pro Phe
65 70 75 80
Val Ser Leu Ala Arg His Lys Phe Ser Asp Asp Ala Glu Ser Ala Ile
85 90 95
Asn Asp Gln Ile Asn Val Glu Tyr Asn Val Ser Tyr Val Tyr His Ala
100 105 110
Leu Tyr Ala Tyr Phe Asp Arg Asp Asn Val Gly Leu Lys Gly Phe Ala
115 120 125
Lys Phe Phe Asn Asp Ser Ser Leu Glu Glu Arg Gly His Ala Glu Met
130 135 140
Phe Met Glu Tyr Gln Asn Lys Arg Gly Gly Arg Val Lys Leu Gln Ser
145 150 155 160
Ile Leu Met Pro Val Ser Glu Phe Asp His Glu Glu Lys Gly Asp Ala
165 170 175
Leu His Ala Met Glu Leu Ala Leu Ser Leu Glu Lys Leu Thr Asn Glu
180 185 190
Lys Leu Leu Lys Leu Gln Ser Val Gly Val Lys Asn Asn Asp Val Gln
195 200 205
Leu Val Asp Phe Val Glu Ser Glu Phe Leu Gly Glu Gln Val Glu Ala
210 215 220
Ile Lys Lys Ile Ser Glu Tyr Val Ala Gln Leu Arg Arg Ile Gly Lys
225 230 235 240
Gly His Gly Val Trp His Phe Asp Gln Met Leu Asn Asp Glu Val
245 250 255

(2) INFORMATION FOR SEQ ID NO:2148:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 253 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1..253
(D) OTHER INFORMATION: / Ceres Seq. ID 1571900

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2148:

Met	Leu	Leu	Lys	Ala	Ser	Pro	Ala	Leu	Ser	Leu	Leu	Ser	Ser	Gly	Ser
1			5					10						15	
Thr	Gly	Gly	Gly	Asn	Leu	Phe	Pro	Pro	Ser	Arg	Asn	Ser	Ser	Asn	Arg
			20					25						30	
Leu	Phe	Ser	Pro	Ser	Gly	Ser	Lys	Phe	Ser	Val	Gln	Ala	Ala	Lys	Gly
			35					40						45	
Thr	Asn	Thr	Lys	Ser	Leu	Thr	Gly	Val	Val	Phe	Glu	Pro	Phe	Glu	Glu
			50					55						60	
Val	Lys	Lys	Glu	Leu	Asp	Leu	Val	Pro	Thr	Thr	Pro	Phe	Val	Ser	Leu
			65					70						80	
Ala	Arg	His	Lys	Phe	Ser	Asp	Asp	Ala	Glu	Ser	Ala	Ile	Asn	Asp	Gln
Ile	Asn	Val	Glu	Tyr	Asn	Val	Ser	Tyr	Val	Tyr	His	Ala	Leu	Tyr	Ala
Tyr	Phe	Asp	Arg	Asp	Asn	Val	Gly	Leu	Lys	Gly	Phe	Ala	Lys	Phe	Phe
Asn	Asp	Ser	Ser	Leu	Glu	Glu	Arg	Gly	His	Ala	Glu	Met	Phe	Met	Glu
Tyr	Gln	Asn	Lys	Arg	Gly	Gly	Arg	Val	Lys	Leu	Gln	Ser	Ile	Leu	Met
Pro	Val	Ser	Glu	Phe	Asp	His	Glu	Glu	Lys	Gly	Asp	Ala	Leu	His	Ala
Met	Glu	Leu	Ala	Leu	Ser	Leu	Glu	Lys	Leu	Thr	Asn	Glu	Lys	Leu	Leu
Lys	Leu	Gln	Ser	Val	Gly	Val	Lys	Asn	Asn	Asp	Val	Gln	Leu	Val	Asp
Phe	Val	Glu	Ser	Glu	Phe	Leu	Gly	Glu	Gln	Val	Glu	Ala	Ile	Lys	Lys
Ile	Ser	Glu	Tyr	Val	Ala	Gln	Leu	Arg	Arg	Ile	Gly	Lys	Gly	His	Gly
Val	Trp	His	Phe	Asp	Gln	Met	Leu	Leu	Asn	Asp	Glu	Val			

(2) INFORMATION FOR SEQ ID NO:2149:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1275 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -
(B) LOCATION: 1..1275
(D) OTHER INFORMATION: / Ceres Seq. ID 1571905

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2149:

aaacaagata	caacacaatt	ggaatctttc	ttctttgaca	aaaaaaaaag	gaatctctct	60
ctttctctga	ttctctcatg	ttcatgcaac	aagaaacgtc	tcacatgacg	gcggctccac	120
agaccaacgg	ccatcaaatc	ttccctgaga	ttgacatgtc	cgccggcgat	ttctctctca	180
tcgtacgagc	tacagtctgc	caagcctcta	cagtcttcta	cgatactccc	gccacgtcga	240
ataaggcaga	gagactgctt	tctgaggcag	cggagaatgg	atctcagcta	gtgggtgtcc	300
cggaggcttt	catcgggtga	tatccacgtg	gctctacctt	tgaattggct	attggtttct	360
gtaccgcgtaa	agggacgagat	gactttcgca	agtaccatgc	ttctgcacct	gatgttctgc	420
gccccgaagt	ggaacgaNtt	agcgtaaatg	gccaaagaagt	acaaagtata	cttggttatg	480
gggtgtgatg	agaggggaag	ctacacgccta	tactgcacgc	ttctttttct	cgattcacaa	540
ggctctgtct	taggtaagca	ccgcaaaactc	atgcctacag	ctcttgaacg	ttgcatttgg	600
ggatttggag	atggatacaac	catccctgtg	ttcgatactc	ctattgggaa	aatcggtgct	660
gctatttgg	gggaaaatag	gatgccttct	ttgagaaccg	caatgtatgc	caaaaggcat	720
gagatttatt	gtgcacctac	tgctgattca	agagaaactt	ggctagcatc	aatgactcat	780

attgcacttg	agggtggatg	ttttgttttg	tcagctaacc	agttttgtcg	tcggaaagac	840
tatcctcttc	cgccggaata	catgttttcc	ggttcagaag	agagcctaac	accggactct	900
gttgtctgcg	ctcttggaag	ctctatcatt	tcacctttgg	gaattgtttt	agctggacca	960
aactatagag	gagaagctct	tatcacagct	gatctagatc	ttggggacat	agcacgagcc	1020
aagtttgatt	tgtatgtggg	cggaacattac	tcgaggcctg	aagtgttttag	cttgaacata	1080
agggagcatt	cgagaaaaagc	ggtcagcttc	aagacgtcaa	aggtaatgga	agatgaatcc	1140
gtctaacaaa	tgatcatctg	ttagacccaa	actttctctg	taatttgatg	aagtttatct	1200
gtagttaact	tcaagacttg	tgttgttaatt	gaaatcgata	aaaaatccaa	accggttagat	1260
tgagtgttgt	cttct					

(2) INFORMATION FOR SEQ ID NO:2150:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 255 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..255

(D) OTHER INFORMATION: / Ceres Seq. ID 1571906

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2150:

Met	Thr	Phe	Ala	Ser	Thr	Met	Leu	Leu	Pro	Leu	Met	Phe	Leu	Ala	Leu
1				5					10				15		
Lys	Trp	Asn	Xaa	Leu	Ala	Leu	Met	Ala	Lys	Lys	Tyr	Lys	Val	Tyr	Leu
				20				25					30		
Val	Met	Gly	Val	Ile	Glu	Arg	Glu	Gly	Tyr	Thr	Leu	Tyr	Cys	Thr	Val
				35				40				45			
Leu	Phe	Phe	Asp	Ser	Gln	Gly	Leu	Phe	Leu	Gly	Lys	His	Arg	Lys	Leu
				50			55				60				
Met	Pro	Thr	Ala	Leu	Glu	Arg	Cys	Ile	Trp	Gly	Phe	Gly	Asp	Gly	Ser
				65			70			75				80	
Thr	Ile	Pro	Val	Phe	Asp	Thr	Pro	Ile	Gly	Lys	Ile	Gly	Ala	Ala	Ile
				85				90					95		
Cys	Trp	Glu	Asn	Arg	Met	Pro	Ser	Leu	Arg	Thr	Ala	Met	Tyr	Ala	Lys
				100				105					110		
Gly	Ile	Glu	Ile	Tyr	Cys	Ala	Pro	Thr	Ala	Asp	Ser	Arg	Glu	Thr	Trp
				115				120					125		
Leu	Ala	Ser	Met	Thr	His	Ile	Ala	Leu	Glu	Gly	Gly	Cys	Phe	Val	Leu
				130			135					140			
Ser	Ala	Asn	Gln	Phe	Cys	Arg	Arg	Lys	Asp	Tyr	Pro	Ser	Pro	Pro	Glu
				145			150				155				160
Tyr	Met	Phe	Ser	Gly	Ser	Glu	Glu	Ser	Leu	Thr	Pro	Asp	Ser	Val	Val
				165				170					175		
Cys	Ala	Gly	Gly	Ser	Ser	Ile	Ile	Ser	Pro	Leu	Gly	Ile	Val	Leu	Ala
				180				185					190		
Gly	Pro	Asn	Tyr	Arg	Gly	Glu	Ala	Leu	Ile	Thr	Ala	Asp	Leu	Asp	Leu
				195			200					205			
Gly	Asp	Ile	Ala	Arg	Ala	Lys	Phe	Asp	Phe	Asp	Val	Val	Gly	His	Tyr
				210			215				220				
Ser	Arg	Pro	Glu	Val	Phe	Ser	Leu	Asn	Ile	Arg	Glu	His	Pro	Arg	Lys
				225			230			235				240	
Ala	Val	Ser	Phe	Lys	Thr	Ser	Lys	Val	Met	Glu	Asp	Glu	Ser	Val	
				245				250					255		

(2) INFORMATION FOR SEQ ID NO:2151:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 249 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1..249
(D) OTHER INFORMATION: / Ceres Seq. ID 1571907

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2151:

Met Leu Leu Pro Leu Met Phe Leu Ala Leu Lys Trp Asn Xaa Leu Ala
1 5 10 15
Leu Met Ala Lys Lys Tyr Lys Val Tyr Leu Val Met Gly Val Ile Glu
20 25 30
Arg Glu Gly Tyr Thr Leu Tyr Cys Thr Val Leu Phe Phe Asp Ser Gln
35 40 45
Gly Leu Phe Leu Gly Lys His Arg Lys Leu Met Pro Thr Ala Leu Glu
50 55 60
Arg Cys Ile Trp Gly Phe Gly Asp Gly Ser Thr Ile Pro Val Phe Asp
65 70 75 80
Thr Pro Ile Gly Lys Ile Gly Ala Ala Ile Cys Trp Glu Asn Arg Met
85 90 95
Pro Ser Leu Arg Thr Ala Met Tyr Ala Lys Gly Ile Glu Ile Tyr Cys
100 105 110
Ala Pro Thr Ala Asp Ser Arg Glu Thr Trp Leu Ala Ser Met Thr His
115 120 125
Ile Ala Leu Glu Gly Gly Cys Phe Val Leu Ser Ala Asn Gln Phe Cys
130 135 140
Arg Arg Lys Asp Tyr Pro Ser Pro Pro Glu Tyr Met Phe Ser Gly Ser
145 150 155 160
Glu Glu Ser Leu Thr Pro Asp Ser Val Val Cys Ala Gly Gly Ser Ser
165 170 175
Ile Ile Ser Pro Leu Gly Ile Val Leu Ala Gly Pro Asn Tyr Arg Gly
180 185 190
Glu Ala Leu Ile Thr Ala Asp Leu Asp Leu Gly Asp Ile Ala Arg Ala
195 200 205
Lys Phe Asp Phe Asp Val Val Gly His Tyr Ser Arg Pro Glu Val Phe
210 215 220
Ser Leu Asn Ile Arg Glu His Pro Arg Lys Ala Val Ser Phe Lys Thr
225 230 235 240
Ser Lys Val Met Glu Asp Glu Ser Val
245

(2) INFORMATION FOR SEQ ID NO:2152:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 244 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1..244
(D) OTHER INFORMATION: / Ceres Seq. ID 1571908

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2152:

Met Phe Leu Ala Leu Lys Trp Asn Xaa Leu Ala Leu Met Ala Lys Lys
1 5 10 15
Tyr Lys Val Tyr Leu Val Met Gly Val Ile Glu Arg Glu Gly Tyr Thr
20 25 30
Leu Tyr Cys Thr Val Leu Phe Phe Asp Ser Gln Gly Leu Phe Leu Gly
35 40 45
Lys His Arg Lys Leu Met Pro Thr Ala Leu Glu Arg Cys Ile Trp Gly
50 55 60
Phe Gly Asp Gly Ser Thr Ile Pro Val Phe Asp Thr Pro Ile Gly Lys
65 70 75 80
Ile Gly Ala Ala Ile Cys Trp Glu Asn Arg Met Pro Ser Leu Arg Thr
85 90 95
Ala Met Tyr Ala Lys Gly Ile Glu Ile Tyr Cys Ala Pro Thr Ala Asp

(2) INFORMATION FOR SEQ ID NO:2153:

(A) LENGTH: 1280 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

{B} LOCATION: 1..1280

(D) OTHER INFORMATION: / Ceres Seq. ID 1571909

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2153:

(A1) - 5000						
tcaaaaagtc	ctctctcggt	caactcttct	cttggctccc	atctctcaaa	atcacaactc	60
tctgttattt	ccaaagagaca	aaaactctgag	aacacacggc	cgactcgaaa	atpgaaactt	120
ctcgtttttac	ctctctctcggt	ctcctctctgt	ccctctcctt	cttctcaact	ctctcgcggc	180
aaatgacggc	aaactctcaac	tgcagtttgg	caaactcgac	gtgtcaatct	ctcgttgattc	240
actccaagaa	gaagccaaca	ctcgttgcca	atattccaaac	ctcttttgcc	gtcagaagac	300
tccgctcgat	ctctcgagctg	aacaaattcc	caactcaaac	ctcagctgac	caacgggtga	360
accgaatca	agtgctacgt	gtcccaactc	attgctcttg	ctccaatgac	accggtgtg	420
cgaacgggga	catctgaatca	accatcaaga	aagacagcat	actctcttct	gtcgcgaact	480
agattttcgt	tgtgtctcgtt	acgtcagaga	agatcagtga	gtgttaaaaa	atccctgacc	540
cgacaaaaat	cgaaatcogtt	caaaagtctt	ggatcccttt	gcctgttagc	tgtgtataat	600
tgaacgggtg	ggatgttgtt	ctaactgcac	attgtagtcaa	actcragraag	tctctcgtgtc	660
agatcgtctg	tcatttttga	actgacaaac	cgacgtctggc	tcagctcaat	ggaaatcattg	720
gtgactctca	ctgtcttggt	gataaaaactc	tcagctcttc	ttccaagaag	tgtagctcgt	780
ctgtgaggaa	cgactcgttg	gatgacaactc	tgcctctctc	taacaaactca	taoqctctca	840
ctgcacaaa	ttggcgtcga	tgtacttggt	acogctttgaa	gaattggact	taagtgtgtc	900
aatcatcaat	ttagatttaag	cccttgaaat	ggcaaaacctg	cccaccattt	tcacaatgtg	960
atcagagctt	gottaaacgcg	ttcttgacag	gaacctctgca	tttgcgtctat	gctgggttat	1020
ccaaacaaac	catctctcaac	acaagctctcc	acagcttgtcc	agattctcgt	gctctgtgta	1080
actatgcatt	aacgctcagc	taagagcttca	gttctcgtgat	tgtgttgatt	caagtgtcgc	1140
tctgttgctg	ctgcctctct	tctaagtgtt	tgtgtgtgtg	ttgatgagtg	tattcaagta	1200
ctgtctcgat	taaaaataaag	acattgtttc	acatgaagca	tcaggtcctt	gtaccattat	1260
tatactggaa	acattttcac					

(2) INFORMATION FOR SEQ ID NO:2154:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 350 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

{ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1..350
(D) OTHER INFORMATION: / Ceres Seq. ID 1571910

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2154:

Met Glu Thr Ser Cys Phe Thr Leu Leu Gly Leu Leu Val Ser Leu Ser
1 5 10 15
Phe Phe Leu Thr Leu Ser Ala Gln Met Thr Gly Asn Phe Asn Cys Ser
20 25 30
Gly Ser Thr Ser Thr Cys Gln Ser Leu Val Gly Tyr Ser Ser Lys Asn
35 40 45
Ala Thr Thr Leu Arg Asn Ile Gln Thr Leu Phe Ala Val Lys Asn Leu
50 55 60
Arg Ser Ile Leu Gly Ala Asn Asn Leu Pro Leu Asn Thr Ser Arg Asp
65 70 75 80
Gln Arg Val Asn Pro Asn Gln Val Val Arg Val Pro Ile His Cys Ser
85 90 95
Cys Ser Asn Gly Thr Gly Val Ser Asn Arg Asp Ile Glu Tyr Thr Ile
100 105 110
Lys Lys Asp Asp Ile Leu Ser Phe Val Ala Thr Glu Ile Phe Gly Gly
115 120 125
Leu Val Thr Tyr Glu Lys Ile Ser Glu Val Asn Lys Ile Pro Asp Pro
130 135 140
Asn Lys Ile Glu Ile Gly Gln Lys Phe Trp Ile Pro Leu Pro Cys Ser
145 150 155 160
Cys Asp Lys Leu Asn Gly Glu Asp Val Val His Tyr Ala His Val Val
165 170 175
Lys Leu Xaa Ser Ser Leu Gly Glu Ile Ala Ala Gln Phe Gly Thr Asp
180 185 190
Asn Thr Thr Leu Ala Gln Leu Asn Gly Ile Ile Gly Asp Ser Gln Leu
195 200 205
Leu Ala Asp Lys Pro Leu Asp Val Pro Leu Lys Ala Cys Ser Ser Ser
210 215 220
Val Arg Asn Asp Ser Leu Asp Ala Pro Leu Leu Ser Asn Asn Ser
225 230 235 240
Tyr Val Phe Thr Ala Asn Asn Cys Val Lys Cys Thr Cys Asp Ala Leu
245 250 255
Lys Asn Trp Thr Leu Ser Cys Gln Ser Ser Ser Glu Ile Lys Pro Ser
260 265 270
Asn Trp Gln Thr Cys Pro Pro Phe Ser Gln Cys Asp Arg Ala Leu Leu
275 280 285
Asn Ala Ser Cys Arg Arg Pro Arg Asp Cys Val Tyr Ala Gly Tyr Ser
290 295 300
Asn Gln Thr Ile Phe Thr Thr Ala Ser Pro Ala Cys Pro Asp Ser Ala
305 310 315 320
Gly Pro Gly Asn Tyr Ala Ser Thr Leu Ser Ser Ser Phe Ser Phe Val
325 330 335
Ile Val Leu Ile Gln Cys Ala Leu Leu Cys Leu Cys Leu Leu
340 345 350

(2) INFORMATION FOR SEQ ID NO:2155:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 326 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1..326
(D) OTHER INFORMATION: / Ceres Seq. ID 1571911

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2155:

Met Thr Gly Asn Phe Asn Cys Ser Gly Ser Thr Ser Thr Cys Gln Ser

1 5 10 15
Leu Val Gly Tyr Ser Ser Lys Asn Ala Thr Thr Leu Arg Asn Ile Gln
20 25 30
Thr Leu Phe Ala Val Lys Asn Leu Arg Ser Ile Leu Gly Ala Asn Asn
35 40 45
Leu Pro Leu Asn Thr Ser Arg Asp Gln Arg Val Asn Pro Asn Gln Val
50 55 60
Val Arg Val Pro Ile His Cys Ser Cys Ser Asn Gly Thr Gly Val Ser
65 70 75 80
Asn Arg Asp Ile Glu Tyr Thr Ile Lys Lys Asp Asp Ile Leu Ser Phe
85 90 95
Val Ala Thr Glu Ile Phe Gly Gly Leu Val Thr Tyr Glu Lys Ile Ser
100 105 110
Glu Val Asn Lys Ile Pro Asp Pro Asn Lys Ile Glu Ile Gly Gln Lys
115 120 125
Phe Trp Ile Pro Leu Pro Cys Ser Cys Asp Lys Leu Asn Gly Glu Asp
130 135 140
Val Val His Tyr Ala His Val Val Lys Leu Xaa Ser Ser Leu Gly Glu
145 150 155 160
Ile Ala Ala Gln Phe Gly Thr Asp Asn Thr Thr Leu Ala Gln Leu Asn
165 170 175
Gly Ile Ile Gly Asp Ser Gln Leu Leu Ala Asp Lys Pro Leu Asp Val
180 185 190
Pro Leu Lys Ala Cys Ser Ser Ser Val Arg Asn Asp Ser Leu Asp Ala
195 200 205
Pro Leu Leu Leu Ser Asn Asn Ser Tyr Val Phe Thr Ala Asn Asn Cys
210 215 220
Val Lys Cys Thr Cys Asp Ala Leu Lys Asn Trp Thr Leu Ser Cys Gln
225 230 235 240
Ser Ser Ser Glu Ile Lys Pro Ser Asn Trp Gln Thr Cys Pro Pro Phe
245 250 255
Ser Gln Cys Asp Arg Ala Leu Leu Asn Ala Ser Cys Arg Arg Pro Arg
260 265 270
Asp Cys Val Tyr Ala Gly Tyr Ser Asn Gln Thr Ile Phe Thr Thr Ala
275 280 285
Ser Pro Ala Cys Pro Asp Ser Ala Gly Pro Gly Asn Tyr Ala Ser Thr
290 295 300
Leu Ser Ser Ser Phe Ser Phe Val Ile Val Leu Ile Gln Cys Ala Leu
305 310 315 320
Leu Cys Leu Cys Leu Leu
325

(2) INFORMATION FOR SEQ ID NO:2156:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 914 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..914
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571912

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2156:

acttcattag	tctccaagaa	gaaaacatct	ctcactctct	aaaatacaca	ctctcatcaa	60
aaaccttctc	ttcgggttcag	aagcatttcaa	gaatccatta	tgagctcatt	tgattccggt	120
aatatacggcg	ttaactcacg	gatgtacttc	cgtaacccga	gtttcagcaa	cgttatcttta	180
aacgataact	ggagcgactt	gcogttaagt	gtcgacgatt	ctcaagacat	ggctattttac	240
aacactctcc	gtgatcgctt	tagctccgcc	tggacaccat	cogttctctc	cgttacctct	300
ccggcgaggag	aagataagcc	tccggcgacg	aaggcgagtg	gctcacacgc	gccgaggcag	360
aagggggatgc	agttacagag	agtgaggagg	aggccgtggg	ggaaattcgc	ggcgagagatt	420
agggatccga	agaagaacgg	agctagggtt	tggtcgggga	cttacgagac	gccggaGgac	480

gcggcggttg cgtacgaccg agcggcggtt cagctcagag gatcgaaagc taagctgaat 540
tttccgcat ttttggttc ttgtaagat gagccgggtta ggattaggcc tcgccgtcgc 600
tcgcccgaac cgtcagtcct cgtcagttta acgtcggagc agaagaggga aagccacgtg 660
gatgacggca agtcagttt gttgttacgg gaggttggatt tcacgggtgga tcagttttac 720
ttcgtatggt gttttattaat ggaccaatca gaattgtctt attctgataa tcggatataa 780
ttagttttaa gattaagcaa aatttgtcca acgagttttg ctgtatgaaa tatctatcga 840
tgactcaaca ggttttgatc atgatcatat gtaatgtgat gaaattataa tattgacggt 900
tggttttttc ttcc

(2) INFORMATION FOR SEQ ID NO:2157:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 226 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..226

(D) OTHER INFORMATION: / Ceres Seq. ID 1571913

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2157:

Met	Ser	Ser	Asp	Ser	Val	Asn	Asn	Gly	Val	Asn	Ser	Arg	Met	Tyr
1			5					10					15	
Phe	Arg	Asn	Pro	Ser	Phe	Ser	Asn	Val	Ile	Leu	Asn	Asp	Asn	Trp
			20					25					30	Ser
Asp	Leu	Pro	Leu	Ser	Val	Asp	Asp	Ser	Gln	Asp	Met	Ala	Ile	Tyr
			35					40					45	Asn
Thr	Leu	Arg	Asp	Ala	Val	Ser	Ser	Ala	Trp	Thr	Pro	Ser	Val	Pro
			50					55					60	Pro
Val	Thr	Ser	Pro	Ala	Glu	Glu	Asp	Lys	Pro	Pro	Ala	Thr	Lys	Ala
			65					70					75	Arg
Gly	Ser	His	Ala	Pro	Arg	Gln	Lys	Gly	Met	Gln	Tyr	Arg	Gly	Val
														80
Arg	Arg	Pro	Trp	Gly	Lys	Phe	Ala	Ala	Glu	Ile	Arg	Asp	Pro	Lys
														85
Asn	Gly	Ala	Arg	Val	Trp	Leu	Gly	Thr	Tyr	Glu	Thr	Pro	Glu	Asp
														90
Ala	Val	Ala	Tyr	Asp	Arg	Ala	Ala	Phe	Gln	Leu	Arg	Gly	Ser	Lys
														95
Lys	Leu	Asn	Phe	Pro	His	Leu	Ile	Gly	Ser	Cys	Lys	Tyr	Glu	Pro
														100
Arg	Ile	Arg	Pro	Arg	Arg	Arg	Ser	Pro	Glu	Pro	Ser	Val	Ser	Asp
														105
Leu	Thr	Ser	Glu	Gln	Lys	Arg	Glu	Ser	His	Val	Asp	Asp	Gly	Lys
														110
Ser	Leu	Val	Val	Pro	Glu	Leu	Asp	Phe	Thr	Val	Asp	Gln	Phe	Tyr
														115
Asp	Gly	Ser	Leu	Leu	Met	Asp	Gln	Ser	Glu	Cys	Ser	Tyr	Ser	Asp
														120
Arg	Ile													125
225														

(2) INFORMATION FOR SEQ ID NO:2158:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 212 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..212

(D) OTHER INFORMATION: / Ceres Seq. ID 1571914

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2158:

Met Tyr Phe Arg Asn Pro Ser Phe Ser Asn Val Ile Leu Asn Asp Asn
1 5 10 15
Trp Ser Asp Leu Pro Leu Ser Val Asp Asp Ser Gln Asp Met Ala Ile
20 25 30
Tyr Asn Thr Leu Arg Asp Ala Val Ser Ser Ala Trp Thr Pro Ser Val
35 40 45
Pro Pro Val Thr Ser Pro Ala Glu Glu Asp Lys Pro Pro Ala Thr Lys
50 55 60
Ala Ser Gly Ser His Ala Pro Arg Gln Lys Gly Met Gln Tyr Arg Gly
65 70 75 80
Val Arg Arg Arg Pro Trp Gly Lys Phe Ala Ala Glu Ile Arg Asp Pro
85 90 95
Lys Lys Asn Gly Ala Arg Val Trp Leu Gly Thr Tyr Glu Thr Pro Glu
100 105 110
Asp Ala Ala Val Ala Tyr Asp Arg Ala Ala Phe Gln Leu Arg Gly Ser
115 120 125
Lys Ala Lys Leu Asn Phe Pro His Leu Ile Gly Ser Cys Lys Tyr Glu
130 135 140
Pro Val Arg Ile Arg Pro Arg Arg Arg Ser Pro Glu Pro Ser Val Ser
145 150 155 160
Asp Gln Leu Thr Ser Glu Gln Lys Arg Glu Ser His Val Asp Asp Gly
165 170 175
Lys Ser Ser Leu Val Val Pro Glu Leu Asp Phe Thr Val Asp Gln Phe
180 185 190
Tyr Phe Asp Gly Ser Leu Leu Met Asp Gln Ser Glu Cys Ser Tyr Ser
195 200 205
Asp Asn Arg Ile
210

(2) INFORMATION FOR SEQ ID NO:2159:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 183 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..183
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571915

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2159:

Met Ala Ile Tyr Asn Thr Leu Arg Asp Ala Val Ser Ser Ala Trp Thr
1 5 10 15
Pro Ser Val Pro Pro Val Thr Ser Pro Ala Glu Glu Asp Lys Pro Pro
20 25 30
Ala Thr Lys Ala Ser Gly Ser His Ala Pro Arg Gln Lys Gly Met Gln
35 40 45
Tyr Arg Gly Val Arg Arg Arg Pro Trp Gly Lys Phe Ala Ala Glu Ile
50 55 60
Arg Asp Pro Lys Lys Asn Gly Ala Arg Val Trp Leu Gly Thr Tyr Glu
65 70 75 80
Thr Pro Glu Asp Ala Ala Val Ala Tyr Asp Arg Ala Ala Phe Gln Leu
85 90 95
Arg Gly Ser Lys Ala Lys Leu Asn Phe Pro His Leu Ile Gly Ser Cys
100 105 110
Lys Tyr Glu Pro Val Arg Ile Arg Pro Arg Arg Arg Ser Pro Glu Pro
115 120 125
Ser Val Ser Asp Gln Leu Thr Ser Glu Gln Lys Arg Glu Ser His Val
130 135 140
Asp Asp Gly Lys Ser Ser Leu Val Val Pro Glu Leu Asp Phe Thr Val
145 150 155 160

Asp Gln Phe Tyr Phe Asp Gly Ser Leu Leu Met Asp Gln Ser Glu Cys
165 170 175
Ser Tyr Ser Asp Asn Arg Ile
180

(2) INFORMATION FOR SEQ ID NO:2160:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1134 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1134
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571920

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2160:

atacgtttgc	tgccccacgt	tgatcttgtt	gtttactctc	tctctctctc	ccatcgccga	60
cgaccaccgg	agatcagcgt	caccgtacca	aaacatcatt	taccttcttt	aagattttgt	120
gttttttaat	cagttgaatc	ggaataaaat	atcgatcag	agatgagtaa	cgagcttctc	180
accatcgatc	ctgtcgacct	tcaattccct	tttgaaattg	agaagcagat	ctctgtgtct	240
ctctatttgg	gtaacaagac	cgataattat	gtcgcttcca	aggtaagac	gacgaatcca	300
aagaagtact	gcgttaggcc	taatactggt	gttggtccat	ccagatcctc	ttctgaagtt	360
ttagtaccac	tgaacagctc	aaaggaagct	cctgctgac	tgccagttaa	agataagttc	420
ttgttccaat	gtgtagtcgc	tagtcccgga	gccaccacca	aggatgttac	tcatgagatg	480
tttagcaaa	agggcaggga	tcgagttgaa	gagactaaat	tgagagttgt	ctatgttgtct	540
ccaccacgac	caccatcacc	ggttcgagaa	ggatctgaa	agggctcttc	accgagggct	600
ctctgtctct	ataatgggaa	gtctctctgat	tttactgtct	ctccaaagat	tagccagcac	660
agggttgatg	ctcaggataa	ctcatctgag	gcaagagctc	tggtcacaaa	actcacccag	720
gaaaagaact	ctcgcggtta	actgaacaac	aggcttcaac	aagaattgga	ccagttgagg	780
cgcgaaaaga	agagaagtga	gagtggttga	atccctttca	tgtaactgtt	tctggtcgcc	840
ctaactcggt	taactctggg	atacattatg	aagaggacat	gatacagatc	cttcaacaaa	900
atactccaaa	agtcctcaag	tgcttaaaaa	agcaattgaa	aggaaagaaa	tcaaattgtg	960
tgaggaggac	atactctctc	tctgccttat	cgtctgcatg	cacctttgtg	taaaatctga	1020
acttagtgcg	ttagaggatt	tgtattacgg	tttcataaag	acttagaatt	gtcaacaaat	1080
ctcctttttc	ctctctctta	ttacaacttt	gtgtagtctt	aaacactttt	gttc	

(2) INFORMATION FOR SEQ ID NO:2161:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 239 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..239
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571921

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2161:

Met Ser Asn Glu Leu Leu Thr Ile Asp	Pro Val Asp Leu Gln Phe Pro	
1	5	10
Phe Glu Leu Lys Lys Gln Ile Ser	Cys Ser Leu Tyr Leu Gly Asn Lys	
15	20	25
Thr Asp Asn Tyr Val Ala Phe Lys Val Lys Thr Thr	Asn Pro Lys Lys	
30	35	40
Tyr Cys Val Arg Pro Asn Thr Gly Val Val His Pro Arg Ser Ser Ser		
45	50	55
Glu Val Leu Val Thr Met Gln Ala Gln Lys Glu Ala Pro Ala Asp Leu		
60	65	70
Gln Cys Lys Asp Lys Phe Leu Leu Gln Cys Val Val Ala Ser Pro Gly		
75	80	85
Ala Thr Pro Lys Asp Val Thr His Glu Met Phe Ser Lys Glu Ala Gly		
90	95	100
		105
		110

His Arg Val Glu Glu Thr Lys Leu Arg Val Val Tyr Val Ala Pro Pro
115 120 125
Arg Pro Pro Ser Pro Val Arg Glu Gly Ser Glu Glu Gly Ser Ser Pro
130 135 140
Arg Ala Ser Val Ser Asp Asn Gly Asn Ala Ser Asp Phe Thr Ala Ala
145 150 155 160
Pro Arg Phe Ser Ala Asp Arg Val Asp Ala Gln Asp Asn Ser Ser Glu
165 170 175
Ala Arg Ala Leu Val Thr Lys Leu Thr Glu Glu Lys Asn Ser Ala Val
180 185 190
Gln Leu Asn Asn Arg Leu Gln Gln Glu Leu Asp Gln Leu Arg Arg Glu
195 200 205
Ser Lys Arg Ser Lys Ser Gly Gly Ile Pro Phe Met Tyr Val Leu Leu
210 215 220
Val Gly Leu Ile Gly Leu Ile Leu Gly Tyr Ile Met Lys Arg Thr
225 230 235

(2) INFORMATION FOR SEQ ID NO:2162:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..170
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571922

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2162:

Met Gln Ala Gln Lys Glu Ala Pro Ala Asp Leu Gln Cys Lys Asp Lys
1 5 10 15
Phe Leu Leu Gln Cys Val Val Ala Ser Pro Gly Ala Thr Pro Lys Asp
20 25 30
Val Thr His Glu Met Phe Ser Lys Glu Ala Gly His Arg Val Glu Glu
35 40 45
Thr Lys Leu Arg Val Val Tyr Val Ala Pro Pro Arg Pro Pro Ser Pro
50 55 60
Val Arg Glu Gly Ser Glu Glu Gly Ser Ser Pro Arg Ala Ser Val Ser
65 70 75 80
Asp Asn Gly Asn Ala Ser Asp Phe Thr Ala Ala Pro Arg Phe Ser Ala
85 90 95
Asp Arg Val Asp Ala Gln Asp Asn Ser Ser Glu Ala Arg Ala Leu Val
100 105 110
Thr Lys Leu Thr Glu Glu Lys Asn Ser Ala Val Gln Leu Asn Asn Arg
115 120 125
Leu Gln Gln Glu Leu Asp Gln Leu Arg Arg Glu Ser Lys Arg Ser Lys
130 135 140
Ser Gly Gly Ile Pro Phe Met Tyr Val Leu Leu Val Gly Leu Ile Gly
145 150 155 160
Leu Ile Leu Gly Tyr Ile Met Lys Arg Thr
165 170

(2) INFORMATION FOR SEQ ID NO:2163:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 134 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..134
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571923

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2163:

```

Met Phe Ser Lys Glu Ala Gly His Arg Val Glu Glu Thr Lys Leu Arg
1      5      10      15
Val Val Tyr Val Ala Pro Pro Arg Pro Pro Ser Pro Val Arg Glu Gly
20      25      30
Ser Glu Glu Gly Ser Ser Pro Arg Ala Ser Val Ser Asp Asn Gly Asn
35      40      45
Ala Ser Asp Phe Thr Ala Ala Pro Arg Phe Ser Ala Asp Arg Val Asp
50      55      60
Ala Gln Asp Asn Ser Ser Glu Ala Arg Ala Leu Val Thr Lys Leu Thr
65      70      75      80
Glu Glu Lys Asn Ser Ala Val Gln Leu Asn Asn Arg Leu Gln Gln Glu
85      90      95
Leu Asp Gln Leu Arg Arg Glu Ser Lys Arg Ser Lys Gly Ile
100      105      110
Pro Phe Met Tyr Val Leu Leu Val Gly Leu Ile Gly Leu Ile Leu Gly
115      120      125

Tyr Ile Met Lys Arg Thr
130

```

(2) INFORMATION FOR SEQ ID NO:2164:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1623 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1623

(D) OTHER INFORMATION: / Ceres Seq. ID 1571927

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2164:

```

attttcgggt attcaagcca caaaacccgt agaatggcgg cagctactca atttctctcc 60
caacctctgt ctctcaatcc acaccaactg aagaacccaaa cctcacaaag ctcacgaagc 120
atccctctgt tgtctcttaa atccacattg aagccactta aacgctctct cgtgaaagcc 180
gccgtgcttt cccaaaactc gtccaaaacc gtgaacgaag Tcgatcacgt tttcaagaaa 240
tcatcagatg ggtttctcta ttgtgaagga actaaagattg aggatatcat ggagtcagtg 300
gagagaagac ccttttacct atatagcaaa cctcagatca ctgaaaacct cgaggtctat 360
aaagaagcat tggaaaggagt gagctctctg attggttacg ctatcaaaag taataacaat 420
cttaagattt tggagcattt gagaagttta ggctgtgggt ctgtgctcgt tagtggaaat 480
gagcttagag ttgctctctg tctgtggttc gatccacaaa agtgcatttt caatggaaat 540
ggcaagctct tggaaagatt agttctagct gctcaagaag gtgttttctg taatgtcgat 600
agtgaagttg acttgaataa catgttgtaa gcttcaagaa tttctgttaa gcaggtcat 660
gtactgctgc gtatcaatgc ttgatgttat cctcaggtgc atccatgatg tgcactagg 720
aacaagaact caaagttttg tatcaggaa cagaagcttc aatggttttc ggaatcaggt 780
aaggcacatc ccaaagagct gaagcttggt ggagctcatt gccatctagg cctcacatt 840
actaagggtg atatatccag agatgcggca gttctcatga tgaatacat tgaagagatc 900
cggtcgtaag gttttgaagt tagttactgt aacattggtg gtggttttag gattgattat 960
taccatgcgc gcgctgtcct tcccacacc atggatctca tcaacactgt aagagagctt 1020
gttctttcac gagacctgaa tctaataatc gagccaggga gatctctgat tgaacaactt 1080
tgctgtttcg tcaacctagt aactggtgtg aagacgaatg gaactagaa ctctcatgct 1140
attgatggaa gtatgggtga gcttatcogt cccagctctt atgatgctta tcagcacatt 1200
gagttggtct cctctccacc ggctgaagca gaggttacca aattogaact cagtggtcct 1260
gtctgtgaat ctgctgattt cctgggcaaa gacagagagc ttccactccc tcaacaggga 1320
ctcgggtctg tggttcatca cgctggtgtc tactgtatga gcattgcttc cacttacaat 1380
ctcaagatgc gtctccggga atactgggtt gaagaagatg ggtcgatcac taagataaag 1440
catgtcgaga cattcgatga ccaattgcgt ttctttgaag tctgatgaac tcttagattt 1500
actcatcatt gtgtcttttt tgattgaatt gtatgattat tccgaatcag gaccataatg 1560
atattgctgt tttagatttt cacattatgt gotttgattc aaagtcaatg aagtgatcat 1620

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(2) INFORMATION FOR SEQ ID NO:2165:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 495 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..495
(D) OTHER INFORMATION: / Ceres Seq. ID 1571928
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2165:

Ile Phe Gly Tyr Gln Ser His Lys Thr Leu Arg Met Ala Ala Ala Thr
1 5 10 15
Gln Phe Leu Ser Gln Pro Ser Ser Leu Asn Pro His Gln Leu Lys Asn
20 25 30
Gln Thr Ser Gln Arg Ser Arg Ser Ile Pro Val Leu Ser Leu Lys Ser
35 40 45
Thr Leu Lys Pro Leu Lys Arg Leu Ser Val Lys Ala Ala Val Val Ser
50 55 60
Gln Asn Ser Ser Lys Thr Val Thr Lys Phe Asp His Cys Phe Lys Lys
65 70 75 80
Ser Ser Asp Gly Phe Leu Tyr Cys Glu Gly Thr Lys Val Glu Asp Ile
85 90 95
Met Glu Ser Val Glu Arg Arg Pro Phe Tyr Leu Tyr Ser Lys Pro Gln
100 105 110
Ile Thr Arg Asn Leu Glu Ala Tyr Lys Glu Ala Leu Glu Gly Val Ser
115 120 125
Ser Val Ile Gly Tyr Ala Ile Lys Ala Asn Asn Asn Leu Lys Ile Leu
130 135 140
Glu His Leu Arg Ser Leu Gly Cys Gly Ala Val Leu Val Ser Gly Asn
145 150 155 160
Glu Leu Arg Leu Ala Leu Arg Ala Gly Phe Asp Pro Thr Lys Cys Ile
165 170 175
Phe Asn Gly Asn Gly Lys Ser Leu Glu Asp Leu Val Leu Ala Ala Gln
180 185 190
Glu Gly Val Phe Val Asn Val Asp Ser Glu Phe Asp Leu Asn Asn Ile
195 200 205
Val Glu Ala Ser Arg Ile Ser Gly Lys Gln Val Asn Val Leu Leu Arg
210 215 220
Ile Asn Pro Asp Val Asp Pro Gln Val His Pro Tyr Val Ala Thr Gly
225 230 235 240
Asn Lys Asn Ser Lys Phe Gly Ile Arg Asn Glu Lys Leu Gln Trp Phe
245 250 255
Leu Asp Gln Val Lys Ala His Pro Lys Glu Leu Lys Leu Val Gly Ala
260 265 270
His Cys His Leu Gly Ser Thr Ile Thr Lys Val Asp Ile Phe Arg Asp
275 280 285
Ala Ala Val Leu Met Ile Glu Tyr Ile Asp Glu Ile Arg Arg Gln Gly
290 295 300
Phe Glu Val Ser Tyr Leu Asn Ile Gly Gly Gly Leu Gly Ile Asp Tyr
305 310 315 320
Tyr His Ala Gly Ala Val Leu Pro Thr Pro Met Asp Leu Ile Asn Thr
325 330 335
Val Arg Glu Leu Val Leu Ser Arg Asp Leu Asn Leu Ile Ile Glu Pro
340 345 350
Gly Arg Ser Leu Ile Ala Asn Thr Cys Cys Phe Val Asn His Val Thr
355 360 365
Gly Val Lys Thr Asn Gly Thr Lys Asn Phe Ile Val Ile Asp Gly Ser
370 375 380
Met Ala Glu Leu Ile Arg Pro Ser Leu Tyr Asp Ala Tyr Gln His Ile
385 390 395 400
Glu Leu Val Ser Pro Pro Ala Glu Ala Glu Val Thr Lys Phe Asp

			405				410						415		
Val	Val	Gly	Pro	Val	Cys	Glu	Ser	Ala	Asp	Phe	Leu	Gly	Lys	Asp	Arg
			420				425						430		
Glu	Leu	Pro	Thr	Pro	Pro	Gln	Gly	Ala	Gly	Leu	Val	Val	His	Asp	Ala
			435				440						445		
Gly	Ala	Tyr	Cys	Met	Ser	Met	Ala	Ser	Thr	Tyr	Asn	Leu	Lys	Met	Arg
			450				455						460		
Pro	Pro	Glu	Tyr	Trp	Val	Glu	Glu	Asp	Gly	Ser	Ile	Thr	Lys	Ile	Arg
			465				470						475		
His	Ala	Glu	Thr	Phe	Asp	Asp	His	Leu	Arg	Phe	Phe	Glu	Gly	Leu	
			485				490						495		

(2) INFORMATION FOR SEQ ID NO:2166:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 484 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..484

(D) OTHER INFORMATION: / Ceres Seq. ID 1571929

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2166:

Met	Ala	Ala	Ala	Thr	Gln	Phe	Leu	Ser	Gln	Pro	Ser	Ser	Leu	Asn	Pro
1			5						10					15	
His	Gln	Leu	Lys	Asn	Gln	Thr	Ser	Gln	Arg	Ser	Arg	Ser	Ile	Pro	Val
			20						25				30		
Leu	Ser	Leu	Lys	Ser	Thr	Leu	Lys	Pro	Leu	Lys	Arg	Leu	Ser	Val	Lys
			35				40					45			
Ala	Ala	Val	Val	Ser	Gln	Asn	Ser	Ser	Lys	Thr	Val	Thr	Lys	Phe	Asp
			50				55				60				
His	Cys	Phe	Lys	Lys	Ser	Ser	Asp	Gly	Phe	Leu	Tyr	Cys	Glu	Gly	Thr
					70				75					80	
Lys	Val	Glu	Asp	Ile	Met	Glu	Ser	Val	Glu	Arg	Arg	Pro	Phe	Tyr	Leu
			85						90				95		
Tyr	Ser	Lys	Pro	Gln	Ile	Thr	Arg	Asn	Leu	Glu	Ala	Tyr	Lys	Glu	Ala
			100					105					110		
Leu	Glu	Gly	Val	Ser	Ser	Val	Ile	Gly	Tyr	Ala	Ile	Lys	Ala	Asn	Asn
			115				120					125			
Asn	Leu	Lys	Ile	Leu	Glu	His	Leu	Arg	Ser	Leu	Gly	Cys	Gly	Ala	Val
			130				135					140			
Leu	Val	Ser	Gly	Asn	Glu	Leu	Arg	Leu	Ala	Leu	Arg	Ala	Gly	Phe	Asp
					150				155					160	
Pro	Thr	Lys	Cys	Ile	Phe	Asn	Gly	Asn	Gly	Lys	Ser	Leu	Glu	Asp	Leu
					165				170				175		
Val	Leu	Ala	Ala	Gln	Glu	Gly	Val	Phe	Val	Asn	Val	Asp	Ser	Glu	Phe
					180			185					190		
Asp	Leu	Asn	Asn	Ile	Val	Glu	Ala	Ser	Arg	Ile	Ser	Gly	Lys	Gln	Val
			195				200					205			
Asn	Val	Leu	Leu	Arg	Ile	Asn	Pro	Asp	Val	Asp	Pro	Gln	Val	His	Pro
			210				215				220				
Tyr	Val	Ala	Thr	Gly	Asn	Lys	Asn	Ser	Lys	Phe	Gly	Ile	Arg	Asn	Glu
					230					235				240	
Lys	Leu	Gln	Trp	Phe	Leu	Asp	Gln	Val	Lys	Ala	His	Pro	Lys	Glu	Leu
					245				250				255		
Lys	Leu	Val	Gly	Ala	His	Cys	His	Leu	Gly	Ser	Thr	Ile	Thr	Lys	Val
			260				265					270			
Asp	Ile	Phe	Arg	Asp	Ala	Ala	Val	Leu	Met	Ile	Glu	Tyr	Ile	Asp	Glu
			275				280					285			
Ile	Arg	Arg	Gln	Gly	Phe	Glu	Val	Ser	Tyr	Leu	Asn	Ile	Gly	Gly	Gly
			290				295					300			

```

Leu Gly Ile Asp Tyr Tyr His Ala Gly Ala Val Leu Pro Thr Pro Met
305                      310                      315                      320
Asp Leu Ile Asn Thr Val Arg Glu Leu Val Leu Ser Arg Asp Leu Asn
                      325                      330                      335
Leu Ile Ile Glu Pro Gly Arg Ser Leu Ile Ala Asn Thr Cys Phe
                      340                      345                      350
Val Asn His Val Thr Gly Val Lys Thr Asn Gly Thr Lys Asn Phe Ile
                      355                      360                      365
Val Ile Asp Gly Ser Met Ala Glu Leu Ile Arg Pro Ser Leu Tyr Asp
                      370                      375                      380
Ala Tyr Gln His Ile Glu Leu Val Ser Pro Pro Pro Ala Glu Ala Glu
385                      390                      395                      400
Val Thr Lys Phe Asp Val Val Gly Pro Val Cys Glu Ser Ala Asp Phe
                      405                      410                      415
Leu Gly Lys Asp Arg Glu Leu Pro Thr Pro Pro Gln Gly Ala Gly Leu
                      420                      425                      430
Val Val His Asp Ala Gly Ala Tyr Cys Met Ser Met Ala Ser Thr Tyr
                      435                      440                      445
Asn Leu Lys Met Arg Pro Pro Glu Tyr Trp Val Glu Glu Asp Gly Ser
450                      455                      460                      465
Ile Thr Lys Ile Arg His Ala Glu Thr Phe Asp Asp His Leu Arg Phe
465                      470                      475                      480
Phe Glu Gly Leu

```

(2) INFORMATION FOR SEQ ID NO:2167:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 399 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..399

(D) OTHER INFORMATION: / Ceres Seq. ID 1571930

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2167:

```

Met Glu Ser Val Glu Arg Arg Pro Phe Tyr Leu Tyr Ser Lys Pro Gln
1                      5                      10                      15
Ile Thr Arg Asn Leu Glu Ala Tyr Lys Glu Ala Leu Glu Gly Val Ser
                      20                      25                      30
Ser Val Ile Gly Tyr Ala Ile Lys Ala Asn Asn Asn Leu Lys Ile Leu
35                      40                      45
Glu His Leu Arg Ser Leu Gly Cys Gly Ala Val Leu Val Ser Gly Asn
50                      55                      60
Glu Leu Arg Leu Ala Leu Arg Ala Gly Phe Asp Pro Thr Lys Cys Ile
65                      70                      75                      80
Phe Asn Gly Asn Gly Lys Ser Leu Glu Asp Leu Val Leu Ala Ala Gln
                      85                      90                      95
Glu Gly Val Phe Val Asn Val Asp Ser Glu Phe Asp Leu Asn Asn Ile
100                      105                      110
Val Glu Ala Ser Arg Ile Ser Gly Lys Gln Val Asn Val Leu Leu Arg
115                      120                      125
Ile Asn Pro Asp Val Asp Pro Gln Val His Pro Tyr Val Ala Thr Gly
130                      135                      140
Asn Lys Asn Ser Lys Phe Gly Ile Arg Asn Glu Lys Leu Gln Trp Phe
145                      150                      155                      160
Leu Asp Gln Val Lys Ala His Pro Lys Glu Leu Lys Leu Val Gly Ala
                      165                      170                      175
His Cys His Leu Gly Ser Thr Ile Thr Lys Val Asp Ile Phe Arg Asp
180                      185                      190
Ala Ala Val Leu Met Ile Glu Tyr Ile Asp Glu Ile Arg Arg Gln Gly

```


(i) SEQUENCE CHARACTERISTICS:

- (ii) MOLECULE TYPE: DNA (genomic)

(A) NAME/KEY: -

- (B) LOCATION: 1..1383
(D) OTHER INFORMATION

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2168:

tec

(2) INFORMATION FOR SEQ ID NO:2169:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 301 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..301

(D) OTHER INFORMATION: / Ceres Seq. ID 1571932

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2169:

Asp Leu Leu Leu Pro Tyr Val Asn Lys Val Arg Glu Leu Asp Asn Thr
1 5 10 15
Thr Leu Tyr Ala Ser Arg Thr Leu Phe Phe Leu Ser Asp Asp Ser Thr
20 25 30
Leu Arg Pro Val Ala Ile Glu Leu Thr Cys Pro Pro Asn Ile Asn Lys
35 40 45
Pro Gln Trp Lys Lys Val Phe Thr Pro Gly Tyr Asp Ala Thr Ser Cys
50 55 60
Trp Leu Trp Asn Leu Ala Lys Thr His Ala Ile Ser His Asp Ala Gly
65 70 75 80
Tyr His Gln Leu Ile Ser His Trp Leu Arg Thr His Ala Cys Thr Glu
85 90 95
Pro Tyr Ile Ile Ala Ala Asn Arg Gln Leu Ser Ala Met His Pro Ile
100 105 110
Tyr Arg Leu Leu His Pro His Phe Arg Tyr Thr Met Glu Ile Asn Ala
115 120 125
Arg Ala Arg Gln Ser Leu Val Asn Gly Gly Gly Ile Ile Glu Thr Cys
130 135 140
Phe Trp Pro Gly Lys Tyr Ala Leu Glu Leu Xaa Ser Ala Val Tyr Gly
145 150 155 160
Lys Leu Trp Arg Phe Asp Gln Glu Gly Leu Pro Ala Asp Leu Ile Lys
165 170 175
Arg Gly Leu Ala Glu Glu Asp Lys Thr Ala Glu His Gly Val Arg Leu
180 185 190
Thr Ile Pro Asp Tyr Pro Phe Ala Asn Asp Gly Leu Ile Leu Trp Asp
195 200 205
Ala Ile Lys Glu Trp Val Thr Asp Tyr Val Lys His Tyr Tyr Pro Asp
210 215 220
Glu Glu Leu Ile Thr Ser Asp Glu Glu Leu Gln Gly Trp Trp Ser Glu
225 230 235 240
Val Arg Asn Ile Gly His Gly Asp Lys Lys Asp Glu Pro Trp Trp Pro
245 250 255
Val Leu Lys Thr Gln Asp Asp Leu Ile Gly Val Val Thr Thr Ile Ala
260 265 270
Trp Val Thr Ser Gly His His Ala Ala Val Asn Phe Gly Gln Arg Ile
275 280 285
Met Glu Asp Thr Phe Pro Thr Asp Gln Arg Gln Gln Gly
290 295 300

(2) INFORMATION FOR SEQ ID NO:2170:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 193 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..193

(D) OTHER INFORMATION: / Ceres Seq. ID 1571933

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2170:

```
Met His Pro Ile Tyr Arg Leu Leu His Pro His Phe Arg Tyr Thr Met
1      5      10      15
Glu Ile Asn Ala Arg Ala Arg Gln Ser Leu Val Asn Gly Gly Gly Ile
20      25      30
Ile Glu Thr Cys Phe Trp Pro Gly Lys Tyr Ala Leu Glu Leu Xaa Ser
35      40      45
Ala Val Tyr Gly Lys Leu Trp Arg Phe Asp Gln Glu Gly Leu Pro Ala
50      55      60
Asp Leu Ile Lys Arg Gly Leu Ala Glu Glu Asp Lys Thr Ala Glu His
65      70      75      80
Gly Val Arg Leu Thr Ile Pro Asp Tyr Pro Phe Ala Asn Asp Gly Leu
85      90      95
Ile Leu Trp Asp Ala Ile Lys Glu Trp Val Thr Asp Tyr Val Lys His
100      105      110
Tyr Tyr Pro Asp Glu Glu Leu Ile Thr Ser Asp Glu Glu Leu Gln Gly
115      120      125
Trp Trp Ser Glu Val Arg Asn Ile Gly His Gly Asp Lys Lys Asp Glu
130      135      140
Pro Trp Trp Pro Val Leu Lys Thr Gln Asp Asp Leu Ile Gly Val Val
145      150      155      160
Thr Thr Ile Ala Trp Val Thr Ser Gly His His Ala Ala Val Asn Phe
165      170      175
Gly Gln Arg Ile Met Glu Asp Thr Phe Pro Thr Asp Gln Arg Gln Gln
180      185      190
Gly
```

(2) INFORMATION FOR SEQ ID NO:2171:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 178 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..178

(D) OTHER INFORMATION: / Ceres Seq. ID 1571934

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2171:

```
Met Glu Ile Asn Ala Arg Ala Arg Gln Ser Leu Val Asn Gly Gly Gly
1      5      10      15
Ile Ile Glu Thr Cys Phe Trp Pro Gly Lys Tyr Ala Leu Glu Leu Xaa
20      25      30
Ser Ala Val Tyr Gly Lys Leu Trp Arg Phe Asp Gln Glu Gly Leu Pro
35      40      45
Ala Asp Leu Ile Lys Arg Gly Leu Ala Glu Glu Asp Lys Thr Ala Glu
50      55      60
His Gly Val Arg Leu Thr Ile Pro Asp Tyr Pro Phe Ala Asn Asp Gly
65      70      75      80
Leu Ile Leu Trp Asp Ala Ile Lys Glu Trp Val Thr Asp Tyr Val Lys
85      90      95
His Tyr Tyr Pro Asp Glu Glu Leu Ile Thr Ser Asp Glu Glu Leu Gln
100      105      110
Gly Trp Trp Ser Glu Val Arg Asn Ile Gly His Gly Asp Lys Lys Asp
115      120      125
Glu Pro Trp Trp Pro Val Leu Lys Thr Gln Asp Asp Leu Ile Gly Val
130      135      140
Val Thr Thr Ile Ala Trp Val Thr Ser Gly His His Ala Ala Val Asn
145      150      155      160
Phe Gly Gln Arg Ile Met Glu Asp Thr Phe Pro Thr Asp Gln Arg Gln
165      170      175
```

Gln Gly

(2) INFORMATION FOR SEQ ID NO:2172:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1229 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1229
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571935

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2172:

gtgcgttcgt	agagactgta	ataaagacgg	agagattctt	ctagagtcag	ttctttctct	60
tcctctctct	cttcccccca	aatcctctct	cgctagggtt	tctcattccg	atccataatt	120
ctagatgtcg	agggttttta	ctgagacctg	tcaataaagc	taaagctctt	tctaaagagt	180
ctaaagaaag	cattgcattg	ttgtagtctt	gtttgtgtcc	acagaagcaa	agaagagtga	240
gaagctcagg	atgtcaaaga	gtcgaaatac	ccactgggtg	cacagatgtc	agcgtgctgt	300
ccgccttcac	ggccaaagag	ctgtatgtct	ttattgcgga	gggtgatttg	ttgaagaact	360
tgatatggct	caagccagcc	cccttgatat	gttttagatc	cacaggggtg	ttgtagaacg	420
tgatcagact	tttgatctca	tggatgcttt	ctctgtgttt	atgaggaacc	gcttagctga	480
aaggagccac	gacagagaaa	tcagaggaag	aacctcagt	tcaggtctcg	aaaactttcc	540
tggtctggcc	cccttgggtg	tcaagtccct	tatagactaa	ctggcgacaa	gtggttaaac	600
tgcatcgaaa	gccctcttca	atggcggtcc	ccctggcatt	ggcatcacac	gtggttaaac	660
cggcgactac	ttcttcggtc	ccggccttga	agaattgttc	gagcaGcttt	cagctggcac	720
tactcgcgca	ggccccacac	ccgcacccag	atcagcaata	ggcgattgac	caactatcaa	780
gatcgcgcag	aggcatctta	ggctcatcga	ctcgaattgt	ccctgtgtga	aagacgaatt	840
cgaactcggg	tcagaagcga	aacagatgcc	gtgtgaaccac	atctatcatt	ctgactgcatt	900
tgctccgttg	ctggttcagc	acaactcttg	cccggtctgt	cgccaagagc	taccatcagc	960
tagcggacct	ctcaagctgc	aaaacagaac	cacccttacc	agaaactaca	gaagcagtag	1020
tagtagtagt	agttagtaac	gtcgtgagaa	cgggaaatga	agaaaggaac	ctttctcttc	1080
cttctggcca	ttccgttctg	cagggttcaag	ctcaagctcc	actcaaaacc	gtggaggcac	1140
aagaaactcg	gatacagcgg	atgagaacca	taactaccat	caacagcaac	atcaacaatt	1200
atatatgggt	tacagtggct	ggccttttg				

(2) INFORMATION FOR SEQ ID NO:2173:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 326 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..326
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571936

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2173:

Met	Ser	Ser	Ser	Arg	Asn	Thr	His	Trp	Cys	His	Arg	Cys	Gln	Arg	Ala
1				5				10					15		
Val	Arg	Leu	His	Gly	Gln	Glu	Pro	Val	Cys	Ser	Tyr	Cys	Gly	Gly	Gly
			20					25					30		
Phe	Val	Glu	Glu	Val	Leu	Asp	Met	Ala	Gln	Ala	Ser	Pro	Phe	Asp	Phe
			35					40					45		
Arg	Ser	His	Arg	Gly	Val	Val	Glu	Arg	Asp	Gln	Thr	Phe	Asp	Leu	Met
			50				55					60			
Asp	Ala	Phe	Ser	Val	Phe	Met	Arg	Asn	Arg	Leu	Ala	Glu	Arg	Ser	His
			65				70			75				80	
Asp	Arg	Glu	Ile	Arg	Gly	Arg	Thr	Ile	Ser	Ser	Gly	Pro	Glu	Asn	Phe
			85				90						95		
Pro	Gly	Leu	Ala	Pro	Leu	Leu	Ile	Phe	Gly	Gly	Gln	Val	Pro	Tyr	Arg
			100				105						110		

Leu Thr Gly Asp Asn Ala Val Glu Ala Leu Phe Asn Gly Gly Ser Pro
115 120 125
Gly Ile Gly Ile Thr Arg Gly Asn Thr Gly Asp Tyr Phe Gly Pro
130 135 140
Gly Leu Glu Glu Leu Phe Glu Gln Leu Ser Ala Gly Thr Thr Arg Arg
145 150 155 160
Gly Pro Pro Pro Ala Pro Arg Ser Ala Ile Asp Ala Leu Pro Thr Ile
165 170 175
Lys Ile Ala Gln Arg His Leu Arg Ser Ser Asp Ser Asn Cys Pro Val
180 185 190
Cys Lys Asp Glu Phe Glu Leu Gly Ser Glu Ala Lys Gln Met Pro Cys
195 200 205
Asn His Ile Tyr His Ser Asp Cys Ile Val Pro Trp Leu Val Gln His
210 215 220
Asn Ser Cys Pro Val Cys Arg Gln Glu Leu Pro Ser Ala Ser Gly Pro
225 230 235 240
Ser Ser Ser Gln Asn Arg Thr Thr Pro Thr Arg Asn Tyr Arg Ser Ser
245 250 255
Ser Ser Ser Ser Ser Ser Asn Ser Arg Glu Asn Gly Asn Glu Arg Arg
260 265 270
Asn Pro Phe Ser Ser Phe Trp Pro Phe Arg Ser Ser Gly Ser Ser Ser
275 280 285
Ser Ser Thr Gln Asn Arg Gly Gly Thr Arg Asn Ser Asp Thr Ser Asp
290 295 300
Glu Asn His Asn Tyr His Gln Gln Gln His Gln Gln Ser Tyr Met Gly
305 310 315 320
Tyr Ser Gly Trp Pro Phe
325

(2) INFORMATION FOR SEQ ID NO:2174:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 288 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..288

(D) OTHER INFORMATION: / Ceres Seq. ID 1571937

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2174:

Met Ala Gln Ala Ser Pro Phe Asp Met Phe Arg Ser His Arg Gly Val
1 5 10 15
Val Glu Arg Asp Gln Thr Phe Asp Leu Met Asp Ala Phe Ser Val Phe
20 25 30
Met Arg Asn Arg Leu Ala Glu Arg Ser His Asp Arg Glu Ile Arg Gly
35 40 45
Arg Thr Ile Ser Ser Gly Pro Glu Asn Phe Pro Gly Leu Ala Pro Leu
50 55 60
Leu Ile Phe Gly Gly Gln Val Pro Tyr Arg Leu Thr Gly Asp Asn Ala
65 70 75 80
Val Glu Ala Leu Phe Asn Gly Gly Ser Pro Gly Ile Gly Ile Thr Arg
85 90 95
Gly Asn Thr Gly Asp Tyr Phe Phe Gly Pro Gly Leu Glu Glu Leu Phe
100 105 110
Glu Gln Leu Ser Ala Gly Thr Thr Arg Arg Gly Pro Pro Pro Ala Pro
115 120 125
Arg Ser Ala Ile Asp Ala Leu Pro Thr Ile Lys Ile Ala Gln Arg His
130 135 140
Leu Arg Ser Ser Asp Ser Asn Cys Pro Val Cys Lys Asp Glu Phe Glu
145 150 155 160
Leu Gly Ser Glu Ala Lys Gln Met Pro Cys Asn His Ile Tyr His Ser

Asp	Cys	Ile	Val	Pro	Trp	Leu	Val	Gln	His	Asn	Ser	Cys	Pro	Val	Cys
			180					185						190	
Arg	Gln	Glu	Leu	Pro	Ser	Ala	Ser	Gly	Pro	Ser	Ser	Ser	Gln	Asn	Arg
		195					200						205		
Thr	Thr	Pro	Thr	Arg	Asn	Tyr	Arg	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Ser
		210				215					220				
Asn	Ser	Arg	Glu	Asn	Gly	Asn	Glu	Arg	Arg	Asn	Pro	Phe	Ser	Ser	Phe
					230					235					240
Trp	Pro	Phe	Arg	Ser	Ser	Gly	Ser	Ser	Ser	Ser	Ser	Thr	Gln	Asn	Arg
					245					250				255	
Gly	Gly	Thr	Arg	Asn	Ser	Asp	Thr	Ser	Asp	Glu	Asn	His	Asn	Tyr	His
			260					265					270		
Gln	Gln	Gln	His	Gln	Gln	Ser	Tyr	Met	Gly	Tyr	Ser	Gly	Trp	Pro	Phe
			275				280					285			

(2) INFORMATION FOR SEQ ID NO:2175:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 280 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..280

(D) OTHER INFORMATION: / Ceres Seq. ID 1571938

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2175:

Met	Phe	Arg	Ser	His	Arg	Gly	Val	Val	Glu	Arg	Asp	Gln	Thr	Phe	Asp
1				5					10					15	
Leu	Met	Asp	Ala	Phe	Ser	Val	Phe	Met	Arg	Asn	Arg	Leu	Ala	Glu	Arg
			20					25					30		
Ser	His	Asp	Arg	Glu	Ile	Arg	Gly	Arg	Thr	Ile	Ser	Ser	Gly	Pro	Glu
			35				40					45			
Asn	Phe	Pro	Gly	Leu	Ala	Pro	Leu	Leu	Ile	Phe	Gly	Gly	Gln	Val	Pro
			50			55				60					
Tyr	Arg	Leu	Thr	Gly	Asp	Asn	Ala	Val	Glu	Ala	Leu	Phe	Asn	Gly	Gly
65				70					75					80	
Ser	Pro	Gly	Ile	Gly	Ile	Thr	Arg	Gly	Asn	Thr	Gly	Asp	Tyr	Phe	Phe
			85						90				95		
Gly	Pro	Gly	Leu	Glu	Glu	Leu	Phe	Glu	Gln	Leu	Ser	Ala	Gly	Thr	Thr
			100					105					110		
Arg	Arg	Gly	Pro	Pro	Pro	Ala	Pro	Arg	Ser	Ala	Ile	Asp	Ala	Leu	Pro
			115				120					125			
Thr	Ile	Lys	Ile	Ala	Gln	Arg	His	Leu	Arg	Ser	Ser	Asp	Ser	Asn	Cys
			130			135					140				
Pro	Val	Cys	Lys	Asp	Glu	Phe	Glu	Leu	Gly	Ser	Glu	Ala	Lys	Gln	Met
145				150						155					160
Pro	Cys	Asn	His	Ile	Tyr	His	Ser	Asp	Cys	Ile	Val	Pro	Trp	Leu	Val
			165						170					175	
Gln	His	Asn	Ser	Cys	Pro	Val	Cys	Arg	Gln	Glu	Leu	Pro	Ser	Ala	Ser
			180					185					190		
Gly	Pro	Ser	Ser	Ser	Gln	Asn	Arg	Thr	Thr	Pro	Thr	Arg	Asn	Tyr	Arg
			195					200				205			
Ser	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Asn	Ser	Arg	Glu	Asn	Gly	Asn
			210				215					220			
Arg	Arg	Asn	Pro	Phe	Ser	Ser	Phe	Trp	Pro	Phe	Arg	Ser	Ser	Gly	Ser
225				230						235					240
Ser	Ser	Ser	Ser	Thr	Gln	Asn	Arg	Gly	Gly	Thr	Arg	Asn	Ser	Asp	Thr
				245						250				255	

Ser Asp Glu Asn His Asn Tyr His Gln Gln Gln His Gln Gln Ser Tyr
260 265 270
Met Gly Tyr Ser Gly Trp Pro Phe
275 280

(2) INFORMATION FOR SEQ ID NO:2176:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1430 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1430

(D) OTHER INFORMATION: / Ceres Seq. ID 1571945

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2176:

ctaaactaaa	atctaaatct	tgcccttcctg	actttctctc	tacgacagaa	tttttgaagc	60
ttctctctgc	ttatcgacac	tatgggttctc	gaggcgacta	tgatatgat	cgacaactcc	120
gaagtggatgc	gaaacggaga	ttactctccg	tctaggttac	aggcgcaaac	ggaagctggt	180
aatcttcttt	gcggagGccaa	aaccacgtcg	aatccggaga	atacggtggg	gattttgaca	240
atggtctggca	aaggagttag	agttattgact	actcctacct	ctgatcttgg	caaaattctg	300
gcctgtatgc	acggcctctga	tgtggggagga	gagatcaact	taaccgcagc	tatccagatc	360
gccacagtag	ctcttaagca	tcgccaataac	aagaatcaac	gccaaaggat	tattgttttt	420
gctggaaagtc	caatcaaagt	ogagaagaag	gcocctagaga	tagttggaaa	aaggctgaag	480
aagaatagtg	tatctcttga	tattgtcaat	ttcggggagg	atgatgatga	ggaaaagctc	540
cagaaaactcg	agggccctctc	tacagctgtg	aataacaatg	acggttagcca	cattgttcat	600
gttctctctg	gagccaatgc	tctctcagat	gtgcttctca	gcacacctgt	attcaccgggt	660
gatgagggtg	caagtggcta	tgtttctgcg	gcagctgctg	cagcgggcgc	aggtggggag	720
ttcgactttg	gtgtggacc	aaatatcgat	ccagaaactg	ctcttgccct	tcgggtctcc	780
atggaggagg	agagagcaag	acaagaagct	gctgccaaaga	agcgggccga	tgaggcatgt	840
cagaaagaca	aagatgggga	cacagcttcc	gcttcacagg	agacagtgtc	taggacaact	900
gacaaagaag	ctgaaccaat	ggatgaggac	agtgctttgc	tagatcaggc	aattgctatg	960
tctgtgtgtg	atgtgaatat	gtcagaagcg	gctgatgagg	accaggatct	ggctttaagt	1020
ctgcaaatgt	caatgagttg	ggaagagtca	agtgaagcta	ctctcatcgc	aaacaacctc	1080
ttgggaaatc	aagccttcct	atcgtctgtt	ctctcatcgc	ttcctggggg	ggatccaaat	1140
gatccggcag	ttaaagaact	actagcgtct	ctgccagacg	agtcaaaagc	tcacgaggag	1200
gaagagagta	gtagcaaaaa	agggcaggat	gagaagaagt	gaasaaggat	ctgagagctc	1260
caataaaaa	tctctctgtt	tcttttggtt	gataagagatt	ggaactgaat	ttaaactaat	1320
tctctgcctt	gtgaaatttg	gttttttctc	tctctctcgc	ctttttataa	tgtgtgtatt	1380
gtacgagtca	aggactagct	tctttttaa	tttttatgg	actttatgcc		

(2) INFORMATION FOR SEQ ID NO:2177:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 386 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..386

(D) OTHER INFORMATION: / Ceres Seq. ID 1571946

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2177:

Met	Val	Leu	Glu	Ala	Thr	Met	Ile	Cys	Ile	Asp	Asn	Ser	Glu	Trp	Met
1															
			5						10				15		
Arg	Asn	Gly	Asp	Tyr	Ser	Pro	Ser	Arg	Leu	Gln	Ala	Gln	Thr	Glu	Ala
			20						25				30		
Val	Asn	Leu	Leu	Cys	Gly	Ala	Lys	Thr	Gln	Ser	Asn	Pro	Glu	Asn	Thr
			35						40				45		
Val	Gly	Ile	Leu	Thr	Met	Ala	Gly	Lys	Gly	Val	Arg	Val	Leu	Thr	Thr
			50						55				60		
Pro	Thr	Ser	Asp	Leu	Gly	Lys	Ile	Leu	Ala	Cys	Met	His	Gly	Leu	Asp

65				70				75				80
Val	Gly	Gly	Glu	Ile	Asn	Leu	Thr	Ala	Ala	Ile	Gln	Ile
				85				90				Gln
Ala	Leu	Lys	His	Arg	Gln	Asn	Lys	Asn	Gln	Arg	Gln	Arg
				100				105				Ile
Phe	Ala	Gly	Ser	Pro	Ile	Lys	Tyr	Glu	Lys	Lys	Ala	Leu
				115				120				Glu
Gly	Lys	Arg	Leu	Lys	Lys	Asn	Ser	Val	Ser	Leu	Asp	Ile
				130				135				Val
Gly	Glu	Asp	Asp	Asp	Glu	Glu	Lys	Pro	Gln	Lys	Leu	Glu
				145				150				Ala
Thr	Ala	Val	Asn	Asn	Asn	Asp	Gly	Ser	His	Ile	Val	His
				165				170				Val
Gly	Ala	Asn	Ala	Leu	Ser	Asp	Val	Leu	Ser	Thr	Pro	Val
				180				185				Phe
Gly	Asp	Glu	Gly	Ala	Ser	Gly	Tyr	Val	Ser	Ala	Ala	Ala
				195				200				Ala
Ala	Ala	Gly	Gly	Asp	Phe	Asp	Phe	Gly	Val	Asp	Pro	Asn
				210				215				Ile
Glu	Leu	Ala	Leu	Ala	Leu	Arg	Val	Ser	Met	Glu	Glu	Glu
				225				230				Arg
Gln	Glu	Ala	Ala	Ala	Lys	Lys	Ala	Ala	Asp	Glu	Ala	Cys
				245				250				Gln
Lys	Asp	Gly	Asp	Thr	Ala	Ser	Ala	Ser	Gln	Glu	Thr	Val
				260				265				Ala
Thr	Asp	Lys	Asn	Ala	Glu	Pro	Met	Asp	Glu	Asp	Ser	Ala
				275				280				Leu
Gln	Ala	Ile	Ala	Met	Ser	Xaa	Gly	Asp	Val	Asn	Met	Ser
				290				295				Glu
Asp	Glu	Asp	Gln	Asp	Leu	Ala	Leu	Ala	Leu	Gln	Met	Ser
				305				310				Met
Glu	Glu	Ser	Ser	Glu	Ala	Thr	Gly	Ala	Gly	Asn	Leu	Leu
				325				330				Gly
Gln	Ala	Phe	Ile	Ser	Ser	Val	Leu	Ser	Ser	Leu	Pro	Gly
				340				345				Val
Asn	Asp	Pro	Ala	Val	Lys	Glu	Leu	Leu	Ala	Ser	Leu	Pro
				355				360				Asp
Lys	Arg	His	Glu	Glu	Glu	Glu	Ser	Ser	Ser	Lys	Lys	Gly
				370				375				Glu
Lys	Lys											

(2) INFORMATION FOR SEQ ID NO:2178:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 380 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..380

(D) OTHER INFORMATION: / Ceres Seq. ID 1571947

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2178:

Met	Ile	Cys	Ile	Asp	Asn	Ser	Glu	Trp	Met	Arg	Asn	Gly	Asp	Tyr	Ser
1				5				10						15	
Pro	Ser	Arg	Leu	Gln	Ala	Gln	Thr	Glu	Ala	Val	Asn	Leu	Leu	Cys	Gly
				20				25						30	
Ala	Lys	Thr	Gln	Ser	Asn	Pro	Glu	Asn	Thr	Val	Gly	Ile	Leu	Thr	Met
				35				40						45	
Ala	Gly	Lys	Gly	Val	Arg	Val	Leu	Thr	Thr	Pro	Thr	Ser	Asp	Leu	Gly
				50				55						60	

Lys Ile Leu Ala Cys Met His Gly Leu Asp Val Gly Gly Glu Ile Asn
65 70 75 80
Leu Thr Ala Ala Ile Gln Ile Ala Gln Leu Ala Leu Lys His Arg Gln
85 90 95
Asn Lys Asn Gln Arg Gln Arg Ile Ile Val Phe Ala Gly Ser Pro Ile
100 105 110
Lys Tyr Glu Lys Lys Ala Leu Glu Ile Val Gly Lys Arg Leu Lys Lys
115 120 125
Asn Ser Val Ser Leu Asp Ile Val Asn Phe Gly Glu Asp Asp Asp Glu
130 135 140
Glu Lys Pro Gln Lys Leu Glu Ala Leu Leu Thr Ala Val Asn Asn Asn
145 150 155 160
Asp Gly Ser His Ile Val His Val Pro Ser Gly Ala Asn Ala Leu Ser
165 170 175
Asp Val Leu Leu Ser Thr Pro Val Phe Thr Gly Asp Glu Gly Ala Ser
180 185 190
Gly Tyr Val Ser Ala Ala Ala Ala Ala Ala Gly Gly Asp Phe
195 200 205
Asp Phe Gly Val Asp Pro Asn Ile Asp Pro Glu Leu Ala Leu Ala Leu
210 215 220
Arg Val Ser Met Glu Glu Glu Arg Ala Arg Gln Gln Ala Ala Ala Lys
225 230 235 240
Lys Ala Ala Asp Glu Ala Cys Gln Lys Asp Lys Asp Gly Asp Thr Ala
245 250 255
Ser Ala Ser Gln Glu Thr Val Ala Arg Thr Thr Asp Lys Asn Ala Glu
260 265 270
Pro Met Asp Glu Asp Ser Ala Leu Leu Asp Gln Ala Ile Ala Met Ser
275 280 285
Xaa Gly Asp Val Asn Met Ser Glu Ala Ala Asp Glu Asp Gln Asp Leu
290 295 300
Ala Leu Ala Leu Gln Met Ser Met Ser Gly Glu Glu Ser Ser Glu Ala
305 310 315 320
Thr Gly Ala Gly Asn Asn Leu Leu Gly Asn Gln Ala Phe Ile Ser Ser
325 330 335
Val Leu Ser Ser Leu Pro Gly Val Asp Pro Asn Asp Pro Ala Val Lys
340 345 350
Glu Leu Leu Ala Ser Leu Pro Asp Glu Ser Lys Arg His Glu Glu Glu
355 360 365
Glu Ser Ser Ser Lys Lys Gly Glu Asp Glu Lys Lys
370 375 380

(2) INFORMATION FOR SEQ ID NO:2179:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 371 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..371

(D) OTHER INFORMATION: / Ceres Seq. ID 1571948

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2179:

Met Arg Asn Gly Asp Tyr Ser Pro Ser Arg Leu Gln Ala Gln Thr Glu
1 5 10 15
Ala Val Asn Leu Leu Cys Gly Ala Lys Thr Gln Ser Asn Pro Glu Asn
20 25 30
Thr Val Gly Ile Leu Thr Met Ala Gly Lys Gly Val Arg Val Leu Thr
35 40 45
Thr Pro Thr Ser Asp Leu Gly Lys Ile Leu Ala Cys Met His Gly Leu
50 55 60
Asp Val Gly Gly Glu Ile Asn Leu Thr Ala Ala Ile Gln Ile Ala Gln

65	70	75	80
Leu Ala Leu Lys His Arg Gln Asn Lys Asn Gln Arg Gln Arg Ile Ile			
	85	90	95
Val Phe Ala Gly Ser Pro Ile Lys Tyr Glu Lys Lys Ala Leu Glu Ile			
	100	105	110
Val Gly Lys Arg Leu Lys Lys Asn Ser Val Ser Leu Asp Ile Val Asn			
	115	120	125
Phe Gly Glu Asp Asp Asp Glu Glu Lys Pro Gln Lys Leu Glu Ala Leu			
	130	135	140
Leu Thr Ala Val Asn Asn Asn Asp Gly Ser His Ile Val His Val Pro			
	145	150	155
Ser Gly Ala Asn Ala Leu Ser Asp Val Leu Leu Ser Thr Pro Val Phe			
	165	170	175
Thr Gly Asp Glu Gly Ala Ser Gly Tyr Val Ser Ala Ala Ala Ala			
	180	185	190
Ala Ala Ala Gly Gly Asp Phe Asp Phe Gly Val Asp Pro Asn Ile Asp			
	195	200	205
Pro Glu Leu Ala Leu Ala Leu Arg Val Ser Met Glu Glu Glu Arg Ala			
	210	215	220
Arg Gln Glu Ala Ala Ala Lys Lys Ala Ala Asp Glu Ala Cys Gln Lys			
	225	230	235
Asp Lys Asp Gly Asp Thr Ala Ser Ala Ser Gln Glu Thr Val Ala Arg			
	245	250	255
Thr Thr Asp Lys Asn Ala Glu Pro Met Asp Glu Asp Ser Ala Leu Leu			
	260	265	270
Asp Gln Ala Ile Ala Met Ser Xaa Gly Asp Val Asn Met Ser Glu Ala			
	275	280	285
Ala Asp Glu Asp Gln Asp Leu Ala Leu Ala Leu Gln Met Ser Met Ser			
	290	295	300
Gly Glu Glu Ser Ser Glu Ala Thr Gly Ala Gly Asn Asn Leu Leu Gly			
	305	310	315
Asn Gln Ala Phe Ile Ser Ser Val Leu Ser Ser Leu Pro Gly Val Asp			
	325	330	335
Pro Asn Asp Pro Ala Val Lys Glu Leu Ala Ser Leu Pro Asp Glu			
	340	345	350
Ser Lys Arg His Glu Glu Glu Glu Ser Ser Ser Lys Lys Gly Glu Asp			
	355	360	365
Glu Lys Lys			
370			

(2) INFORMATION FOR SEQ ID NO:2180:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1140 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1140
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571949

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2180:

atacttgtaa	aagctagagt	caacgcggtt	cagttctcaga	ccagacgaaa	caacgatgct	60
taactctatc	actttaacc	ggaaaccacc	actcccggtc	aactctctgtg	ggttttcagg	120
taatacactc	tcgtcttttt	gtcgaagaac	tataacggaa	ggtagttcga	gcaaggctct	180
ttcgttttgg	tacaaaaatg	ttggttcaat	gaagtgtggt	cggagcaatt	ggccggggcg	240
ttctgggact	gcgtttgggc	atctagtcgg	ggctctctgg	ggtctcaggtg	gaaattcagg	300
tggctctggc	gggttaggtg	gttcaggcgg	tggttgtaat	ggttggttcg	gcggcggttg	360
tggtgatgga	agcgacggaa	aaggaaagaa	cggtgtcaat	ctctcatagt	accaggtctt	420
ttctcacaac	ttctctgttt	tgaccaaaag	tgtgaccgca	gcactttttg	acctcgtgtg	480
agatttgatc	tgtcagctta	caatcaacaa	gacctcatcg	ctggacaaga	agaggacact	540
cactttttacc	ttcttgggct	tagggctagt	cggtccaaca	ttgcattttt	ggtattttga	600

tttgagcaaa	gttgtgacag	cttctggatt	atcaggcgca	gttataccag	ttctactgga	660
tcagtttgtt	tttgtctcta	ttttgtgtgg	agttttctta	tcagcagttg	tgacacttga	720
aggaaaacca	tcaaatgtca	taccgaagct	acaacaggag	tggactgggt	caatgatagc	780
aaattggcag	ctatggatac	catttcagtt	tcttaacttc	agattttgtc	cacagaaacta	840
ccaggtaact	gcttcaaacg	tagtggcctt	ggcttggaa	gtgattttat	cattcaaaagc	900
tcacaaagaa	gttgttgcaa	agtagacatg	tttcttaact	ggagcctaga	ggtgggttgc	960
ggattgttat	cggcagagtt	ttgggggaaac	gttcttgtct	gctgatgcaa	atgtttgtgtg	1020
tttcgaaaca	attatttggg	aacctgtcac	ttgacatttt	cttagagttg	aaacaagctt	1080
ttcttcaagc	acttcaaaata	tttcccccac	atcaatgttt	catatatatta	ttgKtctctc	1140

(2) INFORMATION FOR SEQ ID NO:2181:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 289 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..289
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571950

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2181:

Met	Leu	Asn	Ser	Ile	Thr	Leu	Thr	Arg	Lys	Pro	Pro	Leu	Pro	Phe	Asn
1			5						10					15	
Ser	Val	Gly	Phe	Ser	Gly	Asn	His	Ser	Ser	Ser	Phe	Cys	Arg	Arg	Thr
			20						25					30	
Ile	Thr	Glu	Gly	Ser	Ser	Ser	Lys	Ala	Leu	Ser	Phe	Gly	Tyr	Lys	Asn
			35						40					45	
Val	Gly	Ser	Leu	Lys	Cys	Gly	Arg	Ser	Asn	Trp	Pro	Gly	Arg	Ser	Gly
			50						55					60	
Thr	Ala	Phe	Gly	His	Leu	Val	Arg	Val	Ser	Ala	Val	Ser	Gly	Gly	Asn
			65						70					75	
Ser	Gly	Gly	Ser	Gly	Gly	Leu	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Asn	Gly
									85					90	
Gly	Ser	Gly	Gly	Gly	Gly	Gly	Asp	Gly	Ser	Asp	Gly	Lys	Gly	Lys	Lys
									100					105	
Arg	Ser	Leu	Leu	Ser	Trp	Tyr	Gln	Ala	Leu	Leu	Ser	Asn	Ser	Pro	Val
									115					120	
Leu	Thr	Lys	Ala	Val	Thr	Ala	Ala	Leu	Leu	Asn	Leu	Val	Gly	Asp	Leu
									130					135	
Ile	Cys	Gln	Leu	Thr	Ile	Asn	Lys	Thr	Ser	Ser	Leu	Asp	Lys	Lys	Arg
									145					150	
Thr	Leu	Thr	Phe	Thr	Phe	Leu	Gly	Leu	Gly	Leu	Val	Gly	Pro	Thr	Leu
									165					170	
His	Phe	Trp	Tyr	Leu	Tyr	Leu	Ser	Lys	Val	Val	Thr	Ala	Ser	Gly	Leu
									180					185	
Ser	Gly	Ala	Val	Ile	Arg	Leu	Leu	Leu	Asp	Gln	Phe	Val	Phe	Ala	Pro
									195					200	
Ile	Phe	Val	Gly	Val	Phe	Leu	Ser	Ala	Val	Val	Thr	Leu	Glu	Gly	Lys
									210					215	
Pro	Ser	Asn	Val	Ile	Pro	Lys	Leu	Gln	Gln	Glu	Trp	Thr	Gly	Ala	Met
									225					230	
Ile	Ala	Asn	Trp	Gln	Leu	Trp	Ile	Pro	Phe	Gln	Phe	Leu	Asn	Phe	Arg
									245					250	
Phe	Val	Pro	Gln	Asn	Tyr	Gln	Val	Leu	Ala	Ser	Asn	Val	Val	Ala	Leu
									260					265	
Ala	Trp	Asn	Val	Ile	Leu	Ser	Phe	Lys	Ala	His	Lys	Glu	Val	Val	Ala
									275					280	
														285	

Lys

(2) INFORMATION FOR SEQ ID NO:2182:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 731 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..731
(D) OTHER INFORMATION: / Ceres Seq. ID 1571963

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2182:

attttccaca	acttggaagt	cgaaatccat	ttcgaatttt	ggttagcagc	gatttcaaat	60
tcacaaacgt	agaattatgg	cgaggagtga	tcaggcgtgt	atcttctgtg	agatcgtgcg	120
aaatccaacc	actactcgtc	tccttcacac	cgatgagaaa	gtccatcgct	ttcaagacat	180
caagcctgca	gccagagggc	actattttgt	gattccaaaa	gaacatatcc	ctactgtgaa	240
tgacctttag	agaagagatg	aagactactc	acttgtaaga	cacatgccta	gtgtgggaca	300
acaactgttg	cagaaagatg	ctctccaaag	cattcataga	tttggttttc	accagccacc	360
gatttaacagt	gttgatcatc	tccatctcca	ctgttttgca	ttgccttatg	tgccagatgt	420
gaaagccatc	aagtacaagt	ctttgggacc	tttgggtgga	tttatggaag	ccgagacact	480
gctagagaag	ataaggCctc	ttctttcaaa	gggtMactg	aacccaactt	gtttaaccgc	540
attgcgttgc	ttctcttttg	taaaactgtg	caatatctct	ttctattctt	tttctgtgca	600
aatctgtgaa	caaatgccaa	atattattag	agattttgta	tatgaagaaa	ggatgtgtca	660
agtaattata	tgtaatttct	gccattgtcc	aatagttaac	acttaacacc	aatctcattg	720
tttccatgct	t					

(2) INFORMATION FOR SEQ ID NO:2183:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 209 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..209
(D) OTHER INFORMATION: / Ceres Seq. ID 1571964

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2183:

Met	Ala	Gly	Val	Asn	Gln	Ala	Cys	Ile	Phe	Cys	Glu	Ile	Val	Arg	Asn	
1				5					10					15		
Pro	Thr	Thr	Thr	Arg	Leu	Leu	His	Thr	Asp	Glu	Lys	Val	Ile	Ala	Phe	
			20					25					30			
Gln	Asp	Ile	Lys	Pro	Ala	Ala	Gln	Arg	His	Tyr	Leu	Val	Ile	Pro	Lys	
			35				40					45				
Glu	His	Ile	Pro	Thr	Val	Asn	Asp	Leu	Gln	Arg	Arg	Asp	Glu	Asp	Tyr	
			50			55					60					
Ser	Leu	Val	Arg	His	Met	Leu	Ser	Val	Gly	Gln	Gln	Leu	Leu	Gln	Lys	
			65		70				75					80		
Asp	Ala	Pro	Gln	Ser	Ile	His	Arg	Phe	Gly	Phe	His	Gln	Pro	Pro	Phe	
			85					90					95			
Asn	Ser	Val	Asp	His	Leu	His	Leu	His	Cys	Phe	Ala	Leu	Pro	Tyr	Val	
			100					105					110			
Pro	Arg	Trp	Lys	Ala	Ile	Lys	Tyr	Lys	Ser	Leu	Gly	Pro	Leu	Gly	Gly	
			115			120						125				
Phe	Ile	Glu	Ala	Glu	Thr	Leu	Glu	Lys	Ile	Arg	Pro	Leu	Leu	Ser		
			130			135				140						
Lys	Val	Xaa	Leu	Asn	Pro	Thr	Cys	Leu	Thr	Ala	Leu	Arg	Cys	Phe	Ser	
			145		150					155						
Leu	Leu	Lys	Leu	Cys	Asn	Ile	Ser	Phe	Leu	Phe	Cys	Trp	Gln	Ile		
			165			170						175				
Cys	Glu	Gln	Met	Pro	Asn	Ile	Ile	Arg	Asp	Phe	Val	Tyr	Glu	Arg	Arg	
			180			185						190				
Met	Cys	Gln	Val	Ile	Ile	Cys	Asn	Phe	Cys	His	Cys	Pro	Ile	Val	Asn	

Thr 195 200 205

(2) INFORMATION FOR SEQ ID NO:2184:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 140 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..140
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571965

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2184:

Met	Leu	Ser	Val	Gly	Gln	Gln	Leu	Leu	Lys	Asp	Ala	Pro	Gln	Ser
1			5					10					15	
Ile	His	Arg	Phe	Gly	Phe	His	Gln	Pro	Pro	Phe	Asn	Ser	Val	Asp
			20					25					30	His
Leu	His	Leu	His	Cys	Phe	Ala	Leu	Pro	Tyr	Val	Pro	Arg	Trp	Lys
			35				40					45		Ala
Ile	Lys	Tyr	Lys	Ser	Leu	Gly	Pro	Leu	Gly	Gly	Phe	Ile	Glu	Ala
			50			55				60				Glu
Thr	Leu	Leu	Glu	Lys	Ile	Arg	Pro	Leu	Leu	Ser	Lys	Val	Xaa	Leu
65					70					75				80
Pro	Thr	Cys	Leu	Thr	Ala	Leu	Arg	Cys	Phe	Ser	Leu	Leu	Lys	Leu
					85				90				95	Cys
Asn	Ile	Ser	Phe	Leu	Phe	Phe	Cys	Trp	Gln	Ile	Cys	Glu	Gln	Met
					100			105					110	Pro
Asn	Ile	Ile	Arg	Asp	Phe	Val	Tyr	Glu	Arg	Arg	Met	Cys	Gln	Val
					115			120					125	Ile
Ile	Cys	Asn	Phe	Cys	His	Cys	Pro	Ile	Val	Asn	Thr			
					130			135			140			

(2) INFORMATION FOR SEQ ID NO:2185:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1374 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1374
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571987

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2185:

aacacaaaaga	caataaaaatt	aatcaaaaat	aaacaaagga	gagagacaga	agaacacagag	60
agagtagtga	attccggtgg	ttttctgctc	atctactttc	atccaccttc	atcccttccg	120
ccccaaaatt	caattctctc	ttcctttctc	tctctttctc	cttaaaaaat	ctaactttac	180
tcatctcact	tccaaagtct	caacctttct	tctctaattg	agatctgcac	ttacttcaaa	240
tcacaaccca	cttggtctcc	cattctcttc	gttctggggt	caatctcaat	cttcaaatcc	300
attctcaccc	tctcagatc	tttctacatc	tacttctccc	gaccatccaa	aaacctccgc	360
cgatacgggt	catgggcaat	catcaaccga	ccaacagacg	gaatcggtaa	agctttcgcc	420
tttcagttag	cccagaaaag	tcttaacctt	atactcgttg	ctcgtaaccc	agacaagctc	480
aaagatgtct	ctgattccat	cagatctaa	tatagtcaaa	ctcagatctt	gacogttgtg	540
attgatgtct	ctggagatat	tgatgaaggt	gtgaaacgga	ttaaggagag	tattgaagga	600
ttgatgtgtg	ggattttgat	taataatgct	ggcatgtctt	atccttatgc	taagtatttt	660
catgaggttg	atgaagagtt	gatcaataac	ttgattaaga	tcaatgttga	aggaactaat	720
aaagttaact	aaagtctgtt	gcttaaatat	cttaagagga	agaaaggtgc	tattattaat	780
atgggtcttg	gtgctgtctc	tcttatctct	tcttatctct	tttactctgt	tattgctgtg	840
gtcaaaacgt	acgtggatca	gttcaaaaag	tgtctacatg	ttgagtataa	gaagatgggg	900
attgatgttc	aatgccaggt	tccctgttat	gttgcaacaa	agatgacaaa	aataagaaga	960

gcaccccttct tagttgcatc accagagggg tacgcaaagg cagcacTgcg tttttagggc 1020
tatgaagcgc aatgcacacc gtactggcct cagcgtctca tgggtgcagt tgtctctgca 1080
ttgccgaaa ggcgtttttga atcatttaac atcaagagat gcctccagat ccggaagaag 1140
gggtctccaaa aagactccat gaagaaagaa tgaatcttcc aggttttaag tactaccaag 1200
aatttctctc ttctgaagtt gttggtttct tgaaaagcct ctgttctgaa tcttttgtaa 1260
gactttgact ctttagtttt ctaagttttt tataatttaa gattaaaaac cctaacgtac 1320
acgaataatt tacttctctt gtttctattt ataatattaa cgactgttgt attc

(2) INFORMATION FOR SEQ ID NO:2186:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 318 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..318

(D) OTHER INFORMATION: / Ceres Seq. ID 1571988

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2186:

Met Glu Ile Cys Thr Tyr Phe Lys Ser Gln Pro Thr Trp Leu Leu Ile
1 5 10 15
Leu Phe Val Leu Gly Ser Ile Ser Ile Phe Lys Phe Ile Phe Thr Leu
20 25 30
Leu Arg Ser Phe Tyr Ile Tyr Phe Leu Arg Pro Ser Lys Asn Leu Arg
35 40 45
Arg Tyr Gly Ser Trp Ala Ile Ile Thr Gly Pro Thr Asp Gly Ile Gly
50 55 60
Lys Ala Phe Ala Phe Gln Leu Ala Gln Lys Gly Leu Asn Leu Ile Leu
65 70 75 80
Val Ala Arg Asn Pro Asp Lys Leu Lys Asp Val Ser Asp Ser Ile Arg
85 90 95
Ser Lys Tyr Ser Gln Thr Gln Ile Leu Thr Val Val Met Asp Phe Ser
100 105 110
Gly Asp Ile Asp Glu Gly Val Lys Arg Ile Lys Glu Ser Ile Glu Gly
115 120 125
Leu Asp Val Gly Ile Leu Ile Asn Asn Ala Gly Met Ser Tyr Pro Tyr
130 135 140
Ala Lys Tyr Phe His Glu Val Asp Glu Glu Leu Ile Asn Asn Leu Ile
145 150 155 160
Lys Ile Asn Val Glu Gly Thr Thr Lys Val Thr Gln Ala Val Leu Pro
165 170 175
Asn Met Leu Lys Arg Lys Lys Gly Ala Ile Ile Asn Met Gly Ser Gly
180 185 190
Ala Ala Ala Leu Ile Pro Ser Tyr Pro Phe Tyr Ser Val Tyr Ala Gly
195 200 205
Ala Lys Thr Tyr Val Asp Gln Phe Thr Lys Cys Leu His Val Glu Tyr
210 215 220
Lys Lys Ser Gly Ile Asp Val Gln Cys Gln Val Pro Leu Tyr Val Ala
225 230 235 240
Thr Lys Met Thr Lys Ile Arg Arg Ala Ser Phe Leu Val Ala Ser Pro
245 250 255
Glu Gly Tyr Ala Lys Ala Ala Leu Arg Phe Val Gly Tyr Glu Ala Gln
260 265 270
Cys Thr Pro Tyr Trp Pro His Ala Leu Met Gly Ala Val Val Ser Ala
275 280 285
Leu Pro Glu Ser Val Phe Glu Ser Phe Asn Ile Lys Arg Cys Leu Gln
290 295 300
Ile Arg Lys Lys Gly Leu Gln Lys Asp Ser Met Lys Lys Glu
305 310 315

(2) INFORMATION FOR SEQ ID NO:2187:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 210 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..210
(D) OTHER INFORMATION: / Ceres Seq. ID 1571989
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2187:
Met Asp Phe Ser Gly Asp Ile Asp Glu Gly Val Lys Arg Ile Lys Glu
1 5 10 15
Ser Ile Glu Gly Leu Asp Val Gly Ile Leu Ile Asn Asn Ala Gly Met
20 25 30
Ser Tyr Pro Tyr Ala Lys Tyr Phe His Glu Val Asp Glu Glu Leu Ile
35 40 45
Asn Asn Leu Ile Lys Ile Asn Val Glu Gly Thr Thr Lys Val Thr Gln
50 55 60
Ala Val Leu Pro Asn Met Leu Lys Arg Lys Lys Gly Ala Ile Ile Asn
65 70 75 80
Met Gly Ser Gly Ala Ala Leu Ile Pro Ser Tyr Pro Phe Tyr Ser
85 90 95
Val Tyr Ala Gly Ala Lys Thr Tyr Val Asp Gln Phe Thr Lys Cys Leu
100 105 110
His Val Glu Tyr Lys Lys Ser Gly Ile Asp Val Gln Cys Gln Val Pro
115 120 125
Leu Tyr Val Ala Thr Lys Met Thr Lys Ile Arg Arg Ala Ser Phe Leu
130 135 140
Val Ala Ser Pro Glu Gly Tyr Ala Lys Ala Ala Leu Arg Phe Val Gly
145 150 155 160
Tyr Glu Ala Gln Cys Thr Pro Tyr Trp Pro His Ala Leu Met Gly Ala
165 170 175
Val Val Ser Ala Leu Pro Glu Ser Val Phe Glu Ser Phe Asn Ile Lys
180 185 190
Arg Cys Leu Gln Ile Arg Lys Lys Gly Leu Gln Lys Asp Ser Met Lys
195 200 205
Lys Glu
210

(2) INFORMATION FOR SEQ ID NO:2188:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 179 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1..179
(D) OTHER INFORMATION: / Ceres Seq. ID 1571990

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2188:

Met Ser Tyr Pro Tyr Ala Lys Tyr Phe His Glu Val Asp Glu Glu Leu
1 5 10 15
Ile Asn Asn Leu Ile Lys Ile Asn Val Glu Gly Thr Thr Lys Val Thr
20 25 30
Gln Ala Val Leu Pro Asn Met Leu Lys Arg Lys Lys Gly Ala Ile Ile
35 40 45
Asn Met Gly Ser Gly Ala Ala Ala Leu Ile Pro Ser Tyr Pro Phe Tyr
50 55 60
Ser Val Tyr Ala Gly Ala Lys Thr Tyr Val Asp Gln Phe Thr Lys Cys
65 70 75 80
Leu His Val Glu Tyr Lys Lys Ser Gly Ile Asp Val Gln Cys Gln Val

	85		90		95	
Pro Leu Tyr Val Ala Thr Lys Met Thr Lys Ile Arg Arg Ala Ser Phe						
	100		105		110	
Leu Val Ala Ser Pro Glu Gly Tyr Ala Lys Ala Ala Leu Arg Phe Val						
	115		120		125	
Gly Tyr Glu Ala Gln Cys Thr Pro Tyr Trp Pro His Ala Leu Met Gly						
	130		135		140	
Ala Val Val Ser Ala Leu Pro Glu Ser Val Phe Glu Ser Phe Asn Ile						
	145		150		155	
Lys Arg Cys Leu Gln Ile Arg Lys Lys Gly Leu Gln Lys Asp Ser Met						
	165		170		175	
Lys Lys Glu						

(2) INFORMATION FOR SEQ ID NO:2189:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 917 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..917

(D) OTHER INFORMATION: / Ceres Seq. ID 1571999

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2189:

attctcaactt	actctttttt	ttttttttgt	ttcttgttta	gaagaagcaa	tggccacttc	60
agcaatccaa	cactcttctt	ttgccggcca	aacggctcta	aagccatcca	acgacctcct	120
tgcgaagtc	ggagcctcta	atggtggcgg	cgcggttata	atgcgcgcta	ccgtcaagtc	180
taccctcag	agcatctggt	atggaccaga	cgtcccaaaa	tacctaggac	cattctcggg	240
aaacacacca	tcatacctaa	ctggagaata	ccctggagac	tacggctggg	acaccctggg	300
ttcttcagcc	gattccagaaa	cattcgcaaa	gaatcgtgag	ctcgaagtga	tcacacagta	360
atgggcaatg	ttgggagctt	taggctgcac	cttccctgaa	attctctcaa	aaaaacggagt	420
caaatccggt	gaagccgtgt	ggttcaaggc	aggatatcaa	atcttctcag	aaggaggact	480
tgactacctc	ggaaacccta	acttgatcca	cgcgcgaagc	atattagcta	tatggcgctg	540
tcaagttgtg	ctaattgggat	tcattgaagg	gtacagaaatc	ggaggtggtc	ctcttgggga	600
agggcctgac	ccgcttttacc	cgggcggggc	cttcgaccgc	ttgaacttag	cgtaggatcc	660
agaagcgttt	tcggagttga	aagtgaagga	gcttaaaaaa	ggctgctctg	ctatgtttct	720
aatgtttgga	ttctttgttc	aagccatagt	taccggtaaa	ggctcgatcg	aaaattctgtt	780
cgatcacatt	gcagaccctg	tggtctaaaca	tgcttgGGct	tacgccacca	actctgtccc	840
cggaaaaatg	agtttgatcg	gataatttat	gtaaattata	tcttttaaac	attttatcaat	900
gcattaaagt	tatcccc					

(2) INFORMATION FOR SEQ ID NO:2190:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 217 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..217

(D) OTHER INFORMATION: / Ceres Seq. ID 1572000

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2190:

Phe Ser Leu Thr Ser Phe Leu Phe Leu Cys Ser Cys Leu Glu Glu Ala	
1	5
	10
Met Ala Thr Ser Ala Ile Gln His Ser Ser Phe Ala Gly Gln Thr Ala	
	20
	25
Leu Lys Pro Ser Asn Asp Leu Leu Arg Lys Val Gly Ala Ser Asn Gly	
	35
	40
Gly Gly Arg Val Ile Met Arg Arg Thr Val Lys Ser Thr Pro Gln Ser	
	50
	55
	60

Ile Trp Tyr Gly Pro Asp Arg Pro Lys Tyr Leu Gly Pro Phe Ser Glu
65 70 75 80
Asn Thr Pro Ser Tyr Leu Thr Gly Glu Tyr Pro Gly Asp Tyr Gly Trp
85 90 95
Asp Thr Ala Gly Leu Ser Ala Asp Pro Glu Thr Phe Ala Lys Asn Arg
100 105 110
Glu Leu Gly Val Ile His Ser Arg Trp Ala Met Leu Gly Ala Leu Gly
115 120 125
Cys Thr Phe Pro Glu Ile Leu Ser Lys Asn Gly Val Lys Phe Gly Glu
130 135 140
Ala Val Trp Phe Lys Ala Gly Ser Gln Ile Phe Ser Glu Gly Gly Leu
145 150 155 160
Asp Tyr Leu Gly Asn Pro Asn Leu Ile His Ala Gln Ser Ile Leu Ala
165 170 175
Ile Trp Ala Cys Gln Val Val Leu Met Gly Phe Ile Glu Gly Tyr Arg
180 185 190
Ile Gly Gly Gly Pro Leu Gly Glu Gly Leu Asp Pro Leu Tyr Pro Gly
195 200 205
Gly Ala Phe Asp Pro Leu Asn Leu Ala
210 215

(2) INFORMATION FOR SEQ ID NO:2191:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 201 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..201

(D) OTHER INFORMATION: / Ceres Seq. ID 1572001

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2191:

Met Ala Thr Ser Ala Ile Gln His Ser Ser Phe Ala Gly Gln Thr Ala
1 5 10 15
Leu Lys Pro Ser Asn Asp Leu Leu Arg Lys Val Gly Ala Ser Asn Gly
20 25 30
Gly Gly Arg Val Ile Met Arg Arg Thr Val Lys Ser Thr Pro Gln Ser
35 40 45
Ile Trp Tyr Gly Pro Asp Arg Pro Lys Tyr Leu Gly Pro Phe Ser Glu
50 55 60
Asn Thr Pro Ser Tyr Leu Thr Gly Glu Tyr Pro Gly Asp Tyr Gly Trp
65 70 75 80
Asp Thr Ala Gly Leu Ser Ala Asp Pro Glu Thr Phe Ala Lys Asn Arg
85 90 95
Glu Leu Glu Val Ile His Ser Arg Trp Ala Met Leu Gly Ala Leu Gly
100 105 110
Cys Thr Phe Pro Glu Ile Leu Ser Lys Asn Gly Val Lys Phe Gly Glu
115 120 125
Ala Val Trp Phe Lys Ala Gly Ser Gln Ile Phe Ser Glu Gly Gly Leu
130 135 140
Asp Tyr Leu Gly Asn Pro Asn Leu Ile His Ala Gln Ser Ile Leu Ala
145 150 155 160
Ile Trp Ala Cys Gln Val Val Leu Met Gly Phe Ile Glu Gly Tyr Arg
165 170 175
Ile Gly Gly Gly Pro Leu Gly Glu Gly Leu Asp Pro Leu Tyr Pro Gly
180 185 190
Gly Ala Phe Asp Pro Leu Asn Leu Ala
195 200

(2) INFORMATION FOR SEQ ID NO:2192:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 164 amino acids

(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..164
(D) OTHER INFORMATION: / Ceres Seq. ID 1572002
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2192:
Met Arg Arg Thr Val Lys Ser Thr Pro Gln Ser Ile Trp Tyr Gly Pro
1 5 10 15
Asp Arg Pro Lys Tyr Leu Gly Pro Phe Ser Glu Asn Thr Pro Ser Tyr
20 25 30
Leu Thr Gly Glu Tyr Pro Gly Asp Tyr Gly Trp Asp Thr Ala Gly Leu
35 40 45
Ser Ala Asp Pro Glu Thr Phe Ala Lys Asn Arg Glu Leu Glu Val Ile
50 55 60
His Ser Arg Trp Ala Met Leu Gly Ala Leu Gly Cys Thr Phe Pro Glu
65 70 75 80
Ile Leu Ser Lys Asn Gly Val Lys Phe Gly Glu Ala Val Trp Phe Lys
85 90 95
Ala Gly Ser Gln Ile Phe Ser Glu Gly Gly Leu Asp Tyr Leu Gly Asn
100 105 110
Pro Asn Leu Ile His Ala Gln Ser Ile Leu Ala Ile Trp Ala Cys Gln
115 120 125
Val Val Leu Met Gly Phe Ile Glu Gly Tyr Arg Ile Gly Gly Gly Pro
130 135 140
Leu Gly Glu Gly Leu Asp Pro Leu Tyr Pro Gly Ala Phe Asp Pro
145 150 155 160
Leu Asn Leu Ala

(2) INFORMATION FOR SEQ ID NO:2193:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 932 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..932
(D) OTHER INFORMATION: / Ceres Seq. ID 1572023

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2193:

attacctctc	tctcaattcac	ctctcgctaa	gtgtgcgtta	gcCgttaggg	ttccgatcta	60
atcatggcgg	actctgtttt	gaaggagggt	aactgtggcc	ggcctgaaaa	gattccgaag	120
ttggacaaag	cttgcgaagg	atcgaaatcg	tccctggaac	atctcaagct	aggaaacgtg	180
gaagatgatg	agtatcttcg	acagtatgtg	ttgtttcact	acgaattcca	taaatccgag	240
ggtttcacgg	ttgattggga	gaaatatgac	tacatgttcc	atataaggcc	gttggaaaat	300
taccacaccta	tcagcgatat	acgaaccaat	gctgatgtga	tccgtgatgt	gacactcttt	360
gcatttgaga	aacacaatga	agctcatgga	tctaaacttg	tgtttgtcga	gcattgtctca	420
gctaatttca	aattttgccaa	tggtctcctc	tgctgggtta	cattctgggc	taccgatgatg	480
gcctcatctg	ctctcacatc	gcagatctat	caagtcgaac	tttggcgctg	cggaaaacag	540
tttgaatttc	ccatcttcag	ggtcaagcct	aaggacgaag	agatggatga	tgttgaagtg	600
aaaccacocct	ctccatgcc	ttatgatcac	tatgataaac	caccggttgt	ctttgttcga	660
gcctctcctg	aaagatgggt	ccctttcgtc	tttgatcgaa	ctggagctct	ttatgatctc	720
tatcggtctg	gtttgttaag	aaaaagtata	tataaccattc	ctttggtagc	aaagagatat	780
gatgttagtc	actgactgaa	aaatcaaaat	aggcttgtag	taatatatta	ccctctgaat	840
tttcaacttc	tctatctctc	ctaaatgtac	tagcttctct	tctagagatc	tatgaacaca	900
aatagaattg	atattcaaaa	atccatttgt	tt			

(2) INFORMATION FOR SEQ ID NO:2194:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 224 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..224
(D) OTHER INFORMATION: / Ceres Seq. ID 1572024
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2194:

Met Ala Asp Ser Val Leu Lys Glu Val Asn Cys Gly Arg Pro Glu Lys
1 5 10 15
Ile Pro Lys Leu Asp Lys Ala Cys Glu Gly Ser Lys Ser Ser Trp Lys
20 25 30
His Leu Lys Leu Gly Asn Val Glu Asp Asp Glu Tyr Leu Arg Gln Tyr
35 40 45
Cys Leu Phe His Tyr Glu Phe His Lys Ser Glu Gly Phe Thr Val Asp
50 55 60
Trp Glu Lys Tyr Asp Tyr Met Phe His Ile Arg Pro Leu Glu Asn Ser
65 70 75 80
Pro Pro Ile Ser Asp Ile Arg Thr Asn Ala Asp Val Ile Arg Asp Val
85 90 95
Thr Leu Phe Ala Ile Glu Lys His Asn Glu Ala His Gly Ser Lys Leu
100 105 110
Val Phe Val Glu His Val Ser Ala Asn Phe Lys Phe Ala Asn Gly Leu
115 120 125
Leu Cys Trp Leu Thr Phe Trp Ala Thr Asp Met Ala Ser Ser Ala Pro
130 135 140
Thr Ser Gln Ile Tyr Gln Val Glu Leu Trp Arg Arg Gly Lys Gln Phe
145 150 155 160
Glu Ile Pro Ile Phe Arg Val Lys Pro Lys Asp Glu Glu Met Asp Asp
165 170 175
Val Glu Val Lys Pro Pro Ser Pro Met Pro Tyr Asp Asp Tyr Asp Lys
180 185 190
Pro Pro Val Val Phe Val Arg Ala Ala Pro Glu Asp Gly Val Pro Phe
195 200 205
Val Phe Asp Arg Thr Gly Ala Leu Tyr Asp Leu Tyr Arg Ser Gly Leu
210 215 220

(2) INFORMATION FOR SEQ ID NO:2195:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 154 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide

- (ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..154
(D) OTHER INFORMATION: / Ceres Seq. ID 1572025
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2195:

Met Phe His Ile Arg Pro Leu Glu Asn Ser Pro Pro Ile Ser Asp Ile
1 5 10 15
Arg Thr Asn Ala Asp Val Ile Arg Asp Val Thr Leu Phe Ala Ile Glu
20 25 30
Lys His Asn Glu Ala His Gly Ser Lys Leu Val Phe Val Glu His Val
35 40 45
Ser Ala Asn Phe Lys Phe Ala Asn Gly Leu Leu Cys Trp Leu Thr Phe
50 55 60
Trp Ala Thr Asp Met Ala Ser Ser Ala Pro Thr Ser Gln Ile Tyr Gln

65	70	75	80
Val Glu Leu Trp Arg Arg Gly Lys Gln Phe Glu Ile Pro Ile Phe Arg			
	85	90	95
Val Lys Pro Lys Asp Glu Glu Met Asp Asp Val Glu Val Lys Pro Pro			
	100	105	110
Ser Pro Met Pro Tyr Asp Asp Tyr Asp Lys Pro Pro Val Val Phe Val			
	115	120	125
Arg Ala Ala Pro Glu Asp Gly Val Pro Phe Val Phe Asp Arg Thr Gly			
	130	135	140
Ala Leu Tyr Asp Leu Tyr Arg Ser Gly Leu			
145	150		

(2) INFORMATION FOR SEQ ID NO:2196:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 633 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..633
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572026

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2196:

tcgaaaaaac	atcacccggg	aatctgacgg	cggcttagta	cggccggcta	ctgcacaaaag	60
gactgtgttc	ttcttaggct	tgatacttgc	cttgggaaga	atataacaat	catttttggg	120
gtagctaaaa	cgctaagctc	tatogtcata	tcattatcat	taataacttat	ttgatatcta	180
aatatcataa	aaatggccgc	tcgttcaactc	tcgggtgcgc	ttaaatctct	ttgCtcgcc	240
gcattccgaa	gtctgtcttg	ttccattgtc	ttaaaggagga	gttacgttgc	tacatcgag	300
aatgtaacag	cagcaggatt	gagtaaggga	ggttccacca	gagttatggt	ggggaagatg	360
gaacagagag	gtttagatca	agaggcagag	tcgtcttggg	gaccagatcc	agttactgga	420
tactatagac	cttccaatcg	tcgggctgaa	attgatccag	ctgagctcag	agaattgctt	480
ttgaaaaaca	aagcaaatgc	tttctgagga	ttttgattgg	ttggttgact	tggttccagt	540
ggaagggtgt	cgtaggcgac	tattatgatt	atgtgtgttt	atgtttgtct	tgtatcaact	600
attaagtata	aataaagatc	acattaaacta	gtc			

(2) INFORMATION FOR SEQ ID NO:2197:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..104
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572027

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2197:

Met Ala Ala Arg Ser Leu Ser Gly Ala Val Lys Ser Leu Cys Ser Ala									
1	5	10	15						
Ala Ser Gly Ser Leu Ser Cys Ser Ile Val Leu Arg Arg Ser Tyr Val									
	20	25	30						
Ala Thr Ser Gln Asn Val Thr Ala Ala Gly Leu Ser Lys Gly Gly Ser									
	35	40	45						
Thr Arg Val Met Val Gly Lys Met Glu Gln Arg Gly Leu Asp Gln Glu									
	50	55	60						
Ala Glu Ser Ala Trp Gly Pro Asp Pro Val Thr Gly Tyr Tyr Arg Pro									
	65	70	75						
Ser Asn Arg Ala Ala Glu Ile Asp Pro Ala Glu Leu Arg Glu Leu Leu									
	85	90	95						
Leu Lys Asn Lys Ala Lys Ser Phe									
	100								

(2) INFORMATION FOR SEQ ID NO:2198:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 53 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..53
(D) OTHER INFORMATION: / Ceres Seq. ID 1572028
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2198:
Met Val Gly Lys Met Glu Gln Arg Gly Leu Asp Gln Glu Ala Glu Ser
1 5 10 15
Ala Trp Gly Pro Asp Pro Val Thr Gly Tyr Tyr Arg Pro Ser Asn Arg
20 25 30
Ala Ala Glu Ile Asp Pro Ala Glu Leu Arg Glu Leu Leu Lys Asn
35 40 45
Lys Ala Lys Ser Phe
50

(2) INFORMATION FOR SEQ ID NO:2199:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 790 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..790
(D) OTHER INFORMATION: / Ceres Seq. ID 1572029
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2199:
agaccaccaa gaaaacaaag acctatcgat catgaagatc agacttagca taaccatcat 60
acttttatca tacacagttgg ctacgggtggc cggacaacaa tgcggtcgctc aaggcgggtgg 120
tcgaacttgt cccggtaaca tctgtctgacg tcagtagcgtt tactgtggta ccaccggga 180
ckrcrtgtct ccgaccaaca actgtcagag caattgttgg ggaagtgggc ctagcgggacc 240
aggggagagc gcgtcgaaacg tacgcgccac ctaccatttc tataatccgg cgcagaataa 300
ttgggatttg agagccgtga gtgcttattg ctccacgtgg gatgctgata agccgtacgc 360
atggcggagc aagtatggct ggaccgcctt ctgcggggccg gcaggacctc gtgggtcaagc 420
ttcttgcggc aagtgtttaa ggggtgaagaa cacaagaaca aatgctgcag taactgtgag 480
aatagtggac caatgcagca acggagagctt ggatttggat gtacgaattg tcaatcaaat 540
agacaccgat ggttttggct atcaacaagg ccattctcatt gttgactacc aatttgtctga 600
ctgtggcaat gagctcattg ggcagcctga ttccagaaac atgcttgttt cgccattga 660
tcgctgttga tattatgtta tgattttgag gtcaaatatc atcggtctac ataaaataa 720
taaaagaccg tatatatgta ttgtcagagg atatatgttt cgtatcaata aggaatttt 780
aaatattatt

(2) INFORMATION FOR SEQ ID NO:2200:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 222 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..222
(D) OTHER INFORMATION: / Ceres Seq. ID 1572030
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2200:
Asp His Gln Glu Asn Lys Asp Leu Ser Ile Met Lys Ile Arg Leu Ser
1 5 10 15
Ile Thr Ile Ile Leu Leu Ser Tyr Thr Val Ala Thr Val Ala Gly Gln
20 25 30

Gln Cys Gly Arg Gln Gly Gly Gly Arg Thr Cys Pro Gly Asn Ile Cys
35 40 45
Cys Ser Gln Tyr Gly Tyr Cys Gly Thr Thr Ala Asp Xaa Cys Ser Pro
50 55 60
Thr Asn Asn Cys Gln Ser Asn Cys Trp Gly Ser Gly Pro Ser Gly Pro
65 70 75 80
Gly Glu Ser Ala Ser Asn Val Arg Ala Thr Tyr His Phe Tyr Asn Pro
85 90 95
Ala Gln Asn Asn Trp Asp Leu Arg Ala Val Ser Ala Tyr Cys Ser Thr
100 105 110
Trp Asp Ala Asp Lys Pro Tyr Ala Trp Arg Ser Lys Tyr Gly Trp Thr
115 120 125
Ala Phe Cys Gly Pro Ala Gly Pro Arg Gly Gln Ala Ser Cys Gly Lys
130 135 140
Cys Leu Arg Val Lys Asn Thr Arg Thr Asn Ala Ala Val Thr Val Arg
145 150 155 160
Ile Val Asp Gln Cys Ser Asn Gly Gly Leu Asp Val Ala Met
165 170 175
Phe Asn Gln Ile Asp Thr Asp Gly Phe Gly Tyr Gln Gln Gly His Leu
180 185 190
Ile Val Asp Tyr Gln Phe Val Asp Cys Gly Asn Glu Leu Ile Gly Gln
195 200 205
Pro Asp Ser Arg Asn Met Leu Val Ser Ala Ile Asp Arg Val
210 215 220

(2) INFORMATION FOR SEQ ID NO:2201:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 212 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..212

(D) OTHER INFORMATION: / Ceres Seq. ID 1572031

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2201:

Met Lys Ile Arg Leu Ser Ile Thr Ile Ile Leu Leu Ser Tyr Thr Val
1 5 10 15
Ala Thr Val Ala Gly Gln Gln Cys Gly Arg Gln Gly Gly Gly Arg Thr
20 25 30
Cys Pro Gly Asn Ile Cys Cys Ser Gln Tyr Gly Tyr Cys Gly Thr Thr
35 40 45
Ala Asp Xaa Cys Ser Pro Thr Asn Asn Cys Gln Ser Asn Cys Trp Gly
50 55 60
Ser Gly Pro Ser Gly Pro Gly Glu Ser Ala Ser Asn Val Arg Ala Thr
65 70 75 80
Tyr His Phe Tyr Asn Pro Ala Gln Asn Asn Trp Asp Leu Arg Ala Val
85 90 95
Ser Ala Tyr Cys Ser Thr Trp Asp Ala Asp Lys Pro Tyr Ala Trp Arg
100 105 110
Ser Lys Tyr Gly Trp Thr Ala Phe Cys Gly Pro Ala Gly Pro Arg Gly
115 120 125
Gln Ala Ser Cys Gly Lys Cys Leu Arg Val Lys Asn Thr Arg Thr Asn
130 135 140
Ala Ala Val Thr Val Arg Ile Val Asp Gln Cys Ser Asn Gly Gly Leu
145 150 155 160
Asp Leu Asp Val Ala Met Phe Asn Gln Ile Asp Thr Asp Gly Phe Gly
165 170 175
Tyr Gln Gln Gly His Leu Ile Val Asp Tyr Gln Phe Val Asp Cys Gly
180 185 190
Asn Glu Leu Ile Gly Gln Pro Asp Ser Arg Asn Met Leu Val Ser Ala

195
Ile Asp Arg Val
210

200

205

(2) INFORMATION FOR SEQ ID NO:2202:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 719 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..719
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572040

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2202:

atatattt	gtga	attagtc	gga	tatatata	aa	tacgcg	gttc	ga	tattc	caaa	ttaga	atagt	60
catatag	tca	cgcggt	tata	aacaatt	cgg	tgata	aaatt	gtaagt	caca	cagaaaa	aaga		120
aagaaac	gaa	acgaa	cga	ttatg	gattt	gaagaa	agca	tcctt	gtttt	tattc	ctct		180
ttctgt	gtct	cacot	gcaac	tgcaac	accca	ctttg	ctcac	gcggt	ctcgc	gatct	tcaac		240
aagttag	gcc	ttcgt	tgatc	caaacc	atga	tgatc	ctccg	tttca	agaag	taga	attgaa		300
gccagac	ggt	gacgt	aatcg	aagcca	atttt	accgaa	aat	acagtc	ggtt	gtaaga	aaagg		360
cggcgga	gga	ggagc	agag	gtggag	ggcg	cttcg	gcgga	ggagg	gcga	gtttc	gcggc		420
aggagg	gag	tctag	cagag	gcggt	ggagg	aagtt	ctagc	agagg	cgga	gaggga	gttc		480
tagcaga	gga	ggagga	atac	gtccg	attcc	gattt	atggc	gggtg	gaacg	accgc	asygg		540
tcatcat	tca	agcgc	ggcgc	gggaa	actgc	tagtg	gttgg	ttaggt	ctat	cgatt	tttagc		600
cgggttt	aggt	ttggt	ttttt	aaagc	ttcta	tattt	gattt	accgt	gttag	gttaa	atggt		660
tgatgc	cggt	tttgc	ttccc	actg	gtttgc	tcctc	ggatt	ttatc	agaag	tttgt	tagg		

(2) INFORMATION FOR SEQ ID NO:2203:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 159 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..159
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572041

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2203:

Met	Asp	Leu	Lys	Lys	Ala	Ser	Leu	Phe	Leu	Phe	Leu	Leu	Leu	Cys	Leu
1			5				10							15	
His	Leu	Gln	Leu	Gln	His	His	Phe	Ala	His	Ala	Val	Ser	Arg	Ser	Ser
			20				25							30	
Thr	Ser	Leu	Ala	Phe	Val	Asp	Pro	Asn	His	Asp	Asp	Leu	Pro	Phe	Gln
			35				40					45			
Glu	Val	Glu	Leu	Lys	Pro	Asp	Gly	Asp	Val	Ile	Glu	Ala	Asn	Leu	Pro
			50				55				60				
Lys	Leu	Thr	Val	Val	Val	Lys	Lys	Gly	Gly	Gly	Gly	Gly	Gly	Arg	Gly
			65				70				75			80	
Gly	Gly	Gly	Phe	Gly	Gly	Gly	Arg	Ser	Phe	Gly	Gly	Gly	Gly	Gly	Ser
			85				90				95				
Ser	Ser	Arg	Gly	Gly	Gly	Ser	Ser	Ser	Arg	Gly	Gly	Gly	Gly	Ser	
			100				105				110				
Ser	Ser	Arg	Gly	Gly	Gly	Ile	Arg	Pro	Ile	Pro	Ile	Tyr	Gly	Gly	Gly
			115				120				125				
Thr	His	Arg	Xaa	Gly	His	His	Ser	Ser	Gly	Gly	Arg	Glu	Thr	Ala	Ser
			130				135				140				
Gly	Trp	Leu	Gly	Leu	Ser	Ile	Leu	Ala	Gly	Leu	Gly	Leu	Val	Phe	
			145				150				155				

(2) INFORMATION FOR SEQ ID NO:2204:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1411 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..1411
(D) OTHER INFORMATION: / Ceres Seq. ID 1572046

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2204:

ttctaaagta	acgcgataaa	tctaatgcatt	tcccacgatt	tgtgtttgtc	cctctgacga	60
aaaatcctcg	gatctgttgc	attctotcca	aagcttgaat	cagaagaag	cttttgaaga	120
tcagcctaaa	agtgatctct	cataactgct	taaaagattg	ttgaaactcg	aagatgtctt	180
tggccgagat	aaacaagaat	gaagtgcaga	ttgtatttgg	ggctcttatt	gctgacctta	240
cacagttttt	gaccagctgg	agccctttct	tctccggatt	ccatctgaat	gttgtcaaa	300
atcatgagct	caaggaggaa	ctcaacatcc	cagaaggctt	tgacgtagat	gtctactcta	360
agactgacat	ggaaaagggt	gtggcgcat	ccaattccac	catgttctct	ggctattctt	420
gcagatatatt	cggttatctc	gtatctaaaa	agaagtacat	tgtctctatt	gatgatgatt	480
gtgtcccCtg	ctaaagatcc	gaagggttcc	ctagtggatg	ctgttactca	gcacgtgac	540
aaccttgaaa	accagccacc	gcctctcttc	ttcaacaccc	tttatgatcc	ttactgcgag	600
ggagctggatt	ttgtccgttg	atacccttcc	agcctcagaa	gtgggtgcc	ttgtgctgca	660
tttgtggggc	tttggcttaa	tctagctgat	cttgatgctc	caacacaa	gtctcaagca	720
gagaaaagga	acactgcata	tgttgatgcg	gttatgactg	tcccgcccaa	ggctatgcta	780
cccataacgc	gaatcaacat	tgccttttaac	cgcgagttgg	tgggtccagc	tttgggtcct	840
gcactcagat	tggctggaga	aggaaaagtg	agatgggaaa	cacttgaaga	tggtttgggtg	900
ggagatgttc	tgaacaacat	ctctgatcat	ttgggttatg	gtgtgaaaac	cggactgcct	960
tatgtgtgga	gaacagagag	aggagatgca	gtggagagtt	tgaagaaaga	atgggaagga	1020
atgaagctga	tggagaaaag	tgttccattt	tgcattcat	tgaaattgcc	cgagaactgcg	1080
cttaaaagttg	aagattgtgt	gattgagctt	gtcaaaacgg	tgaagagaga	gttaggttca	1140
gatgatctcg	cctttacgca	agctgctgat	gctatggtta	agtggttcca	gctctggaat	1200
tctgttaatt	ctagcgcctg	aagttagaaca	atctcttgag	gttaggttcc	tttatcactt	1260
ctaagcatat	tatcatgtct	cagagattta	ccaagtcgt	tttcttctct	ttagatcat	1320
catgtttatt	ttctcttttt	atctaaatta	taagcatgtg	ttttgagac	actcaataat	1380
gtaacctgat	gaaccccatc	tgcttggact	c			

(2) INFORMATION FOR SEQ ID NO:2205:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 290 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..290
(D) OTHER INFORMATION: / Ceres Seq. ID 1572047

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2205:

Met	Ser	Thr	Leu	Arg	Leu	Thr	Trp	Lys	Arg	Leu	Trp	Ala	His	Pro	Ile
1				5				10					15		
Pro	Pro	Cys	Ser	Leu	Ala	Ile	Leu	Ala	Asp	Ile	Ser	Val	Ile	Ser	Tyr
			20					25				30			
Leu	Lys	Arg	Ser	Thr	Leu	Ser	Leu	Leu	Met	Met	Ile	Val	Ser	Pro	Ala
			35				40				45				
Lys	Asp	Pro	Lys	Gly	Phe	Leu	Val	Asp	Ala	Val	Thr	Gln	His	Val	Ile
			50				55				60				
Asn	Leu	Glu	Asn	Pro	Ala	Thr	Pro	Leu	Phe	Phe	Asn	Thr	Leu	Tyr	Asp
			65			70			75					80	
Pro	Tyr	Cys	Glu	Gly	Ala	Asp	Phe	Val	Arg	Gly	Tyr	Pro	Phe	Ser	Leu
			85				90						95		
Arg	Ser	Gly	Val	Pro	Cys	Ala	Ala	Ser	Cys	Gly	Leu	Trp	Leu	Asn	Leu
			100				105						110		
Ala	Asp	Leu	Asp	Ala	Pro	Thr	Gln	Ala	Leu	Lys	Thr	Glu	Lys	Arg	Asn


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115              120              125
Thr Ala Tyr Val Asp Ala Val Met Thr Val Pro Ala Lys Ala Met Leu
130              135              140
Pro Ile Ser Gly Ile Asn Ile Ala Phe Asn Arg Glu Leu Val Gly Pro
145              150              155
Ala Leu Val Pro Ala Leu Arg Leu Ala Gly Glu Lys Val Arg Trp
165              170              175
Glu Thr Leu Glu Asp Val Trp Cys Gly Met Cys Leu Lys His Ile Ser
180              185              190
Asp His Leu Gly Tyr Gly Val Lys Thr Gly Leu Pro Tyr Val Trp Arg
195              200              205
Asn Glu Arg Gly Asp Ala Val Glu Ser Leu Arg Lys Lys Trp Glu Gly
210              215              220
Met Lys Leu Met Glu Lys Ser Val Pro Phe Phe Asp Ser Leu Lys Leu
225              230              235
Pro Glu Thr Ala Leu Lys Val Glu Asp Cys Val Ile Glu Leu Ala Lys
245              250              255
Ala Val Lys Glu Gln Leu Gly Ser Asp Asp Pro Ala Phe Thr Gln Ala
260              265              270
Ala Asp Ala Met Val Lys Trp Val Gln Leu Trp Asn Ser Val Asn Ser
275              280              285
Ser Ala
290

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(2) INFORMATION FOR SEQ ID NO:2206:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 249 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..249

(D) OTHER INFORMATION: / Ceres Seq. ID 1572048

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2206:

```

Met Met Ile Val Ser Pro Ala Lys Asp Pro Lys Gly Phe Leu Val Asp
1      5      10      15
Ala Val Thr Gln His Val Ile Asn Leu Glu Asn Pro Ala Thr Pro Leu
20     25     30
Phe Phe Asn Thr Leu Tyr Asp Pro Tyr Cys Glu Gly Ala Asp Phe Val
35     40     45
Arg Gly Tyr Pro Phe Ser Leu Arg Ser Gly Val Pro Cys Ala Ala Ser
50     55     60
Cys Gly Leu Trp Leu Asn Leu Ala Asp Leu Asp Ala Pro Thr Gln Ala
65     70     75     80
Leu Lys Thr Glu Lys Arg Asn Thr Ala Tyr Val Asp Ala Val Met Thr
85     90     95
Val Pro Ala Lys Ala Met Leu Pro Ile Ser Gly Ile Asn Ile Ala Phe
100    105    110
Asn Arg Glu Leu Val Gly Pro Ala Leu Val Pro Ala Leu Arg Leu Ala
115    120    125
Gly Glu Gly Lys Val Arg Trp Glu Thr Leu Glu Asp Val Trp Cys Gly
130    135    140
Met Cys Leu Lys His Ile Ser Asp His Leu Gly Tyr Gly Val Lys Thr
145    150    155    160
Gly Leu Pro Tyr Val Trp Arg Asn Glu Arg Gly Asp Ala Val Glu Ser
165    170    175
Leu Arg Lys Lys Trp Glu Gly Met Lys Leu Met Glu Lys Ser Val Pro
180    185    190
Phe Phe Asp Ser Leu Lys Leu Pro Glu Thr Ala Leu Lys Val Glu Asp
195    200    205

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Cys Val Ile Glu Leu Ala Lys Ala Val Lys Glu Gln Leu Gly Ser Asp
210 215 220
Asp Pro Ala Phe Thr Gln Ala Ala Asp Ala Met Val Lys Trp Val Gln
225 230 235 240
Leu Trp Asn Ser Val Asn Ser Ser Ala
245

(2) INFORMATION FOR SEQ ID NO:2207:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 248 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..248
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572049
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2207:

Met Ile Val Ser Pro Ala Lys Asp Pro Lys Gly Phe Leu Val Asp Ala
1 5 10 15
Val Thr Gln His Val Ile Asn Leu Glu Asn Pro Ala Thr Pro Leu Phe
20 25 30
Phe Asn Thr Leu Tyr Asp Pro Tyr Cys Glu Gly Ala Asp Phe Val Arg
35 40 45
Gly Tyr Pro Phe Ser Leu Arg Ser Gly Val Pro Cys Ala Ala Ser Cys
50 55 60
Gly Leu Trp Leu Asn Leu Ala Asp Leu Asp Ala Pro Thr Gln Ala Leu
65 70 75 80
Lys Thr Glu Lys Arg Asn Thr Ala Tyr Val Asp Ala Val Met Thr Val
85 90 95
Pro Ala Lys Ala Met Leu Pro Ile Ser Gly Ile Asn Ile Ala Phe Asn
100 105 110
Arg Glu Leu Val Gly Pro Ala Leu Val Pro Ala Leu Arg Leu Ala Gly
115 120 125
Glu Gly Lys Val Arg Trp Glu Thr Leu Glu Asp Val Trp Cys Gly Met
130 135 140
Cys Leu Lys His Ile Ser Asp His Leu Gly Tyr Gly Val Lys Thr Gly
145 150 155 160
Leu Pro Tyr Val Trp Arg Asn Glu Arg Gly Asp Ala Val Glu Ser Leu
165 170 175
Arg Lys Lys Trp Glu Gly Met Lys Leu Met Glu Lys Ser Val Pro Phe
180 185 190
Phe Asp Ser Leu Lys Leu Pro Glu Thr Ala Leu Lys Val Glu Asp Cys
195 200 205
Val Ile Glu Leu Ala Lys Ala Val Lys Glu Gln Leu Gly Ser Asp Asp
210 215 220
Pro Ala Phe Thr Gln Ala Ala Asp Ala Met Val Lys Trp Val Gln Leu
225 230 235 240
Trp Asn Ser Val Asn Ser Ser Ala
245

(2) INFORMATION FOR SEQ ID NO:2208:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 652 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..652
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572064

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2208:

attttttcttt	tcatttcatt	tctgattgtc	tttctcagaa	tccttagaac	acactctgat	60
taacgaatca	aagatogatt	tgggattgtg	atcgatcgag	gaagaagatg	acggaggcga	120
tgataaggaa	gaagccagga	atggcgagtg	tgaaggatat	gccgttgcct	caggatggtc	180
caccacccgg	tggattcgca	ccggctccgat	atgctcgccg	gatctctaac	acgggtccaa	240
gcgccatggc	tattttcttt	accgtttcag	gtgcttttgc	tggggggatg	taccaagtgc	300
gtcaggggca	caaaatccgc	agggcggtga	aggaagagaa	atacgtctgc	cgtagagcga	360
ttctaccAat	tcttcaagct	gaagaagatg	aaaggtttgt	gtctgagtgg	aagaagtatc	420
tagaatacga	ggcgagatgt	atgaaggatg	ttcctggatg	gaaagtcggt	gaaaacgtgt	480
acaattctgg	tcgctggatg	cctccagcta	ctggagagct	tcgtctctgat	gtctcggtaaa	540
ttatcaatgg	ctccttttga	tgatgatgaa	tgaatgtttg	tttaagcatt	ttagaacctt	600
gatgtttctt	gtctctcttt	ttccatcgta	taataagaga	attgatacat	ac	

(2) INFORMATION FOR SEQ ID NO:2209:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 143 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..143
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572065

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2209:

Met	Thr	Glu	Ala	Met	Ile	Arg	Lys	Lys	Pro	Gly	Met	Ala	Ser	Val	Lys
1				5					10					15	
Asp	Met	Pro	Leu	Leu	Gln	Asp	Gly	Pro	Pro	Gly	Gly	Phe	Ala	Pro	
			20					25					30		
Val	Arg	Tyr	Ala	Arg	Arg	Ile	Ser	Asn	Thr	Gly	Pro	Ser	Ala	Met	Ala
		35				40					45				
Ile	Phe	Leu	Thr	Val	Ser	Gly	Ala	Phe	Ala	Trp	Gly	Met	Tyr	Gln	Val
	50					55					60				
Gly	Gln	Gly	Asn	Lys	Ile	Arg	Arg	Ala	Leu	Lys	Glu	Glu	Lys	Tyr	Ala
	65			70				75					80		
Ala	Arg	Arg	Ala	Ile	Leu	Pro	Ile	Leu	Gln	Ala	Glu	Glu	Asp	Glu	Arg
			85					90					95		
Phe	Val	Ser	Glu	Trp	Lys	Lys	Tyr	Leu	Glu	Tyr	Glu	Ala	Asp	Val	Met
			100					105					110		
Lys	Asp	Val	Pro	Gly	Trp	Lys	Val	Gly	Glu	Asn	Val	Tyr	Asn	Ser	Gly
		115				120					125				
Arg	Trp	Met	Pro	Pro	Ala	Thr	Gly	Glu	Leu	Arg	Pro	Asp	Val	Trp	
	130					135					140				

(2) INFORMATION FOR SEQ ID NO:2210:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 139 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..139
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572066

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2210:

Met	Ile	Arg	Lys	Lys	Pro	Gly	Met	Ala	Ser	Val	Lys	Asp	Met	Pro	Leu
1				5						10				15	
Leu	Gln	Asp	Gly	Pro	Pro	Pro	Gly	Gly	Phe	Ala	Pro	Val	Arg	Tyr	Ala
		20						25					30		
Arg	Arg	Ile	Ser	Asn	Thr	Gly	Pro	Ser	Ala	Met	Ala	Ile	Phe	Leu	Thr
	35					40					45				
Val	Ser	Gly	Ala	Phe	Ala	Trp	Gly	Met	Tyr	Gln	Val	Gln	Gly	Asn	

50 55 60
Lys Ile Arg Arg Ala Leu Lys Glu Glu Lys Tyr Ala Ala Arg Arg Ala
65 70 75 80
Ile Leu Pro Ile Leu Gln Ala Glu Glu Asp Glu Arg Phe Val Ser Glu
85 90 95
Trp Lys Lys Tyr Leu Glu Tyr Glu Ala Asp Val Met Lys Asp Val Pro
100 105 110
Gly Trp Lys Val Gly Glu Asn Val Tyr Asn Ser Gly Arg Trp Met Pro
115 120 125
Pro Ala Thr Gly Glu Leu Arg Pro Asp Val Trp
130 135

(2) INFORMATION FOR SEQ ID NO:2211:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 132 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..132
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572067

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2211:

Met Ala Ser Val Lys Asp Met Pro Leu Leu Gln Asp Gly Pro Pro Pro
1 5 10 15
Gly Gly Phe Ala Pro Val Arg Tyr Ala Arg Arg Ile Ser Asn Thr Gly
20 25 30
Pro Ser Ala Met Ala Ile Phe Leu Thr Val Ser Gly Ala Phe Ala Trp
35 40 45
Gly Met Tyr Gln Val Gly Gln Gly Asn Lys Ile Arg Arg Ala Leu Lys
50 55 60
Glu Glu Lys Tyr Ala Ala Arg Arg Ala Ile Leu Pro Ile Leu Gln Ala
65 70 75 80
Glu Glu Asp Glu Arg Phe Val Ser Glu Trp Lys Lys Tyr Leu Glu Tyr
85 90 95
Glu Ala Asp Val Met Lys Asp Val Pro Gly Trp Lys Val Gly Glu Asn
100 105 110
Val Tyr Asn Ser Gly Arg Trp Met Pro Pro Ala Thr Gly Glu Leu Arg
115 120 125
Pro Asp Val Trp
130

(2) INFORMATION FOR SEQ ID NO:2212:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 600 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..600
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572082

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2212:

atataaaccc tctcgGcgt gccattgaaa ctctttcaag gagagagctg ctactctgca 60
accatgtcga agcgaggaag aggaggaacc tctggttaaca agttcaggat gtcactgggt 120
cttcagtggt cagccactgt gaactgtgct gacaacaccc gagctaagaa cctttacatc 180
atttcggtta aaggaatcaa gggtcgtctt aaccgtttgc catcagcttg tgttggtgat 240
atggttatgg ctactgttaa gaaaggttaag cctgatctcc gtaagaaggt gctctcctgt 300
gtcattgtta ggcagaggaa gctctggcgc cgaaaggagc gtgtcttcac gtatttcgaa 360
gataatgtgt gtgtcattgt caatccaacg ggtgatatga aaggatctgc tatcactgga 420
ccaatcggaagg agtagtgtgc tgatctgtgg ccaagaatcg caagtgtctgc gaacgccatc 480

gtttaagcaa gcttgagatc tctatgtttt gtgttgaacg tttagcatta tctctatttg 540
ggattgtttt tttgttttct cttagacttt ttttatgcct taaagctgat tctagttctc 600

(2) INFORMATION FOR SEQ ID NO:2213:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 140 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..140
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572083

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2213:

Met	Ser	Lys	Arg	Gly	Arg	Gly	Gly	Thr	Ser	Gly	Asn	Lys	Phe	Arg	Met
1				5										10	15
Ser	Leu	Gly	Leu	Pro	Val	Ala	Ala	Thr	Val	Asn	Cys	Ala	Asp	Asn	Thr
				20				25						30	
Gly	Ala	Lys	Asn	Leu	Tyr	Ile	Ile	Ser	Val	Lys	Gly	Ile	Lys	Gly	Arg
				35				40						45	
Leu	Asn	Arg	Leu	Pro	Ser	Ala	Cys	Val	Gly	Asp	Met	Val	Met	Ala	Thr
				50				55						60	
Val	Lys	Lys	Gly	Lys	Pro	Asp	Leu	Arg	Lys	Lys	Val	Leu	Pro	Ala	Val
				65				70						75	80
Ile	Val	Arg	Gln	Arg	Lys	Pro	Trp	Arg	Arg	Lys	Asp	Gly	Val	Phe	Met
				85				90						95	
Tyr	Phe	Glu	Asp	Asn	Ala	Gly	Val	Ile	Val	Asn	Pro	Lys	Gly	Asp	Met
				100				105						110	
Lys	Gly	Ser	Ala	Ile	Thr	Gly	Pro	Ile	Gly	Lys	Glu	Cys	Ala	Asp	Leu
				115				120						125	
Trp	Pro	Arg	Ile	Ala	Ser	Ala	Ala	Asn	Ala	Ile	Val				
				130				135						140	

(2) INFORMATION FOR SEQ ID NO:2214:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..125
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572084

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2214:

Met	Ser	Leu	Gly	Leu	Pro	Val	Ala	Ala	Thr	Val	Asn	Cys	Ala	Asp	Asn
1				5										10	15
Thr	Gly	Ala	Lys	Asn	Leu	Tyr	Ile	Ile	Ser	Val	Lys	Gly	Ile	Lys	Gly
				20				25						30	
Arg	Leu	Asn	Arg	Leu	Pro	Ser	Ala	Cys	Val	Gly	Asp	Met	Val	Met	Ala
				35				40						45	
Thr	Val	Lys	Lys	Gly	Lys	Pro	Asp	Leu	Arg	Lys	Lys	Val	Leu	Pro	Ala
				50				55						60	
Val	Ile	Val	Arg	Gln	Arg	Lys	Pro	Trp	Arg	Arg	Lys	Asp	Gly	Val	Phe
				65				70						75	80
Met	Tyr	Phe	Glu	Asp	Asn	Ala	Gly	Val	Ile	Val	Asn	Pro	Lys	Gly	Asp
				85				90						95	
Met	Lys	Gly	Ser	Ala	Ile	Thr	Gly	Pro	Ile	Gly	Lys	Glu	Cys	Ala	Asp
				100				105						110	
Leu	Trp	Pro	Arg	Ile	Ala	Ser	Ala	Ala	Asn	Ala	Ile	Val			
				115				120						125	

(2) INFORMATION FOR SEQ ID NO:2215:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 81 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..81

(D) OTHER INFORMATION: / Ceres Seq. ID 1572085

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2215:

Met	Val	Met	Ala	Thr	Val	Lys	Lys	Gly	Lys	Pro	Asp	Leu	Arg	Lys	Lys	
1				5					10					15		
Val	Leu	Pro	Ala	Val	Ile	Val	Arg	Gln	Arg	Lys	Pro	Trp	Arg	Arg	Lys	
				20				25					30			
Asp	Gly	Val	Phe	Met	Tyr	Phe	Glu	Asp	Asn	Ala	Gly	Val	Ile	Val	Asn	
				35			40					45				
Pro	Lys	Gly	Asp	Met	Lys	Gly	Ser	Ala	Ile	Thr	Gly	Pro	Ile	Gly	Lys	
				50		55				60						
Glu	Cys	Ala	Asp	Leu	Trp	Pro	Arg	Ile	Ala	Ser	Ala	Ala	Asn	Ala	Ile	
65				70					75					80		
Val																

(2) INFORMATION FOR SEQ ID NO:2216:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 519 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..519

(D) OTHER INFORMATION: / Ceres Seq. ID 1572094

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2216:

acatccaaaca	acaaaaaacac	aagcgtagaa	ascaaaaactc	aactaattgt	gttatcaccc	60
aaaagagaag	agcaaacacaca	atggCtttcg	ctttgaggtt	cttcacatgc	tttgttttga	120
cagtggtcat	cgttgcatca	gtggatgcag	caataacatg	tggcacagt	gcaagtagct	180
tgagtcacatg	tctaggctac	ctatcgaaagg	gtgggggtgt	gccacctccg	tgctgtgcag	240
gagtcacaaa	gttgaacggt	atggctcaaa	ccacacccga	ccgccaccaa	gcattgcagat	300
gcttacagtc	cqctgcacaaa	ggggttaatc	caagtcNtag	cctctggcct	tcctggaaaag	360
tgccgtgttta	gcattccccCt	atccccCatct	ccacgagcac	caactgcgcc	accatcaagt	420
acgggtgggga	ataacgcacat	catttgccctg	aagagtattg	tttcgtatac	gtaaaataag	480
acgcctatct	aagctgatat	ttaacctgtc	tttgtttgt			

(2) INFORMATION FOR SEQ ID NO:2217:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 122 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..122

(D) OTHER INFORMATION: / Ceres Seq. ID 1572095

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2217:

Ile	Gln	Gln	Gln	Lys	His	Lys	Arg	Arg	Lys	Gln	Asn	Ser	Thr	Asn	Cys	
1				5					10			15				
Val	Ile	Thr	Gln	Lys	Arg	Arg	Ala	Asn	Thr	Met	Ala	Phe	Ala	Leu	Arg	
				20			25					30				

Phe Phe Thr Cys Phe Val Leu Thr Val Phe Ile Val Ala Ser Val Asp
35 40 45
Ala Ala Ile Thr Cys Gly Thr Val Ala Ser Ser Leu Ser Pro Cys Leu
50 55 60
Gly Tyr Leu Ser Lys Gly Gly Val Val Pro Pro Cys Cys Ala Gly
65 70 75 80
Val Lys Lys Leu Asn Gly Met Ala Gln Thr Thr Pro Asp Arg Gln Gln
85 90 95
Ala Cys Arg Cys Leu Gln Ser Ala Ala Lys Gly Val Asn Pro Ser Xaa
100 105 110
Ser Leu Trp Trp Ser Trp Lys Val Arg Cys
115 120

(2) INFORMATION FOR SEQ ID NO:2218:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 96 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..96
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572096

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2218:

Met Ala Phe Ala Leu Arg Phe Phe Thr Cys Phe Val Leu Thr Val Phe
1 5 10 15
Ile Val Ala Ser Val Asp Ala Ala Ile Thr Cys Gly Thr Val Ala Ser
20 25 30
Ser Leu Ser Pro Cys Leu Gly Tyr Leu Ser Lys Gly Gly Val Val Pro
35 40 45
Pro Pro Cys Cys Ala Gly Val Lys Lys Leu Asn Gly Met Ala Gln Thr
50 55 60
Thr Pro Asp Arg Gln Gln Ala Cys Arg Cys Leu Gln Ser Ala Ala Lys
65 70 75 80
Gly Val Asn Pro Ser Xaa Ser Leu Trp Pro Ser Trp Lys Val Arg Cys
85 90 95

(2) INFORMATION FOR SEQ ID NO:2219:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 808 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..808
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572097

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2219:

atcaacccaaa acaaaacata aaaaacaagt ggaagcttta aaacgagagg gatagagcaa 60
aaatggcgac gtccgggaacg tacgtgacgg aagttccgct aaaaggatcg gccgagaaat 120
actacaagag gtggaagaac gagaaaccatg tcttccctga tgctatcgcc caccacatcc 180
aaaatgttac cgttcaacgaa ggccaacatg actctcacgg gtctatcagg agttggaact 240
acacatggga tggaaaaggag gaggtgttca aggaagaaag agagatagac gatgagacca 300
aaacgttgac gttaagagga cttgagggtc acgtgatgga gcagctcaaa gtgtacgacg 360
tcgtctacca attcattccc aatctcgagg atacctgcac ccgcacaaatc actttaatat 420
gggagaagcg caacgatgat tccccgaac caagcggcta catgaaattc gtcaagagct 480
tggttgctga catgggaac cactgttagCC CcAAAAAAAAA AAAAAAAAAa ctaatcatc 540
attcccacag tcgtcgtcat catcatcatc atcatcatca tcatcatcat catcatcatc 600
atcatcatca tcatcatcat catcatcatc atcactatct cgattttataa gttaagatgt 660

tttcagtata ataaatgggg tcttggtgat cgttcatttc tatgtgtaaa cgttttggtt 720
ctgtatgatg cttcgatata ttgttatggt catgatcata tgcggggttc gatataatga 780
ttcttaagat taatttaacta cacatttc

(2) INFORMATION FOR SEQ ID NO:2220:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 195 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..195
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572098

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2220:

Met	Ala	Thr	Ser	Gly	Thr	Tyr	Val	Thr	Glu	Val	Pro	Leu	Lys	Gly	Ser	
1			5					10					15			
Ala	Glu	Lys	Tyr	Tyr	Lys	Arg	Trp	Lys	Asn	Glu	Asn	His	Val	Phe	Pro	
			20				25						30			
Asp	Ala	Ile	Gly	His	His	Ile	Gln	Asn	Val	Thr	Val	His	Glu	Gly	Glu	
			35				40					45				
His	Asp	Ser	His	Gly	Ser	Ile	Arg	Ser	Trp	Asn	Tyr	Thr	Trp	Asp	Gly	
			50				55				60					
Lys	Glu	Glu	Val	Phe	Lys	Glu	Arg	Arg	Glu	Ile	Asp	Asp	Glu	Thr	Lys	
			65				70				75					
Thr	Leu	Thr	Leu	Arg	Gly	Leu	Glu	Gly	His	Val	Met	Glu	Gln	Leu	Lys	
				85					90					95		
Val	Tyr	Asp	Val	Val	Tyr	Gln	Phe	Ile	Pro	Lys	Ser	Glu	Asp	Thr	Cys	
				100					105				110			
Ile	Gly	Lys	Ile	Thr	Leu	Ile	Trp	Glu	Lys	Arg	Asn	Asp	Asp	Ser	Pro	
			115				120					125				
Glu	Pro	Ser	Gly	Tyr	Met	Lys	Phe	Val	Lys	Ser	Leu	Val	Ala	Asp	Met	
			130				135					140				
Gly	Asn	His	Val	Ser	Pro	Lys	Lys	Lys	Lys	Lys	Lys	Leu	Asn	His	His	
			145				150					155			160	
Ser	His	Ser	Arg	Arg	His	His	His	His	His	His	His	His	His	His	His	
			165						170						175	
His	His	His	His	His	His	His	His	His	His	His	His	His	His	His	His	Tyr
			180						185						190	
Leu	Asp	Leu														
			195													

(2) INFORMATION FOR SEQ ID NO:2221:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..104
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572099

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2221:

Met	Glu	Gln	Leu	Lys	Val	Tyr	Asp	Val	Val	Tyr	Gln	Phe	Ile	Pro	Lys	
1			5					10					15			
Ser	Glu	Asp	Thr	Cys	Ile	Gly	Lys	Ile	Thr	Leu	Ile	Trp	Glu	Lys	Arg	
			20					25					30			
Asn	Asp	Asp	Ser	Pro	Glu	Pro	Ser	Gly	Tyr	Met	Lys	Phe	Val	Lys	Ser	
			35				40					45				
Leu	Val	Ala	Asp	Met	Gly	Asn	His	Val	Ser	Pro	Lys	Lys	Lys	Lys	Lys	
			50				55					60				

Lys Leu Asn His His Ser His Ser Arg Arg His His His His His His
65 70 75 80
His His His His His His His His His His His His His His His
85 90 95
His His His His Tyr Leu Asp Leu
100

(2) INFORMATION FOR SEQ ID NO:2222:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1201 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1201

(D) OTHER INFORMATION: / Ceres Seq. ID 1572120

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2222:

ctacatgcc gtcgcctgtt accgtccggt gctattctcc ttcacaaatct cacatttttc 60
gtaccgggta gaagatgaga atcacgcaga tctgttatg tctggtaata gtggcattgt 120
cttcaagctc ccatgtctcg tcgatcaga tcttccacgc tcactagtt ggaacattca 180
gcagaaacaa tcgtgaacca aagtacaaga ttgagttcct tcttgaagat tcaccttttc 240
accgggtgaa taactctggaa tcaatgggta tgttggtata gcattggaat cggtttttat 300
gtactctacc gaaagaggaa aaagcgacga gtggatggac ttctagtcag caaaatatta 360
gtactgtgat gatggaaaca cagcaactgg tgaagctaaa gactcctgat gaattgcttc 420
aaccacttag tgaataatgt ctttttaggc aagagggttg gtggtcttat gagttttggc 480
atcagaagta tgtgcggcag Ccacacgttg aggatgaaaa caagattgtt caagagtatt 540
ttttgggtac ttttgaccga gaggcaActg cggcggttaa tcaaaactgt tctgatgctt 600
caactgatgc atctcagagg tatcactctc atgtatacac caatgggacc acctggtatc 660
ttacagatgc acctcgcgaa gtctgaggtga ggtttgtatg cgcagaaaaa agggcaatgg 720
tcacttcaat cactgaatta tcaacttgca agtacgcact gactgttcag tgcaccaact 780
tgtgcaagca tvscctgttc cagctagaga aaccagtgtc acacacgac cactgcaatg 840
cgatcccagtc ggaagaagac gcaacaagaa acaaggaaga acaagcagta gacgaatcac 900
ctaagatgat agctgattct tgaataaccgc ctaagtgaat accctaagag taagagttaa 960
cagcgactgt atatacaaga actagcatat ctccattttc agtggttacc gctgtagtga 1020
tcatgttttc aattggggtc gcttgcgtgt aggatgatga tactctctct gtaatttttt 1080
gcatacttaa aatagcattt caatagaagg tactgataaa ccactgttga agcaaaagact 1140
gcaagcttca tgtaacacat atgtttccgt ttcactaatg aatttgttcc aagtgtaggg 1200

(2) INFORMATION FOR SEQ ID NO:2223:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 282 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..282

(D) OTHER INFORMATION: / Ceres Seq. ID 1572121

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2223:

Met Arg Ile Thr Gln Ile Leu Leu Cys Leu Val Ile Val Ala Leu Ser
1 5 10 15
Ser Ser Ser His Val Trp Ser Asp Gln Ile Phe Pro Ala His Leu Val
20 25 30
Gly Thr Phe Ser Arg Asn Asn Arg Glu Pro Lys Tyr Lys Ile Glu Phe
35 40 45
Leu Pro Glu Asp Ser Pro Phe His Pro Gly Asp Asn Leu Glu Ser Met
50 55 60
Val Met Leu Asp Lys His Gly Asn Arg Phe Leu Cys Tyr Leu Pro Lys
65 70 75 80

Glu Glu Lys Ala Thr Ser Gly Trp Thr Ser Ser Gln Gln Asn Ile Ser
85 90 95
Thr Val Met Met Glu Thr Gln Gln Leu Val Lys Leu Lys Thr Pro Asp
100 105 110
Glu Leu Leu Gln Pro Leu Ser Glu Lys Cys Leu Phe Arg Gln Glu Gly
115 120 125
Trp Trp Ser Tyr Glu Phe Cys His Gln Lys Tyr Val Arg Gln Leu His
130 135 140
Val Glu Asp Glu Asn Lys Ile Val Gln Glu Phe Phe Leu Gly Thr Phe
145 150 155 160
Asp Pro Glu Ala Thr Ala Ala Phe Asn Gln Thr Val Ser Asp Ala Ser
165 170 175
Thr Asp Ala Ser Gln Arg Tyr His Ser His Val Tyr Thr Asn Gly Thr
180 185 190
Thr Cys Asp Leu Thr Gly Ser Pro Arg Glu Val Glu Val Arg Phe Val
195 200 205
Cys Ala Glu Thr Arg Ala Met Val Thr Ser Ile Thr Glu Leu Ser Thr
210 215 220
Cys Lys Tyr Ala Leu Thr Val Gln Cys Pro Thr Leu Cys Lys His Xaa
225 230 235 240
Leu Phe Gln Leu Glu Lys Pro Val Ser His Thr Ile His Cys Asn Ala
245 250 255
Ile Pro Val Glu Glu Asp Ala Thr Arg Asn Lys Glu Glu Gln Ala Val
260 265 270
Asp Glu Ser Pro Lys Met Ile Ala Asp Ser
275 280

(2) INFORMATION FOR SEQ ID NO:2224:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 219 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..219

(D) OTHER INFORMATION: / Ceres Seq. ID 1572122

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2224:

Met Val Met Leu Asp Lys His Gly Asn Arg Phe Leu Cys Tyr Leu Pro
1 5 10 15
Lys Glu Glu Lys Ala Thr Ser Gly Trp Thr Ser Ser Gln Gln Asn Ile
20 25 30
Ser Thr Val Met Met Glu Thr Gln Gln Leu Val Lys Leu Lys Thr Pro
35 40 45
Asp Glu Leu Leu Gln Pro Leu Ser Glu Lys Cys Leu Phe Arg Gln Glu
50 55 60
Gly Trp Trp Ser Tyr Glu Phe Cys His Gln Lys Tyr Val Arg Gln Leu
65 70 75 80
His Val Glu Asp Glu Asn Lys Ile Val Gln Glu Phe Phe Leu Gly Thr
85 90 95
Phe Asp Pro Glu Ala Thr Ala Ala Phe Asn Gln Thr Val Ser Asp Ala
100 105 110
Ser Thr Asp Ala Ser Gln Arg Tyr His Ser His Val Tyr Thr Asn Gly
115 120 125
Thr Thr Cys Asp Leu Thr Gly Ser Pro Arg Glu Val Glu Val Arg Phe
130 135 140
Val Cys Ala Glu Thr Arg Ala Met Val Thr Ser Ile Thr Glu Leu Ser
145 150 155 160
Thr Cys Lys Tyr Ala Leu Thr Val Gln Cys Pro Thr Leu Cys Lys His
165 170 175
Xaa Leu Phe Gln Leu Glu Lys Pro Val Ser His Thr Ile His Cys Asn

180 185 190
Ala Ile Pro Val Glu Glu Asp Ala Thr Arg Asn Lys Glu Glu Gln Ala
195 200 205
Val Asp Glu Ser Pro Lys Met Ile Ala Asp Ser
210 215

(2) INFORMATION FOR SEQ ID NO:2225:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 217 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..217
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572123

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2225:

Met Leu Asp Lys His Gly Asn Arg Phe Leu Cys Tyr Leu Pro Lys Glu
1 5 10 15
Glu Lys Ala Thr Ser Gly Trp Thr Ser Ser Gln Gln Asn Ile Ser Thr
20 25 30
Val Met Met Glu Thr Gln Gln Leu Val Lys Leu Lys Thr Pro Asp Glu
35 40 45
Leu Leu Gln Pro Leu Ser Glu Lys Cys Leu Phe Arg Gln Glu Gly Trp
50 55 60
Trp Ser Tyr Glu Phe Cys His Gln Lys Tyr Val Arg Gln Leu His Val
65 70 75 80
Glu Asp Glu Asn Lys Ile Val Gln Glu Phe Phe Leu Gly Thr Phe Asp
85 90 95
Pro Glu Ala Thr Ala Phe Asn Gln Thr Val Ser Asp Ala Ser Thr
100 105 110
Asp Ala Ser Gln Arg Tyr His Ser His Val Tyr Thr Asn Gly Thr Thr
115 120 125
Cys Asp Leu Thr Gly Ser Pro Arg Glu Val Glu Val Arg Phe Val Cys
130 135 140
Ala Glu Thr Arg Ala Met Val Thr Ser Ile Thr Glu Leu Ser Thr Cys
145 150 155 160
Lys Tyr Ala Leu Thr Val Gln Cys Pro Thr Leu Cys Lys His Xaa Leu
165 170 175
Phe Gln Leu Glu Lys Pro Val Ser His Thr Ile His Cys Asn Ala Ile
180 185 190
Pro Val Glu Glu Asp Ala Thr Arg Asn Lys Glu Glu Gln Ala Val Asp
195 200 205
Glu Ser Pro Lys Met Ile Ala Asp Ser
210 215

(2) INFORMATION FOR SEQ ID NO:2226:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1662 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1662
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572139

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2226:

aaacctgtat ttatcaatt accacattt gtctaaagcaa aatggattta ttactcatat 60
ccttaaacac tatcataatc gccgcctaca tgcaaaatct acgacgtcgg ggaatccaaca 120
taccgcgggg accaccaacg cgattttctg tcggaaaacct tcatcaactg aaaccattat 180
ggacgcagtc ttctcccgag tggtaacaga ettatggccc catoatatcg gtgtggttag 240

gatcacagct	agctgtgttg	gtctcgagct	ctgacttagc	caaacaagtg	ttgagagaca	300
aagactacca	actctgtaac	cgacacagaa	cgcgaaggat	gactcagaac	ggcagcgatc	360
ttatttggct	tgactacgga	gcacattatg	tgaaaaatgag	aaaactctgt	acactcgagc	420
tcctttcttt	gaaaagcata	gagtggttca	ggctgatgag	agagatggaa	gtaagttcca	480
tggttaaagt	gattttcaat	gacttcatga	gcgatgatca	gaaacccagtg	gtgttgagga	540
actatctaga	ttctgttgtc	ttgaacattg	tttcaagatt	agttatcggg	aaaacattcg	600
aaccccaaaga	tggaagagag	tttagatcaa	ttgtagaaga	ggagactcgc	ttgcccgggc	660
caaccaagat	gcttgattac	accgtttggc	ttaaacgtct	ttcgtcatgg	ttcactagcg	720
caaaagcggt	catgaagcac	atggctcgga	aaagaaattg	gtttaaacga	gctgtaattg	780
atgaagtata	tgagggaaga	gatcaaaagt	gttttgttca	gagtcgtgta	gagttgaaag	840
agaaggatga	gctgaccgag	gagactgtga	tgggactggg	ctggaacatg	ttaactcgag	900
gagctgacac	aaccgcgata	actattgaat	gggcaatggc	agagatgata	agatgccga	960
cogtgaaaga	aaaggtgaga	gatgagcttg	attccgttgg	tggtatccga	cggttaatgt	1020
ctgatgcaga	tatcccaaaa	ctgcggttcc	tgcgaatcgt	actcaaaaga	gcctctcggc	1080
ttcaccctcc	aacaccattg	atgcttccac	acaaggccag	cgaatcagtt	caggtagggt	1140
ggtagcaaat	tcttaaggga	gccacggttt	atgtcaacgt	gcagcgcatg	gctcgagatc	1200
ctgcaaaact	gagtaaccga	gatgagttta	gaccagagag	gtttcttgtg	gaggaacacg	1260
acgttaaaag	tcaagacttt	cggtgtcttc	catttgggtc	gggaagacgg	gtgtgtccag	1320
cogctcaact	cagctcaatt	atgatgacat	tagcactagg	tagtttgttg	cattgtttct	1380
catggacatc	ctctacacct	cgagaaacaca	ttgacatgac	cgagaagcct	gattatgttt	1440
gtttacatgaa	ggctccattg	caggctctag	cttcgtccag	gctgccacaa	gagttatacc	1500
tttaactttt	aactgagata	gattatatta	atcaacataa	gataaagaga	gattctcaat	1560
tgcgaaaaac	agatgtagct	atggcaagat	ttaggacatg	gatgatgaaa	tgggtctgat	1620
aaacagaatg	tagctattga	tagtaataaa	actaaatatt	cc		

(2) INFORMATION FOR SEQ ID NO:2227:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 500 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..500

(D) OTHER INFORMATION: / Ceres Seq. ID 1572140

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2227:

Thr	Cys	Ile	Leu	Ser	Ile	Thr	Thr	Leu	Cys	Leu	Ser	Lys	Met	Asp	Leu
1				5					10					15	
Leu	Leu	Ile	Ser	Leu	Thr	Thr	Ile	Ile	Ile	Ala	Ala	Tyr	Met	Gln	Asn
			20					25					30		
Leu	Arg	Arg	Arg	Gly	Ser	Asn	Ile	Pro	Pro	Gly	Pro	Pro	Thr	Arg	Phe
			35					40				45			
Leu	Val	Gly	Asn	Leu	His	Gln	Leu	Lys	Pro	Leu	Trp	Thr	Gln	Ser	Phe
			50				55				60				
Ser	Glu	Trp	Ser	Gln	Thr	Tyr	Gly	Pro	Ile	Ile	Ser	Val	Trp	Leu	Gly
65				70				75					80		
Ser	Gln	Leu	Ala	Val	Val	Val	Ser	Ser	Ser	Asp	Leu	Ala	Lys	Gln	Val
			85					90					95		
Leu	Arg	Asp	Lys	Asp	Tyr	Gln	Leu	Cys	Asn	Arg	His	Arg	Thr	Ala	Arg
			100					105					110		
Met	Thr	Gln	Asn	Gly	Ser	Asp	Leu	Ile	Trp	Ser	Asp	Tyr	Gly	Ala	His
			115					120					125		
Tyr	Val	Lys	Met	Arg	Lys	Leu	Cys	Thr	Leu	Glu	Leu	Phe	Ser	Leu	Lys
			130				135					140			
Ser	Ile	Glu	Cys	Phe	Arg	Ser	Met	Arg	Glu	Met	Glu	Val	Ser	Ser	Met
145				150				155					160		
Val	Lys	Ser	Ile	Phe	Asn	Asp	Phe	Met	Ser	Asp	Asp	Gln	Lys	Pro	Val
			165					170					175		
Val	Leu	Arg	Asn	Tyr	Leu	Asp	Ser	Val	Ala	Leu	Asn	Ile	Val	Ser	Arg
			180					185					190		
Leu	Val	Ile	Gly	Lys	Thr	Phe	Glu	Pro	Lys	Asp	Gly	Arg	Glu	Phe	Arg

Met	Asp	Leu	Leu	Leu	Ile	Ser	Leu	Thr	Thr	Ile	Ile	Ile	Ala	Ala	Tyr
1				5					10					15	
Met	Gln	Asn	Leu	Arg	Arg	Arg	Gly	Ser	Asn	Ile	Pro	Pro	Gly	Pro	Pro
			20					25					30		
Thr	Arg	Phe	Leu	Val	Gly	Asn	Leu	His	Gln	Leu	Lys	Pro	Leu	Trp	Thr
		35					40					45			
Gln	Ser	Phe	Ser	Glu	Trp	Ser	Gln	Thr	Tyr	Gly	Pro	Ile	Ile	Ser	Val
	50					55				60					
Trp	Leu	Gly	Ser	Gln	Leu	Ala	Val	Val	Val	Ser	Ser	Ser	Asp	Leu	Ala
65					70					75				80	

Lys Gln Val Leu Arg Asp Lys Asp Tyr Gln Leu Cys Asn Arg His Arg
85 90 95
Thr Ala Arg Met Thr Gln Asn Gly Ser Asp Leu Ile Trp Ser Asp Tyr
100 105 110
Gly Ala His Tyr Val Lys Met Arg Lys Leu Cys Thr Leu Glu Leu Phe
115 120 125
Ser Leu Lys Ser Ile Glu Cys Phe Arg Ser Met Arg Glu Met Glu Val
130 135 140
Ser Ser Met Val Lys Ser Ile Phe Asn Asp Phe Met Ser Asp Asp Gln
145 150 155 160
Lys Pro Val Val Leu Arg Asn Tyr Leu Asp Ser Val Ala Leu Asn Ile
165 170 175
Val Ser Arg Leu Val Ile Gly Lys Thr Phe Glu Pro Lys Asp Gly Arg
180 185 190
Glu Phe Arg Ser Ile Val Glu Arg Glu Thr Arg Leu Pro Gly Ala Thr
195 200 205
Lys Met Leu Asp Tyr Thr Val Trp Leu Lys Arg Leu Ser Ser Trp Phe
210 215 220
Thr Ser Asp Lys Ala Phe Met Lys His Met Ala Arg Lys Arg Asn Trp
225 230 235 240
Phe Lys Arg Ala Val Met Asp Glu Val Tyr Gly Gly Arg Asp Gln Lys
245 250 255
Cys Phe Val Gln Ser Leu Leu Glu Leu Lys Glu Lys Asp Glu Leu Thr
260 265 270
Glu Glu Thr Val Met Gly Leu Val Trp Asn Met Leu Thr Ala Gly Ala
275 280 285
Asp Thr Thr Ala Ile Thr Ile Glu Trp Ala Met Ala Glu Met Ile Arg
290 295 300
Cys Pro Thr Val Lys Glu Lys Val Gln Asp Glu Leu Asp Ser Val Val
305 310 315 320
Gly Ser Gly Arg Leu Met Ser Asp Ala Asp Ile Pro Lys Leu Pro Phe
325 330 335
Leu Gln Cys Val Leu Lys Glu Ala Leu Arg Leu His Pro Pro Thr Pro
340 345 350
Leu Met Leu Pro His Lys Ala Ser Glu Ser Val Gln Val Gly Gly Tyr
355 360 365
Lys Val Pro Lys Gly Ala Thr Val Tyr Val Asn Val Gln Ala Ile Ala
370 375 380
Arg Asp Pro Ala Asn Trp Ser Asn Pro Asp Glu Phe Arg Pro Glu Arg
385 390 395 400
Phe Leu Val Glu Glu Thr Asp Val Lys Gly Gln Asp Phe Arg Val Leu
405 410 415
Pro Phe Gly Ser Gly Arg Arg Val Cys Pro Ala Ala Gln Leu Ser Leu
420 425 430
Asn Met Met Thr Leu Ala Leu Gly Ser Leu Leu His Cys Phe Ser Trp
435 440 445
Thr Ser Ser Thr Pro Arg Glu His Ile Asp Met Thr Glu Lys Pro Gly
450 455 460
Leu Val Cys Tyr Met Lys Ala Pro Leu Gln Ala Leu Ala Ser Ser Arg
465 470 475 480
Leu Pro Gln Glu Leu Tyr Leu
485

(2) INFORMATION FOR SEQ ID NO:2229:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 471 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..471

(D) OTHER INFORMATION: / Ceres Seq. ID 1572142

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2229:

Met	Gln	Asn	Leu	Arg	Arg	Arg	Gly	Ser	Asn	Ile	Pro	Pro	Gly	Pro	Pro
1			5						10					15	
Thr	Arg	Phe	Leu	Val	Gly	Asn	Leu	His	Gln	Leu	Lys	Pro	Leu	Trp	Thr
			20					25					30		
Gln	Ser	Phe	Ser	Glu	Trp	Ser	Gln	Thr	Tyr	Gly	Pro	Ile	Ile	Ser	Val
		35					40					45			
Trp	Leu	Gly	Ser	Gln	Leu	Ala	Val	Val	Ser	Ser	Ser	Ser	Asp	Leu	Ala
	50					55				60					
Lys	Gln	Val	Leu	Arg	Asp	Lys	Asp	Tyr	Gln	Leu	Cys	Asn	Arg	His	Arg
65				70						75				80	
Thr	Ala	Arg	Met	Thr	Gln	Asn	Gly	Ser	Asp	Leu	Ile	Trp	Ser	Asp	Tyr
			85					90						95	
Gly	Ala	His	Tyr	Val	Lys	Met	Arg	Lys	Leu	Cys	Thr	Leu	Glu	Leu	Phe
			100					105					110		
Ser	Leu	Lys	Ser	Ile	Glu	Cys	Phe	Arg	Ser	Met	Arg	Glu	Met	Glu	Val
		115					120					125			
Ser	Ser	Met	Val	Lys	Ser	Ile	Phe	Asn	Asp	Phe	Met	Ser	Ser	Asp	Gln
	130						135				140				
Lys	Pro	Val	Val	Leu	Arg	Asn	Tyr	Leu	Asp	Ser	Val	Ala	Leu	Asn	Ile
	145				150				155					160	
Val	Ser	Arg	Leu	Val	Ile	Gly	Lys	Thr	Phe	Glu	Pro	Lys	Asp	Gly	Arg
			165					170					175		
Glu	Phe	Arg	Ser	Ile	Val	Glu	Arg	Glu	Thr	Arg	Leu	Pro	Gly	Ala	Thr
			180					185					190		
Lys	Met	Leu	Asp	Tyr	Thr	Val	Trp	Leu	Lys	Arg	Leu	Ser	Ser	Trp	Phe
	195					200						205			
Thr	Ser	Asp	Lys	Ala	Phe	Met	Lys	His	Met	Ala	Arg	Lys	Arg	Asn	Trp
	210				215					220					
Phe	Lys	Arg	Ala	Val	Met	Asp	Glu	Val	Tyr	Gly	Gly	Arg	Asp	Gln	Lys
	225				230					235				240	
Cys	Phe	Val	Gln	Ser	Leu	Leu	Glu	Leu	Lys	Glu	Lys	Asp	Glu	Leu	Thr
			245						250				255		
Glu	Glu	Thr	Val	Met	Gly	Leu	Val	Trp	Asn	Met	Leu	Thr	Ala	Gly	Ala
			260					265					270		
Asp	Thr	Thr	Ala	Ile	Thr	Ile	Glu	Trp	Ala	Met	Ala	Glu	Met	Ile	Arg
		275					280					285			
Cys	Pro	Thr	Val	Lys	Glu	Lys	Val	Gln	Asp	Glu	Leu	Asp	Ser	Val	Val
	290					295					300				
Gly	Ser	Gly	Arg	Leu	Met	Ser	Asp	Ala	Asp	Ile	Pro	Lys	Leu	Pro	Phe
	305				310					315				320	
Leu	Gln	Cys	Val	Leu	Lys	Glu	Ala	Leu	Arg	Leu	His	Pro	Pro	Thr	Pro
			325						330					335	
Leu	Met	Leu	Pro	His	Lys	Ala	Ser	Glu	Ser	Val	Gln	Val	Gly	Gly	Tyr
			340					345					350		
Lys	Val	Pro	Lys	Gly	Ala	Thr	Val	Tyr	Val	Asn	Val	Gln	Ala	Ile	Ala
		355					360					365			
Arg	Asp	Pro	Ala	Asn	Trp	Ser	Asn	Pro	Asp	Glu	Phe	Arg	Pro	Glu	Arg
	370				375						380				
Phe	Leu	Val	Glu	Glu	Thr	Asp	Val	Lys	Gly	Gln	Asp	Phe	Arg	Val	Leu
	385				390					395				400	
Pro	Phe	Gly	Ser	Gly	Arg	Arg	Val	Cys	Pro	Ala	Ala	Gln	Leu	Ser	Leu
			405					410					415		
Asn	Met	Met	Thr	Leu	Ala	Leu	Gly	Ser	Leu	Leu	His	Cys	Phe	Ser	Trp
			420					425					430		
Thr	Ser	Ser	Thr	Pro	Arg	Glu	His	Ile	Asp	Met	Thr	Glu	Lys	Pro	Gly
		435					440					445			
Leu	Val	Cys	Tyr	Met	Lys	Ala	Pro	Leu	Gln	Ala	Leu	Ala	Ser	Ser	Arg
	450					455					460				

Leu Pro Gln Glu Leu Tyr Leu
465 470

(2) INFORMATION FOR SEQ ID NO:2230:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1390 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1390
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572147

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2230:

aggctccgtcg	cttctcttcc	atttctcttc	attttcgatt	tgtattetta	ttttttcca	60
gtagctcctcg	ctctgtgaat	tcttccgctc	acgatagatc	tgcttatact	ccttacattc	120
aaccttagat	ctgaacatg	ggtgcaggtg	gaagaatgcc	ggttctact	tcttccaaga	180
aatcggaac	cgacaccaca	aagcgtgtgc	cgtgcgagaa	acgccttct	tcggtgggag	240
atctgaagaa	agcaatcccg	cgcattgtt	tcaaacgctc	aatcccttc	tctttctct	300
accttatcag	tgacatcatt	atagcctcat	gcttctacta	cgtgccacc	aattacttct	360
ctctctccc	tcagcctctc	tcttacttgg	cttggccact	ctattggcgc	tgtaagggt	420
gtgtcctaac	tggtatctgg	gtcatagccc	acgaatcgcg	tcaccaagca	tcaagcga	480
accaatggct	ggatgacaca	gttggtctta	tcttccattc	cttctctctc	gtcccttact	540
tctctggaa	gtatagtcat	ggccgtcacc	attccaacac	tggatccctc	gaaagagatg	600
aagttattgt	ccccaaagcg	aaatcagcaa	tcaagtgtta	cgggaaatac	ctcaacaacc	660
ctcttgagcg	catcatgatg	ttaaccgtcc	agtttgcct	cgggtggccc	ttgtacttag	720
cttttaacgt	ctctggcaga	cgttatgacg	ggttcgcttg	ccatttctc	cccaacgctc	780
ccatctacaa	tgaccgagaa	cgctccaga	tatacctctc	tgatcgcggt	attctagccg	840
tctgtttttg	tctttaccgt	tacgctgctg	cacaagggat	ggcctcgatg	attctgcctt	900
acggagtacc	gcttctgata	gtgaatgcgt	tctcgtctt	gatcaactac	ttgcagacaa	960
ctcacctctc	gttgcctcac	tacgattcat	cagagtgagg	ctggctcagg	ggagcttttg	1020
ctaccgtaga	cagagactac	ggaatcttga	acaagtggtt	ccacaacatt	acagacacac	1080
acgtggctca	tcactgttct	tcgacaatgc	cgcattataa	cgcgaatgaa	gctacaagg	1140
cgataaagcc	aattcttgga	gaccattacc	agttcgatgg	aacaccgtgg	tatgtggcga	1200
tgatatgaa	ggcaaaagg	tgatatctatg	tagaaccgga	cagggaagg	gacaaagg	1260
gtgtgtactg	gtacaacaat	aagttatgat	gatgatgggt	aagaaattgt	cgacttttct	1320
cttgtctgtt	tgtcttttgt	taagaagct	atgcttcgtt	ttaataatct	tattgtccat	1380
tttgtgtgc						

(2) INFORMATION FOR SEQ ID NO:2231:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 383 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..383
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572148

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2231:

Met	Gly	Ala	Gly	Gly	Arg	Met	Pro	Val	Pro	Thr	Ser	Ser	Lys	Lys	Ser
1			5					10					15		
Glu	Thr	Asp	Thr	Thr	Lys	Arg	Val	Pro	Cys	Glu	Lys	Pro	Pro	Phe	Ser
			20					25				30			
Val	Gly	Asp	Leu	Lys	Lys	Ala	Ile	Pro	Pro	His	Cys	Phe	Lys	Arg	Ser
			35					40				45			
Ile	Pro	Arg	Ser	Phe	Ser	Tyr	Leu	Ile	Ser	Asp	Ile	Ile	Ile	Ala	Ser
			50				55				60				
Cys	Phe	Tyr	Tyr	Val	Ala	Thr	Asn	Tyr	Phe	Ser	Leu	Leu	Pro	Gln	Pro
			65				70			75			80		
Leu	Ser	Tyr	Leu	Ala	Trp	Pro	Leu	Tyr	Trp	Ala	Cys	Gln	Gly	Cys	Val

(2) INFORMATION FOR SEQ ID NO:2232:

(A) LENGTH: 377 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..377

(D) OTHER INFORMATION: / Ceres Seq. ID 1572149

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2232:

Met	Pro	Val	Pro	Thr	Ser	Ser	Lys	Lys	Ser	Glu	Thr	Asp	Thr	Thr	Lys
1			5						10					15	
Arg	Val	Pro	Cys	Glu	Lys	Pro	Pro	Phe	Ser	Val	Gly	Asp	Leu	Lys	Lys
		20						25					30		
Ala	Ile	Pro	Pro	His	Cys	Phe	Lys	Arg	Ser	Ile	Pro	Arg	Ser	Phe	Ser
		35					40					45			
Tyr	Leu	Ile	Ser	Asp	Ile	Ile	Ile	Ala	Ser	Cys	Phe	Tyr	Tyr	Val	Ala
	50					55					60				
Thr	Asn	Tyr	Phe	Ser	Leu	Leu	Pro	Gln	Pro	Leu	Ser	Tyr	Leu	Ala	Trp
65					70					75				80	
Pro	Leu	Tyr	Trp	Ala	Cys	Gln	Gly	Cys	Val	Leu	Thr	Gly	Ile	Trp	Val
				85					90					95	

Ile Ala His Glu Cys Gly His His Ala Phe Ser Asp Tyr Gln Trp Leu
100 105 110
Asp Asp Thr Val Gly Leu Ile Phe His Ser Phe Leu Leu Val Pro Tyr
115 120 125
Phe Ser Trp Lys Tyr Ser His Arg Arg His His Ser Asn Thr Gly Ser
130 135 140
Leu Glu Arg Asp Glu Val Phe Val Pro Lys Gln Lys Ser Ala Ile Lys
145 150 155 160
Trp Tyr Gly Lys Tyr Leu Asn Asn Pro Leu Gly Arg Ile Met Met Leu
165 170 175
Thr Val Gln Phe Val Leu Gly Trp Pro Leu Tyr Leu Ala Phe Asn Val
180 185 190
Ser Gly Arg Pro Tyr Asp Gly Phe Ala Cys His Phe Phe Pro Asn Ala
195 200 205
Pro Ile Tyr Asn Asp Arg Glu Arg Leu Gln Ile Tyr Leu Ser Asp Ala
210 215 220
Gly Ile Leu Ala Val Cys Phe Gly Leu Tyr Arg Tyr Ala Ala Ala Gln
225 230 235 240
Gly Met Ala Ser Met Ile Cys Leu Tyr Gly Val Pro Leu Leu Ile Val
245 250 255
Asn Ala Phe Leu Val Leu Ile Thr Tyr Leu Gln His Thr His Pro Ser
260 265 270
Leu Pro His Tyr Asp Ser Ser Glu Trp Asp Trp Leu Arg Gly Ala Leu
275 280 285
Ala Thr Val Asp Arg Asp Tyr Gly Ile Leu Asn Lys Val Phe His Asn
290 295 300
Ile Thr Asp Thr His Val Ala His His Leu Phe Ser Thr Met Pro His
305 310 315 320
Tyr Asn Ala Met Glu Ala Thr Lys Ala Ile Lys Pro Ile Leu Gly Asp
325 330 335
His Tyr Gln Phe Asp Gly Thr Pro Trp Tyr Val Ala Met Tyr Arg Glu
340 345 350
Ala Lys Glu Cys Ile Tyr Val Glu Pro Asp Arg Glu Gly Asp Lys Lys
355 360 365
Gly Val Tyr Trp Tyr Asn Asn Lys Leu
370 375

(2) INFORMATION FOR SEQ ID NO:2233:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 204 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..204

(D) OTHER INFORMATION: / Ceres Seq. ID 1572150

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2233:

Met Met Leu Thr Val Gln Phe Val Leu Gly Trp Pro Leu Tyr Leu Ala
1 5 10 15
Phe Asn Val Ser Gly Arg Pro Tyr Asp Gly Phe Ala Cys His Phe Phe
20 25 30
Pro Asn Ala Pro Ile Tyr Asn Asp Arg Glu Arg Leu Gln Ile Tyr Leu
35 40 45
Ser Asp Ala Gly Ile Leu Ala Val Cys Phe Gly Leu Tyr Arg Tyr Ala
50 55 60
Ala Ala Gln Gly Met Ala Ser Met Ile Cys Leu Tyr Gly Val Pro Leu
65 70 75 80
Leu Ile Val Asn Ala Phe Leu Val Leu Ile Thr Tyr Leu Gln His Thr
85 90 95
His Pro Ser Leu Pro His Tyr Asp Ser Ser Glu Trp Asp Trp Leu Arg

	100		105		110	
Gly Ala	Leu Ala Thr Val Asp Arg Asp Tyr Gly Ile	Leu Asn Lys Val				
	115	120			125	
Phe His Asn Ile Thr Asp Thr His Val Ala His His					Leu Phe Ser Thr	
	130	135			140	
Met Pro His Tyr Asn Ala Met Glu Ala Thr Lys Ala Ile Lys Pro Ile						
	145	150			155	160
Leu Gly Asp His Tyr Gln Phe Asp Gly Thr Pro Trp Tyr Val Ala Met						
	165	170			175	
Tyr Arg Glu Ala Lys Glu Cys Ile Tyr Val Glu Pro Asp Arg Glu Gly					190	
	180	185				
Asp Lys Lys Gly Val Tyr Trp Tyr Asn Asn Lys Leu						
	195	200				

(2) INFORMATION FOR SEQ ID NO:2234:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1109 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1109
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572174

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2234:

aaaaaaacca	ataaaattgg	tcgcttcgca	aaaactgaga	tttgagttct	tccttcgggtg	60
gaagagacaa	attttacttt	taagaaattt	gaaacaaaag	tttcattaaa	cagatttggtg	120
ggatttttaa	tttgaatttt	gatcagtgaa	tcaacgataa	acgattcgtc	gttatggaag	180
gagtttggtc	acggttaggc	aggttcctga	cacggtagcg	accggcaacg	gttttcaccg	240
gtccgggtgc	gaagtggaag	aagaagtggg	tacacgtctc	tcctccact	aagaaagaca	300
ataataatag	ctctcccggt	tccgcccgtg	ctgcagcttc	cgctggtta	ggtggttcga	360
attctgacgg	cagtaattga	tcgcatttgc	tgctgtataa	gtgggcacca	ttgtcccgga	420
acggtaacgg	gaatgaagat	ggtaaaagt	agagttaatt	tccgagcgag	gacacgggtg	480
cgacgggtgc	agaagatcct	ccgcggcgga	gattcaaata	cgttccgata	gcagttactg	540
aggaacagaa	gaaggaaatt	acagaaaatt	aggacgatga	taagattgag	gaggaatgaca	600
agattgatga	ggataataag	gtcgagcagg	aagacaaggt	tgatgaggac	aaaactgtag	660
aggagtgcag	cgagaagaaa	gcggaagtgc	aagtggaaat	ggaggaaaag	cctgatataca	720
atgatgttcc	aatggaagat	attcagcagg	atgaagaaaa	aatagtacag	gatgatgaag	780
aaaaagtagt	gcgacaagat	ttgaacgaaa	gcactgtgga	tttaggactg	accttaaatg	840
caaacgatgc	tgatgctgat	gcagaaaaac	acccgaaaga	ggacaagcca	ttagaagaat	900
gataaaactgc	gtgcattggt	ttgttctctc	acctcaact	ctcaatatca	attaggaaga	960
aagacattac	agaaagaaca	aagcagtcac	tagatatgga	cgcagatcct	tgatttggtc	1020
tgtaaccocca	tggcttattc	cttttgatgt	taatgaaat	gactcattga	ttcagactga	1080
tcattcaatt	cataggcaga	ttcttgctc				

(2) INFORMATION FOR SEQ ID NO:2235:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 242 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..242
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572175

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2235:

Met Glu Gly Val Gly Ala Arg Leu Gly Arg Ser Thr Arg Tyr Gly						
	5	10			15	
Pro Ala Thr Val Phe Thr Gly Pro Val Arg Lys Trp Lys Lys Lys Trp						
	20	25			30	
Val His Val Ser Pro Ser Thr Lys Lys Asp Asn Asn Asn Ser Ser Ser						

	35		40		45
Gly	Ser	Ala	Ala	Ala	Ala
50				55	
Asp	Gly	Ser	Asn	Gly	Ser
65			70		
Ser	Gln	Asn	Gly	Asn	Gly
			85		
Pro	Ser	Glu	Asp	Thr	Val
			100		
Arg	Phe	Lys	Tyr	Val	Pro
			115		
Ile	Thr	Glu	Ile	Glu	Asp
130			135		
Asp	Glu	Asp	Asn	Lys	Val
145			150		
Thr	Val	Glu	Glu	Ser	Ser
			165		
Glu	Glu	Lys	Pro	Asp	Ile
			180		
Asp	Glu	Glu	Lys	Ile	Val
195			200		
Asp	Leu	Asn	Glu	Ser	Thr
210			215		
Asp	Ala	Asp	Ala	Asp	Ala
225			230		
Glu	Glu				

(2) INFORMATION FOR SEQ ID NO:2236:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 850 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..850
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572180

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2236:

ctgagctcag	cttcactttg	ctcgacgtta	tcttcttcgt	tcagcgcaca	tgcgctcgat	60
tacgaacetc	gcctcttctc	tctcttcaat	ctcgcttcac	tcccaagtgt	ctcaaagacc	120
taacaccatt	tctctccccc	gcgcgaattc	agtattcgca	ttaccggcga	aatccgcacg	180
ccgcgctctc	ctatctatca	ccgccacggt	atctgctcca	ccggaggagg	aggagatagt	240
tgaactgaag	aaatacgtca	aatcgaggct	tcccgaggga	tttgctgctc	agaagattat	300
tggcactgga	cgacgtaaat	gcgcaatcgc	tagagtttgt	cttcaggaa	gtactgggaa	360
ggttatcatc	aactatcgtg	atgccaaagg	gtacctctac	ggaaatccat	tgtggcttca	420
gtatgttaaa	gtaccatttg	tgacttttag	atatgagaat	agctacgaca	tatttgtgaa	480
agcccatgga	ggcggctctc	caggtccaag	tcaagcaatt	accttgggag	tcgcacgtgc	540
actcctgaag	gtaagtgcag	accacagatc	gcctttgaag	aaggaaaggt	tgctcactag	600
agatgcgaga	gtgggttgaa	gaaagaaggc	cgggctcaa	aaggcgcgta	aagccccaca	660
attctccaag	cggttaagat	tttatatata	attgaatcaa	ctcttcaagt	agaactcctc	720
gcctccattt	ttttttaaaa	cttttcttgt	ctattatcgg	tcttttgttt	catgttaagt	780
tttatgtgta	gacgaactaa	tacaatctct	gttttgtttg	aatggaacgc	aaagttgata	840
tgGcttttgt						

(2) INFORMATION FOR SEQ ID NO:2237:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 208 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..208

(D) OTHER INFORMATION: / Ceres Seq. ID 1572181

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2237:

Met	Ala	Ser	Ile	Thr	Asn	Leu	Ala	Ser	Ser	Leu	Ser	Ser	Leu	Ser	Phe	
1				5					10					15		
Ser	Ser	Gln	Val	Ser	Gln	Arg	Pro	Asn	Thr	Ile	Ser	Phe	Pro	Arg	Ala	
			20					25					30			
Asn	Ser	Val	Phe	Ala	Leu	Pro	Ala	Lys	Ser	Ala	Arg	Arg	Ala	Ser	Leu	
			35				40					45				
Ser	Ile	Thr	Ala	Thr	Val	Ser	Ala	Pro	Pro	Glu	Glu	Glu	Glu	Ile	Val	
			50			55					60					
Glu	Leu	Lys	Lys	Tyr	Val	Ser	Arg	Leu	Pro	Gly	Gly	Phe	Ala	Ala		
65					70					75				80		
Gln	Lys	Ile	Ile	Gly	Thr	Gly	Arg	Arg	Lys	Cys	Ala	Ile	Ala	Arg	Val	
				85					90					95		
Val	Leu	Gln	Glu	Gly	Thr	Gly	Lys	Val	Ile	Ile	Asn	Tyr	Arg	Asp	Ala	
			100					105					110			
Lys	Glu	Tyr	Leu	Gln	Gly	Asn	Pro	Leu	Trp	Leu	Gln	Tyr	Val	Lys	Val	
		115				120						125				
Pro	Leu	Val	Thr	Leu	Gly	Tyr	Glu	Asn	Ser	Tyr	Asp	Ile	Phe	Val	Lys	
		130				135					140					
Ala	His	Gly	Gly	Gly	Leu	Ser	Gly	Gln	Ala	Gln	Ala	Ile	Thr	Leu	Gly	
145					150					155				160		
Val	Ala	Arg	Ala	Leu	Leu	Lys	Val	Ser	Ala	Asp	His	Arg	Ser	Pro	Leu	
				165				170						175		
Lys	Lys	Glu	Gly	Leu	Leu	Thr	Arg	Asp	Ala	Arg	Val	Val	Glu	Arg	Lys	
			180					185					190			
Lys	Ala	Gly	Leu	Lys	Lys	Ala	Arg	Lys	Ala	Pro	Gln	Phe	Ser	Lys	Arg	
		195				200						205				

(2) INFORMATION FOR SEQ ID NO:2238:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 700 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..700

(D) OTHER INFORMATION: / Ceres Seq. ID 1572195

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2238:

acttgtctctc	atattagttt	gttatacaac	tcacttagaa	taattgtagat	tacatttcag	60
ccaaattcatc	attcttgaga	gaaaaagaaat	cgaagatggc	aacaaaatcc	accggaggta	120
ccgagaaaac	caagtcgata	gaagtgaaga	agaaaactaat	caacgtgttg	atcgtcgatg	180
atgatccatt	aaaccgtaga	ctccacgaga	tgatcatcaa	aacgatcgga	ggaattttct	240
agactgcaaa	gaatggcgag	gaggcagtg	tcctccacgc	tgacggcgAa	gcattctttc	300
accttattct	aatggataag	gaaatgcctg	agaggggatg	agtttcgaca	actaagaagc	360
taagagaaat	gaaagtgaac	tcaatgatcg	ttggggtaac	gtcagtagct	gaccaagaag	420
aagagcgtaa	ggctttttat	gaagctgggc	tcaaccattg	cttgaaaaaa	cccttaacca	480
aggccaaagt	cttcccgctc	attagccacc	tcttcgatgc	ttgatgggat	aaggctcatt	540
aatgtatcta	tattttcaat	catgaaatca	cctacacgtg	tatttgacac	aaaaatctgc	600
atttgttgtg	atatagggtt	tctcatatct	atgtttgatt	tattttctta	tcgtccggag	660
taaaatcatg	caagtcattt	ctttgggcta	ataaaatatt			

(2) INFORMATION FOR SEQ ID NO:2239:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 142 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..142
(D) OTHER INFORMATION: / Ceres Seq. ID 1572196
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2239:
Met Ala Thr Lys Ser Thr Gly Gly Thr Glu Lys Thr Lys Ser Ile Glu
1 5 10 15
Val Lys Lys Lys Leu Ile Asn Val Leu Ile Val Asp Asp Asp Pro Leu
20 25 30
Asn Arg Arg Leu His Glu Met Ile Ile Lys Thr Ile Gly Gly Ile Ser
35 40 45
Gln Thr Ala Lys Asn Gly Glu Glu Ala Val Ile Leu His Arg Asp Gly
50 55 60
Glu Ala Ser Phe Asp Leu Ile Leu Met Asp Lys Glu Met Pro Glu Arg
65 70 75 80
Asp Gly Val Ser Thr Thr Lys Lys Leu Arg Glu Met Lys Val Thr Ser
85 90 95
Met Ile Val Gly Val Thr Ser Val Ala Asp Gln Glu Glu Glu Arg Lys
100 105 110
Ala Phe Met Glu Ala Gly Leu Asn His Cys Leu Glu Lys Pro Leu Thr
115 120 125
Lys Ala Lys Ile Phe Pro Leu Ile Ser His Leu Phe Asp Ala
130 135 140

(2) INFORMATION FOR SEQ ID NO:2240:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 104 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..104
(D) OTHER INFORMATION: / Ceres Seq. ID 1572197
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2240:
Met Ile Ile Lys Thr Ile Gly Gly Ile Ser Gln Thr Ala Lys Asn Gly
1 5 10 15
Glu Glu Ala Val Ile Leu His Arg Asp Gly Glu Ala Ser Phe Asp Leu
20 25 30
Ile Leu Met Asp Lys Glu Met Pro Glu Arg Asp Gly Val Ser Thr Thr
35 40 45
Lys Lys Leu Arg Glu Met Lys Val Thr Ser Met Ile Val Gly Val Thr
50 55 60
Ser Val Ala Asp Gln Glu Glu Glu Arg Lys Ala Phe Met Glu Ala Gly
65 70 75 80
Leu Asn His Cys Leu Glu Lys Pro Leu Thr Lys Ala Lys Ile Phe Pro
85 90 95
Leu Ile Ser His Leu Phe Asp Ala
100

(2) INFORMATION FOR SEQ ID NO:2241:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 982 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -

(B) LOCATION: 1..982

(D) OTHER INFORMATION: / Ceres Seq. ID 1572201

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2241:

agaacacaaa	caaaaaacaca	ttgtaacatt	agttaaagca	taaagctctt	ttatgtcgaa	60
taataataat	ctctcgacca	ccgtgaatca	agaaacgacg	acgtctctgt	aagttctcaat	120
cacattgcct	actgatcaat	ctctcacaac	ctcaccagga	tcatctctct	ctccttcaac	180
gagaccttcc	ggtggatcac	cgccgagaag	aacggcgact	ggattattccg	gcaagcactc	240
tatttttcagg	gggattcgac	tacgtaacgg	aaaatgggta	tcggagatta	gagagccacg	300
taaaacgaca	agaatttggc	tcgggactta	tcgggtaccg	gagatggctg	ccgccgttta	360
cgacgtggct	cgcttagctt	taaaaggacc	aggccgtttt	gaattttcct	ggGtttagct	420
ttgacttacg	tggtcccggt	ttcaaaactct	gctgcggata	taagagcgcc	tgctagttaga	480
gcagcgagga	ggaagcaacc	ggatcagggt	ggggatgaga	Aggtattgga	accggttcaa	540
cccgcaaaag	aggaagaatt	agaagaagtg	tcgtgtaact	cgtgttcggt	ggagtttatg	600
gatgaggaag	cgatgttgaa	tatgccgact	ttgttgacgg	agatggctga	agggatgttg	660
atgagttcac	cgagaatgat	gatacatccg	acgatggaaag	atgattcgcc	ggagaatcac	720
gaaggagata	atcttttgag	ttataaatga	atccattgaa	gctgctctct	ttttttattgt	780
tttcggctcg	aatgagattt	tcctccctttt	ttttctcttt	tggttcgctg	ttatggaag	840
tcaaataggt	tattaatatg	atctattaat	atttttgaaa	cataatgagt	ttgaatttga	900
atttttccat	ttttatataa	atatggttta	tatgagggaa	aaatagatac	atatcgaa	960
tataagaatt	gtttttctgc	tt				

(2) INFORMATION FOR SEQ ID NO:2242:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 121 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..121

(D) OTHER INFORMATION: / Ceres Seq. ID 1572202

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2243:

Met	Ser	Asn	Asn	Asn	Asn	Ser	Pro	Thr	Thr	Val	Asn	Gln	Glu	Thr	Thr
1		5							10				15		
Thr	Ser	Arg	Glu	Val	Ser	Ile	Thr	Leu	Pro	Thr	Asp	Gln	Ser	Pro	Gln
		20						25					30		
Thr	Ser	Pro	Gly	Ser	Ser	Ser	Ser	Pro	Ser	Pro	Arg	Pro	Ser	Gly	Gly
		35					40					45			
Ser	Pro	Ala	Arg	Arg	Thr	Ala	Thr	Gly	Leu	Ser	Gly	Lys	His	Ser	Ile
		50				55					60				
Phe	Arg	Gly	Ile	Arg	Leu	Arg	Asn	Gly	Lys	Trp	Val	Ser	Glu	Ile	Arg
		65				70			75				80		
Glu	Pro	Arg	Lys	Thr	Thr	Arg	Ile	Trp	Leu	Gly	Thr	Tyr	Pro	Val	Pro
			85					90					95		
Glu	Met	Ala	Ala	Ala	Ala	Tyr	Asp	Val	Ala	Ala	Leu	Ala	Leu	Lys	Gly
			100				105						110		
Pro	Gly	Arg	Phe	Glu	Phe	Ser	Thr	Val							
		115					120								

(2) INFORMATION FOR SEQ ID NO:2243:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 86 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..86

(D) OTHER INFORMATION: / Ceres Seq. ID 1572203

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2243:

Met Lys Gln Pro Asp Gln Gly Gly Asp Glu Lys Val Leu Glu Pro Val

1	5	10	15
Gln Pro Gly	Lys Glu Glu Glu Leu Glu Glu Val Ser Cys Asn Ser Cys		
	20	25	30
Ser Leu Glu Phe Met Asp Glu Glu Ala Met Leu Asn Met Pro Thr Leu			
	35	40	45
Leu Thr Glu Met Ala Glu Gly Met Leu Met Ser Pro Pro Arg Met Met			
	50	55	60
Ile His Pro Thr Met Glu Asp Asp Ser Pro Glu Asn His Glu Gly Asp			
	65	70	75
Asn Leu Trp Ser Tyr Lys			80
	85		

(2) INFORMATION FOR SEQ ID NO:2244:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 932 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..932

(D) OTHER INFORMATION: / Ceres Seq. ID 1572204

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2244:

aactgtttga	tttctgagga	gaatccatgt	tttccattcg	aagaaaactc	taactttctc	60
gttgaagcgt	tgagctctct	acctctttat	ctccggagat	gtataataac	atgggacctc	120
aaccggggat	gccaaagac	ccaggaacc	ctgagccctg	tccatttgg	aatcctttca	180
ctggagctgg	ctcgggtttt	atccgtgggt	gtttggggag	gtatggggag	agaattttag	240
gatcgartc	tgagtatgtt	cagagcaata	taagccggta	cttctctgat	ccgcaatact	300
atttccaagt	gaatgatcaa	tatgtgagga	ataaactgaa	gggtgttctg	tttcttttcc	360
tacacggggg	acaatggacc	agaatatctg	aaccagttgg	tggtaggctc	tcatacaagc	420
ctccaatata	tgatatcaat	gctccCagac	ttgtacattc	ccatttatgg	atttgggtacc	480
tacgtttttc	ttgctgggtc	ttcattggga	agtttacacc	ggaagcctttg		540
aattggctgt	ttgtgaaagg	attggttgg	tggtttttgc	aagttaagt	cctgaaagta	600
acacttctat	caacttggtag	tgagagggca	ccattactag	ataattgtgg	atacggaggg	660
tatgcttttg	ctggtctgtg	tcttgogggc	tttgccaaaa	taattgtggg	atactcgtac	720
tacgctgtga	tgccatggac	ttgtctatgc	actgggattt	tcttgggtgaa	gacgatgaaa	780
cgtgtttctg	ttgctgaagt	aagaagttac	gattcggagca	aacatcacta	ccttcttctg	840
tttttagcct	tggtccagtt	cccacttttg	atatggcttg	gtaacattag	tgittaattgg	900
cttctttgaa	atgaaaaaag	acgtttttgt	gt			

(2) INFORMATION FOR SEQ ID NO:2245:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 159 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..159

(D) OTHER INFORMATION: / Ceres Seq. ID 1572205

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2245:

Met Ile Ser Met Leu Pro Asp Leu Tyr Ile Pro Phe Met Ala Phe Gly			
1	5	10	15
Thr Tyr Val Val Leu Ala Gly Leu Ser Leu Gly Leu Asn Gly Lys Phe			
	20	25	30
Thr Pro Glu Ala Leu Asn Trp Leu Phe Val Lys Gly Leu Val Gly Trp			
	35	40	45
Phe Leu Gln Val Met Leu Leu Lys Val Thr Leu Leu Ser Leu Gly Ser			
	50	55	60
Gly Glu Ala Pro Leu Leu Asp Ile Val Ala Tyr Gly Gly Tyr Ala Phe			
	65	70	75
			80

Ala Gly Leu Cys Leu Ala Gly Phe Ala Lys Ile Met Trp Gly Tyr Ser
85 90 95
Tyr Tyr Ala Leu Met Pro Trp Thr Cys Leu Cys Thr Gly Ile Phe Leu
100 105 110
Val Lys Thr Met Lys Arg Val Leu Phe Ala Glu Val Arg Ser Tyr Asp
115 120 125
Ser Ser Lys His His Tyr Leu Leu Phe Leu Ala Leu Val Gln Phe
130 135 140
Pro Leu Leu Ile Trp Leu Gly Asn Ile Ser Val Asn Trp Leu Leu
145 150 155

(2) INFORMATION FOR SEQ ID NO:2246:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 156 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..156

(D) OTHER INFORMATION: / Ceres Seq. ID 1572206

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2246:

Met Leu Pro Asp Leu Tyr Ile Pro Phe Met Ala Phe Gly Thr Tyr Val
1 5 10 15
Val Leu Ala Gly Leu Ser Leu Gly Leu Asn Gly Lys Phe Thr Pro Glu
20 25 30
Ala Leu Asn Trp Leu Phe Val Lys Gly Leu Val Gly Trp Phe Leu Gln
35 40 45
Val Met Leu Leu Lys Val Thr Leu Leu Ser Leu Gly Ser Gly Glu Ala
50 55 60
Pro Leu Leu Asp Ile Val Ala Tyr Gly Gly Tyr Ala Phe Ala Gly Leu
65 70 75 80
Cys Leu Ala Gly Phe Ala Lys Ile Met Trp Gly Tyr Ser Tyr Tyr Ala
85 90 95
Leu Met Pro Trp Thr Cys Leu Cys Thr Gly Ile Phe Leu Val Lys Thr
100 105 110
Met Lys Arg Val Leu Phe Ala Glu Val Arg Ser Tyr Asp Ser Ser Lys
115 120 125
His His Tyr Leu Leu Leu Phe Leu Ala Leu Val Gln Phe Pro Leu Leu
130 135 140
Ile Trp Leu Gly Asn Ile Ser Val Asn Trp Leu Leu
145 150 155

(2) INFORMATION FOR SEQ ID NO:2247:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 147 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..147

(D) OTHER INFORMATION: / Ceres Seq. ID 1572207

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2247:

Met Ala Phe Gly Thr Tyr Val Val Leu Ala Gly Leu Ser Leu Gly Leu
1 5 10 15
Asn Gly Lys Phe Thr Pro Glu Ala Leu Asn Trp Leu Phe Val Lys Gly
20 25 30
Leu Val Gly Trp Phe Leu Gln Val Met Leu Leu Lys Val Thr Leu Leu
35 40 45
Ser Leu Gly Ser Gly Glu Ala Pro Leu Leu Asp Ile Val Ala Tyr Gly

50	55	60
Gly Tyr Ala Phe Ala Gly Leu Cys Leu Ala Gly Phe Ala Lys Ile Met		
65	70	75
Trp Gly Tyr Ser Tyr Tyr Ala Leu Met Pro Trp Thr Cys Leu Cys Thr		
	85	90
Gly Ile Phe Leu Val Lys Thr Met Lys Arg Val Leu Phe Ala Glu Val		
	100	105
Arg Ser Tyr Asp Ser Ser Lys His His Tyr Leu Leu Leu Phe Leu Ala		
	115	120
Leu Val Gln Phe Pro Leu Leu Ile Trp Leu Gly Asn Ile Ser Val Asn		
	130	135
Trp Leu Leu		140
145		

(2) INFORMATION FOR SEQ ID NO:2248:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1209 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1209
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572240

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2248:

aaaaatctct	ttactaccag	caagtgtgtt	tcttgctaac	ttcaaaacttc	tctttctctt	60
gttctctctc	aagtcttgat	cttatttacc	gttaactttg	tgaacaaaaa	tcgaatcaaa	120
cacacatgga	gcgcgccacg	cctaagcatc	atcatactca	agccgaccaa	gaagcggcca	180
acaacaacaa	caacaagtcc	ggctctgggt	gttacacgtg	tcgccagacc	agcacgaggt	240
ggacacgcag	gacggagcaa	atcaaaaatc	tcaaagaact	ttactacaac	aatgcaatcc	300
ggtcaccaac	agccgatcag	atccagaaga	tcaactgcaag	gctgagacag	ttcggaaaaa	360
ttgagggcaa	gaagcttctt	tactgtttcc	agaaccataa	ggctcgtgag	cgtcagaaga	420
agagattcaa	cggaacaaac	atgaccacac	catcttcac	accacaactc	gttatgatgg	480
cggctaacga	tcattatcat	cctctacttc	accatcatca	cgggtgtccc	atgcagagac	540
ctgctaattc	cgtaaacggt	aaacttaacc	aagaccatca	tctctatcat	cataacaagc	600
catatccag	cttcaataac	gggaatttaa	atcatgcaag	ctcagggtact	gaatgtggtg	660
ttgttaatgc	ttctaattgc	tacatgagta	gccatgtcta	tggatctatg	gaacaagact	720
gttctatgaa	ttacaacaac	gtaggtggag	gatggggcaa	catggatcat	cattactcat	780
ctgcacctta	caacttcttc	gatagagcaa	agcctctgtt	tgggtctagaa	gggtcatcaag	840
aagaagaaga	atgtggtggc	gatgcttacc	tggaaacatc	acgtacgctt	cctctctctc	900
ctatgcacgg	tgaagatcac	atcaacgggt	gtagtgggtc	catctggaag	ttatggccaat	960
cggaagtctc	cccttcgcgt	tctcttgagc	tacgtctgaa	ctagctctta	cgccggtgtc	1020
gctcggtatt	aaagctcttt	cctctctctc	tctctttcgt	actcgtatgt	tcacaacat	1080
gCttcgctag	tgattaatga	tcagtttgtt	atattagtag	ttaaactagt	atctctcgtt	1140
atgtgtaatt	tgtaattact	agctaagtag	cgtctagggt	ttaatgttaa	ttgacaaccg	1200
ttttatctc						

(2) INFORMATION FOR SEQ ID NO:2249:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 292 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..292
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572241

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2249:

Met Glu Pro Pro Gln His Gln His His His His Gln Ala Asp Gln Glu	
1	5
Ser Gly Asn Asn Asn Asn Lys Ser Gly Ser Gly Gly Tyr Thr Cys	
	10
	15

20										25										30											
Arg	Gln	Thr	Ser	Thr	Arg	Trp	Thr	Pro	Thr	Thr	Glu	Gln	Ile	Lys	Ile																
35										40										45											
Leu	Lys	Glu	Leu	Tyr	Tyr	Asn	Asn	Ala	Ile	Arg	Ser	Pro	Thr	Ala	Asp																
50										55										60											
Gln	Ile	Gln	Lys	Ile	Thr	Ala	Arg	Leu	Arg	Gln	Phe	Gly	Lys	Ile	Glu																
65										70										75											
Gly	Lys	Asn	Val	Phe	Tyr	Trp	Phe	Gln	Asn	His	Lys	Ala	Arg	Glu	Arg																
85										90										95											
Gln	Lys	Lys	Arg	Phe	Asn	Gly	Thr	Asn	Met	Thr	Thr	Pro	Ser	Ser	Ser																
100										105										110											
Pro	Asn	Ser	Val	Met	Met	Ala	Ala	Asn	Asp	His	Tyr	His	Pro	Leu	Leu																
115										120										125											
His	His	His	His	Gly	Val	Pro	Met	Gln	Arg	Pro	Ala	Asn	Ser	Val	Asn																
130										135										140											
Val	Lys	Leu	Asn	Gln	Asp	His	His	Leu	Tyr	His	His	Asn	Lys	Pro	Tyr																
145										150										155											
Pro	Ser	Phe	Asn	Asn	Gly	Asn	Leu	Asn	His	Ala	Ser	Ser	Gly	Thr	Glu																
165										170										175											
Cys	Gly	Val	Val	Asn	Ala	Ser	Asn	Gly	Tyr	Met	Ser	Ser	His	Val	Tyr																
180										185										190											
Gly	Ser	Met	Glu	Gln	Asp	Cys	Ser	Met	Asn	Tyr	Asn	Asn	Val	Gly	Gly																
195										200										205											
Gly	Trp	Ala	Asn	Met	Asp	His	His	Tyr	Ser	Ser	Ala	Pro	Tyr	Asn	Phe																
210										215										220											
Phe	Asp	Arg	Ala	Lys	Pro	Leu	Phe	Gly	Leu	Glu	Gly	His	Gln	Glu	Glu																
225										230										235											
Glu	Glu	Cys	Gly	Gly	Asp	Ala	Tyr	Leu	Glu	His	Arg	Arg	Thr	Leu	Pro																
245										250										255											
Leu	Phe	Pro	Met	His	Gly	Glu	Asp	His	Ile	Asn	Gly	Gly	Ser	Gly	Ala																
260										265										270											
Ile	Trp	Lys	Tyr	Gly	Gln	Ser	Glu	Val	Arg	Pro	Cys	Ala	Ser	Leu	Glu																
275										280										285											
Leu	Arg	Leu	Asn																												
290																															

(2) INFORMATION FOR SEQ ID NO:2250:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 187 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..187

(D) OTHER INFORMATION: / Ceres Seq. ID 1572242

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2250:

Met	Thr	Thr	Pro	Ser	Ser	Ser	Pro	Asn	Ser	Val	Met	Met	Ala	Ala	Asn														
5										10										15									
Asp	His	Tyr	His	Pro	Leu	Leu	His	His	His	His	Gly	Val	Pro	Met	Gln														
20										25										30									
Arg	Pro	Ala	Asn	Ser	Val	Asn	Val	Lys	Leu	Asn	Gln	Asp	His	His	Leu														
35										40										45									
Tyr	His	His	Asn	Lys	Pro	Tyr	Pro	Ser	Phe	Asn	Asn	Gly	Asn	Leu	Asn														
50										55										60									
His	Ala	Ser	Ser	Gly	Thr	Glu	Cys	Gly	Val	Val	Asn	Ala	Ser	Asn	Gly														
65										70										75									
Tyr	Met	Ser	Ser	His	Val	Tyr	Gly	Ser	Met	Glu	Gln	Asp	Cys	Ser	Met														
85										90										95									
Asn	Tyr	Asn	Asn	Val	Gly	Gly	Gly	Trp	Ala	Asn	Met	Asp	His	His	Tyr														
100										105										110									

Ser Ser Ala Pro Tyr Asn Phe Phe Asp Arg Ala Lys Pro Leu Phe Gly
115 120 125
Leu Glu Gly His Gln Glu Glu Cys Gly Gly Asp Ala Tyr Leu
130 135 140
Glu His Arg Arg Thr Leu Pro Leu Phe Pro Met His Gly Glu Asp His
145 150 155 160
Ile Asn Gly Gly Ser Gly Ala Ile Trp Lys Tyr Gly Gln Ser Glu Val
165 170 175
Arg Pro Cys Ala Ser Leu Glu Leu Arg Leu Asn
180 185

(2) INFORMATION FOR SEQ ID NO:2251:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 176 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..176

(D) OTHER INFORMATION: / Ceres Seq. ID 1572243

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2251:

Met Met Ala Ala Asn Asp His Tyr His Pro Leu Leu His His His His
1 5 10 15
Gly Val Pro Met Gln Arg Pro Ala Asn Ser Val Asn Val Lys Leu Asn
20 25 30
Gln Asp His His Leu Tyr His His Asn Lys Pro Tyr Pro Ser Phe Asn
35 40 45
Asn Gly Asn Leu Asn His Ala Ser Ser Gly Thr Glu Cys Gly Val Val
50 55 60
Asn Ala Ser Asn Gly Tyr Met Ser Ser His Val Tyr Gly Ser Met Glu
65 70 75 80
Gln Asp Cys Ser Met Asn Tyr Asn Asn Val Gly Gly Gly Trp Ala Asn
85 90 95
Met Asp His His Tyr Ser Ser Ala Pro Tyr Asn Phe Phe Asp Arg Ala
100 105 110
Lys Pro Leu Phe Gly Leu Glu Gly His Gln Glu Glu Glu Cys Gly
115 120 125
Gly Asp Ala Tyr Leu Glu His Arg Arg Thr Leu Pro Leu Phe Pro Met
130 135 140
His Gly Glu Asp His Ile Asn Gly Gly Ser Gly Ala Ile Trp Lys Tyr
145 150 155 160
Gly Gln Ser Glu Val Arg Pro Cys Ala Ser Leu Glu Leu Arg Leu Asn
165 170 175

(2) INFORMATION FOR SEQ ID NO:2252:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 667 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..667

(D) OTHER INFORMATION: / Ceres Seq. ID 1572244

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2252:

acaacttccc cattttctgc ttctttttgt tcaactccaa tcacacaatt cacaaccat 60
tgagaaacca ataaaaaac ctcaatcaaa aaaaaaaaaa aaaaaagatg aaatctcaa 120
tttagtaag gagaaaaaag ccatttgaa taacttgaaa aggttttggg ttgcagaag 180

aaaatgaagg	agaaggcgga	gagtggtgga	ggagtaggat	acgtgagagc	agatcagata	240
gattttaaga	gtctgggacga	gcaattgacg	agacacttaa	gtaaaagcatg	gacgatggag	300
aagaggaaga	gtttgagtga	tggtgaagat	aacgtcaata	acacccgaca	taaccagaac	360
aacttcggac	atcgacagct	tgtgtttcag	aggccgcttc	Cttggtggtg	gatatagcaa	420
caacaacaac	agcagcaaga	acgacataat	taggtcgacc	gaggttgaga	agtcgaggag	480
agagtgggag	attgatcctt	ctaagcttat	aatcaaaaagt	gtgattgcta	gaggtacttt	540
tggtacggtt	cacogtggaa	tctacgatgg	tcaagatgtc	gccgtaaaac	tactagactg	600
gggagaagag	gggcacaggt	cagacgcaga	gatagCttcg	cttagagctg	cttttcactca	660
agaagtt						

(2) INFORMATION FOR SEQ ID NO:2253:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 77 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..77

(D) OTHER INFORMATION: / Ceres Seq. ID 1572245

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2253:

Met	Lys	Glu	Lys	Ala	Glu	Ser	Gly	Gly	Val	Gly	Tyr	Val	Arg	Ala
1														
				5					10				15	
Asp	Gln	Ile	Asp	Leu	Lys	Ser	Leu	Asp	Glu	Gln	Leu	Gln	Arg	His
				20					25				30	Leu
Ser	Lys	Ala	Trp	Thr	Met	Glu	Lys	Arg	Lys	Ser	Leu	Ser	Asp	Gly
				35					40				45	Glu
Asp	Asn	Val	Asn	Asn	Thr	Arg	His	Asn	Gln	Asn	Asn	Phe	Gly	His
				50				55				60		Arg
Gln	Leu	Val	Phe	Gln	Arg	Pro	Leu	Pro	Trp	Trp	Trp	Ile		
65				70				75						

(2) INFORMATION FOR SEQ ID NO:2254:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 116 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..116

(D) OTHER INFORMATION: / Ceres Seq. ID 1572246

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2254:

Met	Val	Lys	Ile	Thr	Ser	Ile	Thr	Pro	Asp	Ile	Thr	Arg	Thr	Thr
1														Ser
Asp	Ile	Asp	Ser	Leu	Cys	Phe	Arg	Gly	Arg	Phe	Leu	Gly	Gly	Tyr
				20					25				30	
Ser	Asn	Asn	Asn	Asn	Ser	Ser	Lys	Asn	Asp	Ile	Ile	Arg	Ser	Thr
				35				40				45		Glu
Val	Glu	Lys	Ser	Arg	Arg	Glu	Trp	Glu	Ile	Asp	Pro	Ser	Lys	Leu
				50				55			60			Ile
Ile	Lys	Ser	Val	Ile	Ala	Arg	Gly	Thr	Phe	Gly	Thr	Val	His	Arg
65				70				75					80	Gly
Ile	Tyr	Asp	Gly	Gln	Asp	Val	Ala	Val	Lys	Leu	Leu	Asp	Trp	Gly
				85				90					95	Glu
Glu	Gly	His	Arg	Ser	Asp	Ala	Glu	Ile	Ala	Ser	Leu	Arg	Ala	Phe
				100				105					110	
Thr	Gln	Glu	Val											
				115										

(2) INFORMATION FOR SEQ ID NO:2255:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 619 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..619

(D) OTHER INFORMATION: / Ceres Seq. ID 1572298

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2255:

```
atttcggcg  acgtgtgaatt  atgtggctgg  cgacgttato  ttccctctat  ttgtggcttt  60
cttcaccttc  tctacctaat  tacaggaacc  gtatgtttcc  aaagattaaa  gcttcgctct  120
ttaattaccc  tctatcgagc  aaaatcatgg  tcagaaattt  accgttttct  mcaagtgaag  180
attttctaaa  gagagagttt  tcagcttttg  gagagatagc  tgaagtgaag  cttatcaaa  240
atgaggcaat  gcagagatca  aaagggttat  cttttattca  attcacgtct  caagatgatg  300
cttttcttgc  catagagacc  atggaccgtc  ggatgtacaa  tggaagaatg  atttatatag  360
acattgcgaa  acccggtaaa  cgtgattttc  aaggactacc  gaggacttct  ggtccccctg  420
agaagtcgga  tgtgccagaa  gaagccgcta  atgatgaggt  tgcgtattgc  tggattatgt  480
tgttagtatc  aagctcacca  aactgtaact  gaacttgcac  aaatcagatg  tcaaattatg  540
cttcattata  ggaatttgat  caatgtgaag  aatgtgtgtt  actgataaac  aattattgac  600
acggttccag  ttacagctc
```

(2) INFORMATION FOR SEQ ID NO:2256:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 152 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..152

(D) OTHER INFORMATION: / Ceres Seq. ID 1572299

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2256:

```
Met Trp Ser Ala Thr Leu Ser Phe Pro Ser Phe Val Ala Ser Ser Ser
1 5 10 15
Ser Leu Pro Asn Tyr Arg Asn Arg Arg Phe Pro Lys Ile Lys Ala Ser
20 25 30
Leu Phe Asn Tyr Pro Leu Ala Ser Lys Ile Met Val Arg Asn Leu Pro
35 40 45
Phe Ser Xaa Ser Glu Asp Phe Leu Lys Arg Glu Phe Ser Ala Phe Gly
50 55 60
Glu Ile Ala Glu Val Lys Leu Ile Lys Asp Glu Ala Met Gln Arg Ser
65 70 75 80
Lys Gly Tyr Ala Phe Ile Gln Phe Thr Ser Gln Asp Asp Ala Phe Leu
85 90 95
Ala Ile Glu Thr Met Asp Arg Arg Met Tyr Asn Gly Arg Met Ile Tyr
100 105 110
Ile Asp Ile Ala Lys Pro Gly Lys Arg Asp Phe Gln Gly Leu Pro Arg
115 120 125
Thr Ser Gly Pro Pro Glu Lys Ser Asp Val Pro Glu Glu Ala Ala Asn
130 135 140
Asp Glu Val Ala Asp Cys Trp Tyr
145 150
```

(2) INFORMATION FOR SEQ ID NO:2257:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 110 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1..110
(D) OTHER INFORMATION: / Ceres Seq. ID 1572300
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2257:
Met Val Arg Asn Leu Pro Phe Ser Xaa Ser Glu Asp Phe Leu Lys Arg
1 5 10 15
Glu Phe Ser Ala Phe Gly Glu Ile Ala Glu Val Lys Leu Ile Lys Asp
20 25 30
Glu Ala Met Gln Arg Ser Lys Gly Tyr Ala Phe Ile Gln Phe Thr Ser
35 40 45
Gln Asp Asp Ala Phe Leu Ala Ile Glu Thr Met Asp Arg Arg Met Tyr
50 55 60
Asn Gly Arg Met Ile Tyr Ile Asp Ile Ala Lys Pro Gly Lys Arg Asp
65 70 75 80
Phe Gln Gly Leu Pro Arg Thr Ser Gly Pro Pro Glu Lys Ser Asp Val
85 90 95
Pro Glu Glu Ala Ala Asn Asp Glu Val Ala Asp Cys Trp Tyr
100 105 110

(2) INFORMATION FOR SEQ ID NO:2258:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 76 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..76
(D) OTHER INFORMATION: / Ceres Seq. ID 1572301

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2258:

Met Gln Arg Ser Lys Gly Tyr Ala Phe Ile Gln Phe Thr Ser Gln Asp
1 5 10 15
Asp Ala Phe Leu Ala Ile Glu Thr Met Asp Arg Arg Met Tyr Asn Gly
20 25 30
Arg Met Ile Tyr Ile Asp Ile Ala Lys Pro Gly Lys Arg Asp Phe Gln
35 40 45
Gly Leu Pro Arg Thr Ser Gly Pro Pro Glu Lys Ser Asp Val Pro Glu
50 55 60
Glu Ala Ala Asn Asp Glu Val Ala Asp Cys Trp Tyr
65 70 75

(2) INFORMATION FOR SEQ ID NO:2259:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1386 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..1386
(D) OTHER INFORMATION: / Ceres Seq. ID 1572338

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2259:

actgttggtga	atatgctg	cgtttcgcaa	gtatcaccgg	gaattgcгаа	gaagcagagg	60
accatgtacg	gagacgtac	aaactggaat	gaagatgagt	atagagaatc	aattttgaag	120
gagcgagaga	tagagacacg	caccgtcttc	agaacccgct	gggctcctcc	ggcgagaatc	180
ctctaaccag	acgcatttgt	tgtagcctcc	agcgatggaa	ctttagcttt	ccattcaactg	240
aactcgcttg	tgtctcaatc	ggcgagtttt	ggctactcga	aaggccaaga	tgttatgggtg	300
gctgaacctg	agagagtgtg	tagggcacac	gaaggtcctg	cttatgatgt	taagtctcat	360
ggtgaagacg	aagatgcttt	gctacttagt	tgtggtgatg	atggtagagt	taggggatgg	420
aaatggagag	aatttgcgtg	atcagatgtg	tctcttcatt	tgaagaagaa	tcattctgaag	480
ccattgcttg	aactgattaa	tccacaacac	aaaggtccct	ggggtgcgct	ttcacagatg	540

ccctgagatca atgccatgtc tgttgatcct cagtcaggaa gtgtatttac agcagctgggt	600
gattcttgcg catattgttg ggacgtggag agtgcgtaaga ttaaaatgac ctttaaaaggt	660
catccagcat atttgcatac tgtatgttct cgtagttctg caagtccagat attgcacgggt	720
tcagaggatg ggaactgcgag aatctgggat tgcataaacg gaaaaatgtgt taaagtaatt	780
ggttcccgag ataaaaagtc cgcctctgcg gttagtctta tggcccttga tgggagtgaa	840
agctgggttg tttgtggaca gggcaaaaaa ttagtcttat ggaatcttcc cgcctcagaa	900
tgcgtacaaa caataccocat ccctgcacat gtacaggatg tgaatgttga tgaaaagcaa	960
attttgactg taggagcaga accacttcta agacgtttcg acttaaatgg agctttgctt	1020
tctcaaaatt acctgtgctcc ttgttcagta ttttccattt ccttgcatcc agcaggagta	1080
gttgctgtgg gaggttatgg aggtattgtt gatgtcatct ctcaatttgg aagccatctc	1140
tgcaaatctt gtacgaattc attgtaaaac tccttacagt ttcttggattt ggcctgatcac	1200
octaaagagg taaccgaattg tgtcagtcag attattgcag aggttaagaa accottttctt	1260
tgtttttctt aggatctctg tccactactaa agaccaatta gttgtttgggt taagtgtaat	1320
tggttgttgg ttcctgagtt gctatcaaat ttgaaccatt aaaatgcacat tggaccgggt	1380
tagtct	

(2) INFORMATION FOR SEQ ID NO:2260:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 388 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..388

(D) OTHER INFORMATION: / Ceres Seq. ID 1572339

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2260:

Thr	Gly	Asn	Ile	Ala	Gly	Val	Ser	Gln	Val	Ser	Pro	Gly	Ile	Ala
1		5				10							15	
Lys	Lys	Gln	Arg	Thr	Met	Tyr	Gly	Asp	Ala	Thr	Asn	Trp	Asn	Glu
		20					25					30		Asp
Glu	Tyr	Arg	Glu	Ser	Ile	Leu	Lys	Glu	Arg	Glu	Ile	Glu	Thr	Arg
		35					40					45		Thr
Val	Phe	Arg	Thr	Ala	Trp	Ala	Pro	Pro	Ala	Arg	Ile	Ser	Asn	Pro
		50					55					60		Asp
Ala	Phe	Val	Val	Ala	Ser	Ser	Asp	Gly	Thr	Leu	Ala	Phe	His	Ser
		65					70			75				Leu
Asn	Ser	Leu	Val	Ser	Gln	Ser	Ala	Ser	Phe	Gly	Tyr	Ser	Lys	Gly
		85							90				95	Gln
Asp	Val	Met	Val	Ala	Glu	Pro	Glu	Arg	Val	Val	Arg	Ala	His	Glu
		100						105				110		Gly
Pro	Ala	Tyr	Asp	Val	Lys	Phe	Tyr	Gly	Glu	Asp	Glu	Asp	Ala	Leu
		115					120					125		Leu
Leu	Ser	Cys	Gly	Asp	Asp	Gly	Arg	Val	Arg	Gly	Trp	Lys	Trp	Arg
		130					135				140			Glu
Phe	Ala	Glu	Ser	Asp	Val	Ser	Leu	His	Leu	Lys	Glu	Asn	His	Leu
		145					150			155				Lys
Pro	Leu	Leu	Glu	Leu	Ile	Asn	Pro	Gln	His	Lys	Gly	Pro	Trp	Gly
		165							170				175	Ala
Leu	Ser	Pro	Met	Pro	Glu	Ile	Asn	Ala	Met	Ser	Val	Asp	Pro	Gln
		180						185					190	Ser
Gly	Ser	Val	Phe	Thr	Ala	Ala	Gly	Asp	Ser	Cys	Ala	Tyr	Cys	Trp
		195					200				205			Asp
Val	Glu	Ser	Gly	Lys	Ile	Lys	Met	Thr	Phe	Lys	Gly	His	Ser	Asp
		210					215				220			Tyr
Leu	His	Thr	Val	Val	Ser	Arg	Ser	Ser	Ala	Ser	Gln	Ile	Leu	Thr
		225					230			235				Gly
Ser	Glu	Asp	Gly	Thr	Ala	Arg	Ile	Trp	Asp	Cys	Lys	Thr	Gly	Lys
		245							250				255	Cys
Val	Lys	Val	Ile	Gly	Ser	Gln	Asp	Lys	Lys	Ser	Arg	Leu	Arg	Val
		260						265						Ser

Ser Met Ala Leu Asp Gly Ser Glu Ser Trp Leu Val Cys Gly Gln Gly
275 280 285
Lys Asn Leu Ala Leu Trp Asn Leu Pro Ala Ser Glu Cys Val Gln Thr
290 295 300
Ile Pro Ile Pro Ala His Val Gln Asp Val Met Phe Asp Glu Lys Gln
305 310 315 320
Ile Leu Thr Val Gly Ala Glu Pro Leu Leu Arg Arg Phe Asp Leu Asn
325 330 335
Gly Ala Leu Leu Ser Gln Ile His Cys Ala Pro Cys Ser Val Phe Ser
340 345 350
Ile Ser Leu His Pro Ala Gly Val Val Ala Val Gly Gly Tyr Gly Gly
355 360 365
Ile Val Asp Val Ile Ser Gln Phe Gly Ser His Leu Cys Thr Phe Arg
370 375 380
Ser Ser Ser Leu
385

(2) INFORMATION FOR SEQ ID NO:2261:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 367 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..367
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572340

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2261:

Met Tyr Gly Asp Ala Thr Asn Trp Asn Glu Asp Glu Tyr Arg Glu Ser
1 5 10 15
Ile Leu Lys Glu Arg Glu Ile Glu Thr Arg Thr Val Phe Arg Thr Ala
20 25 30
Trp Ala Pro Pro Ala Arg Ile Ser Asn Pro Asp Ala Phe Val Val Ala
35 40 45
Ser Ser Asp Gly Thr Leu Ala Phe His Ser Leu Asn Ser Leu Val Ser
50 55 60
Gln Ser Ala Ser Phe Gly Tyr Ser Lys Gly Gln Asp Val Met Val Ala
65 70 75 80
Glu Pro Glu Arg Val Val Arg Ala His Glu Gly Pro Ala Tyr Asp Val
85 90 95
Lys Phe Tyr Gly Glu Asp Glu Asp Ala Leu Leu Ser Cys Gly Asp
100 105 110
Asp Gly Arg Val Arg Gly Trp Lys Trp Arg Glu Phe Ala Glu Ser Asp
115 120 125
Val Ser Leu His Leu Lys Glu Asn His Leu Lys Pro Leu Leu Glu Leu
130 135 140
Ile Asn Pro Gln His Lys Gly Pro Trp Gly Ala Leu Ser Pro Met Pro
145 150 155 160
Glu Ile Asn Ala Met Ser Val Asp Pro Gln Ser Gly Ser Val Phe Thr
165 170 175
Ala Ala Gly Asp Ser Cys Ala Tyr Cys Trp Asp Val Glu Ser Gly Lys
180 185 190
Ile Lys Met Thr Phe Lys Gly His Ser Asp Tyr Leu His Thr Val Val
195 200 205
Ser Arg Ser Ser Ala Ser Gln Ile Leu Thr Gly Ser Glu Asp Gly Thr
210 215 220
Ala Arg Ile Trp Asp Cys Lys Thr Gly Lys Cys Val Lys Val Ile Gly
225 230 235 240
Ser Gln Asp Lys Lys Ser Arg Leu Arg Val Ser Ser Met Ala Leu Asp
245 250 255
Gly Ser Glu Ser Trp Leu Val Cys Gly Gln Gly Lys Asn Leu Ala Leu

	260		265		270
Trp Asn	Leu Pro	Ala Ser	Glu Cys	Val Gln	Thr Ile
	275		280		285
His Val	Gln Asp	Val Met	Phe Asp	Glu Lys	Gln Ile
	290		295		300
Ala Glu	Pro Leu	Leu Arg	Arg Phe	Asp Leu	Asn Gly
	305		310		315
Gln Ile	His Cys	Ala Pro	Cys Ser	Val Phe	Ser Ile
		325		330	
Ala Gly	Val Val	Ala Val	Gly Gly	Tyr Gly	Gly Ile
	340		345		350
Ser Gln	Phe Gly	Ser His	Leu Cys	Thr Phe	Arg Ser
	355		360		365

(2) INFORMATION FOR SEQ ID NO:2262:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 290 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..290
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572341

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2262:

Met Val	Ala Glu	Pro Glu	Arg Val	Val Arg	Ala His	Glu Gly	Pro Ala
1	5		10		15		
Tyr Asp	Val Lys	Phe Tyr	Gly Glu	Asp Glu	Asp Ala	Leu Leu	Leu Ser
	20		25		30		
Cys Gly	Asp Asp	Gly Arg	Val Arg	Gly Trp	Lys Trp	Arg Glu	Phe Ala
	35		40		45		
Glu Ser	Asp Val	Ser Leu	His Leu	Lys Glu	Asn His	Leu Lys	Pro Leu
	50		55		60		
Leu Glu	Leu Ile	Asn Pro	Gln His	Lys Gly	Pro Trp	Gly Ala	Leu Ser
	65		70		75		80
Pro Met	Pro Glu	Ile Asn	Ala Met	Ser Val	Asp Pro	Gln Ser	Gly Ser
	85		90		95		
Val Phe	Thr Ala	Ala Gly	Asp Ser	Cys Ala	Tyr Cys	Trp Asp	Val Glu
	100		105		110		
Ser Gly	Lys Ile	Lys Met	Thr Phe	Lys Gly	His Ser	Asp Tyr	Leu His
	115		120		125		
Thr Val	Val Ser	Arg Ser	Ser Ala	Ser Gln	Ile Leu	Thr Gly	Ser Glu
	130		135		140		
Asp Gly	Thr Ala	Arg Ile	Trp Asp	Cys Lys	Thr Gly	Lys Cys	Val Lys
	145		150		155		160
Val Ile	Gly Ser	Gln Asp	Lys Lys	Ser Arg	Leu Arg	Val Ser	Ser Met
	165		170		175		
Ala Leu	Asp Gly	Ser Glu	Ser Trp	Leu Val	Cys Gly	Gln Gly	Lys Asn
	180		185		190		
Leu Ala	Leu Trp	Asn Leu	Pro Ala	Ser Glu	Cys Val	Gln Thr	Ile Pro
	195		200		205		
Ile Pro	Ala His	Val Gln	Asp Val	Met Phe	Asp Glu	Lys Gln	Ile Leu
	210		215		220		
Thr Val	Gly Ala	Glu Pro	Leu Leu	Arg Arg	Phe Asp	Leu Asn	Gly Ala
	225		230		235		240
Leu Leu	Ser Gln	Ile His	Cys Ala	Pro Cys	Ser Val	Phe Ser	Ile Ser
	245		250		255		
Leu His	Pro Ala	Gly Val	Val Ala	Val Gly	Gly Tyr	Gly Gly	Ile Val
	260		265		270		
Asp Val	Ile Ser	Gln Phe	Gly Ser	His Leu	Cys Thr	Phe Arg	Ser Ser
	275		280		285		

Ser Leu
290

(2) INFORMATION FOR SEQ ID NO:2263:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1213 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1213
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572349

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2263:

aacaacatct	ttcacacaac	aattcacaca	atctctcggt	tttttttggt	tatcatcaaa	60
agtttttaac	taaattacgt	atcaaaattcc	gagcaagatg	actattcttg	ttgaacattt	120
tgttctcgat	tcaagagtg	atgaaaagaa	agtgatagag	gagagggata	atgaattggg	180
gttgatgga	ggttttggt	ttccaaaatc	aaaggaaact	gatgcattcg	atgctcctga	240
tatgaatttc	ttgggccatt	ccttcaggga	ttatgagaat	gatgaaagcg	agagacaaca	300
agggtgtgag	gaattttaca	ggatgcaaca	cattcaccag	acctatgact	ttgtgaagaa	360
gatgagaaaa	gagtatggaa	aacttaacaa	gatggaaatg	agtatatggg	aatgtttgtg	420
gttattgaac	aatgtgtgtg	atgaaagcga	tccggtatct	gatgagcctc	aaattcaaca	480
ccttctccaa	acgcgtgaag	ccattcgaag	ggactatccc	gacgaagatt	ggctccatct	540
cactgcacct	atccatgatc	ttggcaaggt	tctcctctcg	ccagaattcg	gtggtctctc	600
ccagtgggct	gtcgtggcg	atacatttcc	agttggatgt	accttcgact	cagccaatat	660
tcaccacaag	tatttcaaa	gaacacatga	tatcaacaac	ccaaagtaca	acacaaaaaa	720
tggagtttac	actgaaggat	gtggtttaga	caatgttctc	atgtcatggg	gtcatgacga	780
ctacatgtat	ttggtggcta	agaagaatgg	cacgaccttc	cctcacgctg	ctctctctcat	840
tattcgatat	cattcctttt	atccattgca	caaggcagga	gcctacacac	acttgatgaa	900
cgatgaggac	agagatgatc	tcaagtggtc	ccatgtcttc	aataaatatg	acctatacac	960
taagagcaaa	gttctggtag	atgtcgaaac	agtgaagcct	tactacattt	caactcatca	1020
caagtatttt	ccggcgaaac	taaaatgggt	agataaagct	acgatcaaat	taattcaact	1080
tcttttatga	ggagaacgag	atcgaaggtt	aacgagtttt	ctattgtata	caacggaaga	1140
taaatctatc	tataaaaaa	gttggtgtgt	tcatttgtaa	tttttcccc	catcagttta	1200
aaagttatgt	tgt					

(2) INFORMATION FOR SEQ ID NO:2264:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 317 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..317
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572350

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2264:

Met	Thr	Ile	Leu	Val	Glu	His	Phe	Val	Pro	Asp	Ser	Arg	Val	Asp	Glu
1				5						10				15	
Lys	Lys	Val	Ile	Glu	Glu	Arg	Asp	Asn	Glu	Leu	Val	Leu	Asp	Gly	Gly
				20				25					30		
Phe	Val	Val	Pro	Lys	Ser	Lys	Glu	Thr	Asp	Ala	Phe	Asp	Ala	Pro	Asp
				35			40					45			
Met	Asn	Phe	Leu	Gly	His	Ser	Phe	Arg	Asp	Tyr	Glu	Asn	Asp	Glu	Ser
	50					55					60				
Glu	Arg	Gln	Gln	Gly	Val	Glu	Glu	Phe	Tyr	Arg	Met	Gln	His	Ile	His
	65				70				75					80	
Gln	Thr	Tyr	Asp	Phe	Val	Lys	Lys	Met	Arg	Lys	Glu	Tyr	Gly	Lys	Leu
				85				90						95	
Asn	Lys	Met	Glu	Met	Ser	Ile	Trp	Glu	Cys	Cys	Glu	Leu	Leu	Asn	Asn
				100				105						110	

Val	Val	Asp	Glu	Ser	Asp	Pro	Asp	Leu	Asp	Glu	Pro	Gln	Ile	Gln	His
		115					120					125			
Leu	Leu	Gln	Thr	Ala	Glu	Ala	Ile	Arg	Arg	Asp	Tyr	Pro	Asp	Glu	Asp
		130				135					140				
Trp	Leu	His	Leu	Thr	Ala	Leu	Ile	His	Asp	Leu	Gly	Lys	Val	Leu	Leu
		145				150				155					160
Leu	Pro	Glu	Phe	Gly	Gly	Leu	Pro	Gln	Trp	Ala	Val	Val	Gly	Asp	Thr
				165					170					175	
Phe	Pro	Val	Gly	Cys	Thr	Phe	Asp	Ser	Ala	Asn	Ile	His	His	Lys	Tyr
				180				185					190		
Phe	Lys	Gly	Asn	His	Asp	Ile	Asn	Asn	Pro	Lys	Tyr	Asn	Thr	Lys	Asn
		195					200					205			
Gly	Val	Tyr	Thr	Glu	Gly	Cys	Gly	Leu	Asp	Asn	Val	Leu	Met	Ser	Trp
		210				215					220				
Gly	His	Asp	Asp	Tyr	Met	Tyr	Leu	Val	Ala	Lys	Lys	Asn	Gly	Thr	Thr
		225				230				235					240
Leu	Pro	His	Ala	Gly	Leu	Phe	Ile	Ile	Arg	Tyr	His	Ser	Phe	Tyr	Pro
				245					250					255	
Leu	His	Lys	Ala	Gly	Ala	Tyr	Thr	His	Leu	Met	Asn	Asp	Glu	Asp	Arg
			260					265					270		
Asp	Asp	Leu	Lys	Trp	Leu	His	Val	Phe	Asn	Lys	Tyr	Asp	Leu	Tyr	Ser
		275					280					285			
Lys	Ser	Lys	Val	Leu	Val	Asp	Val	Glu	Gln	Val	Lys	Pro	Tyr	Tyr	Ile
		290				295					300				
Ser	Leu	Ile	Asn	Lys	Tyr	Phe	Pro	Ala	Lys	Leu	Lys	Trp			
		305			310					315					

(2) INFORMATION FOR SEQ ID NO:2265:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 269 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..269

(D) OTHER INFORMATION: / Ceres Seq. ID 1572351

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2265:

Met	Asn	Phe	Leu	Gly	His	Ser	Phe	Arg	Asp	Tyr	Glu	Asn	Asp	Glu	Ser
				5					10					15	
Glu	Arg	Gln	Gln	Gly	Val	Glu	Glu	Phe	Tyr	Arg	Met	Gln	His	Ile	His
			20					25					30		
Gln	Thr	Tyr	Asp	Phe	Val	Lys	Lys	Met	Arg	Lys	Glu	Tyr	Gly	Lys	Leu
		35				40					45				
Asn	Lys	Met	Glu	Met	Ser	Ile	Trp	Glu	Cys	Cys	Glu	Leu	Leu	Asn	Asn
		50				55					60				
Val	Val	Asp	Glu	Ser	Asp	Pro	Asp	Leu	Asp	Glu	Pro	Gln	Ile	Gln	His
		65			70				75					80	
Leu	Leu	Gln	Thr	Ala	Glu	Ala	Ile	Arg	Arg	Asp	Tyr	Pro	Asp	Glu	Asp
			85					90						95	
Trp	Leu	His	Leu	Thr	Ala	Leu	Ile	His	Asp	Leu	Gly	Lys	Val	Leu	Leu
			100					105					110		
Leu	Pro	Glu	Phe	Gly	Gly	Leu	Pro	Gln	Trp	Ala	Val	Val	Gly	Asp	Thr
		115				120						125			
Phe	Pro	Val	Gly	Cys	Thr	Phe	Asp	Ser	Ala	Asn	Ile	His	His	Lys	Tyr
		130				135					140				
Phe	Lys	Gly	Asn	His	Asp	Ile	Asn	Asn	Pro	Lys	Tyr	Asn	Thr	Lys	Asn
		145			150					155				160	
Gly	Val	Tyr	Thr	Glu	Gly	Cys	Gly	Leu	Asp	Asn	Val	Leu	Met	Ser	Trp
			165					170						175	
Gly	His	Asp	Asp	Tyr	Met	Tyr	Leu	Val	Ala	Lys	Lys	Asn	Gly	Thr	Thr

180 185 190
Leu Pro His Ala Gly Leu Phe Ile Arg Tyr His Ser Phe Tyr Pro
195 200 205
Leu His Lys Ala Gly Ala Tyr Thr His Leu Met Asn Asp Glu Asp Arg
210 215 220
Asp Asp Leu Lys Trp Leu His Val Phe Asn Lys Tyr Asp Leu Tyr Ser
225 230 235 240
Lys Ser Lys Val Leu Val Asp Val Glu Gln Val Lys Pro Tyr Tyr Ile
245 250 255
Ser Leu Ile Asn Lys Tyr Phe Pro Ala Lys Leu Lys Trp
260 265

(2) INFORMATION FOR SEQ ID NO:2266:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 242 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..242

(D) OTHER INFORMATION: / Ceres Seq. ID 1572352

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2266:

Met Gln His Ile His Gln Thr Tyr Asp Phe Val Lys Lys Met Arg Lys
1 5 10 15
Glu Tyr Gly Lys Leu Asn Lys Met Glu Met Ser Ile Trp Glu Cys Cys
20 25 30
Glu Leu Leu Asn Asn Val Val Asp Glu Ser Asp Pro Asp Leu Asp Glu
35 40 45
Pro Gln Ile Gln His Leu Leu Gln Thr Ala Glu Ala Ile Arg Arg Asp
50 55 60
Tyr Pro Asp Glu Asp Trp Leu His Leu Thr Ala Leu Ile His Asp Leu
65 70 75 80
Gly Lys Val Leu Leu Pro Glu Phe Gly Gly Leu Pro Gln Trp Ala
85 90 95
Val Val Gly Asp Thr Phe Pro Val Gly Cys Thr Phe Asp Ser Ala Asn
100 105 110
Ile His His Lys Tyr Phe Lys Gly Asn His Asp Ile Asn Asn Pro Lys
115 120 125
Tyr Asn Thr Lys Asn Gly Val Tyr Thr Glu Gly Cys Gly Leu Asp Asn
130 135 140
Val Leu Met Ser Trp Gly His Asp Asp Tyr Met Tyr Leu Val Ala Lys
145 150 155 160
Lys Asn Gly Thr Thr Leu Pro His Ala Gly Leu Phe Ile Ile Arg Tyr
165 170 175
His Ser Phe Tyr Pro Leu His Lys Ala Gly Ala Tyr Thr His Leu Met
180 185 190
Asn Asp Glu Asp Arg Asp Asp Leu Lys Trp Leu His Val Phe Asn Lys
195 200 205
Tyr Asp Leu Tyr Ser Lys Ser Lys Val Leu Val Asp Val Glu Gln Val
210 215 220
Lys Pro Tyr Tyr Ile Ser Leu Ile Asn Lys Tyr Phe Pro Ala Lys Leu
225 230 235 240
Lys Trp

(2) INFORMATION FOR SEQ ID NO:2267:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 629 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..629

(D) OTHER INFORMATION: / Ceres Seq. ID 1572364

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2267:

atccgatttt	attgttttga	taagttcgtg	tcgtcttcgt	ctctctaacc	caattctgtg	60
gtgtctgaag	aaagcagaat	caaaAtccat	gtctttcaga	ggacttagca	ggccaaatgc	120
aatatctgga	atgggtgttg	cagatgagag	caaaaccaca	ttcttagagc	ttcaaaaggaa	180
aaaaactcat	cgctatgttg	ctttcaagat	tgatgaatcc	aaaaaagaag	ttgttgttga	240
aaaaactgga	aacctacag	agagctacga	tgatttctta	gcttcacttc	ctgataatga	300
ctgcagatac	gctgtttatg	acttcgattt	cgttacttot	gagaattgtc	aaaagagcaa	360
aatcttcttc	ttttcttggt	ctccttcgac	ttctccagtt	cgggcgaagg	tgctttactc	420
gacttctaaa	gaccacgctaa	gtaaggagct	tcaagggatt	cactatgaga	ttcaagctac	480
tgatcctact	gaggttgatc	ttgaagtgtt	acgcgaacga	gcgaactgag	agcaagcaag	540
attgctatgt	ctattcaaaa	cttatggtaa	tgtaatgaat	aattcgtatt	ctctgtggat	600
tgattttgtg	aaacacagtt	tcattgttcc				

(2) INFORMATION FOR SEQ ID NO:2268:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 175 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..175

(D) OTHER INFORMATION: / Ceres Seq. ID 1572365

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2268:

Ser	Asp	Phe	Ile	Cys	Leu	Ile	Ser	Ser	Cys	Arg	Leu	Arg	Leu	Ser	Asn	
1				5					10						15	
Pro	Ile	Leu	Trp	Cys	Leu	Lys	Lys	Ala	Glu	Ser	Lys	Ser	Met	Ser	Phe	
			20						25						30	
Arg	Gly	Leu	Ser	Arg	Pro	Asn	Ala	Ile	Ser	Gly	Met	Gly	Val	Ala	Asp	
			35				40						45			
Glu	Ser	Lys	Thr	Thr	Phe	Leu	Glu	Leu	Gln	Arg	Lys	Lys	Thr	His	Arg	
			50				55						60			
Tyr	Val	Val	Phe	Lys	Ile	Asp	Glu	Ser	Lys	Lys	Glu	Val	Val	Val	Glu	
			65			70					75				80	
Lys	Thr	Gly	Asn	Pro	Thr	Glu	Ser	Tyr	Asp	Asp	Phe	Leu	Ala	Ser	Leu	
			85						90						95	
Pro	Asp	Asn	Asp	Cys	Arg	Tyr	Ala	Val	Tyr	Asp	Phe	Asp	Phe	Val	Thr	
			100					105						110		
Ser	Glu	Asn	Cys	Gln	Lys	Ser	Lys	Ile	Phe	Phe	Phe	Ser	Trp	Ser	Pro	
			115					120					125			
Ser	Thr	Ser	Pro	Val	Arg	Ala	Lys	Val	Leu	Tyr	Ser	Thr	Ser	Lys	Asp	
			130				135					140				
Gln	Leu	Ser	Lys	Glu	Leu	Gln	Gly	Ile	His	Tyr	Glu	Ile	Gln	Ala	Thr	
			145				150				155				160	
Asp	Pro	Thr	Glu	Val	Asp	Leu	Glu	Val	Leu	Arg	Glu	Arg	Ala	Asn		
			165						170					175		

(2) INFORMATION FOR SEQ ID NO:2269:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 146 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..146

(D) OTHER INFORMATION: / Ceres Seq. ID 1572366

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2269:

Met Ser Phe Arg Gly Leu Ser Arg Pro Asn Ala Ile Ser Gly Met Gly
1 5 10 15
Val Ala Asp Glu Ser Lys Thr Thr Phe Leu Glu Leu Gln Arg Lys Lys
20 25 30
Thr His Arg Tyr Val Val Phe Lys Ile Asp Glu Ser Lys Lys Glu Val
35 40 45
Val Val Glu Lys Thr Gly Asn Pro Thr Glu Ser Tyr Asp Asp Phe Leu
50 55 60
Ala Ser Leu Pro Asp Asn Asp Cys Arg Tyr Ala Val Tyr Asp Phe Asp
65 70 75 80
Phe Val Thr Ser Glu Asn Cys Gln Lys Ser Lys Ile Phe Phe Phe Ser
85 90 95
Trp Ser Pro Ser Thr Ser Pro Val Arg Ala Lys Val Leu Tyr Ser Thr
100 105 110
Ser Lys Asp Gln Leu Ser Lys Glu Leu Gln Gly Ile His Tyr Glu Ile
115 120 125
Gln Ala Thr Asp Pro Thr Glu Val Asp Leu Glu Val Leu Arg Glu Arg
130 135 140
Ala Asn
145

(2) INFORMATION FOR SEQ ID NO:2270:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 132 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..132

(D) OTHER INFORMATION: / Ceres Seq. ID 1572367

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2270:

Met Gly Val Ala Asp Glu Ser Lys Thr Thr Phe Leu Glu Leu Gln Arg
1 5 10 15
Lys Lys Thr His Arg Tyr Val Val Phe Lys Ile Asp Glu Ser Lys Lys
20 25 30
Glu Val Val Val Glu Lys Thr Gly Asn Pro Thr Glu Ser Tyr Asp Asp
35 40 45
Phe Leu Ala Ser Leu Pro Asp Asn Asp Cys Arg Tyr Ala Val Tyr Asp
50 55 60
Phe Asp Phe Val Thr Ser Glu Asn Cys Gln Lys Ser Lys Ile Phe Phe
65 70 75 80
Phe Ser Trp Ser Pro Ser Thr Ser Pro Val Arg Ala Lys Val Leu Tyr
85 90 95
Ser Thr Ser Lys Asp Gln Leu Ser Lys Glu Leu Gln Gly Ile His Tyr
100 105 110
Glu Ile Gln Ala Thr Asp Pro Thr Glu Val Asp Leu Glu Val Leu Arg
115 120 125
Glu Arg Ala Asn
130

(2) INFORMATION FOR SEQ ID NO:2271:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 798 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -

(B) LOCATION: 1.798

(D) OTHER INFORMATION: / Ceres Seq. ID 1572368

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2271:

ttgtcaaaag	ctgattcttc	gccttatggc	atcgattttg	caccttcgaa	cgcccaaccc	60
acggggaagat	tcactaatgg	tcgaaccatt	tccgatattg	tggtggaagc	cttaggagca	120
aaatcaccac	caccaccata	tcttgaacca	aaactaggag	ctaacacaa	tctcaattgga	180
atcaactatg	cttctgggtc	tgctggaatc	ttggacgaca	ctgactctct	gggtcattcgg	240
ggcgagttcc	gctgagagaa	caagtgaagta	attttgagaa	gagtagagaa	tatatgtgtaa	300
gcgtgattgg	tgaaaatgtg	acaaaagaga	tgttgaagaa	tgcaatgttc	acaatcacaa	360
ttggatcaaa	tgaatttttg	aattatattc	aaccatcaat	acctttcttc	tctcaagaca	420
agctccccc	tgaatgtcct	acaagattcc	atggctctcc	atttTaaaca	cacatcttaa	480
gcgattgcac	cagctaggag	tgaaggaagt	cgtggttggt	ggagtagggc	cacctggttg	540
cataactctt	gctcgagcgt	tgaatttwat	accagccgga	aaatgctccg	aacaAgTcaa	600
ccaagtacgt	CgaggtTata	acatgaAgct	tataactct	cttaagacat	tgaacaatga	660
gttaagatcc	gaagattaca	acactacatt	tgtctacgcc	aactcttacg	acctattctt	720
gaaactagtt	ttgaactatc	aactatttgg	cttgaagaac	gcagacaagc	cgtgtgtgtg	780
cggtactttt	ccaccgtt					

(2) INFORMATION FOR SEQ ID NO:2272:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 84 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1.84

(D) OTHER INFORMATION: / Ceres Seq. ID 1572369

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2272:

Leu	Ser	Lys	Ala	Asp	Ser	Ser	Pro	Tyr	Gly	Ile	Asp	Phe	Ala	Pro	Ser	
1				5				10					15			
Asn	Gly	Gln	Pro	Thr	Gly	Arg	Phe	Thr	Asn	Gly	Arg	Thr	Ile	Ser	Asp	
			20					25					30			
Ile	Val	Gly	Glu	Ala	Leu	Gly	Ala	Lys	Ser	Pro	Pro	Pro	Pro	Tyr	Leu	
			35					40					45			
Glu	Pro	Asn	Thr	Glu	Ala	Asn	Thr	Ile	Leu	Asn	Gly	Ile	Asn	Tyr	Ala	
			50					55					60			
Ser	Gly	Ala	Ala	Gly	Ile	Leu	Asp	Asp	Thr	Gly	Leu	Leu	Val	His	Arg	
			65					70					75		80	
Gly	Glu	Phe	Arg													

(2) INFORMATION FOR SEQ ID NO:2273:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 121 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1.121

(D) OTHER INFORMATION: / Ceres Seq. ID 1572370

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2273:

Met	Ser	Tyr	Lys	Ile	Pro	Trp	Ser	Ser	Ile	Leu	Thr	Thr	His	Leu	Lys	
1			5					10					15			
Arg	Leu	His	Gln	Leu	Gly	Gly	Arg	Lys	Phe	Val	Val	Val	Gly	Val	Gly	
			20					25					30			
Pro	Leu	Gly	Cys	Ile	Pro	Phe	Ala	Arg	Ala	Leu	Asn	Xaa	Ile	Pro	Ala	
			35					40					45			
Gly	Lys	Cys	Ser	Glu	Gln	Val	Asn	Gln	Val	Val	Arg	Gly	Tyr	Asn	Met	
			50					55					60			

Lys Leu Ile His Ser Leu Lys Thr Leu Asn Asn Glu Leu Arg Ser Glu
65 70 75 80
Asp Tyr Asn Thr Thr Phe Val Tyr Ala Asn Ser Tyr Asp Leu Phe Leu
85 90 95
Lys Leu Val Leu Asn Tyr Gln Leu Phe Gly Leu Lys Asn Ala Asp Lys
100 105 110
Pro Cys Cys Gly Gly Tyr Phe Pro Pro
115 120

(2) INFORMATION FOR SEQ ID NO:2274:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1080 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1080

(D) OTHER INFORMATION: / Ceres Seq. ID 1572375

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2274:

gatcacaaaa aattagaatc atggaggctc agagagacca gcacaagcct ccgttgtctc 60
tacaagaacaa caaatcccca tcatcacaaa acttccagct cgtcgacctc agcaacacca 120
atggggagct cgtggcgctg aaagtggcaa agcgagcgca agagtgggga attttcagg 180
tagttaacca cgggatccca acogaactaa tccggagggt gcacaagggt gatacacagt 240
tctttgagct cccagagtcc aagaagaag cgtggcccaa accagcgaa cccaaagaga 300
tacaaggata tgagattgat gatgtacaag gtagaaggag tcatatcttc cataatctat 360
atcatcatc gtacgtcaat tatgattctt ggcctaagaa tctctcgtga tacagagagg 420
tgactgagga gtttgcaaa cgtgcaaaag agctagcgga agagatcttc cgtttgctat 480
ccgaagKtt aggtttacaa cgtgagatgt tgaagttagc attcggggag gatagtgtgt 540
gttatcttat gaagatcaac tattaccggt cgtgtccaga gccagattgg gtcattggaa 600
taaaagccca cactgatttc aatgaactca cacttctcat tcccaatgaa attttcggac 660
ttcaagtgtt caaggaagac cgtcggcttg atgtagatta tatatattccc gcggttatta 720
tcatcatcgg agatcagatc atgaagatga gcaacggaag gtacaacaat gtgttgcata 780
gaaccttgat ggataaaaa aaaaacgagga tgtgtcggt ggttcatatc aagcctcctt 840
atgatattgt tgtgaagcca ttcccgaac tcaccagcgg cgataaatctt cccaagttag 900
agcctttaac ttaccaggat tacatagaca ttgaagtcct caagctttct cgactgatca 960
agaattgact tctttgtcgt tgtatgtatg ttgtttgttg ttgtctctgt tcatttggcc 1020
gtttgcatc gtgtgaacgg gtttctatta attgaagttc aaacaaaaaa aatttgactc 1080

(2) INFORMATION FOR SEQ ID NO:2275:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 321 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..321

(D) OTHER INFORMATION: / Ceres Seq. ID 1572376

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2275:

Ser Gln Lys Ile Arg Ile Met Glu Val Glu Arg Asp Gln His Lys Pro
1 5 10 15
Pro Leu Ser Leu Gln Asn Asn Lys Ile Pro Ser Ser Gln Asn Phe Pro
20 25 30
Val Val Asp Leu Ser Asn Thr Asn Gly Glu Leu Val Ala Arg Lys Val
35 40 45
Ala Lys Ala Ser Glu Glu Trp Gly Ile Phe Gln Val Val Asn His Gly
50 55 60
Ile Pro Thr Glu Leu Ile Arg Arg Leu His Lys Val Asp Thr Gln Phe
65 70 75 80

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Phe Glu Leu Pro Glu Ser Lys Lys Glu Ala Val Ala Lys Pro Ala Asn
      85                      90                      95
Ser Lys Glu Ile Gln Gly Tyr Glu Met Asp Asp Val Gln Gly Arg Arg
      100                      105                      110
Ser His Ile Phe His Asn Leu Tyr Pro Ser Ser Ser Val Asn Tyr Ala
      115                      120                      125
Phe Trp Pro Lys Asn Pro Pro Glu Tyr Arg Glu Val Thr Glu Glu Phe
      130                      135                      140
Ala Lys His Ala Lys Gln Leu Ala Glu Glu Ile Leu Gly Leu Leu Ser
      145                      150                      155                      160
Glu Xaa Leu Gly Leu Gln Arg Glu Met Leu Lys Leu Ala Phe Gly Asp
      165                      170                      175
Asp Ser Ala Gly Tyr Leu Met Lys Ile Asn Tyr Tyr Arg Pro Cys Pro
      180                      185                      190
Glu Pro Asp Trp Val Met Gly Ile Lys Ala His Thr Asp Phe Asn Glu
      195                      200                      205
Leu Thr Leu Leu Ile Pro Asn Glu Ile Phe Gly Leu Gln Val Phe Lys
      210                      215                      220
Glu Asp Arg Trp Leu Asp Val Asp Tyr Ile Tyr Pro Ala Val Ile Ile
      225                      230                      235                      240
Ile Ile Gly Asp Gln Ile Met Lys Met Ser Asn Gly Arg Tyr Asn Asn
      245                      250                      255
Val Leu His Arg Thr Leu Met Asp Lys Lys Thr Arg Met Ser Ser
      260                      265                      270
Val Val His Ile Lys Pro Pro Tyr Asp Met Val Val Lys Pro Phe Pro
      275                      280                      285
Glu Leu Thr Ser Gly Asp Asn Pro Pro Lys Phe Glu Pro Leu Thr Tyr
      290                      295                      300
Gln Asp Tyr Ile Asp Ile Glu Val Pro Lys Leu Ser Arg Leu Ile Lys
      305                      310                      315                      320
Asn

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(2) INFORMATION FOR SEQ ID NO:2276:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 315 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..315
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572377

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2276:

```

Met Glu Val Glu Arg Asp Gln His Lys Pro Pro Leu Ser Leu Gln Asn
1      5                      10                      15
Asn Lys Ile Pro Ser Ser Gln Asn Phe Pro Val Val Asp Leu Ser Asn
      20                      25                      30
Thr Asn Gly Glu Leu Val Ala Arg Lys Val Ala Lys Ala Ser Glu Glu
      35                      40                      45
Trp Gly Ile Phe Gln Val Val Asn His Gly Ile Pro Thr Glu Leu Ile
      50                      55                      60
Arg Arg Leu His Lys Val Asp Thr Gln Phe Phe Glu Leu Pro Glu Ser
      65                      70                      75                      80
Lys Lys Glu Ala Val Ala Lys Pro Ala Asn Ser Lys Glu Ile Gln Gly
      85                      90                      95
Tyr Glu Met Asp Asp Val Gln Gly Arg Arg Ser His Ile Phe His Asn
      100                      105                      110
Leu Tyr Pro Ser Ser Ser Val Asn Tyr Ala Phe Trp Pro Lys Asn Pro
      115                      120                      125
Pro Glu Tyr Arg Glu Val Thr Glu Glu Phe Ala Lys His Ala Lys Gln

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130	135	140
Leu Ala Glu Glu Ile	Leu Gly Leu Leu Ser	Glu Xaa Leu Gly Leu Gln
145	150	155
Arg Glu Met Leu Lys	Leu Ala Phe Gly Asp	Asp Ser Ala Gly Tyr Leu
165	170	175
Met Lys Ile Asn Tyr	Tyr Arg Pro Cys Pro	Glu Pro Asp Trp Val Met
180	185	190
Gly Ile Lys Ala His	Thr Asp Phe Asn Glu Leu Thr	Leu Leu Ile Pro
195	200	205
Asn Glu Ile Phe Gly	Leu Gln Val Phe Lys Glu Asp	Arg Trp Leu Asp
210	215	220
Val Asp Tyr Ile Tyr	Pro Ala Val Ile Ile	Ile Gly Asp Gln Ile
225	230	235
Met Lys Met Ser Asn	Gly Arg Tyr Asn Asn Val	Leu His Arg Thr Leu
245	250	255
Met Asp Lys Lys Lys	Thr Arg Met Ser Ser Val	Val His Ile Lys Pro
260	265	270
Pro Tyr Asp Met Val	Val Lys Pro Phe Pro Glu	Leu Thr Ser Gly Asp
275	280	285
Asn Pro Pro Lys Phe	Glu Pro Leu Thr Tyr Gln	Asp Tyr Ile Asp Ile
290	295	300
Glu Val Pro Lys Leu	Ser Arg Leu Ile Lys Asn	
305	310	315

(2) INFORMATION FOR SEQ ID NO:2277:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 217 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..217

(D) OTHER INFORMATION: / Ceres Seq. ID 1572378

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2277:

Met Asp Asp Val Gln Gly Arg Arg Ser His Ile Phe His Asn Leu Tyr	1	5	10	15
Pro Ser Ser Ser Val Asn Tyr Ala Phe Trp Pro Lys Asn Pro Pro Glu	20	25	30	
Tyr Arg Glu Val Thr Glu Glu Phe Ala Lys His Ala Lys Gln Leu Ala	35	40	45	
Glu Glu Ile Leu Gly Leu Leu Ser Glu Xaa Leu Gly Leu Gln Arg Glu	50	55	60	
Met Leu Lys Leu Ala Phe Gly Asp Asp Ser Ala Gly Tyr Leu Met Lys	65	70	75	80
Ile Asn Tyr Tyr Arg Pro Cys Pro Glu Pro Asp Trp Val Met Gly Ile	85	90	95	
Lys Ala His Thr Asp Phe Asn Glu Leu Thr Leu Leu Ile Pro Asn Glu	100	105	110	
Ile Phe Gly Leu Gln Val Phe Lys Glu Asp Arg Trp Leu Asp Val Asp	115	120	125	
Tyr Ile Tyr Pro Ala Val Ile Ile Ile Gly Asp Gln Ile Met Lys	130	135	140	
Met Ser Asn Gly Arg Tyr Asn Asn Val Leu His Arg Thr Leu Met Asp	145	150	155	160
Lys Lys Lys Thr Arg Met Ser Ser Val Val His Ile Lys Pro Pro Tyr	165	170	175	
Asp Met Val Val Lys Pro Phe Pro Glu Leu Thr Ser Gly Asp Asn Pro	180	185	190	
Pro Lys Phe Glu Pro Leu Thr Tyr Gln Asp Tyr Ile Asp Ile Glu Val	195	200	205	

Pro Lys Leu Ser Arg Leu Ile Lys Asn
210 215

(2) INFORMATION FOR SEQ ID NO:2278:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 729 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..729
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572397

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2278:

acactcatct	octaattccc	ttacataata	ttttcttaag	ataagcaaaa	aatcatggcg	60
agaagcgctc	agtttgggtg	ggaaacttga	gacagaagtg	gagatcaaa	cttcggccaa	120
aaagttccat	cacatgttta	ccgagagacc	acaccatgtc	tccaaagcaa	ctccagataa	180
aattcatgga	tgtgagctgc	acgaaggcga	ctggggccaa	gtcggctcta	tcgtcatctg	240
gaaatacgtt	catgatggaa	agttacacgt	ggggaagaat	aagatcgagg	cggtggatcc	300
ggagaagaac	ctgatcacgt	tcaaggtttt	agaaggtgat	ctgatgaatg	agtacaagag	360
cttcgcattt	acactccaag	tgacccttaa	gcaaggggag	tcaggaggta	ttgcgcactg	420
gcacctggag	tatgagaaaa	ttagcggagg	ggtagctcat	cccgaacc	ttctccaatt	480
ctgtgtcgag	atctccaaag	agatcgacga	acatctcttg	gccgaggaat	agaaaaatac	540
tcctcgtctg	tgtgtgggtc	tttgaactt	aagcaagtc	ttgaaactgc	aataataaat	600
gaacgggtcg	gtctttatgt	aagagaaaa	agatatatat	atatgtgttg	gtgtgtgtaa	660
tgctgttatg	ctactacta	cggttgagtt	atgttggaa	agtaaaaRgc	atataatcta	720
ttttgtcc						

(2) INFORMATION FOR SEQ ID NO:2279:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 158 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..158
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572398

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2279:

Met	Ala	Glu	Ala	Ser	Ser	Leu	Val	Gly	Lys	Leu	Glu	Thr	Glu	Val	Glu
1		5						10			15				
Ile	Lys	Ala	Ser	Ala	Lys	Lys	Phe	His	His	Met	Phe	Thr	Glu	Arg	Pro
		20						25				30			
His	His	Val	Ser	Lys	Ala	Thr	Pro	Asp	Lys	Ile	His	Gly	Cys	Glu	Leu
		35						40				45			
His	Glu	Gly	Asp	Trp	Gly	Lys	Val	Gly	Ser	Ile	Val	Ile	Trp	Lys	Tyr
		50						55			60				
Val	His	Asp	Gly	Lys	Leu	Thr	Val	Gly	Lys	Asn	Lys	Ile	Glu	Ala	Val
		65						70			75			80	
Asp	Pro	Glu	Lys	Asn	Leu	Ile	Thr	Phe	Lys	Val	Leu	Glu	Gly	Asp	Leu
		85						90					95		
Met	Asn	Glu	Tyr	Lys	Ser	Phe	Ala	Phe	Thr	Leu	Gln	Val	Thr	Pro	Lys
		100						105				110			
Gln	Gly	Glu	Ser	Gly	Ser	Ile	Ala	His	Trp	His	Leu	Glu	Tyr	Glu	Lys
		115						120				125			
Ile	Ser	Glu	Glu	Val	Ala	His	Pro	Glu	Thr	Leu	Leu	Gln	Phe	Cys	Val
		130						135				140			
Glu	Ile	Ser	Lys	Glu	Ile	Asp	Glu	His	Leu	Leu	Ala	Glu	Glu		
		145						150				155			

(2) INFORMATION FOR SEQ ID NO:2280:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 132 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..132
(D) OTHER INFORMATION: / Ceres Seq. ID 1572399
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2280:
Met Phe Thr Glu Arg Pro His His Val Ser Lys Ala Thr Pro Asp Lys
1 5 10 15
Ile His Gly Cys Glu Leu His Glu Gly Asp Trp Gly Lys Val Gly Ser
20 25 30
Ile Val Ile Trp Lys Tyr Val His Asp Gly Lys Leu Thr Val Gly Lys
35 40 45
Asn Lys Ile Glu Ala Val Asp Pro Glu Lys Asn Leu Ile Thr Phe Lys
50 55 60
Val Leu Glu Gly Asp Leu Met Asn Glu Tyr Lys Ser Phe Ala Phe Thr
65 70 75 80
Leu Gln Val Thr Pro Lys Gln Gly Glu Ser Gly Ser Ile Ala His Trp
85 90 95
His Leu Glu Tyr Glu Lys Ile Ser Glu Val Ala His Pro Glu Thr
100 105 110
Leu Leu Gln Phe Cys Val Glu Ile Ser Lys Glu Ile Asp Glu His Leu
115 120 125
Leu Ala Glu Glu
130

(2) INFORMATION FOR SEQ ID NO:2281:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 572 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..572

(D) OTHER INFORMATION: / Ceres Seq. ID 1572400

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2281:

attcataaat	ctctcaaaag	aagaactaag	agctttacta	cagtcctact	ctctacacat	60
cttctcttct	ctctcaagag	ctagtcgatg	ccaaactcat	aacttttttt	ctcttaactca	120
caattttatt	caactttcgt	tgtctcacta	tgtcaaaaaga	agctgagtag	catccagaaa	180
gtgtgaagttt	ttattttttg	gtaaaaataga	aagttatgga	ccagggaagtc	tgaatcatca	240
ccaatgtgga	ggacaatgca	caaggagatg	tagcaataca	aagtatcata	agccatgcac	300
gttctcttcgc	caaaaagtgt	gtgctaagt	cctttgtgtc	cctccaggca	cgtacggcaa	360
caaaacaagt	tgtctcttgt	acaacaactg	gaagactcaa	caaggtggac	caaaatgtcc	420
ataaacaaaa	agagagaaaac	ccaatctgt	ttctattttt	atttaattat	ttccagtagt	480
cttttgttgt	cgtgatggtt	aaattatagt	gtttttgcag	gtatcattta	tcatcgataa	540
acaatatcat	ataaaaattct	ctatgtttct	tg			

(2) INFORMATION FOR SEQ ID NO:2282:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..40

(D) OTHER INFORMATION: / Ceres Seq. ID 1572401

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2282:

Met Ala Lys Leu Ile Thr Ser Phe Leu Leu Thr Ile Leu Phe Thr
1 5 10 15
Phe Val Cys Leu Thr Met Ser Lys Glu Ala Glu Tyr His Pro Glu Ser
20 25 30
Val Ser Phe Tyr Phe Leu Val Lys
35 40

(2) INFORMATION FOR SEQ ID NO:2283:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..41
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572402

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2283:

Met Phe Phe Cys Gln Lys Cys Cys Ala Lys Cys Leu Cys Val Pro Pro
1 5 10 15
Gly Thr Tyr Gly Asn Lys Gln Val Cys Pro Cys Tyr Asn Asn Trp Lys
20 25 30
Thr Gln Gln Gly Gly Pro Lys Cys Pro
35 40

(2) INFORMATION FOR SEQ ID NO:2284:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 55 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..55
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572403

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2284:

Met Pro Leu Cys Pro Ser Arg His Val Arg Gln Gln Thr Ser Val Ser
1 5 10 15
Leu Leu Gln Gln Leu Glu Asp Ser Thr Arg Trp Thr Lys Met Ser Ile
20 25 30
Asn Lys Lys Arg Glu Thr Pro Ile Cys Phe Leu Phe Tyr Leu Ile Ile
35 40 45
Ser Ser Met Leu Leu Leu Ser
50 55

(2) INFORMATION FOR SEQ ID NO:2285:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1459 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1459
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572404

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2285:

cggagggtgat cggttgctct tgggtaaatg aagctgccac gaattggcgt atttagatt 60
gatacgctcaa agctcctctc cgcgcacgtt agctaaagga atgtcttgta ctctttttgt 120
tggtgtgtgtt gattttttga acaagaaaag aaactaatca aaaagacgaa gaggaagagg 180
aagctcacccg tttctatctc tcattttaac cactgatctt ctcgattgc gtcttgcttc 240

tcgtcggttg	cttcgcgatc	ctctctggat	ttcttcaatt	tcgtacggat	taggttaatt	300
gtgtataaag	gagtttagtt	gatcatttgt	ttgtacattt	gggtagatga	tgcgtactgt	360
tgctttacca	ttgtcccatg	atctgaatgt	tcataagatc	catgaagctt	ctggattcca	420
taatagtgtc	gctggtaaaa	atcgtgtgta	tctgactcgg	actggttctt	catcatgtgc	480
cacgagacaa	gacgttttga	gtcttcagct	actagagagc	ttgagtgggt	caatagtacc	540
tgtatcatct	agggtgtaag	catttgtttg	ccggtcagct	ctctctctcg	ggaatggaaa	600
tgaaggccct	attcttaaat	caactgcagt	aattattcaca	agggttatatg	atgcttttag	660
tggaaatcct	catttagtga	aactaattcc	agcgggtggg	attcttgcat	tgtctacatg	720
gggtcttaga	ccccttctgc	gccttgccag	aactaccctg	tttgagaagg	ggaatgatgc	780
aaatttcacag	aagagttagca	cgcagtagat	tgttgtgtca	tatcttcaac	ctttgctgct	840
ttggagcgga	gcaattccttt	tatgcagaac	attggaccaca	atagattatgc	cttcaagtgc	900
cggccaggtc	attaaacagc	gtcttctgat	ctttgctcgg	tccatatcaa	cgggtgtggc	960
attttctctgc	tgtttatcaa	gcctacttca	gcagggtcag	aaatttttta	tggagacaaa	1020
taatcctctg	gataccagaa	atatgggttt	cagttttgct	ggaaaagctg	tttacaactg	1080
tcgctgggtt	gctgtgctgt	cattgtttat	ggaaactgtta	ggcttctcta	ccccaaaagt	1140
gcataacggt	gggggtctcg	ggacagtact	gctaactctt	gctggccctg	agataactact	1200
taactttctt	tcaagcatta	tgatttcagc	tacacggccc	tttgttctga	atgagtggat	1260
ccagaccaag	ataggaggct	atgaagtctt	tggcacagta	gagcaagctg	gttggtggct	1320
acctacaatt	atcagagggt	atgaccggga	agcagttcat	attcctaacc	accagttcag	1380
tgtaaatatt	gtgagaatac	tcactcagaa	gacgcattgg	cgcatacaaa	cacatcttgc	1440
catcagtcac	cttgatgtc					

(2) INFORMATION FOR SEQ ID NO:2286:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 372 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..372

(D) OTHER INFORMATION: / Ceres Seq. ID 1572405

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2286:

Met	Met	Met	Arg	Thr	Val	Ala	Leu	Pro	Leu	Ser	His	Asp	Leu	Asn	Val
1			5					10						15	
His	Lys	Ile	His	Glu	Ala	Ser	Gly	Phe	His	Asn	Ser	Ala	Ala	Gly	Lys
			20				25						30		
Asn	Arg	Val	Tyr	Leu	Thr	Arg	Thr	Gly	Leu	Ser	Ser	Cys	Ala	Thr	Arg
			35				40					45			
Gln	Asp	Val	Trp	Ser	Leu	Gln	Leu	Leu	Glu	Ser	Leu	Ser	Gly	Ser	Ile
			50				55					60			
Val	Pro	Val	Ser	Ser	Arg	Cys	Asn	Ala	Phe	Val	Cys	Arg	Ser	Ala	Leu
			65				70					75			80
Ser	Pro	Gly	Asn	Gly	Asn	Glu	Gly	Pro	Ile	Leu	Lys	Ser	Thr	Ala	Val
			85				90							95	
Ile	Phe	Thr	Arg	Val	Tyr	Asp	Ala	Leu	Gly	Gly	Asn	Pro	His	Leu	Val
			100				105						110		
Lys	Leu	Ile	Pro	Ala	Val	Gly	Ile	Leu	Ala	Phe	Ala	Thr	Thr	Gly	Leu
			115				120					125			
Arg	Pro	Leu	Leu	Arg	Leu	Ala	Arg	Thr	Thr	Leu	Phe	Glu	Lys	Gly	Asn
			130				135					140			
Asp	Ala	Asn	Ser	Gln	Lys	Ser	Ser	Thr	Gln	Tyr	Ile	Val	Val	Ser	Tyr
			145				150				155			160	
Leu	Gln	Pro	Leu	Leu	Trp	Ser	Gly	Ala	Ile	Leu	Leu	Cys	Arg	Thr	
			165				170						175		
Leu	Asp	Pro	Ile	Val	Leu	Pro	Ser	Ser	Ala	Gly	Gln	Ala	Ile	Lys	Gln
			180				185						190		
Arg	Leu	Leu	Ile	Phe	Ala	Arg	Ser	Ile	Ser	Thr	Val	Leu	Ala	Phe	Ser
			195				200						205		
Cys	Cys	Leu	Ser	Ser	Leu	Gln	Gln	Val	Gln	Lys	Phe	Phe	Met	Glu	
			210				215						220		

Thr Asn Asn Pro Ala Asp Thr Arg Asn Met Gly Phe Ser Phe Ala Gly
225 230 235 240
Lys Ala Val Tyr Thr Thr Ala Ala Trp Val Ala Ala Ser Leu Phe Met
245 250 255
Glu Leu Leu Gly Phe Ser Thr Gln Lys Trp Leu Thr Ala Gly Gly Leu
260 265 270
Gly Thr Val Leu Leu Thr Leu Ala Gly Arg Glu Ile Leu Thr Asn Phe
275 280 285
Leu Ser Ser Ile Met Ile His Ala Thr Arg Pro Phe Val Leu Asn Glu
290 295 300
Trp Ile Gln Thr Lys Ile Gly Gly Tyr Glu Val Ser Gly Thr Val Glu
305 310 315 320
Gln Val Gly Trp Trp Ser Pro Thr Ile Ile Arg Gly Asp Asp Arg Glu
325 330 335
Ala Val His Ile Pro Asn His Gln Phe Ser Val Asn Ile Val Arg Asn
340 345 350
Leu Thr Gln Lys Thr His Trp Arg Ile Lys Thr His Leu Ala Ile Ser
355 360 365
His Leu Asp Val
370

(2) INFORMATION FOR SEQ ID NO:2287:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 371 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..371
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572406

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2287:

Met Met Arg Thr Val Ala Leu Pro Leu Ser His Asp Leu Asn Val His
1 5 10 15
Lys Ile His Glu Ala Ser Gly Phe His Asn Ser Ala Ala Gly Lys Asn
20 25 30
Arg Val Tyr Leu Thr Arg Thr Gly Leu Ser Ser Cys Ala Thr Arg Gln
35 40 45
Asp Val Trp Ser Leu Gln Leu Leu Glu Ser Leu Ser Gly Ser Ile Val
50 55 60
Pro Val Ser Ser Arg Cys Asn Ala Phe Val Cys Arg Ser Ala Leu Ser
65 70 75 80
Pro Gly Asn Gly Asn Glu Gly Pro Ile Leu Lys Ser Thr Ala Val Ile
85 90 95
Phe Thr Arg Val Tyr Asp Ala Leu Gly Gly Asn Pro His Leu Val Lys
100 105 110
Leu Ile Pro Ala Val Gly Ile Leu Ala Phe Ala Thr Trp Gly Leu Arg
115 120 125
Pro Leu Leu Arg Leu Ala Arg Thr Thr Leu Phe Glu Lys Gly Asn Asp
130 135 140
Ala Asn Ser Gln Lys Ser Ser Thr Gln Tyr Ile Val Val Ser Tyr Leu
145 150 155 160
Gln Pro Leu Leu Leu Trp Ser Gly Ala Ile Leu Leu Cys Arg Thr Leu
165 170 175
Asp Pro Ile Val Leu Pro Ser Ser Ala Gly Gln Ala Ile Lys Gln Arg
180 185 190
Leu Leu Ile Phe Ala Arg Ser Ile Ser Thr Val Leu Ala Phe Ser Cys
195 200 205
Cys Leu Ser Ser Leu Leu Gln Gln Val Gln Lys Phe Phe Met Glu Thr
210 215 220
Asn Asn Pro Ala Asp Thr Arg Asn Met Gly Phe Ser Phe Ala Gly Lys

(2) INFORMATION FOR SEQ ID NO:2288:

(A) LENGTH: 370 amino acids

(B) TYPE: amino acid

(B) TYPE: amino acid
(C) STRENGTHENING:

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..370

(D) OTHER INFORMATION: / Ceres Seq. ID 1572407

{xi} SEQUENCE DESCRIPTION: SEQ ID NO:2288:

Met	Arg	Thr	Val	Ala	Leu	Pro	Leu	Ser	His	Asp	Leu	Asn	Val	His	Lys
1				5					10					15	
Ile	His	Glu	Ala	Ser	Gly	Phe	His	Asn	Ser	Ala	Ala	Gly	Lys	Asn	Arg
			20					25					30		
Val	Tyr	Leu	Thr	Arg	Thr	Gly	Leu	Ser	Ser	Cys	Ala	Thr	Arg	Gln	Asp
		35					40					45			
Val	Trp	Ser	Leu	Gln	Leu	Leu	Glu	Ser	Leu	Ser	Gly	Ser	Ile	Val	Pro
		50				55					60				
Val	Ser	Ser	Arg	Cys	Asn	Ala	Phe	Val	Cys	Arg	Ser	Ala	Leu	Ser	Pro
65					70					75					80
Gly	Asn	Gly	Asn	Glu	Gly	Pro	Ile	Leu	Lys	Ser	Thr	Ala	Val	Ile	Phe
				85					90				95		
Thr	Arg	Val	Tyr	Asp	Ala	Leu	Gly	Gly	Asn	Pro	His	Leu	Val	Lys	Leu
				100				105					110		
Ile	Pro	Ala	Val	Gly	Ile	Leu	Ala	Phe	Ala	Thr	Trp	Gly	Leu	Arg	Pro
		115					120					125			
Leu	Leu	Arg	Leu	Ala	Arg	Thr	Thr	Leu	Phe	Glu	Lys	Gly	Asn	Asp	Ala
						135					140				
Asn	Ser	Gln	Lys	Ser	Ser	Thr	Gln	Tyr	Ile	Val	Val	Ser	Tyr	Leu	Gln
145					150					155					160
Pro	Leu	Leu	Leu	Trp	Ser	Gly	Ala	Ile	Leu	Leu	Cys	Arg	Thr	Leu	Asp
				165					170					175	
Pro	Ile	Val	Leu	Pro	Ser	Ser	Ala	Gly	Gln	Ala	Ile	Lys	Gln	Arg	Leu
			180					185					190		
Leu	Ile	Phe	Ala	Arg	Ser	Ile	Ser	Thr	Val	Leu	Ala	Phe	Ser	Cys	Cys
		195					200					205			
Leu	Ser	Ser	Leu	Leu	Gln	Gln	Val	Gln	Lys	Phe	Phe	Met	Glu	Thr	Asn
		210				215					220				
Asn	Pro	Ala	Asp	Thr	Arg	Asn	Met	Gly	Phe	Ser	Phe	Ala	Gly	Lys	Ala
225					230					235					240

Val Tyr Thr Ala Ala Trp Val Ala Ala Ala Ser Leu Phe Met Glu Leu
245 250 255
Leu Gly Phe Ser Thr Gln Lys Trp Leu Thr Ala Gly Gly Leu Gly Thr
260 265 270
Val Leu Leu Thr Leu Ala Gly Arg Glu Ile Leu Thr Asn Phe Leu Ser
275 280 285
Ser Ile Met Ile His Ala Thr Arg Pro Phe Val Leu Asn Glu Trp Ile
290 295 300
Gln Thr Lys Ile Gly Gly Tyr Glu Val Ser Gly Thr Val Glu Gln Val
305 310 315 320
Gly Trp Trp Ser Pro Thr Ile Ile Arg Gly Asp Asp Arg Glu Ala Val
325 330 335
His Ile Pro Asn His Gln Phe Ser Val Asn Ile Val Arg Asn Leu Thr
340 345 350
Gln Lys Thr His Trp Arg Ile Lys Thr His Leu Ala Ile Ser His Leu
355 360 365
Asp Val
370

(2) INFORMATION FOR SEQ ID NO:2289:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 605 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..605
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572448

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2289:

gcaccoccttt	tattgtagcg	acgcaagaag	aagcagctat	agcgtacgat	atcgcagcta	60
tcgagtaccg	tggaactaac	gccgttaacta	acttcgacat	cagccgttat	ctgaaactcc	120
cgggtgccga	gaaccctatc	gataccgcga	ataatctcct	cgagagtcgc	cattctgatc	180
ttagcccat	tataaaacct	aaccacgagt	ctgaactatc	acagagtcac	tcttcgtcag	240
aggacaacga	tgatcggaaa	acaaagctct	tgaagtctgc	acctttagtg	gcagaggagg	300
taatcggaac	atcgacgcca	cctgagattg	ctccgcctcg	tcggagcttc	ccggaagata	360
tccagacgta	tttcgggtgt	caaaaactccg	gcaagttaac	ggcggaggaa	gatgatgta	420
ctcttcggtga	tttagattct	ttccttaacg	ctgatttcta	cagcgagtta	aatgatgtg	480
aaagtgtgt	tctctcgata	agttttgttt	tttagttgtt	cagaatctcg	gtttcgaaat	540
tcaacattga	cacatcgatt	attctttctt	gtgacaatct	tataataata	agtttgaatc	600
ttttt						

(2) INFORMATION FOR SEQ ID NO:2290:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 159 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..159
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572449

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2290:

Thr	Pro	Phe	Ile	Val	Ala	Thr	Gln	Glu	Glu	Ala	Ala	Ile	Ala	Tyr	Asp
1				5				10				15			
Ile	Ala	Ala	Ile	Glu	Tyr	Arg	Gly	Leu	Asn	Ala	Val	Thr	Asn	Phe	Asp
			20				25				30				
Ile	Ser	Arg	Tyr	Leu	Lys	Leu	Pro	Val	Pro	Glu	Asn	Pro	Ile	Asp	Thr
		35				40				45					
Ala	Asn	Asn	Leu	Leu	Glu	Ser	Pro	His	Ser	Asp	Leu	Ser	Pro	Phe	Ile
	50				55					60					

Lys Pro Asn His Glu Ser Asp Leu Ser Gln Ser Gln Ser Ser Ser Glu
65 70 75 80
Asp Asn Asp Asp Arg Lys Thr Lys Leu Leu Lys Ser Ser Pro Leu Val
85 90 95
Ala Glu Glu Val Ile Gly Pro Ser Thr Pro Pro Glu Ile Ala Pro Pro
100 105 110
Arg Arg Ser Phe Pro Glu Asp Ile Gln Thr Tyr Phe Gly Cys Gln Asn
115 120 125
Ser Gly Lys Leu Thr Ala Glu Glu Asp Asp Val Ile Phe Gly Asp Leu
130 135 140
Asp Ser Phe Leu Thr Pro Asp Phe Tyr Ser Glu Leu Asn Asp Cys
145 150 155

(2) INFORMATION FOR SEQ ID NO:2291:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1393 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..1393
(D) OTHER INFORMATION: / Ceres Seq. ID 1572450

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2291:

aagccataga tattgaacaa atacactttt tgtctttttg ttgctgtgca acgtcataga 60
tctaactccg gaagaagaag aagatgagtg acgaaacgac gtcactcccg tccccagctc 120
cgcggaagaa gaagcagaat ctgggatgga tggagtgatg gaggggatgg agcagtggtt 180
tcggggagat tctctccag aggatcacag ctctcattt ggagaatcct ctctctcttc 240
cttcgcgtcaa cgacctcaat tgcgttgtca ctggtccac cagcggtcatt gccgtgaaa 300
ccgcgagga gcttgacaga gctgggtgctc atgttgtgat gccgtaagg aacaaaaagg 360
cggtctcagga gctgatactg caatggcaga acgaatggct tggtaaaagt ctcccactca 420
atattgagcc aatggagatt gatctactct cactggattc tgtcgcgaga ttgtgtgagg 480
ctttcaacgc tcggttagga cotttgcatg ttctgattaa caatgctggg atgtttgcta 540
tgggagaggg gcaaaaattc tcagaggaag gatatgagca gcacatgcaa gtgaatcatt 600
tagctccagc gctgctttca tacttcttt tgcgctctct gctccgaggg tctcctagcc 660
gaatcattaa tgtgaattcc gttatgcata gtgtcggttt tgttgaccgg gatgacatga 720
atgtgtgttc tggtagagct aagtactcaa gccttatagg atactcaag agcaagcttg 780
cccgattatt gtttagtagc attcttttca aaaagcttcc tctgaaaaca ggagtcagcg 840
tcgtatgtct atccccctgg tttgtcctaa caaatgttgc cagggatcta tccaggattc 900
ttcaagctct ttacgcagtg ataccttatt tcatattttc accccaagaa ggtttagaaa 960
gttctctatt ctccgcacaa gactctcaga ttccagagta ctgggaaaca ctaaaaaacg 1020
atgattggcc tgtttgccca tcatctctc aagattgccg cctcgcaaat ccttccgaag 1080
aagcacacaa cacagaaact gcacagagag tgtgaaaaaa gacgttagag cgttggtgct 1140
ttcctctcga tgcagttgag aagctcatag aaggggaaaa tatccaatgc cgttagggag 1200
cacacacaga atagtctttc aaaattacca caggttaagt gacccattac agatcaaaag 1260
gtaggtaatt gagaaaaata cttttttttt tgtttcctg tatcaattca cagatcacag 1320
tggggaatgg atcccccagg catgtagttt gcttgagaat gtttgattgt tggataaaaag 1380
tcaagcttta gct

(2) INFORMATION FOR SEQ ID NO:2292:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 376 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..376
(D) OTHER INFORMATION: / Ceres Seq. ID 1572451

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2292:

Met Ser Asp Glu Thr Thr Ser Ser Pro Ser Pro Ala Pro Ala Lys Lys

(2) INFORMATION FOR SEQ ID NO:2293:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 354 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

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{ix} FEATURE:
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(A) NAME/KEY: peptide

(B) LOCATION: 1..354

(D) OTHER INFORMATION: / Ceres Seq. ID 1572452

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2293:

Met Glu Trp Met Arg Gly Trp Ser Ser Val Phe Gly Glu Ile Leu Phe
1 5 10 15

Gln Arg Ile Thr Ala Ser His Leu Glu Asn Pro Leu Pro Leu Pro Ser
20 25 30
Val Asn Asp Leu Thr Cys Val Val Thr Gly Ser Thr Ser Gly Ile Gly
35 40 45
Arg Glu Thr Ala Arg Gln Leu Ala Glu Ala Gly Ala His Val Val Met
50 55 60
Ala Val Arg Asn Thr Lys Ala Ala Gln Glu Leu Ile Leu Gln Trp Gln
65 70 75 80
Asn Glu Trp Ser Gly Lys Gly Leu Pro Leu Asn Ile Glu Ala Met Glu
85 90 95
Ile Asp Leu Leu Ser Leu Asp Ser Val Ala Arg Phe Ala Glu Ala Phe
100 105 110
Asn Ala Arg Leu Gly Pro Leu His Val Leu Ile Asn Asn Ala Gly Met
115 120 125
Phe Ala Met Gly Glu Ala Gln Lys Phe Ser Glu Glu Gly Tyr Glu Gln
130 135 140
His Met Gln Val Asn His Leu Ala Pro Ala Leu Leu Ser Val Leu Leu
145 150 155 160
Leu Pro Ser Leu Ile Arg Gly Ser Pro Ser Arg Ile Ile Asn Val Asn
165 170 175
Ser Val Met His Ser Val Gly Phe Val Asp Pro Asp Met Asn Val
180 185 190
Val Ser Gly Arg Arg Lys Tyr Ser Ser Leu Ile Gly Tyr Ser Ser Ser
195 200 205
Lys Leu Ala Gln Ile Met Phe Ser Ser Ile Leu Phe Lys Lys Leu Pro
210 215 220
Leu Glu Thr Gly Val Ser Val Val Cys Leu Ser Pro Gly Val Val Leu
225 230 235 240
Thr Asn Val Ala Arg Asp Leu Ser Arg Ile Leu Gln Ala Leu Tyr Ala
245 250 255
Val Ile Pro Tyr Phe Ile Phe Ser Pro Gln Glu Gly Cys Arg Ser Ser
260 265 270
Leu Phe Ser Ala Thr Asp Pro Gln Ile Pro Glu Tyr Trp Glu Thr Leu
275 280 285
Lys Asn Asp Asp Trp Pro Val Cys Pro Phe Ile Ser Gln Asp Cys Arg
290 295 300
Pro Ala Asn Pro Ser Glu Glu Ala His Asn Thr Glu Thr Ala Gln Arg
305 310 315 320
Val Trp Lys Lys Thr Leu Glu Leu Val Gly Leu Pro Leu Asp Ala Val
325 330 335
Glu Lys Leu Ile Glu Gly Glu Asn Ile Gln Cys Arg Tyr Gly Ala Gln
340 345 350
His Glu

(2) INFORMATION FOR SEQ ID NO:2294:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 351 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..351
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572453

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2294:

Met Arg Gly Trp Ser Ser Val Phe Gly Glu Ile Leu Phe Gln Arg Ile
1 5 10 15
Thr Ala Ser His Leu Glu Asn Pro Leu Pro Leu Pro Ser Val Asn Asp
20 25 30
Leu Thr Cys Val Val Thr Gly Ser Thr Ser Gly Ile Gly Arg Glu Thr

35	40	45
Ala Arg Gln Leu	Ala Glu Ala Gly	Ala His Val Val Met Ala Val Arg
50	55	60
Asn Thr Lys Ala	Ala Gln Glu Leu Ile	Leu Gln Trp Gln Asn Glu Trp
65	70	75
Ser Gly Lys Gly	Leu Pro Leu Asn Ile	Glu Ala Met Glu Ile Asp Leu
85	90	95
Leu Ser Leu Asp	Ser Val Ala Arg Phe	Ala Glu Ala Phe Asn Ala Arg
100	105	110
Leu Gly Pro Leu	His Val Leu Ile	Asn Asn Ala Gly Met Phe Ala Met
115	120	125
Gly Glu Ala Gln	Lys Phe Ser Glu	Glu Gly Tyr Glu Gln His Met Gln
130	135	140
Val Asn His Leu	Ala Pro Ala Leu	Leu Ser Val Leu Leu Pro Ser
145	150	155
Leu Ile Arg Gly	Ser Pro Ser Arg Ile	Ile Asn Val Asn Ser Val Met
165	170	175
His Ser Val Gly	Phe Val Asp Pro	Asp Asp Met Asn Val Val Ser Gly
180	185	190
Arg Arg Lys Tyr	Ser Ser Leu Ile	Gly Tyr Ser Ser Ser Lys Leu Ala
195	200	205
Gln Ile Met Phe	Ser Ser Ile Leu	Phe Lys Lys Leu Pro Leu Glu Thr
210	215	220
Gly Val Ser Val	Val Cys Leu Ser	Pro Gly Val Val Leu Thr Asn Val
225	230	235
Ala Arg Asp Leu	Ser Arg Ile Leu	Gln Ala Leu Tyr Ala Val Ile Pro
245	250	255
Tyr Phe Ile Phe	Ser Pro Gln Glu	Gly Cys Arg Ser Ser Leu Phe Ser
260	265	270
Ala Thr Asp Pro	Gln Ile Pro Glu	Tyr Trp Glu Thr Leu Lys Asn Asp
275	280	285
Asp Trp Pro Val	Cys Pro Phe Ile	Ser Gln Asp Cys Arg Pro Ala Asn
290	295	300
Pro Ser Glu Glu	Ala His Asn Thr	Glu Thr Ala Gln Arg Val Trp Lys
305	310	315
Lys Thr Leu Glu	Leu Val Gly Leu	Pro Leu Asp Ala Val Glu Lys Leu
325	330	335
Ile Glu Gly Glu	Asn Ile Gln Cys	Arg Tyr Gly Ala Gln His Glu
340	345	350

(2) INFORMATION FOR SEQ ID NO:2295:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1506 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1506
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572458

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2295:

accgagaaat	gggtagctga	gcgaatacac	aaaccaacgg	caacgcacgg	ccaccgtcgt	60
cgaatcaaaa	gcctccggct	acgaacggcg	ttgatgggtc	tcattcctct	cctcctcctt	120
taactctcga	tcaagctatt	atagagtctg	atccgtcgaa	gaagaggaaa	atggggatgc	180
ttcctctaga	agtggtgat	cgtgtgatgt	gtcgggtggg	agacggggaa	caccatccgg	240
tgaagaataat	tgaagcgcgg	cggataYcat	aacggcggtc	aaaatgatta	cgagtattac	300
gttcattaca	ctgagtttaa	taggaggtcg	gatgaatgga	ctcagctgga	ccaactggac	360
cttgattcag	tagagtgcgc	tgtagatgaa	aaattggaag	acaagtgaa	acagcttgaa	420
gatgacacgt	caccagaaga	ggaagatcga	tgaGgacaca	tatagagggg	catgaagagc	480
tggtatcagc	aagtttgcgt	gaacatgaag	agtttcacga	agtgaagaac	atatacaaaa	540
ttgatcttgg	aaaatatgat	attgagactt	ggtacttctc	cccttttcgc	ccagaatata	600

atgactgtgtg	gaagctcttt	ttttgtgagt	tttgccgtgaa	cttcatgaaa	cgcaaaagagc	660
agcttcaaaag	gcataatgag	aagtgtgacc	tgaagcaccc	acctgtgtgat	gaaatttacc	720
atctctgcta	cttgcacaatg	tttgaggtag	atggcaaaaa	gaacaaggtt	tatgcacaga	780
gaagtgtgat	cttgcgcaaa	ttatttcttg	accacaaaaac	tctttactac	gatgtgtatt	840
atctctgcta	cttgcgcaaa	ttatttcttg	accacaaaaac	atgccacatg	gttgggtact	900
tttcaaaaga	gaagcattcg	gaagaagcat	acaacttagc	ttgcattcta	acctgcctt	960
catatacaaa	aaaagcgtat	ggaaggttct	taatagcctt	ttcctatgaa	ctgtcaaaaga	1020
aagaggga	agttgggaca	ccggRaaaga	cccttgcgg	atctaggctt	actaagctac	1080
agagggtatt	ggactcgtgt	tcattatgaa	atcttgaaaa	aacataaggg	aaacatttct	1140
atcaaggagc	tgagcgacgt	gacagcaatc	aaagcggaag	atatattaag	cacacttcag	1200
agcctagaag	tgatacagta	caggaaagga	cagcatgtga	ctgtgcgga	tcacaaaggtt	1260
ctggaccgac	atctgaaagc	tgacggccga	ggtgtgtctt	atgtagatgc	tagcaaatcg	1320
atttgacac	cttacaagga	ccagagttaa	gagtaagtac	actcctcttg	tgccatttga	1380
tttgatttga	gtgtgtaagt	aaggggctgt	cttattctcc	tgaaatgtaa	gtgtacttta	1440
cttgtaaatg	ttgaaatcgt	acttggaaatg	gtgtttgttt	acaactNctt	ataatgagga	1500
aatttg						

(2) INFORMATION FOR SEQ ID NO:2296:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 225 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..225
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572459

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2296:

Met	Arg	Thr	His	Ile	Glu	Gly	His	Glu	Glu	Leu	Asp	Ala	Ala	Ser	Leu
1			5					10						15	
Arg	Glu	His	Glu	Glu	Phe	Thr	Lys	Val	Lys	Asn	Ile	Ser	Thr	Ile	Glu
			20					25					30		
Leu	Gly	Lys	Tyr	Glu	Ile	Glu	Thr	Trp	Tyr	Phe	Ser	Pro	Phe	Pro	Pro
		35					40					45			
Glu	Tyr	Asn	Asp	Cys	Val	Lys	Leu	Phe	Phe	Cys	Glu	Phe	Cys	Leu	Asn
		50				55					60				
Phe	Met	Lys	Arg	Lys	Glu	Gln	Leu	Gln	Arg	His	Met	Xaa	Lys	Cys	Asp
			70						75					80	
Leu	Lys	His	Pro	Pro	Gly	Asp	Glu	Ile	Tyr	Arg	Ser	Gly	Thr	Leu	Ser
			85						90				95		
Met	Phe	Glu	Val	Asp	Gly	Lys	Lys	Asn	Lys	Val	Tyr	Ala	Gln	Asn	Leu
		100						105					110		
Cys	Tyr	Leu	Ala	Lys	Leu	Phe	Leu	Asp	His	Lys	Thr	Leu	Tyr	Tyr	Asp
		115						120				125			
Val	Asp	Leu	Phe	Leu	Phe	Tyr	Val	Leu	Cys	Glu	Cys	Asp	Asp	Arg	Gly
		130				135					140				
Cys	His	Met	Val	Gly	Tyr	Phe	Ser	Lys	Glu	Lys	His	Ser	Glu	Glu	Ala
		145				150				155				160	
Tyr	Asn	Leu	Ala	Cys	Ile	Leu	Thr	Leu	Pro	Ser	Tyr	Gln	Arg	Lys	Gly
			165						170					175	
Tyr	Gly	Lys	Phe	Leu	Ile	Ala	Phe	Ser	Tyr	Glu	Leu	Ser	Lys	Lys	Glu
			180					185					190		
Gly	Lys	Val	Gly	Thr	Pro	Xaa	Lys	Thr	Leu	Val	Gly	Ser	Arg	Leu	Thr
		195						200				205			
Lys	Leu	Gln	Arg	Leu	Leu	Asp	Ser	Cys	Ser	Ile	Arg	Asn	Leu	Glu	Lys
		210				215					220				

Thr
225

(2) INFORMATION FOR SEQ ID NO:2297:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 160 amino acids

- (B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1..160
(D) OTHER INFORMATION: / Ceres Seq. ID 1572460

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2297:

Met	Lys	Arg	Lys	Glu	Gln	Leu	Gln	Arg	His	Met	Xaa	Lys	Cys	Asp	Leu	
1			5				10							15		
Lys	His	Pro	Pro	Gly	Asp	Glu	Ile	Tyr	Arg	Ser	Gly	Thr	Leu	Ser	Met	
			20				25						30			
Phe	Glu	Val	Asp	Gly	Lys	Lys	Asn	Lys	Val	Tyr	Ala	Gln	Asn	Leu	Cys	
			35				40					45				
Tyr	Leu	Ala	Lys	Leu	Phe	Leu	Asp	His	Lys	Thr	Leu	Tyr	Tyr	Asp	Val	
			50				55				60					
Asp	Leu	Phe	Leu	Phe	Tyr	Val	Leu	Cys	Glu	Cys	Asp	Asp	Arg	Gly	Cys	
65					70					75				80		
His	Met	Val	Gly	Tyr	Phe	Ser	Lys	Glu	Lys	His	Ser	Glu	Glu	Ala	Tyr	
					85					90				95		
Asn	Leu	Ala	Cys	Ile	Leu	Thr	Leu	Pro	Ser	Tyr	Gln	Arg	Lys	Gly	Tyr	
			100							105				110		
Gly	Lys	Phe	Leu	Ile	Ala	Phe	Ser	Tyr	Glu	Leu	Ser	Lys	Lys	Glu	Gly	
			115							120				125		
Lys	Val	Gly	Thr	Pro	Xaa	Lys	Thr	Leu	Val	Gly	Ser	Arg	Leu	Thr	Lys	
			130							135				140		
Leu	Gln	Arg	Leu	Leu	Asp	Ser	Cys	Ser	Ile	Arg	Asn	Leu	Glu	Lys	Thr	
145					150					155				160		

(2) INFORMATION FOR SEQ ID NO:2298:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 150 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide
(ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1..150
(D) OTHER INFORMATION: / Ceres Seq. ID 1572461

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2298:

Met	Xaa	Lys	Cys	Asp	Leu	Lys	His	Pro	Pro	Gly	Asp	Glu	Ile	Tyr	Arg	
1					5					10				15		
Ser	Gly	Thr	Leu	Ser	Met	Phe	Glu	Val	Asp	Gly	Lys	Lys	Asn	Lys	Val	
					20					25				30		
Tyr	Ala	Gln	Asn	Leu	Cys	Tyr	Leu	Ala	Lys	Leu	Phe	Leu	Asp	His	Lys	
					35					40				45		
Thr	Leu	Tyr	Tyr	Asp	Val	Asp	Leu	Phe	Leu	Phe	Tyr	Val	Leu	Cys	Glu	
					50					55				60		
Cys	Asp	Asp	Arg	Gly	Cys	His	Met	Val	Gly	Tyr	Phe	Ser	Lys	Glu	Lys	
65					70					75				80		
His	Ser	Glu	Glu	Ala	Tyr	Asn	Leu	Ala	Cys	Ile	Leu	Thr	Leu	Pro	Ser	
					85					90				95		
Tyr	Gln	Arg	Lys	Gly	Tyr	Gly	Lys	Phe	Leu	Ile	Ala	Phe	Ser	Tyr	Glu	
					100					105				110		
Leu	Ser	Lys	Lys	Glu	Gly	Lys	Val	Gly	Thr	Pro	Xaa	Lys	Thr	Leu	Val	
					115					120				125		
Gly	Ser	Arg	Leu	Thr	Lys	Leu	Gln	Arg	Leu	Leu	Asp	Ser	Cys	Ser	Ile	
130							135							140		

Arg Asn Leu Glu Lys Thr
145 150

(2) INFORMATION FOR SEQ ID NO:2299:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 889 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..889

(D) OTHER INFORMATION: / Ceres Seq. ID 1572462

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2299:

aaaacgaact agagacagtt tgattcgaaa atcttgcg	60
ccagaatta agcaattact gggaaacctag ctcttgc	120
cgacagctcg cctttggaag aagccatttc tgggtcg	180
agctgcttcg tcgcccgtct ctaagaatat tgttcg	240
taaccagaga ctcttgcctc ttcgatcagt tgttccca	300
ctcaataatc aaagatgcta ttgattacat agaaggat	360
cgaagctgag atcagagaa	420
atcttgcagc tgatttact gttcctgtca catccaag	480
gttcttcac	540
caatggtggt gaggtaaca tgtaataaga ggacagat	600
ctcttgcagc attgaatctc aaaatcctca ctccaat	660
ttctccacac tgtctttatt gaggcgagtg aagaaga	720
tagaaacagg aatgagagct tataatgaaa ctcaa	780
tttctaata atactttttt tcttctttt ttggttc	840
aatgatgtgc tctcttttca ttttatgat ctctacg	

(2) INFORMATION FOR SEQ ID NO:2300:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 141 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..141

(D) OTHER INFORMATION: / Ceres Seq. ID 1572463

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2300:

Lys Arg Thr Arg Asp Ser Leu Ile Arg Lys Ser Cys Arg Lys Met Glu	
1 5 10 15	
Asp Ile Val Asp Gln Glu Leu Ser Asn Tyr Trp Glu Pro Ser Ser Leu	
20 25 30	
Leu Gln Asn Glu Tyr Phe Glu Tyr Asp Ser Trp Pro Leu Glu Glu Ala	
35 40 45	
Ile Ser Gly Ser Tyr Asp Ser Ser Pro Asp Gly Ala Ala Ser Ser	
50 55 60	
Pro Ala Ser Lys Asn Ile Val Ser Glu Arg Asn Arg Arg Gln Lys Leu	
65 70 75 80	
Asn Gln Arg Leu Phe Ala Leu Arg Ser Val Val Pro Asn Ile Thr Lys	
85 90 95	
Met Asp Lys Ala Ser Ile Ile Lys Asp Ala Ile Ser Tyr Ile Glu Gly	
100 105 110	
Leu Gln Tyr Glu Glu Lys Lys Leu Glu Ala Glu Ile Arg Glu Leu Glu	
115 120 125	
Ser Thr Pro Lys Ser Ser Leu Ser Phe Ser Lys Gly Phe	
130 135 140	

(2) INFORMATION FOR SEQ ID NO:2301:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 127 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..127
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1572464
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2301:

Met	Glu	Asp	Ile	Val	Asp	Gln	Glu	Leu	Ser	Asn	Tyr	Trp	Glu	Pro	Ser	
1			5						10					15		
Ser	Leu	Leu	Gln	Asn	Glu	Tyr	Phe	Glu	Tyr	Asp	Ser	Trp	Pro	Leu	Glu	
			20						25				30			
Glu	Ala	Ile	Ser	Gly	Ser	Tyr	Asp	Ser	Ser	Ser	Pro	Asp	Gly	Ala	Ala	
			35				40					45				
Ser	Ser	Pro	Ala	Ser	Lys	Asn	Ile	Val	Ser	Glu	Arg	Asn	Arg	Arg	Gln	
			50			55				60						
Lys	Leu	Asn	Gln	Arg	Leu	Phe	Ala	Leu	Arg	Ser	Val	Val	Pro	Asn	Ile	
65				70					75				80			
Thr	Lys	Met	Asp	Lys	Ala	Ser	Ile	Ile	Lys	Asp	Ala	Ile	Ser	Tyr	Ile	
			85					90					95			
Glu	Gly	Leu	Gln	Tyr	Glu	Glu	Lys	Lys	Leu	Glu	Ala	Glu	Ile	Arg	Glu	
			100				105						110			
Leu	Glu	Ser	Thr	Pro	Lys	Ser	Ser	Leu	Ser	Phe	Ser	Lys	Gly	Phe		
			115			120						125				

- (2) INFORMATION FOR SEQ ID NO:2302:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 147 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..147
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1572465
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2302:

Met	Lys	Lys	Arg	Ser	Ser	Lys	Leu	Arg	Ser	Glu	Asn	Leu	Asn	Leu	His	
1			5						10					15		
Gln	Arg	Val	Ala	Leu	Val	Ser	Ala	Lys	Asp	Arg	Asp	Arg	Leu	Leu		
			20					25				30				
Val	Pro	Val	Thr	Ser	Lys	Lys	Met	Lys	Gln	Leu	Asp	Ser	Gly	Ser	Ser	
			35				40				45					
Thr	Ser	Leu	Ile	Glu	Val	Leu	Glu	Leu	Lys	Val	Thr	Phe	Met	Gly	Glu	
			50			55				60						
Arg	Thr	Met	Val	Val	Ser	Val	Thr	Cys	Asn	Lys	Arg	Thr	Asp	Thr	Met	
65				70					75				80			
Val	Lys	Leu	Cys	Glu	Val	Phe	Glu	Ser	Leu	Asn	Leu	Lys	Ile	Leu	Thr	
			85					90					95			
Ser	Asn	Leu	Thr	Ser	Phe	Ser	Gly	Met	Ile	Phe	His	Thr	Val	Phe	Ile	
			100				105						110			
Glu	Ala	Asp	Glu	Glu	Glu	Gln	Glu	Val	Leu	Arg	Leu	Lys	Ile	Glu	Thr	
			115				120					125				
Gly	Ile	Gly	Ala	Tyr	Asn	Glu	Thr	Gln	Ser	Pro	Thr	Leu	Ser	Ile	Asp	
			130			135						140				
Ser	Leu	Tyr														
145																

- (2) INFORMATION FOR SEQ ID NO:2303:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1010 base pairs

- (B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..1010
(D) OTHER INFORMATION: / Ceres Seq. ID 1572487

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2303:

atccattaga	ggaggagcgc	atgtttctgc	ttccatggta	acgcctctcgt	ctccattctcc	60
ctcgcctctc	tgcgttagaga	acgtgacatg	taaattctct	cacgtttctc	gggttctaat	120
ctccggtacc	gataatatta	atcacgggtga	atcgtcggaa	gccaaaaaac	tgagagatgt	180
tcattctcta	gaaagggtat	tggaggagatt	cactgagcgt	gcaagagaga	acactgagaa	240
ggacctcgag	actctgtgga	ctctcgtcgc	ctttcttgaa	agaggaattt	tttatgtaac	300
cactctgata	atacctaagc	aagaatcaac	ttctaattct	tgctcaggcta	tgaatgaagt	360
ggaagtgttt	tcattcaaaa	acgaagaaga	actctatccc	gtagGatgga	ttcatactca	420
tcctctctcg	ggttctttca	tgtcatctgt	agatctgcat	acacattatt	cttatcaggt	480
aatggtgcca	gaggcttttg	caatcgtcgt	agctccaact	gatagctcta	attacgggat	540
atttaagcta	acggaccctg	gaggaaatgga	ggtagctgaga	ggctgctcag	agactggatt	600
ccaccgcgac	aaagaaccag	aagatgggaa	cccagtttat	gagcattgct	caaacgtcta	660
caagaactcg	aaccttaggt	tcgagatttt	tgatctacgt	taaggtaacg	actctgtggt	720
acttatcagt	aaaaagggtc	aaactttatc	cactgtgggc	taaggatgtc	aataataaac	780
gtcatcataa	ccaccaccct	ccttctatta	agcttagcaa	tgtaaataaa	ttgtcatgtc	840
cgggttatga	acacaaggta	ccttctatta	agcttagcaa	tgtaaataaa	ttgtcatgtc	900
cttagatttg	gatcaattgg	ttccattatg	gaagaacaac	aatgaccata	gacataagac	960
attgtattgg	cgtatgcaat	tggtatatat	ctgtacacaa	gtatacattg		

(2) INFORMATION FOR SEQ ID NO:2304:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 233 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..233

(D) OTHER INFORMATION: / Ceres Seq. ID 1572488

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2304:

Ser	Ile	Arg	Gly	Gly	Ala	Asp	Val	Ser	Ala	Ser	Met	Val	Thr	Leu	Ser
1				5								10			15
Ser	Pro	Ser	Pro	Ser	Leu	Ser	Cys	Val	Glu	Asn	Val	Thr	Cys	Lys	Ser
			20					25					30		
Ser	His	Val	Ser	Arg	Val	Leu	Ile	Ser	Gly	Thr	Asp	Asn	Ile	Asn	His
			35				40					45			
Gly	Glu	Ser	Ser	Glu	Ala	Lys	Ile	Leu	Arg	Asp	Val	His	Ile	Ser	Glu
			50				55				60				
Arg	Leu	Leu	Glu	Asp	Phe	Thr	Glu	Leu	Ala	Arg	Glu	Asn	Thr	Glu	Lys
65					70					75				80	
Asp	Leu	Glu	Thr	Cys	Gly	Thr	Leu	Ala	Ala	Phe	Leu	Glu	Arg	Gly	Ile
				85					90					95	
Phe	Tyr	Val	Thr	Thr	Leu	Ile	Ile	Pro	Lys	Gln	Glu	Ser	Thr	Ser	Asn
			100					105					110		
Ser	Cys	Gln	Ala	Met	Asn	Glu	Val	Glu	Val	Phe	Ser	Ile	Gln	Asn	Glu
			115				120					125			
Arg	Glu	Leu	Tyr	Pro	Val	Gly	Trp	Ile	His	Thr	His	Pro	Ser	Gln	Gly
			130				135					140			
Cys	Phe	Met	Ser	Ser	Val	Asp	Leu	His	Thr	His	Tyr	Ser	Tyr	Gln	Val
145					150					155				160	
Met	Val	Pro	Glu	Ala	Phe	Ala	Ile	Val	Val	Ala	Pro	Thr	Asp	Ser	Ser
					165					170				175	
Asn	Tyr	Gly	Ile	Phe	Lys	Leu	Thr	Asp	Pro	Gly	Gly	Met	Glu	Val	Leu

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(2) INFORMATION FOR SEQ ID NO:2305:

(A) LENGTH: 222 amino acids

(C) STRANDEDNESS:

(D) TOPOLOGY: linear
MOLECULE TYPE: peptid

(1x) FEATURE:
(2x) NAME:

(B) LOCATION: 1.222

SEQUENCE DESCRIPTION: SEQ ID NO:2305:

1	5	10	15

20 25 30

35 40 45

50 55 60

65 70 75 80

85 90 95

100	105	110
-----	-----	-----

115	120	125
-----	-----	-----

130 135 140

[illegible]

165 170 175

Gly Met Glu Val Leu Arg Gly Cys Ser Glu Thr Gly Phe His Leu Val
180 185 190

Lys Glu Pro Glu Asp Gly Asn Phe Val Tyr Glu His Cys Ser Asn Val
195 200 205

Tyr Lys Asn Ser Asn Leu Arg Phe Glu Ile Phe Asp Leu Arg
210 215 220

(2) INFORMATION FOR SEQ ID NO:2306:
 (1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 117 amino acids
(B) TYPE: amino acid

(D) TOPOLOGY: linear

```
(ii) MOLECULE TYPE: peptide
(iii) FEATURE:
```

(A) NAME/KEY: peptide
(B) LOCATION: 1-117

(D) OTHER INFORMATION: / Ceres Seq. ID 1572490
SEQUENCE DESCRIPTION: SEQ ID NO: 3306:

Met Asn Glu Val Glu Val Phe Ser Ile Gln Asn Glu Arg Glu Leu Tyr
10 15

1	5	10	15
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Pro Val Gly Trp Ile His Thr His Pro Ser Gln Gly Cys Phe Met Ser
20 25 30
Ser Val Asp Leu His Thr His Tyr Ser Tyr Gln Val Met Val Pro Glu
35 40 45
Ala Phe Ala Ile Val Val Ala Pro Thr Asp Ser Ser Asn Tyr Gly Ile
50 55 60
Phe Lys Leu Thr Asp Pro Gly Gly Met Glu Val Leu Arg Gly Cys Ser
65 70 75 80
Glu Thr Gly Phe His Pro His Lys Glu Pro Glu Asp Gly Asn Pro Val
85 90 95
Tyr Glu His Cys Ser Asn Val Tyr Lys Asn Ser Asn Leu Arg Phe Glu
100 105 110
Ile Phe Asp Leu Arg
115

(2) INFORMATION FOR SEQ ID NO:2307:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 868 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..868
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572495

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2307:

aatacacttg	taattctaa	cttctctct	ttccaaaaat	ggcgctcatca	tcggcctttag	60
ctctcaaggag	actctctct	tcttccaccg	tcggcgctccc	tcgcgccttta	agagccggttc	120
gtccgggtgtc	tgcttcttct	cgctctctca	ataccaacgc	cgccagaaaac	atgaagacg	180
gtgtcgatag	gaaccatcac	tcaaaccgac	atgtttctcg	ccacggcgccg	gatttcttct	240
cagatataact	cgatccgttt	actccaacga	gaagcttgag	ccagatgctg	aatttcatgg	300
accaggttaag	cgaatccct	ttggtatcac	ctactctggg	aatgggagct	tctggagtta	360
gacgtggttg	gaacgtgaaa	gagaaagacg	acgcgttgca	tctaaggata	gatagccgg	420
gactaagcag	agaggtatgt	aaattgacct	tggaacagaa	cacatttggtg	attagaggag	480
aaggggaaac	agaggagggg	gaagatgttt	ctggagatgg	acggagggtt	accagtagga	540
ttgagttacc	ggagaaaagta	tacaagactg	atgagatTAA	ggcggaaAtg	aagaatgggt	600
tgtTgaaAgt	ggtgatTCa	aagattaaAg	agGatgagcg	taAcaAtatT	cgtcacataa	660
acgttgacta	gagtggttta	ttttggattg	tttgagatgg	aatggaagta	agtgaagtga	720
ttttgaaact	ttaaggtgtc	ctttggtgaa	tcaaggagaa	tgacatttcc	cacggtccta	780
tgtgttcggg	attttgactt	ttttcgttac	atcaatgata	tatgtacggt	tgactacttt	840
catatcatag	gttcggattt	gtttctcc				

(2) INFORMATION FOR SEQ ID NO:2308:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 222 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..222
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572496

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2308:

Ser	Leu	Val	Asn	Ser	Lys	Leu	Leu	Leu	Phe	Pro	Lys	Met	Ala	Ser	Ser
1			5					10					15		
Ser	Ala	Leu	Ala	Leu	Arg	Arg	Leu	Leu	Ser	Ser	Ser	Thr	Val	Ala	Val
			20					25					30		
Pro	Arg	Ala	Leu	Arg	Ala	Val	Arg	Pro	Val	Ser	Ala	Ser	Ser	Arg	Leu
			35				40					45			
Phe	Asn	Thr	Asn	Ala	Ala	Arg	Asn	Tyr	Glu	Asp	Gly	Val	Asp	Arg	Asn
			50			55						60			

His His Ser Asn Arg His Val Ser Arg His Gly Gly Asp Phe Phe Ser
65 70 75 80
Asp Ile Leu Asp Pro Phe Thr Pro Thr Arg Ser Leu Ser Gln Met Leu
85 90 95
Asn Phe Met Asp Gln Val Ser Glu Ile Pro Leu Val Ser Ala Thr Arg
100 105 110
Gly Met Gly Ala Ser Gly Val Arg Arg Gly Trp Asn Val Lys Glu Lys
115 120 125
Asp Asp Ala Leu His Leu Arg Ile Asp Met Pro Gly Leu Ser Arg Glu
130 135 140
Asp Val Lys Leu Ala Leu Glu Gln Asn Thr Leu Val Ile Arg Gly Glu
145 150 155 160
Gly Glu Thr Glu Glu Gly Glu Asp Val Ser Gly Asp Gly Arg Arg Phe
165 170 175
Thr Ser Arg Ile Glu Leu Pro Glu Lys Val Tyr Lys Thr Asp Glu Ile
180 185 190
Lys Ala Glu Met Lys Asn Gly Val Leu Lys Val Val Ile Pro Lys Ile
195 200 205
Lys Glu Asp Glu Arg Asn Asn Ile Arg His Ile Asn Val Asp
210 215 220

(2) INFORMATION FOR SEQ ID NO:2309:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 210 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..210
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572497

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2309:

Met Ala Ser Ser Ser Ala Leu Ala Leu Arg Arg Leu Leu Ser Ser Ser
1 5 10 15
Thr Val Ala Val Pro Arg Ala Leu Arg Ala Val Arg Pro Val Ser Ala
20 25 30
Ser Ser Arg Leu Phe Asn Thr Asn Ala Ala Arg Asn Tyr Glu Asp Gly
35 40 45
Val Asp Arg Asn His His Ser Asn Arg His Val Ser Arg His Gly Gly
50 55 60
Asp Phe Phe Ser Asp Ile Leu Asp Pro Phe Thr Pro Thr Arg Ser Leu
65 70 75 80
Ser Gln Met Leu Asn Phe Met Asp Gln Val Ser Glu Ile Pro Leu Val
85 90 95
Ser Ala Thr Arg Gly Met Gly Ala Ser Gly Val Arg Arg Gly Trp Asn
100 105 110
Val Lys Glu Lys Asp Asp Ala Leu His Leu Arg Ile Asp Met Pro Gly
115 120 125
Leu Ser Arg Glu Asp Val Lys Leu Ala Leu Glu Gln Asn Thr Leu Val
130 135 140
Ile Arg Gly Glu Gly Glu Thr Glu Glu Gly Glu Asp Val Ser Gly Asp
145 150 155 160
Gly Arg Arg Phe Thr Ser Arg Ile Glu Leu Pro Glu Lys Val Tyr Lys
165 170 175
Thr Asp Glu Ile Lys Ala Glu Met Lys Asn Gly Val Leu Lys Val Val
180 185 190
Ile Pro Lys Ile Lys Glu Asp Glu Arg Asn Asn Ile Arg His Ile Asn
195 200 205
Val Asp
210

(2) INFORMATION FOR SEQ ID NO:2310:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 128 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..128
(D) OTHER INFORMATION: / Ceres Seq. ID 1572498
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2310:

Met	Leu	Asn	Phe	Met	Asp	Gln	Val	Ser	Glu	Ile	Pro	Leu	Val	Ser	Ala
1				5					10					15	
Thr	Arg	Gly	Met	Gly	Ala	Ser	Gly	Val	Arg	Arg	Gly	Trp	Asn	Val	Lys
			20					25					30		
Glu	Lys	Asp	Asp	Ala	Leu	His	Leu	Arg	Ile	Asp	Met	Pro	Gly	Leu	Ser
			35				40					45			
Arg	Glu	Asp	Val	Lys	Leu	Ala	Leu	Glu	Gln	Asn	Thr	Leu	Val	Ile	Arg
			50			55				60					
Gly	Glu	Gly	Glu	Thr	Glu	Glu	Gly	Glu	Asp	Val	Ser	Gly	Asp	Gly	Arg
65				70					75				80		
Arg	Phe	Thr	Ser	Arg	Ile	Glu	Leu	Pro	Glu	Lys	Val	Tyr	Lys	Thr	Asp
			85					90					95		
Glu	Ile	Lys	Ala	Glu	Met	Lys	Asn	Gly	Val	Leu	Lys	Val	Val	Ile	Pro
			100				105						110		
Lys	Ile	Lys	Glu	Asp	Glu	Arg	Asn	Asn	Ile	Arg	His	Ile	Asn	Val	Asp
			115				120					125			

- (2) INFORMATION FOR SEQ ID NO:2311:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 911 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..911
(D) OTHER INFORMATION: / Ceres Seq. ID 1572503
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2311:

agtgaaccgg	aggagacag	cgagatgagg	ccggagatag	ttctgttcgg	ogaactcgac	60
acggcgcgagt	cttttaggtc	cgcggtttgg	ggatctgctc	ttgccgacgc	ttactctcgc	120
aaggctgatg	ttgtgtgttc	aggctacggc	ggctacaaca	cccgatgggc	tctctctctg	180
cttcatcaca	tcttccctct	gggtctcttg	tctctctctg	ttgtctacgac	gatattcttc	240
gggtgcaaacg	atgcagctct	caaaggaaga	accagtgata	gacaacatgt	gccggtggaa	300
gagtaacacag	ataatgtcag	aaagattgtt	cagcatttga	agaaaatgtc	acctacaagt	360
ctaattgtgc	ttataactcc	accaccaatt	gatgaagctg	gacgGtcaaa	gttatgcaga	420
atcaaatctac	gggtgagaag	ctatgaaaga	gcctgagaga	acaaacgaaa	caacaggggt	480
atatgcacaa	cattgtgttg	cattggccga	ggaaactcgt	ctgcgatgtg	tcaacttatg	540
gtctcaagat	caggaaacca	attattggca	gaaaaagtac	ctaagtgtatg	ggctccatct	600
caagcctgaa	ggcaatgggg	tagtttttga	tgaagtctcg	agagttttta	gagaagcttg	660
gctctctctcc	gaagaaatgc	cgtttgattt	cccccatcat	tcccatatcg	atggtaaaaa	720
cccatgaaaa	gotttttgag	agcgttgctt	ataacgatca	tccccaattt	aatgagcagg	780
tttgttttga	tttaaaattg	tgaacacgtt	tcaatgtgtg	gatttgaaga	actctcgcat	840
gtgaataaat	acctaaaagg	tgcacatcca	ctagagatcg	ttttcaagag	aaatgaactt	900
atgatgtact	t					

- (2) INFORMATION FOR SEQ ID NO:2312:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 144 amino acids
(B) TYPE: amino acid

- (C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..144
(D) OTHER INFORMATION: / Ceres Seq. ID 1572504
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2312:

Ser	Glu	Pro	Glu	Gly	Asp	Ser	Glu	Met	Arg	Pro	Glu	Ile	Val	Leu	Phe	
1			5					10						15		
Gly	Asp	Ser	Ile	Thr	Ala	Gln	Ser	Phe	Arg	Ser	Gly	Gly	Trp	Gly	Ser	
			20					25					30			
Ala	Leu	Ala	Asp	Ala	Tyr	Ser	Arg	Lys	Ala	Asp	Val	Val	Val	Arg	Gly	
			35					40					45			
Tyr	Gly	Gly	Tyr	Asn	Thr	Arg	Trp	Ala	Leu	Phe	Leu	Leu	His	His	Ile	
			50			55					60					
Phe	Pro	Leu	Gly	Ser	Ser	Ser	Pro	Pro	Val	Ala	Thr	Thr	Ile	Phe	Phe	
65				70						75				80		
Gly	Ala	Asn	Asp	Ala	Ala	Leu	Lys	Gly	Arg	Thr	Ser	Asp	Arg	Gln	His	
			85					90						95		
Val	Pro	Val	Glu	Glu	Tyr	Thr	Asp	Asn	Val	Arg	Lys	Ile	Val	Gln	His	
			100					105					110			
Leu	Lys	Lys	Cys	Ser	Pro	Thr	Met	Leu	Ile	Val	Leu	Ile	Thr	Pro	Pro	
			115				120						125			
Pro	Ile	Asp	Glu	Ala	Gly	Arg	Ser	Lys	Leu	Cys	Arg	Ile	Asn	Leu	Arg	
			130				135					140				

(2) INFORMATION FOR SEQ ID NO:2313:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 136 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..136
(D) OTHER INFORMATION: / Ceres Seq. ID 1572505
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2313:

Met	Arg	Pro	Glu	Ile	Val	Leu	Phe	Gly	Asp	Ser	Ile	Thr	Ala	Gln	Ser	
1			5					10						15		
Phe	Arg	Ser	Gly	Gly	Trp	Gly	Ser	Ala	Leu	Ala	Asp	Ala	Tyr	Ser	Arg	
			20					25					30			
Lys	Ala	Asp	Val	Val	Val	Arg	Gly	Tyr	Gly	Gly	Tyr	Asn	Thr	Arg	Trp	
			35				40					45				
Ala	Leu	Phe	Leu	Leu	His	His	Ile	Phe	Pro	Leu	Gly	Ser	Ser	Ser	Pro	
			50			55					60					
Pro	Val	Ala	Thr	Thr	Ile	Phe	Phe	Gly	Ala	Asn	Asp	Ala	Ala	Leu	Lys	
65				70				75						80		
Gly	Arg	Thr	Ser	Asp	Arg	Gln	His	Val	Pro	Val	Glu	Glu	Tyr	Thr	Asp	
			85					90					95			
Asn	Val	Arg	Lys	Ile	Val	Gln	His	Leu	Lys	Lys	Cys	Ser	Pro	Thr	Met	
			100					105					110			
Leu	Ile	Val	Leu	Ile	Thr	Pro	Pro	Pro	Ile	Asp	Glu	Ala	Gly	Arg	Ser	
			115				120						125			
Lys	Leu	Cys	Arg	Ile	Asn	Leu	Arg									
			130			135										

(2) INFORMATION FOR SEQ ID NO:2314:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 120 amino acids

(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..120
(D) OTHER INFORMATION: / Ceres Seq. ID 1572506
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2314:
Met Lys Leu Asp Gly Gln Ser Tyr Ala Glu Ser Ile Tyr Gly Glu Lys
1 5 10 15
Ala Met Lys Glu Pro Glu Arg Thr Asn Glu Thr Thr Gly Val Tyr Ala
20 25 30
Gln His Cys Val Ala Leu Ala Glu Leu Gly Leu Arg Cys Val Asn
35 40 45
Leu Trp Ser Lys Met Gln Glu Thr Asn Tyr Trp Gln Lys Lys Tyr Leu
50 55 60
Ser Asp Gly Leu His Leu Thr Pro Glu Gly Asn Gly Val Val Phe Asp
65 70 75 80
Glu Val Ser Arg Val Phe Arg Glu Ala Trp Leu Ser Pro Glu Glu Met
85 90 95
Pro Phe Asp Phe Pro His His Ser His Ile Asp Gly Lys Asn Pro Trp
100 105 110
Lys Ala Phe Glu Glu Arg Cys Leu
115 120

(2) INFORMATION FOR SEQ ID NO:2315:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 538 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..538
(D) OTHER INFORMATION: / Ceres Seq. ID 1572524

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2315:

atcaaaacRa tcacatacac tatttttctc ctctccttat tgtctatata ttttctctct 60
ttagcttttt catttcgaaa tggccaccgt tgagggttgaa caagtcactc cagtagcagt 120
agagaacggt gaggtaccaa caaagacagt ggaggagaca gtggtggaga cagagaagaa 180
agatgaagaa accgagaaga aaacagagga gaaagacgag aagacagaag tgatcacgga 240
aactccggtg gttgaggagg aggagaagaa agctgaggaa gtgaccgaaa ctccggcggt 300
tgtggaggag gagaagaaga cagaggtggt tgaggagaaa cagactgagg ttgcggctgc 360
tgaggaagtc gcggttgaga aggccgagga gtaaaagagga aggaagaagc tatatatgac 420
cttttttggt ctcatactgt tttctgttta ttttatttta tcaacatttc ataagtattt 480
tctatgtttg ttgggtttgt tatgatgaaa tcagatggtt ggatctttta atggttgc

(2) INFORMATION FOR SEQ ID NO:2316:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..104
(D) OTHER INFORMATION: / Ceres Seq. ID 1572525

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2316:

Met Ala Thr Val Glu Val Glu Gln Val Thr Pro Val Ala Val Glu Asn
1 5 10 15
Val Glu Val Pro Thr Lys Thr Val Glu Glu Thr Val Val Glu Thr Glu

	20					25						30							
Lys	Lys	Asp	Glu	Glu	Thr	Glu	Lys	Lys	Thr	Glu	Glu	Lys	Asp	Glu	Lys				
	35					40						45							
Thr	Glu	Val	Ile	Thr	Glu	Thr	Pro	Val	Val	Glu	Glu	Glu	Glu	Lys	Lys				
	50					55						60							
Ala	Glu	Glu	Val	Thr	Glu	Thr	Pro	Ala	Val	Val	Glu	Glu	Glu	Lys	Lys				
	65					70					75								
Thr	Glu	Val	Val	Glu	Glu	Lys	Gln	Thr	Glu	Val	Ala	Ala	Ala	Glu	Glu				
					85				90					95					
Val	Ala	Val	Glu	Lys	Ala	Glu	Glu												
					100														

(2) INFORMATION FOR SEQ ID NO:2317:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1465 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1465
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572526

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2317:

gcagtgaggaga	gagagcagatg	gaataaaaaag	cgtgaagcgtt	tttgatatct	ctttctcttc	60
ctctctcttt	ctctctcgat	agatttcgcc	ggcgatggcg	gtggactcct	tagaaaacgga	120
gattgacaacg	gcggtgcggt	ttgtccacct	cgcttctct	ctctgtgtta	aagttcaaga	180
gaagcttcat	ctctctaacg	gtggtcacgt	taagtctaaa	gacgatgatt	ccctgtcac	240
cgctcgctgat	tttgggtgac	aagcaattgt	gagctggggt	ttagctgaag	tgtttgggtga	300
tcaaaacctct	tcaattgttg	ctgaagaaga	cactgagaca	ctctctgagg	ctgattcttt	360
aggtctattta	ggagctgtgt	cgaatgcggt	taatgaagca	ttgtccgaag	ctcagaacta	420
cggtgctccg	aagccagtta	agccattggg	gtctagttaa	attcttaagg	ctattagtag	480
atgtaactct	gttggaggac	ctaaagggaag	gcattggggt	cttgatccgt	ttgatggaaac	540
gttaggggtt	gttcgtgggg	atcagtatgc	tgttgcctta	gctttgatag	agaatggtaa	600
agttcttttg	ggtgtactag	gatgtcctaa	ttatccggtt	aagaaagaat	gtttaagtaa	660
tggttgtaac	caagctatga	agacgaaagc	tgttgctggt	tcagtatcga	aaggatggt	720
tatgtatgca	aagagaggta	gtggtcgaac	ttggatgcaa	cccttgatcg	ttggaggaaat	780
accagaatct	gcaacacttc	ttaaggtttc	ttcagttgat	gatccgggtt	tagctacagt	840
ttgtgagcca	gtagagagag	caaaactcaa	ccacttgctc	actgcaggac	ttgccaatag	900
catgggagtt	agaaaagcag	ctatgcgagt	gtatagcatg	gtgaaatatg	cagcgatTgc	960
acgtggagac	gctgaagtgt	ttatgaagtt	tgacagatca	agttacaaag	agaagatatg	1020
ggaatcacgca	gctggagttg	ttatttgga	agaagctggt	gggtgtgtga	ctgatgcggg	1080
agggagaaac	ttagactttc	cgaaaaggtg	ttacttgga	ggtcttgacc	gtggaatcat	1140
cgcatcttgt	ggctcaagttt	tacatgagaa	gattataggt	gctgtttatg	ctagtggga	1200
atctctccgt	ctctgaaaaa	gcttatccac	aatccgtagt	ttggtgcagc	atcatcgagc	1260
caaaagcaag	gagggaacag	ggccattacg	gtttaggatg	agcaagggcc	agtttaaatg	1320
aatgtgaatg	gcggagaagt	aaataatgct	gagggaacag	cggtaaaagt	aagaatctag	1380
tttatttacc	tatctaaagag	taataaagct	gctgcatttc	acgaacccct	atgttctatg	1440
atctttaatg	gatgatatac	ttttt				

(2) INFORMATION FOR SEQ ID NO:2318:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 373 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..373
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572527

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2318:

Met Ala Val Asp Ser Leu Glu Thr Glu Ile Asp Thr Ala Val Arg Val

1	5	10	15
Val His Leu Ala Ser Ser Leu Cys Val Lys Val Gln Glu Lys Leu His			
	20	25	30
Leu Pro Asn Gly Gly His Val Lys Ser Lys Asp Asp Asp Ser Pro Val			
	35	40	45
Thr Val Ala Asp Phe Gly Val Gln Ala Ile Val Ser Trp Val Leu Ala			
	50	55	60
Glu Val Phe Gly Asp Gln Asn Leu Ser Ile Val Ala Glu Glu Asp Thr			
65	70	75	80
Glu Thr Leu Ser Glu Ala Asp Ser Leu Gly Leu Gly Ala Val Ser			
	85	90	95
Asn Ala Val Asn Glu Ala Leu Ser Glu Ala Gln Asn Tyr Gly Leu Pro			
	100	105	110
Lys Pro Val Lys Pro Leu Gly Ser Ser Glu Ile Leu Lys Ala Ile Ser			
	115	120	125
Arg Cys Asn Ser Val Gly Gly Pro Lys Gly Arg His Trp Val Leu Asp			
	130	135	140
Pro Val Asp Gly Thr Leu Gly Phe Val Arg Gly Asp Gln Tyr Ala Val			
145	150	155	160
Ala Leu Ala Leu Ile Glu Asn Gly Lys Val Leu Leu Gly Val Leu Gly			
	165	170	175
Cys Pro Asn Tyr Pro Val Lys Lys Glu Cys Leu Ser Asn Gly Cys Asn			
	180	185	190
Gln Ala Met Lys Thr Lys Ala Val Ala Gly Ser Val Ser Lys Gly Cys			
	195	200	205
Val Met Tyr Ala Lys Arg Gly Ser Gly Gln Ala Trp Met Gln Pro Leu			
	210	215	220
Ile Val Gly Gly Ile Pro Glu Ser Ala Thr Leu Leu Lys Val Ser Ser			
225	230	235	240
Val Asp Asp Pro Val Leu Ala Thr Val Cys Glu Pro Val Glu Arg Ala			
	245	250	255
Asn Ser Asn His Leu Phe Thr Ala Gly Leu Ala Asn Ser Met Gly Val			
	260	265	270
Arg Lys Gln Pro Met Arg Val Tyr Ser Met Val Lys Tyr Ala Ala Ile			
	275	280	285
Ala Arg Gly Asp Ala Glu Val Phe Met Lys Phe Ala Gln Ser Ser Tyr			
	290	295	300
Lys Glu Lys Ile Trp Asp His Ala Ala Gly Val Val Ile Val Glu Glu			
305	310	315	320
Ala Gly Gly Val Val Thr Asp Ala Gly Gly Arg Asn Leu Asp Phe Ser			
	325	330	335
Lys Gly Val Tyr Leu Glu Gly Leu Asp Arg Gly Ile Ile Ala Cys Ser			
	340	345	350
Gly Gln Val Leu His Glu Lys Ile Gly Ala Val Tyr Ala Ser Trp			
	355	360	365
Glu Ser Ser Ser Leu			
370			

(2) INFORMATION FOR SEQ ID NO:2319:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1270 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1270
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572528

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2319:

atctacaact ttcattcttc cactacattt ctctccttga gtatcttctt atctattttt
ccaaattcca aaacaattca caaaatggct acatgctggc ctgagccgat tgttttcgctg

60
120

caatccttgt	cccaaacccg	tgtaccaact	gtaccaaacc	gctatgtgaa	gccggctcat	180
cagagaccgg	tctttaaacc	caccacaatc	gatgctggga	tagaaatccc	tggtctagac	240
atgaacgacg	tgtgggggaa	accagagggg	ctaaggctcg	tgaggagcgc	gtgtgaggag	300
tggggtttct	tccaaatggt	gaaccatggt	gtgacccact	cgttgatgga	gagagtgaga	360
ggagcgtgac	gagagttctt	cgagctaccg	ctagaggaga	aacggaaagta	tgcaaatcta	420
ccggacacgt	accaggggata	tggaaagcgc	cctgggggtg	tgagagatgc	taaattagat	480
tggaagtatt	atttcttctt	caattacttg	ccttcttcca	taagaaaccc	ttccagatgg	540
ccatActcag	ctccttaaga	tcagagaatt	gatcgaaaag	tacggagaag	aagtggagaa	600
actgtgcgaa	aggctaacag	agacgttgtc	agagagttaa	ggtttaaaac	caaacaagct	660
catgcaggct	ttaggaggag	gcgacaaagt	cggagcttct	ctgaggacaa	actcttacc	720
aaaaatgcct	cagccgcagc	tcaactttag	tctctcttct	cattctgacc	ctggaggcat	780
caccattctt	ctcccgagc	agaaggtcgc	tgcccttcag	gtccgtcggt	gtgatggctg	840
ggtcaccatt	aaatcagtc	ctaactgctt	gatcgtaaac	attggagatc	aaacttcagat	900
acttagcaat	ggaattttaca	aaagcgtgga	acatcaagtg	atcgtaatt	ccggtatgga	960
acgagctctt	ttggcattct	tcataaaccc	gagaagtgat	atcccggttg	gaccaatcga	1020
agaactagta	actgcaaac	gacctgtctt	ttataaaacca	atcaggttgc	acgagtaccg	1080
ttctctgata	aggcaaaagg	gtccttggtg	aaaaaaaccaa	gtcgactcac	tggtattatac	1140
tagataataa	ttgataaaca	ttccaagtat	tatctgttat	tcttatgtcc	ttgatattgt	1200
cggtactaaa	taatatgtga	accgtatctt	cactttttct	tattatattg	ctgctctctc	1260
ttgaggtttg						

(2) INFORMATION FOR SEQ ID NO:2320:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 185 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..185
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1572529
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2320:

Ile	Tyr	Asn	Phe	His	Ser	Ser	Thr	Thr	Phe	Leu	Ser	Leu	Ser	Ile	Phe
1				5					10					15	
Leu	Ser	Tyr	Phe	Pro	Asn	Ser	Lys	Thr	Ile	His	Lys	Met	Ala	Thr	Cys
				20					25				30		
Trp	Pro	Glu	Pro	Ile	Val	Ser	Val	Gln	Ser	Leu	Ser	Gln	Thr	Gly	Val
				35			40					45			
Pro	Thr	Val	Pro	Asn	Arg	Tyr	Val	Lys	Pro	Ala	His	Gln	Arg	Pro	Val
				50			55				60				
Phe	Asn	Thr	Thr	Gln	Ser	Asp	Ala	Gly	Ile	Glu	Ile	Pro	Val	Leu	Asp
65				70					75				80		
Met	Asn	Asp	Val	Trp	Gly	Lys	Pro	Glu	Gly	Leu	Arg	Leu	Val	Arg	Ser
				85					90				95		
Ala	Cys	Glu	Glu	Trp	Gly	Phe	Phe	Gln	Met	Val	Asn	His	Gly	Val	Thr
				100				105					110		
His	Ser	Leu	Met	Glu	Arg	Val	Arg	Gly	Ala	Trp	Arg	Glu	Phe	Phe	Glu
				115				120				125			
Leu	Pro	Leu	Glu	Glu	Lys	Arg	Lys	Tyr	Ala	Asn	Ser	Pro	Asp	Thr	Tyr
				130			135				140				
Glu	Gly	Tyr	Gly	Ser	Arg	Leu	Gly	Val	Val	Arg	Asp	Ala	Lys	Leu	Asp
145				150					155					160	
Trp	Ser	Asp	Tyr	Phe	Phe	Leu	Asn	Tyr	Leu	Pro	Ser	Ser	Ile	Arg	Asn
				165					170					175	
Pro	Ser	Lys	Trp	Pro	Tyr	Ser	Ala	Ser							
				180				185							

(2) INFORMATION FOR SEQ ID NO:2321:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 157 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:

- (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..157
 (D) OTHER INFORMATION: / Ceres Seq. ID 1572530

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2321:

Met	Ala	Thr	Cys	Trp	Pro	Glu	Pro	Ile	Val	Ser	Val	Gln	Ser	Leu	Ser	
1				5				10						15		
Gln	Thr	Gly	Val	Pro	Thr	Val	Pro	Asn	Arg	Tyr	Val	Lys	Pro	Ala	His	
			20					25					30			
Gln	Arg	Pro	Val	Phe	Asn	Thr	Thr	Gln	Ser	Asp	Ala	Gly	Ile	Glu	Ile	
			35					40					45			
Pro	Val	Leu	Asp	Met	Asn	Asp	Val	Trp	Gly	Lys	Pro	Glu	Gly	Leu	Arg	
			50				55					60				
Leu	Val	Arg	Ser	Ala	Cys	Glu	Glu	Trp	Gly	Phe	Phe	Gln	Met	Val	Asn	
65					70					75				80		
His	Gly	Val	Thr	His	Ser	Leu	Met	Glu	Arg	Val	Arg	Gly	Ala	Trp	Arg	
				85					90					95		
Glu	Phe	Phe	Glu	Leu	Pro	Leu	Glu	Glu	Lys	Arg	Lys	Tyr	Ala	Asn	Ser	
			100					105					110			
Pro	Asp	Thr	Tyr	Glu	Gly	Tyr	Gly	Ser	Arg	Leu	Gly	Val	Val	Arg	Asp	
			115				120						125			
Ala	Lys	Leu	Asp	Trp	Ser	Asp	Tyr	Phe	Phe	Leu	Asn	Tyr	Leu	Pro	Ser	
			130				135					140				
Ser	Ile	Arg	Asn	Pro	Ser	Lys	Trp	Pro	Tyr	Ser	Ala	Ser				
145				150						155						

(2) INFORMATION FOR SEQ ID NO:2322:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 161 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..161
(D) OTHER INFORMATION: / Ceres Seq. ID 1572531

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2322:

Met	Gln	Ala	Leu	Gly	Gly	Gly	Asp	Lys	Val	Gly	Ala	Ser	Leu	Arg	Thr	
1				5				10					15			
Asn	Phe	Tyr	Pro	Lys	Cys	Pro	Gln	Pro	Gln	Leu	Thr	Leu	Gly	Leu	Ser	
			20					25					30			
Ser	His	Ser	Asp	Pro	Gly	Gly	Ile	Thr	Ile	Leu	Leu	Pro	Asp	Glu	Lys	
			35				40						45			
Val	Ala	Gly	Leu	Gln	Val	Arg	Arg	Gly	Asp	Gly	Trp	Val	Thr	Ile	Lys	
			50				55				60					
Ser	Val	Pro	Asn	Ala	Leu	Ile	Val	Asn	Ile	Gly	Asp	Gln	Leu	Gln	Ile	
65					70					75				80		
Leu	Ser	Asn	Gly	Ile	Tyr	Lys	Ser	Val	Glu	His	Gln	Val	Ile	Val	Asn	
			85					90					95			
Ser	Gly	Met	Glu	Arg	Val	Ser	Leu	Ala	Phe	Phe	Tyr	Asn	Pro	Arg	Ser	
			100					105				110				
Asp	Ile	Pro	Val	Gly	Pro	Ile	Glu	Glu	Leu	Val	Thr	Ala	Asn	Arg	Pro	
			115				120					125				
Ala	Leu	Tyr	Lys	Pro	Ile	Arg	Phe	Asp	Glu	Tyr	Arg	Ser	Leu	Ile	Arg	
			130				135					140				
Gln	Lys	Gly	Pro	Cys	Gly	Lys	Asn	Gln	Val	Asp	Ser	Leu	Leu	Leu	Thr	
145				150						155					160	

Arg

(2) INFORMATION FOR SEQ ID NO:2323:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1178 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1178
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572538

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2323:

acaagtca	ca	ccccaccat	gc	atgtcata	tct	ttttt	cg	tat	cctcaat	att	tttttt	60
ctcttctca	cat	caaccat	tt	gtatttc	c	gggtaca	ac	ccacaac	ctc	gaagc	ctccg	120
gcaccacgc	ccc	acagaga	gc	tctccgc	g	attactac	t	ccaagaa	aatg	tct	cagctt	180
gaaactctg	tc	gttccgt	ca	cttctcag	c	gttcaaa	g	aagtc	cccat	ctc	agctcca	240
gccaccattc	gc	cttctct	tc	acgactgc	tt	cgttgag	g	gttgtg	atgg	gtc	gatattg	300
atagaaacaa	aga	aaaggaag	ca	gaaatga	gc	agagagag	a	agcatat	ga	ga	taaggaa	360
ttgagagagg	aag	gatttga	ta	gtatcatc	a	aagcgaa	g	g	gtgtg	gtc	gaattgc	420
ccttctctg	tct	Ttctct	tg	atattctc	gc	tattg	ccg	ctc	gagatt	cat	tcatctg	480
gcaggtgggc	ctt	actatca	agt	gaaaaaa	g	gaaggtg	ggg	acg	gaaaa	at	caacggca	540
aagaacgtcc	ctc	caaacat	ac	ctcgatca	aa	actccac	ccg	ttg	atcaact	cat	caagctc	600
ttcgcgtcca	aag	gactaac	ct	gtagagg	aa	ctgctgt	ctc	ttt	ctggttc	cca	caccatc	660
ggttgcgcca	ttg	taaaaat	tt	cttgggtc	gt	ctctacga	ca	ctaca	aaagg	ac	aaaacgac	720
ccgaccgcag	tct	taccacaa	ag	attactaa	aa	agagctccg	g	gat	gtctt	gtg	ctttttccg	780
gcggaagctc	tg	gaagtcgc	ct	ctccgctc	ac	gctacac	ac	tc	ggtt	gtg	tttgataatg	840
gatatctcac	agg	cttagga	ac	caacatgg	gc	cttctcgg	g	gtc	ggacc	caa	gctttgtctc	900
ttgaccgcag	gc	gaagccc	att	gcaattg	ag	atggg	caa	ag	ataa	agc	ga	960
agggcgtttg	ag	acgctatg	ga	ataaaatg	gt	tccattg	g	tg	taaa	gaga	gggaagagac	1020
atggggaat	ac	gtacggat	tg	tcgagctc	tt	ttatagat	tt	ct	tttatt	gt	ctgtgtctg	1080
atgggttttt	tct	gtatctt	gat	gtgttct	gt	gcatgtg	t	tc	tttaatt	tatt	agcatt	1140
ttcgtgattg	ttt	gttgat	agt	ataaagt	att	ttttt						

(2) INFORMATION FOR SEQ ID NO:2324:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 249 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..249
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572539

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2324:

Thr	Ser	His	Asn	Pro	Thr	Met	His	Val	Ile	Ser	Leu	Ser	Leu	Ser	Ser
1			5					10					15		
Ile	Phe	Phe	Phe	Leu	Phe	Leu	Thr	Ser	Thr	Ile	Leu	Ile	Ser	Pro	Val
			20					25					30		
Gln	Pro	Thr	Thr	Ser	Lys	Pro	Pro	Ala	Pro	Arg	Pro	His	Arg	Glu	Leu
			35				40					45			
Ser	Ala	Asp	Tyr	Tyr	Ser	Lys	Lys	Cys	Pro	Gln	Leu	Glu	Thr	Leu	Val
			50			55				60					
Gly	Ser	Val	Thr	Ser	Gln	Arg	Phe	Lys	Glu	Val	Pro	Ile	Ser	Ala	Pro
			65			70			75					80	
Ala	Thr	Ile	Arg	Leu	Phe	Phe	His	Asp	Cys	Phe	Val	Glu	Gly	Cys	Asp
			85					90						95	
Gly	Ser	Ile	Leu	Ile	Glu	Thr	Lys	Lys	Gly	Ser	Lys	Lys	Leu	Ala	Glu
			100				105						110		
Arg	Glu	Ala	Tyr	Glu	Asn	Lys	Glu	Leu	Arg	Glu	Glu	Gly	Phe	Asp	Ser
			115			120				125					
Ile	Ile	Lys	Ala	Lys	Ala	Leu	Val	Glu	Ser	His	Cys	Pro	Ser	Leu	Val

130	135	140
Ser Xaa Ser Asp Ile Leu Ala Ile Ala Ala Arg Asp Phe Ile His Leu		
145	150	155
Ala Gly Gly Pro Tyr Tyr Gln Val Lys Lys Gly Arg Trp Asp Gly Lys		160
	165	170
Arg Ser Thr Ala Lys Asn Val Pro Pro Asn Ile Pro Arg Ser Asn Ser		175
	180	185
Thr Val Asp Gln Leu Ile Lys Leu Phe Ala Ser Lys Gly Leu Thr Val		190
	195	200
Glu Glu Leu Val Val Leu Ser Gly Ser His Thr Ile Gly Ser Pro Ile		205
	210	215
Val Lys Ile Ser Leu Val Val Ser Thr Thr Thr Lys Ala Gln Asn Asp		220
225	230	235
Pro Thr Arg Val Leu Thr Lys Asp Tyr		240
	245	

(2) INFORMATION FOR SEQ ID NO:2325:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 243 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..243

(D) OTHER INFORMATION: / Ceres Seq. ID 1572540

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2325:

Met His Val Ile Ser Leu Ser Leu Ser Ser Ile Phe Phe Leu Phe	
1	5
	10
Leu Thr Ser Thr Ile Leu Ile Ser Pro Val Gln Pro Thr Thr Ser Lys	15
	20
	25
Pro Pro Ala Pro Arg Pro His Arg Glu Leu Ser Ala Asp Tyr Tyr Ser	30
	35
	40
Lys Lys Cys Pro Gln Leu Glu Thr Leu Val Gly Ser Val Thr Ser Gln	45
	50
	55
Arg Phe Lys Glu Val Pro Ile Ser Ala Pro Ala Thr Ile Arg Leu Phe	60
	65
	70
Phe His Asp Cys Phe Val Glu Gly Cys Asp Gly Ser Ile Leu Ile Glu	75
	80
	85
	90
Thr Lys Lys Gly Ser Lys Lys Leu Ala Glu Arg Glu Ala Tyr Glu Asn	95
	100
	105
Lys Glu Leu Arg Glu Glu Gly Phe Asp Ser Ile Ile Lys Ala Lys Ala	110
	115
	120
Leu Val Glu Ser His Cys Pro Ser Leu Val Ser Xaa Ser Asp Ile Leu	125
	130
	135
Ala Ile Ala Ala Arg Asp Phe Ile His Leu Ala Gly Gly Pro Tyr Tyr	140
	145
	150
Gln Val Lys Lys Gly Arg Trp Asp Gly Lys Arg Ser Thr Ala Lys Asn	155
	160
	165
	170
Val Pro Pro Asn Ile Pro Arg Ser Asn Ser Thr Val Asp Gln Leu Ile	175
	180
	185
Lys Leu Phe Ala Ser Lys Gly Leu Thr Val Glu Glu Leu Val Val Leu	190
	195
	200
Ser Gly Ser His Thr Ile Gly Ser Pro Ile Val Lys Ile Ser Leu Val	205
	210
	215
Val Ser Thr Thr Thr Lys Ala Gln Asn Asp Pro Thr Arg Val Leu Thr	220
225	230
	235
Lys Asp Tyr	240

(2) INFORMATION FOR SEQ ID NO:2326:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1239 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..1239
(D) OTHER INFORMATION: / Ceres Seq. ID 1572569

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2326:

acaattcaga	ttccaaatttt	ctcaaaactct	aaaatcaatc	tctcaaatct	ctcaaccgtg	60
atcaaggtag	atttctgagt	tcttattgta	ttctctcgat	ttgtttcggt	cgatcgcaat	120
ttaggctctg	tcttttgatt	ttgatctcgt	taatctctga	tccgaggcaa	attacatagt	180
ttcatcggtta	gatctctctt	tatttctcga	ttagggttgg	tatttttcgc	agatctgttt	240
attttcttgt	tgtttccttg	tatttgatcc	gatttgttga	aagaatttgt	gtgttctcga	300
ttatttatgc	tttgatctgt	gattttttatc	tagatttggt	gttagttttc	tgtttgtgcg	360
atcgaatttg	tcgattaatc	tcggtttttc	tgattaacag	atgcagatct	tcgttaagac	420
gtctaccgga	aagactatca	ccctcgaggt	ggaaagctct	gacaccatcg	acaacgtaa	480
ggccaagatc	caggataaag	aaggtattcc	tccggatcag	cagagggtta	tcttcgcggg	540
aaagcagttg	gaggatggcc	gcacgttggc	ggattacaat	atccagaagg	aatccaccct	600
ccacttggtt	ctcaggctcc	gtggtgggtat	gcagattttc	gttaaaaccc	taacgggaaa	660
gaagattact	cttgagggtg	agagctctga	caccattgac	aacgtcaagg	ccaagatcca	720
agataaggag	ggtattctct	cggaccagca	gaggttgatc	ttgcgcggaa	agcaactgtt	780
ggacggcaga	accttggcgg	attacaacat	ccagaaggag	tctacgcttc	atttggctTt	840
tcgctctgcg	tggagggtatg	cagatcttcg	taaaagacttt	gacccggaaa	acatcaactc	900
ttgaagtgtg	gagctccgag	accattgata	acgtgaagcg	taagatccag	gacaagggaag	960
cgattctctc	ggaccagcag	cgtctcatct	tcgctggaaa	gcagcttgag	gatggacgtg	1020
ctttggcoga	ctacaacatc	cagaaggagt	ctactcttca	ctctgtctcc	cgctcccgta	1080
gtggttttcta	aaactgtgtct	ctctctctta	tggttactga	accaagtcca	tgatctcggt	1140
catctagatc	tttgggtggt	tatgttttgg	ggccatgtac	agcctctgat	aaataatgtg	1200
tcgactatgt	ttcgtttctt	ttcatctctc	ttttctttc			

(2) INFORMATION FOR SEQ ID NO:2327:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 167 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..167
(D) OTHER INFORMATION: / Ceres Seq. ID 1572570

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2327:

Met	Gln	Ile	Phe	Val	Lys	Thr	Leu	Thr	Gly	Lys	Thr	Ile	Thr	Leu	Glu
1				5					10					15	
Val	Glu	Ser	Ser	Asp	Thr	Ile	Asp	Asn	Val	Lys	Ala	Lys	Ile	Gln	Asp
				20				25					30		
Lys	Glu	Gly	Ile	Pro	Pro	Asp	Gln	Gln	Arg	Leu	Ile	Phe	Ala	Gly	Lys
				35				40				45			
Gln	Leu	Glu	Asp	Gly	Arg	Thr	Leu	Ala	Asp	Tyr	Asn	Ile	Gln	Lys	Glu
				50				55			60				
Ser	Thr	Leu	His	Leu	Val	Leu	Arg	Leu	Arg	Gly	Gly	Met	Gln	Ile	Phe
				65			70			75				80	
Val	Lys	Thr	Leu	Thr	Gly	Lys	Thr	Ile	Thr	Leu	Glu	Val	Glu	Ser	Ser
				85				90					95		
Asp	Thr	Ile	Asp	Asn	Val	Lys	Ala	Lys	Ile	Gln	Asp	Lys	Glu	Gly	Ile
				100				105					110		
Pro	Pro	Asp	Gln	Gln	Arg	Leu	Ile	Phe	Ala	Gly	Lys	Gln	Leu	Glu	Asp
				115			120					125			
Gly	Arg	Thr	Leu	Ala	Asp	Tyr	Asn	Ile	Gln	Lys	Glu	Ser	Thr	Leu	His
				130			135					140			

Leu Val Phe Ala Ser Ala Trp Arg Tyr Ala Asp Leu Arg Lys Asp Phe
145 150 155 160
Asp Arg Lys Asp His His Ser
165

(2) INFORMATION FOR SEQ ID NO:2328:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 91 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..91

(D) OTHER INFORMATION: / Ceres Seq. ID 1572571

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2328:

Met Thr Ile Phe Val Lys Thr Leu Thr Gly Lys Thr Ile Thr Leu Glu	
1 5 10 15	
Val Glu Ser Ser Asp Thr Ile Asp Asn Val Lys Ala Lys Ile Gln Asp	
20 25 30	
Lys Glu Gly Ile Pro Pro Asp Gln Gln Arg Leu Ile Phe Ala Gly Lys	
35 40 45	
Gln Leu Glu Asp Gly Arg Thr Leu Ala Asp Tyr Asn Ile Gln Lys Glu	
50 55 60	
Ser Thr Leu His Leu Val Phe Ala Ser Ala Trp Arg Tyr Ala Asp Leu	
65 70 75 80	
Arg Lys Asp Phe Asp Arg Lys Asp His His Ser	
85 90	

(2) INFORMATION FOR SEQ ID NO:2329:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1597 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1597

(D) OTHER INFORMATION: / Ceres Seq. ID 1572576

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2329:

aaaaataaaga	accttgacaa	cttctctaca	acactcaatt	tttctctcta	atgggtggaag	60
caagaagctt	gaagaaaacca	atccaattgg	gtaataaaga	agatcaaaaac	octagaaaaat	120
tctactcttc	attcatcttt	aaagctcttta	tcctcacogt	gctctgcgac	gtcgatccotg	180
tcttctcttc	tcagacacca	gagcttgcta	accaaacaag	actctcgag	cttctccacc	240
tgtttttcgt	cggtatcgca	gtctcttaac	gtctcttacc	ccgcaggaag	tacgacggag	300
gaggaggttg	aggaacaacg	aatagtgatc	acaacaaggc	tgatcatagt	aataataatt	360
cgcatctata	tgtgcctaa	attcttgaag	tatctctgtt	ttttacacgt	gggtcacgaga	420
gtgaactcga	accgtccgat	gattctctcg	gtgatcaacg	taagtctcag	acatggaaga	480
acaagtacca	catgaaaatc	cccgagggtg	agactcggtt	cggtgatcga	gttagttcag	540
aaaacagaga	gaagcctctg	cttttgcggg	ttcggagcgt	gaattattct	cgtgtttctg	600
attcttccgg	cgataattcc	ggctgatggg	agaaagtga	attcaagaga	gaacttctga	660
agactcttat	cgatgataat	agtgatgtgc	ttccttctcc	gattccatgg	aggtcaagat	720
catcttcttc	atcatcatca	tcatcaaaag	aggttggaatc	tctaccgtcc	gttaagaatc	780
tgactacagt	tgaatcacag	ccggttgatca	agaactctgac	accatcttct	tctttctctt	840
ctccaagaaa	gtcgaaatct	atacctaata	tgcgatctga	gttccatcca	tctccgcccac	900
cgctctctcc	gccgcgcgca	ccactaccgg	cggttttata	ctctctcgct	agaaaagagt	960
atcccggaat	ttacacgggt	gagagagagag	aatcatcagt	tcacaagaag	aaattttcag	1020
gaggtgtagt	tcattctctc	ccgcctctct	ctccaccacc	tcctggtggag	tattataagt	1080
cactctcgac	aaaattcaga	ctaagtaaac	aacggagaaa	gtctctcgag	caaaagatgw	1140
aaagaaacgc	tcctaaaaag	ggttggtggt	ccgatccaat	cgtggaatcg	aaggaacaa	1200
acacagagaa	gaatgatcaa	agaagtaact	tgaggagcaa	ggcagctgga	gaatcccgaga	1260

(2) INFORMATION FOR SEQ ID NO:2330:

(i) SEQUENCE CHARACTERISTICS:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 473 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

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(ix) FEATURE:
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(A) NAME/KEY: peptide

(B) LOCATION: 1..473

(D) OTHER INFORMATION: / Ceres Seq. ID 1572577

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2330:

Met	Val	Glu	Ala	Arg	Ser	Leu	Lys	Lys	Pro	Ile	Gln	Leu	Gly	Asn	Lys
1				5					10					15	
Glu	Asp	Gln	Asn	Pro	Arg	Lys	Phe	Tyr	Ser	Arg	Phe	Ile	Phe	Lys	Ala
			20					25					30		
Leu	Ile	Leu	Thr	Val	Leu	Cys	Ala	Val	Val	Pro	Val	Phe	Leu	Ser	Gln
		35					40					45			
Thr	Pro	Glu	Leu	Ala	Asn	Gln	Thr	Arg	Leu	Leu	Glu	Leu	Leu	His	Leu
		50				55					60				
Val	Phe	Val	Gly	Ile	Ala	Val	Ser	Tyr	Gly	Leu	Phe	Ser	Arg	Arg	Asn
65					70					75					80
Tyr	Asp	Gly	Gly	Gly	Gly	Gly	Gly	Thr	Ser	Asn	Ser	Asp	His	Asn	Lys
				85					90					95	
Ala	Asp	His	Ser	Asn	Asn	Asn	Ser	His	Ser	Tyr	Val	Pro	Lys	Ile	Leu
				100				105						110	
Glu	Val	Ser	Ser	Val	Phe	Asn	Val	Gly	His	Glu	Ser	Glu	Ser	Glu	Pro
				115				120				125			
Ser	Asp	Asp	Ser	Ser	Gly	Asp	Gln	Arg	Lys	Phe	Gln	Thr	Trp	Lys	Asn
		130					135				140				
Lys	Tyr	His	Met	Lys	Ile	Pro	Glu	Val	Glu	Thr	Arg	Phe	Val	Asp	Arg
145					150					155					160
Val	Ser	Ser	Glu	Asn	Arg	Glu	Lys	Pro	Leu	Leu	Leu	Pro	Val	Arg	Ser
				165					170					175	
Leu	Asn	Tyr	Ser	Arg	Val	Ser	Asp	Ser	Ser	Gly	Asp	Asn	Ser	Gly	Arg
				180				185					190		
Trp	Glu	Lys	Val	Arg	Ser	Lys	Arg	Glu	Leu	Leu	Lys	Thr	Leu	Gly	Asp
		195					200					205			
Asp	Asn	Ser	Asp	Val	Leu	Pro	Ser	Pro	Ile	Pro	Trp	Arg	Ser	Arg	Ser
					215						220				
Ser	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Lys	Glu	Val	Glu	Ser	Leu	Pro	Ser
225					230					235					240
Val	Lys	Asn	Leu	Thr	Thr	Val	Glu	Ser	Gln	Pro	Leu	Ile	Lys	Asn	Leu
				245					250					255	
Thr	Pro	Ser	Ser	Ser	Phe	Ser	Ser	Pro	Arg	Lys	Ser	Asn	Pro	Ile	Pro
				260				265					270		
Asn	Leu	Ala	Ser	Glu	Phe	His	Pro	Ser	Pro	Pro	Pro	Pro	Pro	Pro	Pro
				275			280					285			
Pro	Pro	Pro	Leu	Pro	Ala	Phe	Tyr	Asn	Ser	Ser	Ser	Arg	Lys	Asp	His
					295						300				
Pro	Gly	Ile	Tyr	Arg	Val	Glu	Arg	Arg	Glu	Ser	Ser	Val	His	Lys	Thr
305					310					315					320
Lys	Phe	Ala	Gly	Gly	Glu	Phe	His	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro
				325					330					335	
Pro	Pro	Val	Glu	Tyr	Tyr	Lys	Ser	Pro	Pro	Thr	Lys	Phe	Arg	Leu	Ser

340 345 350
Asn Glu Arg Arg Lys Ser Ser Glu Gln Lys Met Xaa Arg Asn Ala Pro
355 360 365
Lys Lys Val Trp Trp Ser Asp Pro Ile Val Glu Ser Lys Glu Gln Asp
370 375
Thr Glu Lys Asn Asp Gln Arg Ser Asn Leu Gly Ser Lys Ala Val Glu
385 390 395 400
Glu Ser Glu Asn Gly Glu Gln Arg Arg Gly Glu Asn Glu Ile His Asp
405 410 415
Glu Val Glu Lys Lys Ile Val Glu Glu Glu Gly Val Ser Glu Ile Asn
420 425 430
Asn Gly Ser Asp Val Asp Lys Lys Ala Asp Glu Phe Ile Ala Lys Phe
435 440 445
Arg Glu Gln Ile Arg Leu Gln Arg Ile Glu Ser Ile Lys Arg Ser Thr
450 455 460
Asn Lys Ile Ser Ala Asn Ser Ser Arg
465 470
(2) INFORMATION FOR SEQ ID NO:2331:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 326 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..326
(D) OTHER INFORMATION: / Ceres Seq. ID 1572578
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2331:
Met Lys Ile Pro Glu Val Glu Thr Arg Phe Val Asp Arg Val Ser Ser
1 5 10 15
Glu Asn Arg Glu Lys Pro Leu Leu Leu Pro Val Arg Ser Leu Asn Tyr
20 25 30
Ser Arg Val Ser Asp Ser Ser Gly Asp Asn Ser Gly Arg Trp Glu Lys
35 40 45
Val Arg Ser Lys Arg Glu Leu Leu Lys Thr Leu Gly Asp Asp Asn Ser
50 55 60
Asp Val Leu Pro Ser Pro Ile Pro Trp Arg Ser Arg Ser Ser Ser Ser
65 70 75 80
Ser Ser Ser Ser Ser Lys Glu Val Glu Ser Leu Pro Ser Val Lys Asn
85 90 95
Leu Thr Thr Val Glu Ser Gln Pro Leu Ile Lys Asn Leu Thr Pro Ser
100 105 110
Ser Ser Phe Ser Ser Pro Arg Lys Ser Asn Pro Ile Pro Asn Leu Ala
115 120 125
Ser Glu Phe His Pro Ser Pro Pro Pro Pro Pro Pro Pro Pro Pro
130 135 140
Leu Pro Ala Phe Tyr Asn Ser Ser Ser Arg Lys Asp His Pro Gly Ile
145 150 155 160
Tyr Arg Val Glu Arg Arg Glu Ser Ser Val His Lys Thr Lys Phe Ala
165 170 175
Gly Gly Glu Phe His Pro Pro Pro Pro Pro Pro Pro Pro Pro Val
180 185 190
Glu Tyr Tyr Lys Ser Pro Pro Thr Lys Phe Arg Leu Ser Asn Glu Arg
195 200 205
Arg Lys Ser Ser Glu Gln Lys Met Xaa Arg Asn Ala Pro Lys Lys Val
210 215 220
Trp Trp Ser Asp Pro Ile Val Glu Ser Lys Glu Gln Asp Thr Glu Lys
225 230 235 240
Asn Asp Gln Arg Ser Asn Leu Gly Ser Lys Ala Val Glu Glu Ser Glu
245 250 255

Asn Gly Glu Gln Arg Arg Gly Glu Asn Glu Ile His Asp Glu Val Glu
260 265 270
Lys Lys Ile Val Glu Glu Glu Gly Val Ser Glu Ile Asn Asn Gly Ser
275 280 285
Asp Val Asp Lys Lys Ala Asp Glu Phe Ile Ala Lys Phe Arg Glu Gln
290 295 300
Ile Arg Leu Gln Arg Ile Glu Ser Ile Lys Arg Ser Thr Asn Lys Ile
305 310 315 320
Ser Ala Asn Ser Ser Arg
325

(2) INFORMATION FOR SEQ ID NO:2332:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 783 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..783

(D) OTHER INFORMATION: / Ceres Seq. ID 1572627

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2332:

attgaagtct	gcgtctgtga	gatacagctt	tagctttgtg	gatgcagaat	tcgagactat	60
acattctttt	ttaagttctt	gagcttgga	caataacctt	ttcactctag	ttgtttcttc	120
aactaaatgg	atactgggtg	gtttgttag	gaaaaagggt	agaacagatt	atatgttga	180
aacctggatc	ttagaataaa	cgaggcttcg	ttgataaaaa	tgttttctcc	atatgggaag	240
atcatatcag	aagactctct	ttggcacaca	cgcgggccaa	agaagggaga	acctcggggt	300
tatgctttca	ttcaatacac	ccttaaaag	tgagcataca	ggaagctgaa	ttggcgaaag	360
agaagatgca	tgggagatta	gcttgttgta	ggcctttagt	ggtgcgtcta	gctagtgaga	420
agcaactaga	agattctctc	catgatcaat	ccaaaagatc	attaccagaa	ggaacagaa	480
ccagatttgt	aaacggggagc	agotcaggac	aaatgagccg	agacgaaaaa	gtaactgcc	540
ttaaagaacaa	actcaaaagct	ttggaagaag	atgagaaaacg	tgatccCaag	aaacagaaaa	600
tttaagaaaa	cggttttcaa	acacacaact	ttgggtctat	gtgactctgt	gactctgacc	660
atttttcagt	tttggtttga	tttgatttgg	tttaccgggt	taatcgaaac	caattttgat	720
ttaatatattc	ggtttggtct	agtgatgat	ataaaatttg	taatggaaag	caaaagtga	780

cg

(2) INFORMATION FOR SEQ ID NO:2333:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..68

(D) OTHER INFORMATION: / Ceres Seq. ID 1572628

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2333:

Met	Asp	Thr	Gly	Gly	Phe	Val	Asp	Glu	Lys	Gly	Glu	Asn	Arg	Leu	Tyr
1			5					10			15				
Val	Gly	Asn	Leu	Asp	Leu	Arg	Ile	Asn	Glu	Ala	Ser	Leu	Ile	Lys	Met
			20					25					30		
Phe	Ser	Pro	Tyr	Gly	Lys	Ile	Ile	Ser	Glu	Asp	Phe	Leu	Trp	His	Thr
			35					40				45			
Arg	Gly	Pro	Lys	Lys	Gly	Glu	Pro	Arg	Gly	Tyr	Ala	Phe	Ile	Gln	Tyr
			50					55				60			
Ser	Leu	Lys	Glu												

65

(2) INFORMATION FOR SEQ ID NO:2334:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 79 amino acids

(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..79
(D) OTHER INFORMATION: / Ceres Seq. ID 1572629
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2334:
Met His Gly Arg Leu Ala Cys Gly Arg Pro Leu Val Val Arg Leu Ala
1 5 10 15
Ser Glu Lys His Leu Glu Asp Ser Ser His Asp His Ser Lys Arg Ser
20 25 30
Leu Pro Glu Gly Asn Arg Thr Arg Phe Val Asn Gly Ser Ser Ser Gly
35 40 45
Gln Met Ser Arg Asp Glu Lys Val Thr Ala Ile Lys Asn Lys Leu Lys
50 55 60
Ala Leu Glu Glu Asp Glu Lys Arg Asp Pro Lys Lys Gln Lys Ile
65 70 75

(2) INFORMATION FOR SEQ ID NO:2335:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 58 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..58
(D) OTHER INFORMATION: / Ceres Seq. ID 1572630
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2335:
Met Arg Asn Val Ile Pro Arg Asn Arg Lys Phe Lys Lys Thr Val Phe
1 5 10 15
Lys His Thr Thr Leu Gly Leu Cys Asp Ser Val Thr Leu Thr Ile Phe
20 25 30
Gln Phe Trp Phe Asp Leu Ile Trp Phe Thr Gly Leu Ile Glu Thr Asn
35 40 45
Phe Asp Leu Ile Phe Arg Phe Gly Ser Val
50 55

(2) INFORMATION FOR SEQ ID NO:2336:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 910 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..910
(D) OTHER INFORMATION: / Ceres Seq. ID 1572643
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2336:
atcaactctc tctctcaatt tcacaactct ccttttctat ttctctctct agaaaaatat 60
catcatctat caattatata gaggacttat tttagattcat ttcatataaa tggagaaaag 120
agaaagttagt ggtggttctg gatcaggaga tgcagaggtg agaaaaggcg catggacgat 180
ggaagaagat ttgatttcca tcaattatat cgccaatcat ggtgaagggt tttggaactc 240
tctgcacaaa tctgcaggac taaaacgcac cgggaaaagt tgccggctcc ggtggctgaa 300
ctacctccga cctgatgtgc gacggggaaa tatcacacca gaagaacagc tcaccatcat 360
ggaacttcat gcaaaatggg gaaatagggt gtcaaaaatt gcaaaagcatt taccaggaag 420
gaccgacaat gagataaaga acttttgagg gactaagatc cagaaatata tcatcaagag 480
cgagaaaacg acgaccgttg gatcacaaag ctccgagttt ataaaccatc atgcgcacaac 540
gagccatgtc atgaatgata ctcaagaaac Catggatgat tattctccaa cgacgtcgta 600

tcaacatgcc	agcaatatta	atcagcagct	taattatggt	aattatgtgc	ctgaatccag	660
ttcgatcatg	atgccattat	ctgttgatca	atccgaacaa	aactattgga	gcgtcgatga	720
tccttggccc	atgaatatat	ataatggtaa	ttaataaata	agttcggtaa	aacttatata	780
taattacggt	ccaagagggt	ttctatatata	acagagtact	gtatgggttt	gcctcattgt	840
ttagaggtag	gtacttaata	taaggttgga	gatcttatat	gaattaataa	ataactcgta	900
tttactagat						

(2) INFORMATION FOR SEQ ID NO:2337:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 214 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..214

(D) OTHER INFORMATION: / Ceres Seq. ID 1572644

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2337:

Met	Glu	Lys	Arg	Glu	Glu	Ser	Ser	Gly	Gly	Ser	Gly	Ser	Gly	Asp	Ala	Glu	
1				5					10						15		
Val	Arg	Lys	Gly	Pro	Trp	Thr	Met	Glu	Glu	Asp	Leu	Ile	Leu	Ile	Asn		
			20					25					30				
Tyr	Ile	Ala	Asn	His	Gly	Glu	Gly	Val	Trp	Asn	Ser	Leu	Ala	Lys	Ser		
			35				40					45					
Ala	Gly	Leu	Lys	Arg	Thr	Gly	Lys	Ser	Cys	Arg	Leu	Arg	Trp	Leu	Asn		
			50				55					60					
Tyr	Leu	Arg	Pro	Asp	Val	Arg	Arg	Gly	Asn	Ile	Thr	Pro	Glu	Glu	Gln		
			65				70					75			80		
Leu	Thr	Ile	Met	Glu	Leu	His	Ala	Lys	Trp	Gly	Asn	Arg	Trp	Ser	Lys		
			85					90					95				
Ile	Ala	Lys	His	Leu	Pro	Gly	Arg	Thr	Asp	Asn	Glu	Ile	Lys	Asn	Phe		
			100					105					110				
Trp	Arg	Thr	Lys	Ile	Gln	Lys	Tyr	Ile	Ile	Lys	Ser	Gly	Glu	Thr	Thr		
			115					120					125				
Thr	Val	Gly	Ser	Gln	Ser	Ser	Glu	Phe	Ile	Asn	His	His	Ala	Thr	Thr		
			130				135					140					
Ser	His	Val	Met	Asn	Asp	Thr	Gln	Glu	Thr	Met	Asp	Met	Tyr	Ser	Pro		
			145				150				155				160		
Thr	Thr	Ser	Tyr	Gln	His	Ala	Ser	Asn	Ile	Asn	Gln	Gln	Leu	Asn	Tyr		
			165					170					175				
Gly	Asn	Tyr	Val	Pro	Glu	Ser	Ser	Ser	Ile	Met	Met	Pro	Leu	Ser	Val		
			180					185					190				
Asp	Gln	Ser	Glu	Gln	Asn	Tyr	Trp	Ser	Val	Asp	Asp	Leu	Trp	Pro	Met		
			195				200					205					
Asn	Ile	Tyr	Asn	Gly	Asn												
			210														

(2) INFORMATION FOR SEQ ID NO:2338:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 191 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..191

(D) OTHER INFORMATION: / Ceres Seq. ID 1572645

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2338:

Met	Glu	Glu	Asp	Leu	Ile	Leu	Ile	Asn	Tyr	Ile	Ala	Asn	His	Gly	Glu	
1				5				10					15			
Gly	Val	Trp	Asn	Ser	Leu	Ala	Lys	Ser	Ala	Gly	Leu	Lys	Arg	Thr	Gly	

(2) INFORMATION FOR SEO ID NO:2339:

(A) LENGTH: 131 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(A) NAME/KEY: peptide
(B) LOCATION: 1..131

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2339:

(2) INFORMATION FOR SEQ ID NO:2340:

(A) LENGTH: 1928 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(A) NAME/KEY: -
(B) LOCATION: 1..1928

(D) OTHER INFORMATION: / Ceres Seq. ID 1572647
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2340:

ttctctcttc	ttccattctc	acaaattcca	aacatctctc	ttcttttctc	totcacacac	60
aaaattgcag	aagaagaaga	gtcatgaatg	gtgaagaaga	ctttgtagaa	gattgtctcg	120
ttttttgtga	gattgatctc	tctggaagat	atggaagata	cgatgaaata	cttggaaga	180
gagcttcaaa	gacagtatac	agagcatttg	atgagtaga	aggtagatga	gtagcatgga	240
accaagtaaa	gcttcgaaat	ttcacaagga	atcctgagga	attagagaag	tttttcagag	300
agattcatct	ttccaagact	ttgaatcatc	aaaacattat	gaaattctac	actctctggg	360
ttgataccaa	caatttatca	atcaattttg	tcaactgaact	cttcacacct	ggtagcttca	420
gacagtatag	gttgagacat	agaagagtag	atattagagc	agtgaagcaa	tgggtgcaagc	480
agatttttaa	agggctcttc	tattttacata	ctgctttctc	accaattata	catagagatc	540
tcaaatgtga	taacattttt	atcaatggaa	accaaggtga	agtcgaagtc	ggtagacctg	600
gactcgctgc	gattctctcg	aaatcacatg	ccgttcgttg	cggttggaac	cctgagttta	660
tggtctcaga	agtgtagatg	gaggaatata	atgagttggt	tgatgtatat	gcttttgcca	720
tgtgtgtgtt	ggagatgggt	acttttgatt	atccttacag	tgaatgtact	caaccggcac	780
aaatctacaa	gaaagttaac	tccgggaaaa	agcctgaagc	tttttactta	gtgaaggatc	840
ctgaggttgc	tgaagtttgt	gagaagtgtt	tagctaacgt	gacgtgtagg	ctaacggcat	900
tgtagctttt	acaagacctc	tttctacaa	atgataatat	ggatggattt	gttatgagac	960
ctattgatta	ctacaatgtg	tatgatgaaa	ctgggtgtgt	ccttagacat	cctttgattg	1020
ctagctctct	ttaccatgat	cagtttgagt	cgtcacagat	atgtgagatc	gatctttctg	1080
ctaagcatga	tgaagatcat	gtcgacattt	cgattaaagg	gaagagaaac	ggtagctgat	1140
ggatattctt	gagactttga	atatctgatg	ctgaaggacg	gataaggaa	atttactctc	1200
cgtttgagac	ggctattggt	actgcagtga	gtgtagcggt	tgagatgggt	ctcagagctcg	1260
acataacgaa	tcaagatgat	gcgaaaatcg	cggagatgat	cgatgcagag	attgtcgcac	1320
tgggtgcctga	ttggaaaaat	gatacagaaa	gtTccaaaa	tgtatacaac	acaaagaaca	1380
acaaactctc	aggattctct	ggagagtggt	cttcaaacgg	gtatatacaa	gagactgtat	1440
catcaggaga	aaaattctat	cataatcatc	atgagttcga	tagttctgaa	gacagagact	1500
tgtctctcgt	tcaacggtagg	tttgccgata	tgtgggggtt	gcgagaatca	tattctgatg	1560
atggagaaaa	acagagctca	aggaaggtta	gaagtggacg	gtggctggag	aatgagatga	1620
gacgagaact	gagatggcct	aaggcaagcg	acaaattaca	acttatgaaa	attgagaggtc	1680
aaaacgatctg	cgagacacgc	atagagatct	ctcttacacc	gggaacttca	gtttcgctac	1740
ctcttcttta	cagggcctata	tcacttctct	tggatgccgt	ggatatgtga	cattattgtg	1800
aagtcctgat	atagttatca	cttatatttg	tatgtttcga	catttttaac	ttttgttaag	1860
ttaaaagtta	atgacatagt	gtactttatt	taaagagaag	aagagtaaac	gaaaaacata	1920
aattagtc						

(2) INFORMATION FOR SEQ ID NO:2341:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 595 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..595
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1572648

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2341:

Ser	Ser	Ser	Ser	Ile	Ser	Thr	Asn	Ser	Lys	His	Leu	Ser	Leu	Phe	Leu
1				5					10					15	
Ser	His	Thr	Gln	Asn	Cys	Ser	Arg	Arg	Arg	Val	Met	Asn	Gly	Glu	Glu
			20						25				30		
Ser	Phe	Val	Glu	Asp	Cys	Ser	Val	Phe	Val	Glu	Ile	Asp	Pro	Ser	Gly
			35				40					45			
Arg	Tyr	Gly	Arg	Tyr	Asp	Glu	Ile	Leu	Gly	Lys	Gly	Ala	Ser	Lys	Thr
			50			55					60				
Val	Tyr	Arg	Ala	Phe	Asp	Glu	Tyr	Glu	Gly	Ile	Glu	Val	Ala	Trp	Asn
			65			70				75				80	
Gln	Val	Lys	Leu	Arg	Asn	Phe	Thr	Arg	Asn	Pro	Glu	Glu	Leu	Glu	Lys
			85					90					95		
Phe	Thr	Arg	Glu	Ile	His	Leu	Leu	Lys	Thr	Leu	Asn	His	Gln	Asn	Ile
			100					105					110		

Met	Lys	Phe	Tyr	Thr	Ser	Trp	Val	Asp	Thr	Asn	Asn	Leu	Ser	Ile	Asn
	115						120					125			
Phe	Val	Thr	Glu	Leu	Phe	Thr	Ser	Gly	Thr	Leu	Arg	Gln	Tyr	Arg	Leu
	130					135					140				
Arg	His	Arg	Arg	Val	Asn	Ile	Arg	Ala	Val	Lys	Gln	Trp	Cys	Lys	Gln
145					150					155					160
Ile	Leu	Lys	Gly	Leu	Leu	Tyr	Leu	His	Ser	Arg	Ser	Pro	Pro	Ile	Ile
				165					170					175	
His	Arg	Asp	Leu	Lys	Cys	Asp	Asn	Ile	Phe	Ile	Asn	Gly	Asn	Gln	Gly
			180					185					190		
Glu	Val	Lys	Ile	Gly	Asp	Leu	Gly	Leu	Ala	Ala	Ile	Leu	Arg	Lys	Ser
			195				200					205			
His	Ala	Val	Arg	Cys	Val	Gly	Thr	Pro	Glu	Phe	Met	Ala	Pro	Glu	Val
	210					215					220				
Tyr	Asp	Glu	Glu	Tyr	Asn	Glu	Leu	Val	Asp	Val	Tyr	Ala	Phe	Gly	Met
225					230					235					240
Cys	Val	Leu	Glu	Met	Val	Thr	Phe	Asp	Tyr	Pro	Tyr	Ser	Glu	Cys	Thr
				245					250					255	
His	Pro	Ala	Gln	Ile	Tyr	Lys	Lys	Val	Thr	Ser	Gly	Lys	Lys	Pro	Glu
			260					265					270		
Ala	Phe	Tyr	Leu	Val	Lys	Asp	Pro	Glu	Val	Arg	Glu	Phe	Val	Glu	Lys
	275					280						285			
Cys	Leu	Ala	Asn	Val	Thr	Cys	Arg	Leu	Thr	Ala	Leu	Glu	Leu	Leu	Gln
	290					295					300				
Asp	Pro	Phe	Leu	Gln	Asp	Asn	Met	Asp	Gly	Phe	Val	Met	Arg	Pro	
305					310				315					320	
Ile	Asp	Tyr	Tyr	Asn	Gly	Tyr	Asp	Glu	Thr	Gly	Val	Phe	Leu	Arg	His
				325					330					335	
Pro	Leu	Ile	Asp	Asp	Pro	Leu	Tyr	His	Asp	Gln	Phe	Glu	Ser	Ser	Gln
			340					345					350		
Ile	Cys	Glu	Ile	Asp	Leu	Phe	Ala	Asn	Asp	Asp	Glu	Asp	His	Val	Asp
		355				360						365			
Ile	Ser	Ile	Lys	Gly	Lys	Arg	Asn	Gly	Asp	Asp	Gly	Ile	Phe	Leu	Arg
	370					375					380				
Leu	Arg	Ile	Ser	Asp	Ala	Glu	Gly	Arg	Ile	Arg	Asn	Ile	Tyr	Phe	Pro
385					390					395					400
Phe	Glu	Thr	Ala	Ile	Asp	Thr	Ala	Trp	Ser	Val	Ala	Val	Glu	Met	Val
				405				410						415	
Ser	Glu	Leu	Asp	Ile	Thr	Asn	Gln	Asp	Val	Ala	Lys	Ile	Ala	Glu	Met
			420					425					430		
Ile	Asp	Ala	Glu	Ile	Ala	Ala	Leu	Val	Pro	Asp	Trp	Lys	Asn	Asp	Thr
	435					440						445			
Glu	Ser	Ser	Gln	Asn	Val	Asn	Asn	Asn	Lys	Asn	Asn	Asn	Thr	Ala	Gly
	450					455					460				
Phe	Cys														

595

(2) INFORMATION FOR SEQ ID NO:2342:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 568 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..568
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572649

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2342:

Met	Asn	Gly	Glu	Glu	Ser	Phe	Val	Glu	Asp	Cys	Ser	Val	Phe	Val	Glu
1			5						10					15	
Ile	Asp	Pro	Ser	Gly	Arg	Tyr	Gly	Arg	Tyr	Asp	Glu	Ile	Leu	Gly	Lys
			20					25					30		
Gly	Ala	Ser	Lys	Thr	Val	Tyr	Arg	Ala	Phe	Asp	Glu	Tyr	Glu	Gly	Ile
			35				40					45			
Glu	Val	Ala	Trp	Asn	Gln	Val	Lys	Leu	Arg	Asn	Phe	Thr	Arg	Asn	Pro
			50				55				60				
Glu	Glu	Leu	Glu	Lys	Phe	Phe	Arg	Glu	Ile	His	Leu	Leu	Lys	Thr	Leu
			65				70				75				80
Asn	His	Gln	Asn	Ile	Met	Lys	Phe	Tyr	Thr	Ser	Trp	Val	Asp	Thr	Asn
			85						90					95	
Asn	Leu	Ser	Ile	Asn	Phe	Val	Thr	Glu	Leu	Phe	Thr	Ser	Gly	Thr	Leu
			100					105					110		
Arg	Gln	Tyr	Arg	Leu	Arg	His	Arg	Arg	Val	Asn	Ile	Arg	Ala	Val	Lys
			115					120					125		
Gln	Trp	Cys	Lys	Gln	Ile	Leu	Lys	Gly	Leu	Leu	Tyr	Leu	His	Ser	Arg
			130				135					140			
Ser	Pro	Pro	Ile	Ile	His	Arg	Asp	Leu	Lys	Cys	Asp	Asn	Ile	Phe	Ile
			145				150				155				160
Asn	Gly	Asn	Gln	Gly	Glu	Val	Lys	Ile	Gly	Asp	Leu	Gly	Leu	Ala	Ala
			165						170					175	
Ile	Leu	Arg	Lys	Ser	His	Ala	Val	Arg	Cys	Val	Gly	Thr	Pro	Glu	Phe
			180					185					190		
Met	Ala	Pro	Glu	Val	Tyr	Asp	Glu	Glu	Tyr	Asn	Glu	Leu	Val	Asp	Val
			195					200					205		
Tyr	Ala	Phe	Gly	Met	Cys	Val	Leu	Glu	Met	Val	Thr	Phe	Asp	Tyr	Pro
			210				215						220		
Tyr	Ser	Glu	Cys	Thr	His	Pro	Ala	Gln	Ile	Tyr	Lys	Lys	Val	Thr	Ser
			225				230				235				240
Gly	Lys	Lys	Pro	Glu	Ala	Phe	Tyr	Leu	Val	Lys	Asp	Pro	Glu	Val	Arg
			245						250					255	
Glu	Phe	Val	Glu	Lys	Cys	Leu	Ala	Asn	Val	Thr	Cys	Arg	Leu	Thr	Ala
			260					265					270		
Leu	Glu	Leu	Leu	Gln	Asp	Pro	Phe	Leu	Gln	Asp	Asp	Asn	Met	Asp	Gly
			275					280					285		
Phe	Val	Met	Arg	Pro	Ile	Asp	Tyr	Tyr	Asn	Gly	Tyr	Asp	Glu	Thr	Gly
			290				295					300			
Val	Phe	Leu	Arg	His	Pro	Leu	Ile	Asp	Asp	Pro	Leu	Tyr	His	Asp	Gln
			305				310				315				320
Phe	Glu	Ser	Ser	Gln	Ile	Cys	Glu	Ile	Asp	Leu	Phe	Ala	Asn	Asp	Asp
			325						330					335	
Glu	Asp	His	Val	Asp	Ile	Ser	Ile	Lys	Gly	Lys	Arg	Asn	Gly	Asp	Asp
			340					345					350		
Gly	Ile	Phe	Leu	Arg	Leu	Arg	Ile	Ser	Asp	Ala	Glu	Gly	Arg	Ile	Arg
			355					360					365		
Asn	Ile	Tyr	Phe	Pro	Phe	Glu	Thr	Ala	Ile	Asp	Thr	Ala	Trp	Ser	Val
			370				375						380		

Ala Val Glu Met Val Ser Glu Leu Asp Ile Thr Asn Gln Asp Val Ala
385 390 395 400
Lys Ile Ala Glu Met Ile Asp Ala Glu Ile Ala Leu Val Pro Asp
405 410 415
Trp Lys Asn Asp Thr Glu Ser Ser Gln Asn Val Asn Asn Asn Lys Asn
420 425 430
Asn Asn Thr Ala Gly Phe Cys Gly Glu Cys Ala Ser Asn Gly Tyr Ile
435 440 445
Gln Glu Thr Val Ser Ser Gly Glu Lys Ser His His Asn His His Glu
450 455 460
Phe Asp Ser Ser Glu Asp Lys Ser Cys Ser Ser Val His Gly Arg Phe
465 470 475 480
Ala Asp Met Trp Gly Leu Arg Glu Ser Tyr Ser Asp Asp Gly Glu Lys
485 490 495
Gln Ser Ser Arg Lys Val Arg Ser Gly Arg Trp Ser Glu Asn Glu Met
500 505 510
Arg Arg Glu Leu Arg Trp Leu Lys Ala Arg His Lys Ile Gln Leu Met
515 520 525
Lys Met Arg Gly Gln Thr Ile Cys Glu Thr Pro Ile Glu Ile Ser Leu
530 535 540
Thr Pro Gly Thr Ser Val Ser Leu Pro Leu Leu Tyr Arg Ala Ile Ser
545 550 555 560
Leu Pro Val Asp Ala Val Asp Met
565

(2) INFORMATION FOR SEQ ID NO:2343:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 483 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..483

(D) OTHER INFORMATION: / Ceres Seq. ID 1572650

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2343:

Met Lys Phe Tyr Thr Ser Trp Val Asp Thr Asn Asn Leu Ser Ile Asn
1 5 10 15
Phe Val Thr Glu Leu Phe Thr Ser Gly Thr Leu Arg Gln Tyr Arg Leu
20 25 30
Arg His Arg Arg Val Asn Ile Arg Ala Val Lys Gln Trp Cys Lys Gln
35 40 45
Ile Leu Lys Gly Leu Leu Tyr Leu His Ser Arg Ser Pro Pro Ile Ile
50 55 60
His Arg Asp Leu Lys Cys Asp Asn Ile Phe Ile Asn Gly Asn Gln Gly
65 70 75 80
Glu Val Lys Ile Gly Asp Leu Gly Leu Ala Ile Leu Arg Lys Ser
85 90 95
His Ala Val Arg Cys Val Gly Thr Pro Glu Phe Met Ala Pro Glu Val
100 105 110
Tyr Asp Glu Glu Tyr Asn Glu Leu Val Asp Val Tyr Ala Phe Gly Met
115 120 125
Cys Val Leu Glu Met Val Thr Phe Asp Tyr Pro Tyr Ser Glu Cys Thr
130 135 140
His Pro Ala Gln Ile Tyr Lys Lys Val Thr Ser Gly Lys Lys Pro Glu
145 150 155 160
Ala Phe Tyr Leu Val Lys Asp Pro Glu Val Arg Glu Phe Val Glu Lys
165 170 175
Cys Leu Ala Asn Val Thr Cys Arg Leu Thr Ala Leu Glu Leu Leu Gln
180 185 190
Asp Pro Phe Leu Gln Asp Asp Asn Met Asp Gly Phe Val Met Arg Pro

	195		200		205														
Ile	Asp	Tyr	Tyr	Asn	Gly	Tyr	Asp	Glu	Thr	Gly	Val	Phe	Leu	Arg	His				
210					215														
Pro	Leu	Ile	Asp	Asp	Pro	Leu	Tyr	His	Asp	Gln	Phe	Glu	Ser	Ser	Gln				
225					230					235					240				
Ile	Cys	Glu	Ile	Asp	Leu	Phe	Ala	Asn	Asp	Asp	Glu	Asp	His	Val	Asp				
				245						250				255					
Ile	Ser	Ile	Lys	Gly	Lys	Arg	Asn	Gly	Asp	Asp	Gly	Ile	Phe	Leu	Arg				
			260					265					270						
Leu	Arg	Ile	Ser	Asp	Ala	Glu	Gly	Arg	Ile	Arg	Asn	Ile	Tyr	Phe	Pro				
			275				280						285						
Phe	Glu	Thr	Ala	Ile	Asp	Thr	Ala	Trp	Ser	Val	Ala	Val	Glu	Met	Val				
					295						300								
Ser	Glu	Leu	Asp	Ile	Thr	Asn	Gln	Asp	Val	Ala	Lys	Ile	Ala	Glu	Met				
305					310					315				320					
Ile	Asp	Ala	Glu	Ile	Ala	Ala	Leu	Val	Pro	Asp	Trp	Lys	Asn	Asp	Thr				
				325					330					335					
Glu	Ser	Ser	Gln	Asn	Val	Asn	Asn	Asn	Lys	Asn	Asn	Asn	Thr	Ala	Gly				
			340					345					350						
Phe	Cys	Gly	Glu	Cys	Ala	Ser	Asn	Gly	Tyr	Ile	Gln	Glu	Thr	Val	Ser				
			355				360					365							
Ser	Gly	Glu	Lys	Ser	His	His	Asn	His	His	Glu	Phe	Asp	Ser	Ser	Glu				
	370				375						380								
Asp	Lys	Ser	Cys	Ser	Ser	Val	His	Gly	Arg	Phe	Ala	Asp	Met	Trp	Gly				
385					390					395					400				
Leu	Arg	Glu	Ser	Tyr	Ser	Asp	Asp	Gly	Glu	Lys	Gln	Ser	Ser	Arg	Lys				
				405					410					415					
Val	Arg	Ser	Gly	Arg	Trp	Ser	Glu	Asn	Glu	Met	Arg	Arg	Glu	Leu	Arg				
				420				425					430						
Trp	Leu	Lys	Ala	Arg	His	Lys	Ile	Gln	Leu	Met	Lys	Met	Arg	Gly	Gln				
		435				440					445								
Thr	Ile	Cys	Glu	Thr	Pro	Ile	Glu	Ile	Ser	Leu	Thr	Pro	Gly	Thr	Ser				
	450				455						460								
Val	Ser	Leu	Pro	Leu	Leu	Tyr	Arg	Ala	Ile	Ser	Leu	Pro	Val	Asp	Ala				
465					470					475				480					
Val	Asp	Met																	

(2) INFORMATION FOR SEQ ID NO:2344:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 931 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..931
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572662

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2344:

aagatgggga	cgaaattgag	ctggatatag	aagctgtcga	caatgagact	ctatggggagc	60
tgtatcgttt	tgtgacgaac	tacaagaaga	tggctagcaa	aatcaagcgc	caagggtttaa	120
tcaggaaagt	gtcaactcca	cttaggaaca	tggcttcggt	agcagaaatg	ggtagtgcgg	180
agaagagaac	aaggagagga	gatgcagggg	aagaggatgt	tgacattgga	gaggacatcac	240
caatcgaaga	ttatccattc	stagagatcg	aaagagatgg	Gtactgcagt	tcagctgct	300
gctagttagt	gttctagttc	ttcaggcgagt	tcacgttcta	gtgggtgtagt	ttcctcgctt	360
atgtagttcag	ggtcagggtg	gagtttcac	ggtagtgtat	ctgatgcaga	tagtgttcaa	420
tcgctcattg	tggagacaaa	agaagcccaa	tgttaaaatc	atttgggaat	ttaacogttg	480
attctgtcct	gaagtactag	gaacgtttag	ctgaggggtg	aaaggggagga	atgaaggggga	540
aaactgaag	aaaggatttg	ttttttcttt	cgatgataaa	cttaggaagc	agatgtagtt	600
agaagamaa	aatgtaatat	gtagatagaa	agagaatgct	agtttaaagc	agaagaagag	660
ttcggttatt	aatacccttt	acatttagga	gttggtttag	gtatttgtag	gatgctgaac	720

agagggtgag agtgagtggg taggtactgt aggagaagaa gaagaagaaa agagctctttt 780
taggttctat gactttattt atttttcttt gttagtagtg ttaaagagtc tgggtgtggt 840
aggaaaaatg gtgatagaag agaagaaga aatcaatgca atgtatcaga tgtaaatggt 900
tggcatatta aaaaagaaaa gttgattttc c

(2) INFORMATION FOR SEQ ID NO:2345:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 100 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..100

(D) OTHER INFORMATION: / Ceres Seq. ID 1572663

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2345:

Asp Gly Asp Glu Ile Glu Leu Asp Ile Glu Ala Val Asp Asn Glu Thr
1 5 10 15
Leu Trp Glu Leu Asp Arg Phe Val Thr Asn Tyr Lys Lys Met Ala Ser
20 25 30
Lys Ile Lys Arg Gln Gly Phe Ile Arg Asn Val Ser Thr Pro Leu Arg
35 40 45
Asn Met Ala Ser Val Ala Glu Met Gly Ser Ala Glu Lys Arg Thr Arg
50 55 60
Arg Gly Asp Ala Gly Glu Asp Val Asp Ile Gly Glu Asp Ile Pro
65 70 75 80
Ile Glu Asp Tyr Pro Ser Xaa Glu Ile Glu Arg Asp Gly Tyr Cys Ser
85 90 95
Cys Ser Cys Cys
100

(2) INFORMATION FOR SEQ ID NO:2346:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..71

(D) OTHER INFORMATION: / Ceres Seq. ID 1572664

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2346:

Met Ala Ser Lys Ile Lys Arg Gln Gly Phe Ile Arg Asn Val Ser Thr
1 5 10 15
Pro Leu Arg Asn Met Ala Ser Val Ala Glu Met Gly Ser Ala Glu Lys
20 25 30
Arg Thr Arg Arg Gly Asp Ala Gly Glu Glu Asp Val Asp Ile Gly Glu
35 40 45
Asp Ile Pro Ile Glu Asp Tyr Pro Ser Xaa Glu Ile Glu Arg Asp Gly
50 55 60
Tyr Cys Ser Cys Ser Cys Cys
65 70

(2) INFORMATION FOR SEQ ID NO:2347:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide

Met Gln Gly Gly Gly Gly Arg Asp Pro Phe Gly Gly Gly Phe Gly Gly
1 5 10 15
Pro Phe Gly Gly Phe Gly Gly Gly Ser Phe Gly Gly Phe Gly Arg Gly
20 25 30

```

Ser Phe Gly Gly Phe Gly Gly Pro Asn Gly Pro Pro Ser Leu Met Ser
    35                                40                                45
Asn Phe Phe Gly Gly Arg Asp Pro Phe Asp Asp Pro Phe Phe Thr Gln
    50                                55                                60
Pro Phe Gly Gly Gly Met Phe Gln Ser Asn Phe Phe Gly Pro Ser Met
    65                                70                                75                                80
Asn Pro Phe Ala Glu Met His Arg Leu Pro Gln Gly Phe Ile Glu Asn
    85                                90                                95
Asn Gln Pro Pro Gly Pro Ser Arg Ser Arg Gly Pro Val Ile Glu Glu
    100                               105                               110
Ile Asp Ser Asp Asp Glu Lys Glu Gly Glu Gly Asp Lys Glu Lys Lys
    115                               120                               125
Gly Ser Leu Gly Lys His Gly Arg Ser Ser Ser Glu Ala Glu Thr Glu
    130                               135                               140
Asp Ala Arg Val Arg Glu Arg Arg Asn Arg Gln Met Gln Ser Met Asn
    145                               150                               155                               160
Val Asn Ala Glu Arg Arg Asn Arg Glu Met Gln Asn Met Asn Val Asn
    165                               170                               175
Ala Glu Arg Arg Asn Pro Gln Met Gln Asn Met Asn Val Asn Ala Met
    180                               185                               190
Val Asn Asn Gly Gln Trp Gln Pro Gln Thr Gly Ser Tyr Ser Phe Gln
    195                               200                               205
Ser Ser Thr Val Thr Tyr Gly Gly Gln Asn Gly Asn Tyr Tyr Thr Ser
    210                               215                               220
Ser Lys Thr Arg Arg Thr Gly Ser Asp Gly Leu Thr Leu Glu Glu Ser
    225                               230                               235                               240
Arg Glu Ala Asn Thr Ala Thr Arg Glu Ala Ala His Met Ile Ser Arg
    245                               250                               255
Gly Leu His Asn Lys Gly His Thr Val Ala Arg Lys Leu Asn Ser Asp
    260                               265                               270
Gly Arg Val Asp Thr Thr Gln Thr Leu His Asn Leu Asn Glu Asp Glu
    275                               280                               285
Leu Ala Gly Phe Glu Gln Ser Trp Ser Gly Asn Ala Arg Arg Gln Met
    290                               295                               300
Gln Leu Pro Ser Arg Ser Gly Ser Phe Gly Ser Gly Leu Val Asn Arg
    305                               310                               315                               320
Glu Gln Pro Met Leu Leu Pro Xaa Thr Asp Pro Ser Pro Ser His Ala
    325                               330                               335
Arg Ala Glu Ser Ser Arg Arg Pro Xaa Ala Ala Met Asn Val Arg Gly
    340                               345                               350
His Gly Thr Asn
    355

```

(2) INFORMATION FOR SEQ ID NO:2350:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 310 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..310
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572696

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2350:

```

Met Ser Asn Phe Phe Gly Gly Arg Asp Pro Phe Asp Asp Pro Phe Phe
1      5      10      15
Thr Gln Pro Phe Gly Gly Gly Met Phe Gln Ser Asn Phe Phe Gly Pro
20     25     30
Ser Met Asn Pro Phe Ala Glu Met His Arg Leu Pro Gln Gly Phe Ile
35     40     45
Glu Asn Asn Gln Pro Pro Gly Pro Ser Arg Ser Arg Gly Pro Val Ile

```

Figure 1

(i) SEQUENCE CHARACTERISTICS:

- | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Phe | Gln | Ser | Asn | Phe | Phe | Gly | Pro | Ser | Met | Asn | Pro | Phe | Ala | Glu |
| 1 | | | 5 | | | | | 10 | | | | | | 15 | |
| Met | His | Arg | Leu | Pro | Gln | Gly | Phe | Ile | Glu | Asn | Asn | Gln | Pro | Pro | Gly |
| | | 20 | | | | | | 25 | | | | | 30 | | |
| Pro | Ser | Arg | Ser | Arg | Gly | Pro | Val | Ile | Glu | Glu | Ile | Asp | Ser | Asp | Asp |
| | | 35 | | | | | 40 | | | | | 45 | | | |
| Glu | Lys | Glu | Gly | Glu | Gly | Asp | Lys | Glu | Lys | Lys | Gly | Ser | Leu | Gly | Lys |
| | | 50 | | | | 55 | | | | | 60 | | | | |
| His | Gly | Arg | Ser | Ser | Ser | Glu | Ala | Glu | Thr | Glu | Asp | Ala | Arg | Val | Arg |
| 65 | | | | | 70 | | | | | 75 | | | | 80 | |
| Glu | Arg | Arg | Asn | Arg | Gln | Met | Gln | Ser | Met | Asn | Val | Asn | Ala | Glu | Arg |
| | | | | 85 | | | | | 90 | | | | | 95 | |
| Arg | Asn | Arg | Glu | Met | Gln | Asn | Met | Asn | Val | Asn | Ala | Glu | Arg | Arg | Asn |
| | | | 100 | | | | | 105 | | | | | 110 | | |
| Pro | Gln | Met | Gln | Asn | Met | Asn | Val | Asn | Ala | Met | Val | Asn | Asn | Gly | Gln |
| | | 115 | | | | | 120 | | | | | 125 | | | |

Trp Gln Pro Gln Thr Gly Ser Tyr Ser Phe Gln Ser Ser Thr Val Thr
130 135 140
Tyr Gly Gly Gln Asn Gly Asn Tyr Tyr Thr Ser Ser Lys Thr Arg Arg
145 150 155 160
Thr Gly Ser Asp Gly Leu Thr Leu Glu Glu Ser Arg Glu Ala Asn Thr
165 170 175
Ala Thr Arg Glu Ala Ala His Met Ile Ser Arg Gly Leu His Asn Lys
180 185 190
Gly His Thr Val Ala Arg Lys Leu Asn Ser Asp Gly Arg Val Asp Thr
195 200 205
Thr Gln Thr Leu His Asn Leu Asn Glu Asp Glu Leu Ala Gly Phe Glu
210 215 220
Gln Ser Trp Ser Gly Asn Ala Arg Arg Gln Met Gln Leu Pro Ser Arg
225 230 235 240
Ser Gly Ser Phe Gly Ser Gly Leu Val Asn Arg Glu Gln Pro Met Leu
245 250 255
Leu Pro Xaa Thr Asp Pro Ser Pro Ser His Ala Arg Ala Glu Ser Ser
260 265 270
Arg Arg Pro Xaa Ala Ala Met Asn Val Arg Gly His Gly Thr Asn
275 280 285

(2) INFORMATION FOR SEQ ID NO:2352:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 629 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..629
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572706

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2352:

tccacacttt	catatccaca	aaataaaata	aaaaaatggc	ctcaagagc	tcaaccacca	60
tttccctcat	catecatcctc	ctcatcagcc	tcgcagaagc	aaatctctta	agctcgccca	120
caccgaccaa	caacttttggc	tcattgtccca	gaacccatt	gcaactagcc	gtatgtgccca	180
acgtccttgg	cctagccaat	gttacagctg	gcgacccag	agcacgacag	tgttgcactg	240
ccctcaatgg	cctcactaat	gttcaagtaa	ccgattgtct	ctgttttacc	tccaggccga	300
ttccgttggt	tttcggtatt	gatgtggccg	ttagagaaat	cttttttgc	tgcaataggg	360
tttttccat	cggtttccag	tgtccaccac	cacagtaact	actacttaat	tcccctaaat	420
aagagcccta	tccggtgttt	ccttgcaacta	taagtgttgc	ggtaccacaaa	gtatgggttt	480
atctattaat	gttttacagt	gttggtgtgt	gtttcgttgt	tgattagaac	gtaattataa	540
ggactatcga	tgcttactaa	aaagtgtgta	agcatatcta	ttaatgtcta	Mtgaagaata	600
atattaaata	aagtataaca	ctttgtgtc				

(2) INFORMATION FOR SEQ ID NO:2353:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..120
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572707

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2353:

Met	Ala	Ser	Lys	Ser	Ser	Thr	Thr	Ile	Ser	Leu	Ile	Ile	Ile	Leu	Leu
1				5				10					15		
Ile	Ser	Leu	Ala	Glu	Ala	Asn	Leu	Leu	Ser	Ser	Pro	Thr	Pro	Thr	Asn
			20				25					30			
Asn	Phe	Gly	Ser	Cys	Pro	Arg	Asn	Pro	Leu	Gln	Leu	Gly	Val	Cys	Ala
			35				40					45			

Asn Val Leu Gly Leu Ala Asn Val Thr Ala Gly Asp Pro Arg Ala Arg
50 55 60
Gln Cys Cys Thr Ala Leu Asn Gly Leu Thr Asn Val Gln Val Thr Asp
65 70 75 80
Cys Leu Cys Phe Ile Phe Arg Pro Ile Pro Leu Val Phe Gly Ile Asp
85 90 95
Val Ala Val Arg Glu Ile Phe Phe Ala Cys Asn Arg Val Phe Pro Ile
100 105 110
Gly Phe Gln Cys Pro Pro Pro Gln
115 120

(2) INFORMATION FOR SEQ ID NO:2354:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 954 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..954

(D) OTHER INFORMATION: / Ceres Seq. ID 1572750

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2354:

acattaccgaa	aagtactagt	ttattggtgt	tattcatcgc	tgctcaagggt	ggcaaaccaa	60
ggagaacaag	aagagtcag	ggccaatgag	cotgagggta	tcaaatcagt	gattgatgac	120
atctacaatt	ttgaagacga	cctgtggtt	gatagattca	atagatttgg	aacggagatg	180
tttgccatgg	ttctggcctt	gacacagggt	gtttctgctc	gctctcagac	tgaagctgaa	240
gggtctcaact	cttcttcttc	ctcggctgga	cataagagag	aatggcttgg	aatcgattct	300
gttctctattc	ctctcatcatt	tgctcgtgta	gactcttcac	ataatccgat	cgaagaatcc	360
ataagaaagg	catttccaga	ggaagcaagg	gagaaaaaaa	ggaggtagac	aggagtaggt	420
cagagaccat	ggggcaaatg	ggcagctgag	atacgtgatc	cacatagagc	cgctaRggtt	480
tggctcgggg	cgtttgatac	agcggaggcc	gogcgtagag	cctacgacga	ggctgcactc	540
cggttccgtg	gaaataaagg	aaagctaaat	ttcccagagg	atgtaaggat	ttctctcctt	600
ccccctcttc	ttcttcgttc	accagctgac	acggtggcga	ataaagcaga	agaggatctg	660
ataaaattatt	ggagttatc	aaagtgtgtg	caaagtctac	gccaacggctc	atttctcgag	720
cgaggacaag	aagagagtaa	taacataatt	gaacatttcac	caatggaaca	acctctgcct	780
ccttcaagtt	ctgggtccaa	ttctcttaatt	tttctctgac	cttctctacc	taatacatag	840
tttctacttt	attaaagctc	tacaaataca	attaaataca	tagctaaatg	aaaatgattt	900
ctctgtctgt	ataccttctt	aagtgtctaaa	caatatattg	tactctttgt	ttcc	

(2) INFORMATION FOR SEQ ID NO:2355:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 279 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..279

(D) OTHER INFORMATION: / Ceres Seq. ID 1572751

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2355:

Thr	Leu	Arg	Lys	Val	Leu	Val	Tyr	Trp	Cys	Tyr	Ser	Ser	Leu	Leu	Lys
1			5					10					15		
Val	Ala	Asn	Gln	Gly	Glu	Gln	Glu	Glu	Ser	Arg	Ala	Asn	Glu	Pro	Glu
			20					25					30		
Gly	Ile	Lys	Ser	Val	Ile	Asp	Asp	Ile	Tyr	Asn	Phe	Glu	Asp	Asp	Pro
			35				40					45			
Val	Val	Asp	Arg	Phe	Asn	Arg	Phe	Gly	Thr	Glu	Met	Ser	Ala	Met	Val
			50			55					60				
Ser	Ala	Leu	Thr	Gln	Val	Val	Ser	Ala	Arg	Ser	Gln	Thr	Glu	Ala	Glu
			65			70				75			80		
Gly	Ala	His	Ser	Ser	Ser	Ser	Ala	Gly	His	Lys	Arg	Glu	Trp	Leu	

CONCLUSIONS

(i) SEQUENCE CHARACTERISTICS:

- (ii) MOLECULE TYPE: peptide

- (A) NAME/KEY: peptide

- (B) LOCATION: 1..220

- (D) OTHER INFORMATION: / Ceres Seq. ID 1572752

Met	Ser	Ala	Met	Val	Ser	Ala	Leu	Thr	Gln	Val	Val	Ser	Ala	Arg	Ser
1			5					10						15	
Gln	Thr	Glu	Ala	Glu	Gly	Ala	His	Ser	Ser	Ser	Ser	Ser	Ala	Gly	His
			20					25					30		
Lys	Arg	Glu	Trp	Leu	Gly	Ile	Asp	Ser	Val	Pro	Ile	Pro	Ser	Ser	Phe
			35				40					45			
Ala	Arg	Val	Asp	Ser	Ser	His	Asn	Pro	Ile	Glu	Glu	Ser	Ile	Arg	Lys
			50			55					60				
Ala	Phe	Pro	Glu	Glu	Ala	Arg	Glu	Lys	Lys	Arg	Arg	Tyr	Arg	Gly	Val
65					70					75				80	
Arg	Gln	Arg	Pro	Trp	Gly	Lys	Trp	Ala	Ala	Glu	Ile	Arg	Asp	Pro	His
				85				90						95	
Arg	Ala	Ala	Xaa	Val	Trp	Leu	Gly	Thr	Phe	Asp	Thr	Ala	Glu	Ala	Ala
			100					105					110		
Ala	Arg	Ala	Tyr	Asp	Glu	Ala	Ala	Leu	Arg	Phe	Arg	Gly	Asn	Lys	Ala
			115				120					125			
Lys	Leu	Asn	Phe	Pro	Glu	Asp	Val	Arg	Ile	Leu	Pro	Pro	Pro	Pro	Pro
			130			135					140				
Leu	Leu	Arg	Ser	Pro	Ala	Asp	Thr	Val	Ala	Asn	Lys	Ala	Glu	Glu	Asp
145					150					155				160	
Leu	Ile	Asn	Tyr	Trp	Ser	Tyr	Thr	Lys	Leu	Leu	Gln	Ser	Ser	Gly	Gln
				165					170					175	
Arg	Ser	Phe	Leu	Glu	Arg	Gly	Gln	Glu	Glu	Ser	Asn	Asn	Ile	Phe	Glu
			180					185					190		

His Ser Pro Met Glu Gln Pro Leu Pro Pro Ser Ser Ser Gly Pro Ser
195 200 205
Ser Ser Asn Phe Pro Ala Pro Ser Leu Pro Asn Thr
210 215 220

(2) INFORMATION FOR SEQ ID NO:2357:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 217 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..217

(D) OTHER INFORMATION: / Ceres Seq. ID 1572753

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2357:

Met	Val	Ser	Ala	Leu	Thr	Gln	Val	Val	Ser	Ala	Arg	Ser	Gln	Thr	Glu
1				5						10				15	
Ala	Glu	Gly	Ala	His	Ser	Ser	Ser	Ser	Ser	Ala	Gly	His	Lys	Arg	Glu
			20					25					30		
Trp	Leu	Gly	Ile	Asp	Ser	Val	Pro	Ile	Pro	Ser	Ser	Phe	Ala	Arg	Val
		35					40						45		
Asp	Ser	Ser	His	Asn	Pro	Ile	Glu	Glu	Ser	Ile	Arg	Lys	Ala	Phe	Pro
		50				55					60				
Glu	Glu	Ala	Arg	Glu	Lys	Lys	Arg	Arg	Tyr	Arg	Gly	Val	Arg	Gln	Arg
		65				70				75				80	
Pro	Trp	Gly	Lys	Trp	Ala	Ala	Glu	Ile	Arg	Asp	Pro	His	Arg	Ala	Ala
				85					90					95	
Xaa	Val	Trp	Leu	Gly	Thr	Phe	Asp	Thr	Ala	Glu	Ala	Ala	Ala	Arg	Ala
			100					105						110	
Tyr	Asp	Glu	Ala	Ala	Leu	Arg	Phe	Arg	Gly	Asn	Lys	Ala	Lys	Leu	Asn
			115					120					125		
Phe	Pro	Glu	Asp	Val	Arg	Ile	Leu	Pro	Pro	Pro	Pro	Pro	Leu	Leu	Arg
			130				135						140		
Ser	Pro	Ala	Asp	Thr	Val	Ala	Asn	Lys	Ala	Glu	Glu	Asp	Leu	Ile	Asn
			145			150				155				160	
Tyr	Trp	Ser	Tyr	Thr	Lys	Leu	Leu	Gln	Ser	Ser	Gly	Gln	Arg	Ser	Phe
				165				170						175	
Leu	Glu	Arg	Gly	Gln	Glu	Ser	Asn	Asn	Ile	Phe	Glu	His	Ser	Ser	Pro
				180				185					190		
Met	Glu	Gln	Pro	Leu	Pro	Pro	Ser	Ser	Ser	Gly	Pro	Ser	Ser	Ser	Asn
			195					200					205		
Phe	Pro	Ala	Pro	Ser	Leu	Pro	Asn	Thr							
			210				215								

(2) INFORMATION FOR SEQ ID NO:2358:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1072 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1072

(D) OTHER INFORMATION: / Ceres Seq. ID 1572762

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2358:

acacatctca	ctgctcacta	ctctcactgt	aatcccttag	atcttctttt	caaatctcaa	60
tggcgctcgg	tgatgttgag	tatcggtgct	tcgttgagg	tctagcatgg	gccactgatg	120
acagagctct	tgagactgcc	tctgctcaat	acggcgactg	tattgattcc	aaggctctgt	180
acacgcagag	atcgactccc	gagtgatata	gatgatctca	tctcgcagcg	atctgtctcg	240
atcttgtgtt	tctctgtttac	ttgattcgat	tactctgtta	ctattctcgt	tctttgtttac	300

tactactact	actactgtta	cttgtatatt	cccaaatcgg	tacgttcac	ttcctgcttc	360
tgtgagcccg	gagatcgatc	ggattttttt	gtatttttga	tattttgtgt	agatcataat	420
gctttttgttc	agttttgttg	gattgttttg	ctgatctggg	ttttgtatta	tttggaatac	480
agatcattaa	cgatcgtgag	actggaagat	caaggggatt	cggattcgtc	acctccaagg	540
atgagaaagc	catgaaggat	gcgattgagg	gaatgaacgg	acaagatctc	gatggccgta	600
gcatacactgt	taacgaggct	cagtcacgag	gaagcgggtg	cgccggaggc	caccgtggag	660
gtggtggcgg	tggatacgcg	agcggcggtg	gtggagggtta	ctccggtgga	ggtggtagct	720
acggaggttc	cggcggttaga	cgcgagggtg	gaggaggata	cagcggcgcc	ggcggttaact	780
cctcaagagg	tgggtgtggc	ggaagctacg	gtggtggaag	acgtgaggga	ggaggaggat	840
acgggtgtgg	tgaaggagga	ggttacggag	gaagcgggtg	tggtggagga	tggtaattcc	900
tttaattagg	tttgggatta	ccaatgaatg	ttctctctct	cgcttggtat	gcttctactt	960
ggttttgtgt	gtttctctatt	ttgttctggt	tctgctttag	atttgatga	acagttcgtg	1020
attaggtatt	ttgtatctct	gaaacgtaat	gttaagtcac	ttgtcaattct	cc	

(2) INFORMATION FOR SEQ ID NO:2359:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 114 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..114
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572763

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2359:

Met	Lys	Asp	Ala	Ile	Glu	Gly	Met	Asn	Gly	Gln	Asp	Leu	Asp	Gly	Arg
1				5					10					15	
Ser	Ile	Thr	Val	Asn	Glu	Ala	Gln	Ser	Arg	Gly	Ser	Gly	Gly	Gly	Gly
			20					25					30		
Gly	His	Arg	Gly	Gly	Gly	Gly	Gly	Tyr	Arg	Ser	Gly	Gly	Gly	Gly	Gly
			35				40				45				
Gly	Tyr	Ser	Gly	Gly	Gly	Ser	Tyr	Gly	Gly	Gly	Gly	Gly	Arg	Arg	
			50			55				60					
Glu	Gly	Gly	Gly	Gly	Tyr	Ser	Gly	Gly	Gly	Tyr	Ser	Ser	Arg	Gly	
			65			70				75				80	
Gly	Gly	Gly	Gly	Ser	Tyr	Gly	Gly	Gly	Arg	Glu	Gly	Gly	Gly	Gly	
			85					90					95		
Tyr	Gly	Gly	Gly	Glu	Gly	Gly	Gly	Tyr	Gly	Gly	Ser	Gly	Gly	Gly	Gly
			100					105					110		

Gly Trp

(2) INFORMATION FOR SEQ ID NO:2360:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..107
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572764

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2360:

Met	Asn	Gly	Gln	Asp	Leu	Asp	Gly	Arg	Ser	Ile	Thr	Val	Asn	Glu	Ala
1				5					10					15	
Gln	Ser	Arg	Gly	Ser	Gly	Gly	Gly	Gly	Gly	His	Arg	Gly	Gly	Gly	Gly
			20					25					30		
Gly	Gly	Tyr	Arg	Ser	Gly	Gly	Gly	Gly	Gly	Tyr	Ser	Gly	Gly	Gly	Gly
			35				40				45				
Ser	Tyr	Gly	Gly	Gly	Gly	Gly	Arg	Arg	Glu	Gly	Gly	Gly	Gly	Tyr	Ser
			50				55				60				

Gly Gly Gly Gly Tyr Ser Ser Arg Gly Gly Gly Gly Ser Tyr Gly
65 70 75 80
Gly Gly Arg Arg Glu Gly Gly Gly Tyr Gly Gly Glu Gly Gly
85 90 95
Gly Tyr Gly Gly Ser Gly Gly Gly Gly Trp
100 105

(2) INFORMATION FOR SEQ ID NO:2361:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..105

(D) OTHER INFORMATION: / Ceres Seq. ID 1572765

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2361:

Met Ala Val Ala Ser Leu Leu Thr Arg Leu Ser His Glu Glu Ala Val
1 5 10 15
Ala Ala Glu Ala Thr Val Glu Val Val Ala Val Asp Thr Ala Ala Ala
20 25 30
Val Val Glu Val Thr Pro Val Glu Val Val Ala Thr Glu Val Ala Ala
35 40 45
Val Asp Ala Arg Val Glu Glu Asp Thr Ala Ala Ala Val Thr Pro
50 55 60
Gln Glu Val Val Val Ala Glu Ala Thr Val Val Glu Asp Val Arg Glu
65 70 75 80
Glu Glu Asp Thr Val Val Lys Glu Glu Val Thr Glu Glu Ala Val
85 90 95
Val Val Glu Asp Gly Asn Ser Phe Asn
100 105

(2) INFORMATION FOR SEQ ID NO:2362:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 629 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..629

(D) OTHER INFORMATION: / Ceres Seq. ID 1572774

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2362:

ggtttctctag ggtttcagcg accagactca aacagagagt gaaaatgccg gcgggacacg 60
gagtgagggc gagaacaaga gatctgttcg cgagaccatt gaggagaag gggtatatc 120
cactctccac ttacctcaga acctccaagg tcggcgatta cgtcgatgct aagggttaag 180
gagctatcca caagggtatg cctcataagt tctaccatgg tegtactggt cgcactctgga 240
atgtcactaa gcgtgccgtt ggtgttgaag tcaacaaaca gattgggaac agaatacataa 300
ggaagaggat acatgtgcgt gtggagcatg tgcaacagtc aaggtgtgct gaggagtta 360
aactcagaaa gaagcagaac gatgtgctta aggcgtatgc taaagccaga ggagagacta 420
tcagcaccaa gagacagcct aaaggtccta aaccgggttt catggctgaa ggtatgacat 480
tggagactgt cactccatt ccttacgatg ttgtcaacga tctcaagggt ggtattgag 540
tttttccat tttattatca ttctttactc agaatttttg cacttgcttt tttaatgatg 600
ttttgtatc aattaagact aattBStct

(2) INFORMATION FOR SEQ ID NO:2363:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 178 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..178

(D) OTHER INFORMATION: / Ceres Seq. ID 1572775

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2363:

Phe	Ser	Arg	Val	Ser	Ala	Thr	Arg	Leu	Lys	Gln	Arg	Val	Lys	Met	Pro
1			5					10						15	
Ala	Gly	His	Gly	Val	Arg	Ala	Arg	Thr	Arg	Asp	Leu	Phe	Ala	Arg	Pro
			20					25					30		
Phe	Arg	Lys	Lys	Gly	Tyr	Ile	Pro	Leu	Ser	Thr	Tyr	Leu	Arg	Thr	Phe
			35				40					45			
Lys	Val	Gly	Asp	Tyr	Val	Asp	Val	Lys	Val	Asn	Gly	Ala	Ile	His	Lys
			50				55				60				
Gly	Met	Pro	His	Lys	Phe	Tyr	His	Gly	Arg	Thr	Gly	Arg	Ile	Trp	Asn
			65				70				75			80	
Val	Thr	Lys	Arg	Ala	Val	Gly	Val	Glu	Val	Asn	Lys	Gln	Ile	Gly	Asn
			85					90						95	
Arg	Ile	Ile	Arg	Lys	Arg	Ile	His	Val	Arg	Val	Glu	His	Val	Gln	Gln
			100					105					110		
Ser	Arg	Cys	Ala	Glu	Glu	Phe	Lys	Leu	Arg	Lys	Lys	Gln	Asn	Asp	Val
			115				120					125			
Leu	Lys	Ala	Asp	Ala	Lys	Ala	Arg	Gly	Glu	Thr	Ile	Ser	Thr	Lys	Arg
			130				135					140			
Gln	Pro	Lys	Gly	Pro	Lys	Pro	Gly	Phe	Met	Val	Glu	Gly	Met	Thr	Leu
			145				150				155			160	
Glu	Thr	Val	Thr	Pro	Ile	Pro	Tyr	Asp	Val	Val	Asn	Asp	Leu	Lys	Gly
			165					170					175		

Gly Tyr

(2) INFORMATION FOR SEQ ID NO:2364:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 164 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..164

(D) OTHER INFORMATION: / Ceres Seq. ID 1572776

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2364:

Met	Pro	Ala	Gly	His	Gly	Val	Arg	Ala	Arg	Thr	Arg	Asp	Leu	Phe	Ala
1			5					10					15		
Arg	Pro	Phe	Arg	Lys	Lys	Gly	Tyr	Ile	Pro	Leu	Ser	Thr	Tyr	Leu	Arg
			20					25					30		
Thr	Phe	Lys	Val	Gly	Asp	Tyr	Val	Asp	Val	Lys	Val	Asn	Gly	Ala	Ile
			35					40					45		
His	Lys	Gly	Met	Pro	His	Lys	Phe	Tyr	His	Gly	Arg	Thr	Gly	Arg	Ile
			50				55					60			
Trp	Asn	Val	Thr	Lys	Arg	Ala	Val	Gly	Val	Glu	Val	Asn	Lys	Gln	Ile
			65				70				75			80	
Gly	Asn	Arg	Ile	Ile	Arg	Lys	Arg	Ile	His	Val	Arg	Val	Glu	His	Val
			85					90					95		
Gln	Gln	Ser	Arg	Cys	Ala	Glu	Glu	Phe	Lys	Leu	Arg	Lys	Lys	Gln	Asn
			100					105					110		
Asp	Val	Leu	Lys	Ala	Asp	Ala	Lys	Ala	Arg	Gly	Glu	Thr	Ile	Ser	Thr
			115				120					125			
Lys	Arg	Gln	Pro	Lys	Gly	Pro	Lys	Pro	Gly	Phe	Met	Val	Glu	Gly	Met
			130				135					140			

Thr Leu Glu Thr Val Thr Pro Ile Pro Tyr Asp Val Val Asn Asp Leu

145 150 155 160
Lys Gly Gly Tyr

(2) INFORMATION FOR SEQ ID NO:2365:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..113

(D) OTHER INFORMATION: / Ceres Seq. ID 1572777

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2365:

Met	Pro	His	Lys	Phe	Tyr	His	Gly	Arg	Thr	Gly	Arg	Ile	Trp	Asn	Val
1			5					10					15		
Thr	Lys	Arg	Ala	Val	Gly	Val	Glu	Val	Asn	Lys	Gln	Ile	Gly	Asn	Arg
			20					25					30		
Ile	Ile	Arg	Lys	Arg	Ile	His	Val	Arg	Val	Glu	His	Val	Gln	Gln	Ser
			35				40					45			
Arg	Cys	Ala	Glu	Glu	Phe	Lys	Leu	Arg	Lys	Lys	Gln	Asn	Asp	Val	Leu
			50				55					60			
Lys	Ala	Asp	Ala	Lys	Ala	Arg	Gly	Glu	Thr	Ile	Ser	Thr	Lys	Arg	Gln
			65				70					75			80
Pro	Lys	Gly	Pro	Lys	Pro	Gly	Phe	Met	Val	Glu	Gly	Met	Thr	Leu	Glu
							85					90			95
Thr	Val	Thr	Pro	Ile	Pro	Tyr	Asp	Val	Val	Asn	Asp	Leu	Lys	Gly	Gly
			100					105					110		

Tyr

(2) INFORMATION FOR SEQ ID NO:2366:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1472 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1472

(D) OTHER INFORMATION: / Ceres Seq. ID 1572785

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2366:

aaaaaagtca	atcatatcaa	atccaaaatc	ctccagatg	tttttatcat	cttcttcttc	60
ctgaagattt	gatttcattt	tctctcttt	cagatcccta	ttctcatggc	ttctggatct	120
tactgggtgc	atagtttgt	cagattcgtt	tgggtttcgc	attcaatctc	ttgcctgat	180
tgcgacggtg	gttttctcga	actcatccaa	gagcctctcg	atttcacacc	ttccgatctc	240
ttcaccacca	ccaccaccac	tcaacatcgc	agccccaact	gcttccctcc	tctctctctc	300
tctctctcca	ccccatccgc	ttctatgcac	gccgataaca	gtcccaactc	taccatcggt	360
actcgtacac	gaagcaatcg	atctcctaatt	ccagttattg	ttctccgtgg	atctcgtcgt	420
gctccttctt	ctgatgttgt	ttccgaaggt	ttagatcgat	ctgcttttca	gatgtattac	480
gatgatggta	ctgattctgtg	tcttagacct	ttaccaccga	gtatgactga	gtttttgtta	540
ggttctggat	ttgatcgttt	gttagatcag	atctctcaga	tcgagcttaa	caccaatcgg	600
aatcttctgt	cttctgaaaca	tccaccggct	tctaaatcgg	ccattgaagc	tttgccctcg	660
attgaaatcg	atccgactca	tctcttatcg	gattctcaat	ctcattgcgc	gttttgcaaa	720
gagaaatttc	ttttgaaatc	atctgctcgc	gagatgcctt	gtaatcacat	ctatcatcct	780
gattgtattc	ttccttgggt	tcggaatcgt	aactctgtc	cggtttgcgc	tcattgageta	840
ccggcggagg	atctcaccga	cggaaaccgg	gctgctttga	ctgctgtttac	cgctactcga	900
gaggaaagag	aagactcagc	tcgctgggta	acgatttggg	ggttacacgg	tgagagattc	960
gctgtaggga	gaatccctcg	tgggtggaga	ggtggagata	gaatgatgcc	gggtggtttac	1020
acggagggtt	atgggtggtag	actcgggtgat	gagagacttc	cgagaagagt	agcttgggggt	1080

tcgagaagag	gtggaagaga	tggtggaggt	agtagagagC	agaggtgggtg	gctttgcggg	1140
tcggatcatg	aggtcttttcg	gatgttttag	tgatcatct	ggatccattg	ctgctgctgc	1200
tgctgcatca	tcgggtgccg	ggtccagaat	tcgggttact	cgtagaacca	ggtcgtcttc	1260
tatgttcagt	acggcgctcg	cttcgtcaa	gagacgaaat	tggttagcgt	gattactaga	1320
attaccaagc	tctctttcca	ggtgaaaaat	aaacacgaaa	gaacacactc	ttctcttggt	1380
taaaatttttc	ctatgttctc	tattaagtgt	ttgtctattt	cagtgtaatg	attatattca	1440
ttctctaaat	ttgaatctat	gcgagtaaat	tg			

(2) INFORMATION FOR SEQ ID NO:2367:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 354 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..354

(D) OTHER INFORMATION: / Ceres Seq. ID 1572786

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2367:

Met	Ala	Ser	Gly	Ser	Tyr	Trp	Cys	Tyr	Ser	Cys	Ser	Arg	Phe	Val	Trp
1			5				10						15		
Val	Ser	Asp	Ser	Ile	Ser	Cys	Pro	Asp	Cys	Asp	Gly	Gly	Phe	Leu	Glu
			20					25					30		
Leu	Ile	Gln	Glu	Pro	Leu	Asp	Phe	Thr	Pro	Ser	Asp	Ser	Phe	Thr	Thr
			35				40					45			
Thr	Thr	Thr	Thr	Gln	His	Arg	Ser	Pro	Thr	Arg	Phe	Pro	Pro	Pro	Ser
			50			55					60				
Ser	Ser	Ser	Ser	Thr	Pro	Ser	Ala	Ser	Met	His	Ala	Asp	Asn	Ser	Pro
			65			70				75				80	
Thr	Pro	Thr	Ile	Val	Thr	Arg	Thr	Arg	Ser	Asn	Arg	Ser	Pro	Asn	Pro
			85					90					95		
Val	Ile	Val	Leu	Arg	Gly	Ser	Ala	Ala	Ala	Pro	Ser	Ser	Asp	Val	Val
			100				105						110		
Ser	Glu	Gly	Leu	Asp	Arg	Ser	Ala	Phe	Gln	Met	Tyr	Tyr	Asp	Asp	Gly
			115				120					125			
Thr	Asp	Ser	Gly	Leu	Arg	Pro	Leu	Pro	Pro	Ser	Met	Thr	Glu	Phe	Leu
			130				135				140				
Leu	Gly	Ser	Gly	Phe	Asp	Arg	Leu	Leu	Asp	Gln	Ile	Ser	Gln	Ile	Glu
			145			150				155					160
Leu	Asn	Thr	Asn	Arg	Asn	Leu	Arg	Ser	Cys	Glu	His	Pro	Pro	Ala	Ser
			165						170					175	
Lys	Ser	Ala	Ile	Glu	Ala	Leu	Pro	Leu	Ile	Glu	Ile	Asp	Pro	Thr	His
			180						185					190	
Leu	Leu	Ser	Asp	Ser	Gln	Ser	His	Cys	Ala	Val	Cys	Lys	Glu	Asn	Phe
			195				200					205			
Val	Leu	Lys	Ser	Ser	Ala	Arg	Glu	Met	Pro	Cys	Asn	His	Ile	Tyr	His
			210			215					220				
Pro	Asp	Cys	Ile	Leu	Pro	Trp	Leu	Ala	Ile	Arg	Asn	Ser	Cys	Pro	Val
			225			230				235				240	
Cys	Arg	His	Glu	Leu	Pro	Ala	Glu	Asp	Leu	Thr	Asp	Gly	Thr	Gly	Ala
			245						250					255	
Ala	Leu	Thr	Ala	Val	Thr	Ala	Thr	Ala	Glu	Glu	Glu	Glu	Asp	Ser	Ala
			260				265						270		
Ala	Gly	Leu	Thr	Ile	Trp	Arg	Leu	Pro	Gly	Gly	Gly	Phe	Ala	Val	Gly
			275				280					285			
Arg	Ile	Pro	Gly	Gly	Trp	Arg	Gly	Gly	Asp	Arg	Met	Met	Pro	Val	Val
			290				295				300				
Tyr	Thr	Glu	Val	Asp	Gly	Gly	Arg	Leu	Gly	Asp	Glu	Arg	Leu	Pro	Arg
			305			310				315				320	
Arg	Val	Ala	Trp	Gly	Ser	Arg	Arg	Gly	Gly	Arg	Asp	Gly	Gly	Gly	Ser
			325						330						

Arg Glu Gln Arg Trp Trp Leu Cys Gly Ser Asp His Glu Ala Phe Arg
340 345 350
Met Phe

(2) INFORMATION FOR SEQ ID NO:2368:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 281 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..281
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572787

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2368:

Met	His	Ala	Asp	Asn	Ser	Pro	Thr	Pro	Thr	Ile	Val	Thr	Arg	Thr	Arg
1				5					10					15	
Ser	Asn	Arg	Ser	Pro	Asn	Pro	Val	Ile	Val	Leu	Arg	Gly	Ser	Ala	Ala
			20				25					30			
Ala	Pro	Ser	Ser	Asp	Val	Val	Ser	Glu	Gly	Leu	Asp	Arg	Ser	Ala	Phe
		35					40					45			
Gln	Met	Tyr	Tyr	Asp	Asp	Gly	Thr	Asp	Ser	Gly	Leu	Arg	Pro	Leu	Pro
	50					55					60				
Pro	Ser	Met	Thr	Glu	Phe	Leu	Leu	Gly	Ser	Gly	Phe	Asp	Arg	Leu	Leu
	65				70					75				80	
Asp	Gln	Ile	Ser	Gln	Ile	Glu	Leu	Asn	Thr	Asn	Arg	Asn	Leu	Arg	Ser
			85						90					95	
Cys	Glu	His	Pro	Pro	Ala	Ser	Lys	Ser	Ala	Ile	Glu	Ala	Leu	Pro	Leu
			100					105					110		
Ile	Glu	Ile	Asp	Pro	Thr	His	Leu	Leu	Ser	Asp	Ser	Gln	Ser	His	Cys
			115				120					125			
Ala	Val	Cys	Lys	Glu	Asn	Phe	Val	Leu	Lys	Ser	Ser	Ala	Arg	Glu	Met
	130					135						140			
Pro	Cys	Asn	His	Ile	Tyr	His	Pro	Asp	Cys	Ile	Leu	Pro	Trp	Leu	Ala
	145				150					155				160	
Ile	Arg	Asn	Ser	Cys	Pro	Val	Cys	Arg	His	Glu	Leu	Pro	Ala	Glu	Asp
			165						170					175	
Leu	Thr	Asp	Gly	Thr	Gly	Ala	Ala	Leu	Thr	Ala	Val	Thr	Ala	Thr	Ala
			180					185					190		
Glu	Glu	Glu	Glu	Asp	Ser	Ala	Ala	Gly	Leu	Thr	Ile	Trp	Arg	Leu	Pro
			195				200					205			
Gly	Gly	Gly	Phe	Ala	Val	Gly	Arg	Ile	Pro	Gly	Gly	Trp	Arg	Gly	Gly
	210					215						220			
Asp	Arg	Met	Met	Pro	Val	Val	Tyr	Thr	Glu	Val	Asp	Gly	Gly	Arg	Leu
	225				230					235				240	
Gly	Asp	Glu	Arg	Leu	Pro	Arg	Arg	Val	Ala	Trp	Gly	Ser	Arg	Arg	Gly
			245						250					255	
Gly	Arg	Asp	Gly	Gly	Gly	Ser	Arg	Glu	Gln	Arg	Trp	Trp	Leu	Cys	Gly
			260					265						270	
Ser	Asp	His	Glu	Ala	Phe	Arg	Met	Phe							
		275					280								

(2) INFORMATION FOR SEQ ID NO:2369:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 232 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide

(B) LOCATION: 1..232

(D) OTHER INFORMATION: / Ceres Seq. ID 1572788

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2369:

```
Met Tyr Tyr Asp Asp Gly Thr Asp Ser Gly Leu Arg Pro Leu Pro Pro
1      5      10      15
Ser Met Thr Glu Phe Leu Leu Gly Ser Gly Phe Asp Arg Leu Leu Asp
      20      25      30
Gln Ile Ser Gln Ile Glu Leu Asn Thr Asn Arg Asn Leu Arg Ser Cys
      35      40      45
Glu His Pro Pro Ala Ser Lys Ser Ala Ile Glu Ala Leu Pro Leu Ile
      50      55      60
Glu Ile Asp Pro Thr His Leu Ser Asp Ser Gln Ser His Cys Ala
      65      70      75      80
Val Cys Lys Glu Asn Phe Val Leu Lys Ser Ser Ala Arg Glu Met Pro
      85      90      95
Cys Asn His Ile Tyr His Pro Asp Cys Ile Leu Pro Trp Leu Ala Ile
      100      105      110
Arg Asn Ser Cys Pro Val Cys Arg His Glu Leu Pro Ala Glu Asp Leu
      115      120      125
Thr Asp Gly Thr Gly Ala Ala Leu Thr Ala Val Thr Ala Thr Ala Glu
      130      135      140
Glu Glu Glu Asp Ser Ala Ala Gly Leu Thr Ile Trp Arg Leu Pro Gly
      145      150      155      160
Gly Gly Phe Ala Val Gly Arg Ile Pro Gly Gly Trp Arg Gly Gly Asp
      165      170      175
Arg Met Met Pro Val Val Tyr Thr Glu Val Asp Gly Gly Arg Leu Gly
      180      185      190
Asp Glu Arg Leu Pro Arg Arg Val Ala Trp Gly Ser Arg Arg Gly Gly
      195      200      205
Arg Asp Gly Gly Gly Ser Arg Glu Gln Arg Trp Trp Leu Cys Gly Ser
      210      215      220
Asp His Glu Ala Phe Arg Met Phe
      225      230
```

(2) INFORMATION FOR SEQ ID NO:2370:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 944 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..944

(D) OTHER INFORMATION: / Ceres Seq. ID 1572796

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2370:

```
acagtcgtcaca ctcaccacct caccgacctc accgttcctt atccatttgg ctgacgcaaaa      60
atcgaaatcgg aaccctaaaaa tctctccgaa agccatgtct cctcctcctg ctgtagtcaac      120
tgaatctgcgc gatggacaac ctaggcaacc accggttacc gccattgctg aagagctgcac      180
gaaaagcttcca gactgatgaa ccgattgtag aagatgttaa agatgatgaa gacgatgatg      240
atgatgacga agaagaggaa gacgacgatg ctcaagggtg aagtggaaag tcaaagcaga      300
tagaagtgca aaagaagagt aggaagcgca tggttgaagct cggtatgaaa cctgtcactg      360
gtgttagtcgc agtaaccatc aagagaacga aaaacgttct ctcttatttc tctaagcctg      420
attgtcttaa gagcccgcat tcagaaaacct atgttatatt cggtgaggcc aagatcgagg      480
atttgagctc tcagcttcaa acgcaagcgt ctcaacagtt taggatgcct gMaattggag      540
ccacatctca gagagcagag gcattcgacag ccactgtaga agcacagggt gaagaagatg      600
aagaggaata ccatgagacc ggtgtggagg ctgcgtgacat tgacttggct atgactcagg      660
ctggagcttcc gcgtagcaaa gcggtttaaag cactcaagag tcacgatgga gacattgttaa      720
gtgcaataat ggaactcact acttaagagt taagagagat tgagctctca tgccttattc      780
actctgcagat tgttttcaaa tacttttggg tttatcagga aattgatta ttgttgtctc      840
taccgagtac taatctagtt tgtttgttat gatgcttatg cagtatctga gttgtactgt      900
gtttttcacg acaatgtatt ggagaaaaata catatcaaaa ttgcg
```

(2) INFORMATION FOR SEQ ID NO:2371:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 204 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..204

(D) OTHER INFORMATION: / Ceres Seq. ID 1572797

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2371:

Met	Asp	Asn	Leu	Ser	Asn	His	Arg	Leu	Pro	Leu	Leu	Lys	Ser	Trp
1			5					10				15		
Arg	Lys	Leu	Gln	Thr	Asp	Glu	Pro	Ile	Val	Glu	Asp	Val	Lys	Asp
			20					25				30		
Glu	Asp	Asp	Asp	Asp	Asp	Asp	Glu	Glu	Glu	Asp	Asp	Asp	Ala	Gln
			35				40				45			
Gly	Val	Ser	Gly	Ser	Ser	Lys	Gln	Ser	Arg	Ser	Glu	Lys	Lys	Arg
			50			55					60			
Lys	Ala	Met	Leu	Lys	Leu	Gly	Met	Lys	Pro	Val	Thr	Gly	Val	Ser
65					70				75				80	
Val	Thr	Ile	Lys	Arg	Thr	Lys	Asn	Val	Leu	Phe	Ile	Ser	Lys	Pro
			85					90				95		
Asp	Val	Phe	Lys	Ser	Pro	His	Ser	Glu	Thr	Tyr	Val	Ile	Phe	Gly
			100					105				110		
Ala	Lys	Ile	Glu	Asp	Leu	Ser	Ser	Gln	Leu	Gln	Thr	Gln	Ala	Ala
			115				120					125		
Gln	Phe	Arg	Met	Pro	Xaa	Ile	Gly	Ala	Thr	Ser	Gln	Arg	Ala	Glu
			130				135					140		
Ser	Thr	Ala	Thr	Val	Glu	Ala	Gln	Val	Glu	Glu	Asp	Glu	Glu	Ile
145					150				155					160
Asp	Glu	Thr	Gly	Val	Glu	Ala	Arg	Asp	Ile	Asp	Leu	Val	Met	Thr
			165					170					175	
Ala	Gly	Val	Ser	Arg	Ser	Lys	Ala	Val	Lys	Ala	Leu	Lys	Ser	His
			180					185					190	
Gly	Asp	Ile	Val	Ser	Ala	Ile	Met	Glu	Leu	Thr	Thr			
			195				200							

(2) INFORMATION FOR SEQ ID NO:2372:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 138 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..138

(D) OTHER INFORMATION: / Ceres Seq. ID 1572798

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2372:

Met	Leu	Lys	Leu	Gly	Met	Lys	Pro	Val	Thr	Gly	Val	Ser	Arg	Val	Thr
1			5					10				15			
Ile	Lys	Arg	Thr	Lys	Asn	Val	Leu	Phe	Phe	Ile	Ser	Lys	Pro	Asp	Val
			20					25				30			
Phe	Lys	Ser	Pro	His	Ser	Glu	Thr	Tyr	Val	Ile	Phe	Gly	Glu	Ala	Lys
			35				40					45			
Ile	Glu	Asp	Leu	Ser	Ser	Gln	Leu	Gln	Thr	Gln	Ala	Ala	Gln	Gln	Phe
			50			55					60				
Arg	Met	Pro	Xaa	Ile	Gly	Ala	Thr	Ser	Gln	Arg	Ala	Glu	Ala	Ser	Thr
65					70				75					80	
Ala	Thr	Val	Glu	Ala	Gln	Val	Glu	Glu	Asp	Glu	Glu	Glu	Ile	Asp	Glu

85 90 95
Thr Gly Val Glu Ala Arg Asp Ile Asp Leu Val Met Thr Gln Ala Gly
100 105 110
Val Ser Arg Ser Lys Ala Val Lys Ala Leu Lys Ser His Asp Gly Asp
115 120 125
Ile Val Ser Ala Ile Met Glu Leu Thr Thr
130 135

(2) INFORMATION FOR SEQ ID NO:2373:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 133 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..133
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572799

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2373:

Met Lys Pro Val Thr Gly Val Ser Arg Val Thr Ile Lys Arg Thr Lys
1 5 10 15
Asn Val Leu Phe Phe Ile Ser Lys Pro Asp Val Phe Lys Ser Pro His
20 25 30
Ser Glu Thr Tyr Val Ile Phe Gly Glu Ala Lys Ile Glu Asp Leu Ser
35 40 45
Ser Gln Leu Gln Thr Gln Ala Ala Gln Gln Phe Arg Met Pro Xaa Ile
50 55 60
Gly Ala Thr Ser Gln Arg Ala Glu Ala Ser Thr Ala Thr Val Glu Ala
65 70 75 80
Gln Val Glu Glu Asp Glu Glu Glu Ile Asp Glu Thr Gly Val Glu Ala
85 90 95
Arg Asp Ile Asp Leu Val Met Thr Gln Ala Gly Val Ser Arg Ser Lys
100 105 110
Ala Val Lys Ala Leu Lys Ser His Asp Gly Asp Ile Val Ser Ala Ile
115 120 125
Met Glu Leu Thr Thr
130

(2) INFORMATION FOR SEQ ID NO:2374:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1793 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1793
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572800

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2374:

ctctcgatt	tttatttctt	atatacaat	ccctaaaacc	ctatagcctt	ctttcttcac	60
caactactac	taactccaag	ctcaagcccc	tctgttttct	ctgctttgtg	ttaaaaatca	120
tttcagacac	agtgcctttg	atgactctct	gcaacaaaac	acagcagctg	cagacaaaagc	180
ttatacgaag	ctgtatctac	tgactttgat	ggtgaaatat	caaaaaccct	aaattaaatt	240
aaaaaataaaa	aacacatttt	ttttcttctt	ttggtttttc	ctctgagggg	atccatcatc	300
aatgcttaca	aagtacagtg	ggtaaacaaa	acaaaaacaa	aaaaccattt	ttttctctct	360
tccttataat	ccaaatccat	ctctaaagtt	tgattttttt	ttttgggggg	accacaaaaa	420
aaacaaaacc	ccaatttttt	ttcttttagt	atgagattat	tggtgatgat	gaaatgattg	480
gagatctaat	gaagaataac	aacaatggcg	acgttgttga	taacgaagtg	aacacccggg	540
taagccgggt	gcatacaaat	tcttcocgga	taattagggt	ttcacgagct	tcgggttgta	600
aagatcgaca	cagcaaaatc	ttgacttcta	aaggaccacg	tgaccgtcgt	gtccggttat	660
cagttctccac	cgcttcttca	ttctatgatc	ttcaagatcg	gttaggttat	gatcaacctc	720

gcaaagctgt	tgaatggtta	atcaaagctg	ctgaagattc	aatctbtgag	cttccttcac	780
tcaacaacac	ttcttttccg	accgatgacg	agaatcacca	gaatcagaca	ttacaacacg	840
ttgtgctgt	ttccttggct	aaatctgctt	gtagtaccaa	ttcagacacg	agcaagaact	900
cttttgctt	YYtthataca	gatcggagct	tagagataaa	gctagagaga	gagctagaga	960
gagaacagct	aaagagacca	aggagagaga	tcataaccac	acttcgttta	cogatttgtt	1020
aaattccggt	tcagatccgg	ttaaactcaa	ccggcaatgg	atggctttcg	ctcctttctt	1080
atctccaatg	gagtatttta	gttcgggttt	aattctcggg	tcgggtcaac	aaacccattt	1140
cccgatttgc	acaaattctc	atcctttctc	atcaatctcc	gatcatcatc	atcctcatca	1200
tcagacccaa	gagttttcat	tcgttcccca	ccatttgata	tcaccgcgag	aatccaacgg	1260
cgagacattc	aatcttgatt	ttaatatgtc	gacacccctc	ggcgccggag	ctgcgctctc	1320
cgcccatccc	gggtggtggg	tcagtggttt	caacaggggg	acccttcagt	ccaattcaac	1380
aaatcagctc	cagtcatctt	tcgctaattc	acagaggttt	ccaacatcag	aaagtggagg	1440
aggctccacg	ttcttattcg	gtgcactgcc	tcgacagaa	caccaccaca	atcaccagtt	1500
tcagctttac	tatgaaaatg	gatgcagaaa	ctcatcagac	cataagggtg	aaggcagaag	1560
ctgattgata	taattattgc	atctttggtt	ttgttcaaat	cctcattttg	tatgtttatc	1620
ttttggttat	ttcaaaacaa	atgttaatct	cttttgttgt	ctgatgtgtg	ttagggtttt	1680
ttctcacata	tgtattgagg	gtctttggaa	atctttttgc	attgtgcttg	taattgttga	1740
tttttgata	atagcatttt	gtttgtgagt	ttataattca	atttttgaat	ggt	

(2) INFORMATION FOR SEQ ID NO:2375:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 182 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..182

(D) OTHER INFORMATION: / Ceres Seq. ID 1572801

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2375:

Met	Ile	Gly	Asp	Leu	Met	Lys	Asn	Asn	Asn	Asn	Gly	Asp	Val	Val	Asp
1			5				10				15				
Asn	Glu	Val	Asn	Asn	Arg	Leu	Ser	Arg	Trp	His	His	Asn	Ser	Ser	Arg
			20					25				30			
Ile	Ile	Arg	Val	Ser	Arg	Ala	Ser	Gly	Gly	Lys	Asp	Arg	His	Ser	Lys
			35				40				45				
Val	Leu	Thr	Ser	Lys	Gly	Pro	Arg	Asp	Arg	Arg	Val	Arg	Leu	Ser	Val
			50			55					60				
Ser	Thr	Ala	Leu	Gln	Phe	Tyr	Asp	Leu	Gln	Asp	Arg	Leu	Gly	Tyr	Asp
			65		70		75				80				
Gln	Pro	Ser	Lys	Ala	Val	Glu	Trp	Leu	Ile	Lys	Ala	Ala	Glu	Asp	Ser
			85				90				95				
Ile	Xaa	Glu	Leu	Pro	Ser	Leu	Asn	Asn	Thr	His	Phe	Pro	Thr	Asp	Asp
			100				105				110				
Glu	Asn	His	Gln	Asn	Gln	Thr	Leu	Thr	Thr	Val	Ala	Ala	Asn	Ser	Leu
			115				120				125				
Ser	Lys	Ser	Ala	Cys	Ser	Ser	Asn	Ser	Asp	Thr	Ser	Lys	Asn	Ser	Leu
			130			135					140				
Val	Xaa	Xaa	Xaa	Gln	Asp	Arg	Ser	Leu	Glu	Ile	Lys	Leu	Glu	Arg	Glu
			145		150				155						160
Leu	Glu	Arg	Glu	Gln	Leu	Lys	Arg	Pro	Arg	Arg	Glu	Ile	Ile	Thr	Thr
			165				170								175
Leu	Arg	Leu	Pro	Ile	Cys										
			180												

(2) INFORMATION FOR SEQ ID NO:2376:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 177 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..177

(D) OTHER INFORMATION: / Ceres Seq. ID 1572802

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2376:

```
Met Lys Asn Asn Asn Asn Gly Asp Val Val Asp Asn Glu Val Asn Asn
1      5      10      15
Arg Leu Ser Arg Trp His His Asn Ser Ser Arg Ile Ile Arg Val Ser
      20      25      30
Arg Ala Ser Gly Gly Lys Asp Arg His Ser Lys Val Leu Thr Ser Lys
      35      40      45
Gly Pro Arg Asp Arg Arg Val Arg Leu Ser Val Ser Thr Ala Leu Gln
      50      55      60
Phe Tyr Asp Leu Gln Asp Arg Leu Gly Tyr Asp Gln Pro Ser Lys Ala
      65      70      75      80
Val Glu Trp Leu Ile Lys Ala Ala Glu Asp Ser Ile Xaa Glu Leu Pro
      85      90      95
Ser Leu Asn Asn Thr His Phe Pro Thr Asp Asp Glu Asn His Gln Asn
      100      105      110
Gln Thr Leu Thr Thr Val Ala Ala Asn Ser Leu Ser Lys Ser Ala Cys
      115      120      125
Ser Ser Asn Ser Asp Thr Ser Lys Asn Ser Leu Val Xaa Xaa Xaa Gln
      130      135      140
Asp Arg Ser Leu Glu Ile Lys Leu Glu Arg Glu Leu Glu Arg Glu Gln
      145      150      155      160
Leu Lys Arg Pro Arg Glu Ile Ile Thr Thr Leu Arg Leu Pro Ile
      165      170      175
Cys
```

(2) INFORMATION FOR SEQ ID NO:2377:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 167 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..167

(D) OTHER INFORMATION: / Ceres Seq. ID 1572803

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2377:

```
Met Ala Ser Ala Pro Ser Ser Ser Pro Met Glu Tyr Phe Ser Ser Gly
1      5      10      15
Leu Ile Leu Gly Ser Gly Gln Gln Thr His Phe Pro Ile Ser Thr Asn
      20      25      30
Ser His Pro Phe Ser Ser Ile Ser Asp His His His Pro His His Gln
      35      40      45
His Gln Glu Phe Ser Phe Val Pro Asp His Leu Ile Ser Pro Ala Glu
      50      55      60
Ser Asn Gly Gly Ala Phe Asn Leu Asp Phe Asn Met Ser Thr Pro Ser
      65      70      75      80
Gly Ala Gly Ala Ala Val Ser Ala Ala Ser Gly Gly Gly Phe Ser Gly
      85      90      95
Phe Asn Arg Gly Thr Leu Gln Ser Asn Ser Thr Asn Gln His Gln Ser
      100      105      110
Phe Leu Ala Asn Leu Gln Arg Phe Pro Thr Ser Glu Ser Gly Gly Gly
      115      120      125
Pro Gln Phe Leu Phe Gly Ala Leu Pro Ala Glu Asn His His His Asn
      130      135      140
His Gln Phe Gln Leu Tyr Tyr Glu Asn Gly Cys Arg Asn Ser Ser Asp
      145      150      155      160
```

His Lys Gly Lys Gly Lys Asn
165

(2) INFORMATION FOR SEQ ID NO:2378:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 493 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..493
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572804

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2378:

aagttacact	ataaactcaa	acacatctat	cggaagtc	taacacacga	agatttccaa	60
aatggctaag	gccgaagGtc	ttttcttct	tggtttagta	gttatttcaa	gtttatgtat	120
gttaaccgag	agccgactcg	caagaaaaga	ctgggggatt	gacctaggtg	ggattggaat	180
cggtttgggc	gttggtattg	ggattggtct	tggcggcg	tcgggctccg	gtgctgggtc	240
aggttctgga	tcagggticag	gttcagatc	atcatctagc	tccagctcat	catcaagtc	300
gagttctagt	gggtcgggtg	gttcagctg	tcatctgcc	ggttcattg	ctggctctag	360
agctggatca	ggatctggga	actaaattat	ataaattact	tttcgactta	aagtgtagaa	420
caataagtat	gttttatgtt	tttggttcgt	cgtagttaat	atcgtatgta	cggaatggaa	480
tgataaattt	ggt					

(2) INFORMATION FOR SEQ ID NO:2379:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..107
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572805

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2379:

Met	Ala	Lys	Ala	Glu	Gly	Leu	Phe	Leu	Leu	Gly	Leu	Val	Val	Ile	Ser
1		5				10				15					
Ser	Leu	Val	Met	Leu	Thr	Glu	Ser	Arg	Leu	Ala	Arg	Lys	Asp	Leu	Gly
		20				25				30					
Ile	Asp	Leu	Gly	Gly	Ile	Gly	Ile	Gly	Leu	Gly	Val	Gly	Leu	Gly	Ile
		35				40				45					
Gly	Leu	Gly	Gly	Gly	Ser	Gly	Ser	Gly	Ala	Gly	Ala	Gly	Ser	Gly	Ser
		50				55				60					
Gly	Ser	Gly	Ser	Arg	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Ser
		65				70				75					
Ser	Ser	Ser	Gly	Ser	Gly	Gly	Ser	Ala	Gly	Ser	Ser	Ala	Gly	Ser	Phe
			85			90				95					
Ala	Gly	Ser	Arg	Ala	Gly	Ser	Gly	Ser	Gly	Asn					
			100			105									

(2) INFORMATION FOR SEQ ID NO:2380:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 88 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..88
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572806

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2380:

Met Leu Thr Glu Ser Arg Leu Ala Arg Lys Asp Leu Gly Ile Asp Leu
1 5 10 15
Gly Gly Ile Gly Ile Gly Leu Gly Val Gly Leu Gly Ile Gly Leu Gly
20 25 30
Gly Gly Ser Gly Ser Gly Ala Gly Ala Gly Ser Gly Ser Gly Ser Gly
35 40 45
Ser Arg Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser
50 55 60
Gly Ser Gly Gly Ser Ala Gly Ser Ser Ala Gly Ser Phe Ala Gly Ser
65 70 75 80
Arg Ala Gly Ser Gly Ser Gly Asn
85

(2) INFORMATION FOR SEQ ID NO:2381:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1491 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1491
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572807

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2381:

aattgtcaaa aactcacaag gcattatcat gtggacatgc aaaccttttt ttctatacgc 60
attacagaaa tgaaaaacaat gattaggatc gcattgcacgt caagaaaaaa acctatagta 120
gtactttgat atactaactc aatcattgtc ttggctcaag cacacaagct tctagctaga 180
tacaactgca aacatatatg atggctttgt ctaataaaga gacgacgact tgggcaccgc 240
tttgaccagt caatacacca aatctgtatg tatcatttat ataatattta tcttccacca 300
gttggtgaag aatcacatatg acagcacaca cggattccat ggagactaaa cagagtattc 360
ctctctcatc gccctataag atgggacccct toaatcttct tccacagggtt gttttggcgc 420
cattgacag atcagagatcg tatggttaaca ttctctacgc taatgccaaa ttatattaca 480
ctcagagaa acacactcgtt ggtcttctta ttctcgaatc ctgtgtatgc tccgagacat 540
cattgggcta tcgggattta ctctggattt ggaacagaga ccaagtggag gcattggaagc 600
ccatcgtgga tcgggtttcat tcgaaaaggcg gtatcttctt ctgccagatt tggcattggtg 660
gcagagtttt tcatcaagac cagccaaatg ggggaagcacc cgtctctctt acagacaagc 720
cattgatgtg caagaacatg tatggaggtc agtttaagcc tccacggcgg ttaaggagcg 780
acgagcttcc cgccattgtc aacgacttta gaatcgtcgc acgaaacgct atcgaagctg 840
gcttcgatgg agtgaggatt caccggcgac atggttacct agatgatcac tctccgaaag 900
acaaagtga tgcagaagt gaccaatatg gtggGtcatt agagaaaccg ttagatattg 960
ctcttgaagt aatcagaagc gtggtaaacg agatcgggtt agatogttgt ggaatcacag 1020
tctcgcattt tgcagattac atggagtcag gagactcgaa tccagaagca ttagggctct 1080
acctgtgcca agctatgaac aagcatggca tggagtcgtc tacggctaca tggttgaacc 1140
tagaatgaaa acccttgaag gaattctcga atgcacggaa tcgtttacgc ccatcgcaaa 1200
agccttcaaa ggtacgttca tagtagcagg aggatattct agagaagacg ggaacaagcg 1260
gggtgaagag ggaagaaccg atcttctggc ttattggacg cgttctctgg ggaatccggg 1320
tctcagagag agattagcaac tcaatgagcc gttgaatagg tacgatagat caactgttca 1380
caactcagat cctgtatgtg gctatacaga ctacccttct ctcgagacca cagatacaac 1440
aacctgctaa ggggtttatt catagtcatt attagcaaaa catatttttc c

(2) INFORMATION FOR SEQ ID NO:2382:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 269 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..269
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572808

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2382:

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```

Met Glu Thr Lys Gln Ser Ile Pro Leu Leu Met Pro Tyr Lys Met Gly
1      5      10      15
Pro Phe Asn Leu Ser His Arg Val Val Leu Ala Pro Leu Thr Arg Ser
20      25      30
Arg Ser Tyr Gly Asn Ile Pro Gln Pro Asn Ala Lys Leu Tyr Tyr Thr
35      40      45
Gln Arg Thr Thr Pro Gly Gly Leu Leu Ile Ser Glu Ser Cys Val Val
50      55      60
Ser Glu Thr Ser Leu Gly Tyr Pro Asp Leu Pro Gly Leu Trp Asn Arg
65      70      75      80
Asp Gln Val Glu Ala Trp Lys Pro Ile Val Asp Ala Val His Ser Lys
85      90      95
Gly Gly Ile Phe Phe Cys Gln Ile Trp His Gly Gly Arg Val Phe His
100      105      110
Gln Asp Gln Pro Asn Gly Glu Ala Pro Val Ser Ser Thr Asp Lys Pro
115      120      125
Leu Met Cys Lys Asn Met Tyr Gly Gly Gln Phe Lys Pro Pro Arg Arg
130      135      140
Leu Arg Ser Asp Glu Leu Pro Ala Ile Val Asn Asp Phe Arg Ile Ala
145      150      155      160
Ala Arg Asn Ala Ile Glu Ala Gly Phe Asp Gly Val Glu Val His Gly
165      170      175
Ala His Gly Tyr Leu Ile Asp Gln Phe Leu Lys Asp Lys Val Asn Asp
180      185      190
Arg Ser Asp Gln Tyr Gly Gly Ser Leu Glu Asn Arg Cys Arg Phe Ala
195      200      205
Leu Glu Val Ile Glu Ala Val Val Asn Glu Ile Gly Ser Asp Arg Val
210      215      220
Gly Ile Arg Leu Ser Pro Phe Ala Asp Tyr Met Glu Ser Gly Asp Ser
225      230      235      240
Asn Pro Glu Ala Leu Gly Leu Tyr Leu Val Gln Ala Met Asn Lys His
245      250      255
Gly Met Glu Ser Ser Thr Val Thr Trp Leu Asn Leu Glu
260      265

```

(2) INFORMATION FOR SEQ ID NO:2383:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 259 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..259

(D) OTHER INFORMATION: / Ceres Seq. ID 1572809

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2383:

```

Met Pro Tyr Lys Met Gly Pro Phe Asn Leu Ser His Arg Val Val Leu
1      5      10      15
Ala Pro Leu Thr Arg Ser Arg Ser Tyr Gly Asn Ile Pro Gln Pro Asn
20      25      30
Ala Lys Leu Tyr Tyr Thr Gln Arg Thr Thr Pro Gly Gly Leu Leu Ile
35      40      45
Ser Glu Ser Cys Val Val Ser Glu Thr Ser Leu Gly Tyr Pro Asp Leu
50      55      60
Pro Gly Leu Trp Asn Arg Asp Gln Val Glu Ala Trp Lys Pro Ile Val
65      70      75      80
Asp Ala Val His Ser Lys Gly Gly Ile Phe Phe Cys Gln Ile Trp His
85      90      95
Gly Gly Arg Val Phe His Gln Asp Gln Pro Asn Gly Glu Ala Pro Val
100      105      110
Ser Ser Thr Asp Lys Pro Leu Met Cys Lys Asn Met Tyr Gly Gln

```

(2) INFORMATION FOR SEQ ID NO:2384:

(A) LENGTH: 255 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

$\langle \underline{1x} \rangle$ FEATURE:

(B) LOCATION: 1..255

(D) OTHER INFORMATION:

SEQUENCE DESCRIPTION: SEQ ID NO:2384:

Gly Pro Phe Asn Leu Ser His Arg Val Val Le

1					5					10					15	
Arg	Ser	Arg	Ser	Tyr	Gly	Asn	Ile	Pro	Gln	Pro	Asn	Ala	Lys	Leu	Tyr	
				20				25					30			
Tyr	Thr	Gln	Arg	Thr	Thr	Pro	Gly	Gly	Leu	Leu	Ile	Ser	Glu	Ser	Cys	
				35				40				45				
Val	Val	Ser	Glu	Thr	Ser	Leu	Gly	Tyr	Pro	Asp	Leu	Pro	Gly	Leu	Trp	
				50				55			60					
Asn	Arg	Asp	Gln	Val	Glu	Ala	Trp	Lys	Pro	Ile	Val	Asp	Ala	Val	His	
					70					75					80	
Ser	Lys	Gly	Gly	Ile	Phe	Phe	Cys	Gln	Ile	Trp	His	Gly	Gly	Arg	Val	
				85					90					95		
Phe	His	Gln	Asp	Gln	Pro	Asn	Gly	Glu	Ala	Pro	Val	Ser	Ser	Thr	Asp	
				100				105					110			
Lys	Pro	Leu	Met	Cys	Lys	Asn	Met	Tyr	Gly	Gly	Gln	Phe	Lys	Pro	Pro	
				115				120				125				
Arg	Arg	Leu	Arg	Ser	Asp	Glu	Leu	Pro	Ala	Ile	Val	Asn	Asp	Phe	Arg	
						135					140					
Ile	Ala	Ala	Arg	Asn	Ala	Ile	Glu	Ala	Gly	Phe	Asp	Gly	Val	Glu	Val	
					150					155					160	
His	Gly	Ala	His	Gly	Tyr	Leu	Ile	Asp	Gln	Phe	Leu	Lys	Asp	Lys	Val	
				165					170					175		
Asn	Asp	Arg	Ser	Asp	Gln	Tyr	Gly	Gly	Ser	Leu	Glu	Asn	Arg	Cys	Arg	
				180				185					190			
Phe	Ala	Leu	Glu	Val	Ile	Glu	Ala	Val	Val	Asn	Glu	Ile	Gly	Ser	Asp	
				195				200				205				
Arg	Val	Gly	Ile	Arg	Leu	Ser	Pro	Phe	Ala	Asp	Tyr	Met	Glu	Ser	Gly	
				210				215			220					
Asp	Ser	Asn	Pro	Glu	Ala	Leu	Gly	Leu	Tyr	Leu	Val	Gln	Ala	Met	Asn	
					230					235					240	

Lys His Gly Met Glu Ser Ser Thr Val Thr Trp Leu Asn Leu Glu
245 250 255

(2) INFORMATION FOR SEQ ID NO:2385:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 342 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..342
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572811

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2385:

aatgctattg	ttgggttcca	tggacgggta	ggttcttg	ttgatagat	cgggtcatat	60
tacgtccgt	ttctcccttc	tctccacct	acagagaaac	tagagggaca	aggtggat	120
ggaggagatt	cttgggacga	tgggtcttcc	ctaaatgtaa	agaaagtata	tgttggacaa	180
ggctcgaacg	gtattgtcgc	cgtaaagttt	gagtacgaga	acgacgtag	tgaggttggt	240
gttggagatg	aacatggaaa	gactacattg	cttggatacg	aaKgTggtga	tgactactcc	300
ttactttaat	tgtttaaagt	ttcaaaacta	tactatatat	cg		

(2) INFORMATION FOR SEQ ID NO:2386:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..102
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572812

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2386:

Asn	Ala	Ile	Val	Gly	Phe	His	Gly	Arg	Val	Gly	Ser	Cys	Val	Asp	Ser	
1			5					10			15					
Ile	Gly	Ala	Tyr	Tyr	Ala	Pro	Phe	Ser	Pro	Ser	Pro	Pro	Pro	Thr	Glu	
			20					25						30		
Lys	Leu	Glu	Gly	Gln	Gly	Gly	Asp	Gly	Gly	Asp	Ser	Trp	Asp	Asp	Gly	
			35				40				45					
Ala	Phe	Leu	Asn	Val	Lys	Lys	Val	Tyr	Val	Gly	Gln	Gly	Ser	Asn	Gly	
			50			55				60						
Ile	Val	Ala	Val	Lys	Phe	Glu	Tyr	Glu	Asn	Asp	Ala	Ser	Glu	Val	Val	
			65		70			75						80		
Val	Gly	Asp	Glu	His	Gly	Lys	Thr	Thr	Leu	Leu	Gly	Tyr	Glu	Xaa	Gly	
			85					90					95			
Asp	Asp	Tyr	Ser	Leu	Leu											
			100													

(2) INFORMATION FOR SEQ ID NO:2387:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..57
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572813

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2387:

Met	Leu	Asp	Lys	Ala	Arg	Thr	Val	Leu	Ser	Pro	Leu	Ser	Leu	Ser	Thr	
1			5					10				15				
Arg	Thr	Thr	Leu	Val	Arg	Leu	Leu	Leu	Glu	Met	Asn	Met	Glu	Arg	Leu	

20 25 30
His Cys Leu Asp Thr Xaa Val Val Met Thr Thr Pro Tyr Phe Asn Cys
35 40 45
Leu Lys Phe Gln Asn Tyr Thr Ile Tyr
50 55

(2) INFORMATION FOR SEQ ID NO:2388:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1125 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1125

(D) OTHER INFORMATION: / Ceres Seq. ID 1572814

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2388:

```
cmcraracca ttmcctagat catcctaaat caaaagtctt tcaaaaatca aaatcccttc 60
ctctctctct ctcaccgagc cggcgagccc gttctctcgg tgtttttaa gatgcttatg 120
atgatgatgg ggagtaatat cagaaatcaa gctttttcac aaatctcagaa attgtagtag 180
agtttgggga ttttatcaac ctccggaaca agctctctct tcttcgtttt actcttgtea 240
tcctgtaaaKg ggttgtttcc attccacggc tgccagagaa ttcccgatc acgaaaaacc 300
tgtgaagctt gcttctgaga ctgcttttag tgttagtgaa tgtgaagcat tgtatgaatt 360
gttcaagagc ataagcagct cgggtgttga cgatggcttg ataaacaagg aagagttttc 420
acttgctttg tcaagaaca gaaagaaga aaatttgttt gccaatagga tatttgattt 480
atttgatgtt aaacgaaaag gcgtaattga ttttgagac tttgtgagat cactcaatgt 540
tttccatcct aatgcttccc tagaggagaa aacagacttt acctttaggc ttacagacat 600
ggaactgcaca ggcctcattg agcgccaaga ggtgaagcag atgttgattg cacttctctg 660
cgaatctgaa atgaaactcg ctgatgatac aatagagatg atacttgatc agacatttga 720
ggagcgcagat gtggatcggt atggaaagat tgataagaca gaatggagca atttcgttat 780
caaaaaccca tctttgttta aaatcatgac tcttcogtat ctacgggata taacagcgac 840
atttccgagt ttctgtattta actcggaggt ggacgagatt gcgacgtgaa agagacaaga 900
caagctggtt tatagagacc aagtctgtag ctggaccaag aataaaaaag aagattgatt 960
ccaacaatgt tatatagcag gatcgagctc tatttccttt ggaattttta gtctatttga 1020
tttcaatttc tatatgtggt attactttt gctctcttct tttaacagtt ttgaatactc 1080
aagttgtagt tctacgaaaa gattaatata aaaccacaat ttctgt
```

(2) INFORMATION FOR SEQ ID NO:2389:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 96 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..96

(D) OTHER INFORMATION: / Ceres Seq. ID 1572815

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2389:

```
Met Asp Cys Thr Gly Phe Ile Glu Arg Gln Glu Val Lys Gln Met Leu
1 5 10 15
Ile Ala Leu Leu Cys Glu Ser Glu Met Lys Leu Ala Asp Asp Thr Ile
20 25 30
Glu Met Ile Leu Asp Gln Thr Phe Glu Asp Ala Asp Val Asp Arg Asp
35 40 45
Gly Lys Ile Asp Lys Thr Glu Trp Ser Asn Phe Val Ile Lys Asn Pro
50 55 60
Ser Leu Leu Lys Ile Met Thr Leu Pro Tyr Leu Arg Asp Ile Thr Thr
65 70 75 80
Thr Phe Pro Ser Phe Val Phe Asn Ser Glu Val Asp Glu Ile Ala Thr
85 90 95
```

(2) INFORMATION FOR SEQ ID NO:2390:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 82 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..82

(D) OTHER INFORMATION: / Ceres Seq. ID 1572816

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2390:

Met	Leu	Ile	Ala	Leu	Leu	Cys	Glu	Ser	Glu	Met	Lys	Leu	Ala	Asp	Asp
1				5					10					15	
Thr	Ile	Glu	Met	Ile	Leu	Asp	Gln	Thr	Phe	Glu	Asp	Ala	Asp	Val	Asp
		20					25					30			
Arg	Asp	Gly	Lys	Ile	Asp	Lys	Thr	Glu	Trp	Ser	Asn	Phe	Val	Ile	Lys
		35					40					45			
Asn	Pro	Ser	Leu	Leu	Lys	Ile	Met	Thr	Leu	Pro	Tyr	Leu	Arg	Asp	Ile
		50				55					60				
Thr	Thr	Thr	Phe	Pro	Ser	Phe	Val	Phe	Asn	Ser	Glu	Val	Asp	Glu	Ile
65					70				75					80	
Ala	Thr														

(2) INFORMATION FOR SEQ ID NO:2391:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 72 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..72

(D) OTHER INFORMATION: / Ceres Seq. ID 1572817

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2391:

Met	Lys	Leu	Ala	Asp	Asp	Thr	Ile	Glu	Met	Ile	Leu	Asp	Gln	Thr	Phe
1				5					10					15	
Glu	Asp	Ala	Asp	Val	Asp	Arg	Asp	Gly	Lys	Ile	Asp	Lys	Thr	Glu	Trp
		20					25					30			
Ser	Asn	Phe	Val	Ile	Lys	Asn	Pro	Ser	Leu	Leu	Lys	Ile	Met	Thr	Leu
		35					40					45			
Pro	Tyr	Leu	Arg	Asp	Ile	Thr	Thr	Thr	Phe	Pro	Ser	Phe	Val	Phe	Asn
		50				55					60				
Ser	Glu	Val	Asp	Glu	Ile	Ala	Thr								
65					70										

(2) INFORMATION FOR SEQ ID NO:2392:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 950 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..950

(D) OTHER INFORMATION: / Ceres Seq. ID 1572826

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2392:

acatcaaaaa	ctaaacaata	aaccatatac	cataaaaaac	atgaaaatcc	tctcactttc	60
acttctcttg	ctcttggccg	ctacgggtctc	tgcattcatt	ccagagctca	tcgaactcgt	120

```
cgattcgaac accatcttta cgaacgaagc cgaactctta gagaaagaga aactttccat 180
caactacgcc aactcgagaa gctggcacct tgggtgtgag acctctaata tcatagacct 240
cgacacggtg cccgcaaat gcaaaagacta tgttgaagac tacttgatca ctccaacaca 300
gtaccaaatc gactccaaaa ccgtgtgcaa agaggcttat tcttatgcca aaggacttgc 360
ctaaagaac gacaccgtta atgtttggat ctttgaccta gatgataccc tccctcttag 420
tattccctac tacgcaaaat atggatacgg gacagagaag accgaccggg gggcgtagctg 480
gtgttggtta gggacccggg catcaacccc tggactcccg gagGccttgc atctttacca 540
aaacatcata gagctcgagg ttgaacccat catactcagt gacgcttggg aattgtggaa 600
gaatgtcact ctogacaatc tcgaagctgc tggcgtggcc tactggaagc atctcatatt 660
gaagcctaatt ggttcgaact tgaggcaagt ggtttacaag tcaaaaggtga ggaagagtct 720
cgtaagaana ggatacaaca tcgttgccaa tatcggagac caatgggctg atttggttga 780
ggataccctt ggaagggttt ttaagctccc aaatccactc tactacgtac ctctctaagc 840
atttatcttc atggcatttt ccccttggat ccacttccata tctatgtcgt ttctgtttatc 900
tttgtagccg tttttggacc gttgcataaa taaaatttct atcctatcgc
```

(2) INFORMATION FOR SEQ ID NO:2393:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 278 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..278
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572827

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2393:

```
His Gln Lys Leu Asn Asn Lys Pro Tyr Thr Ile Lys Asn Met Lys Ile
1 5 10 15
Leu Ser Leu Ser Leu Leu Leu Leu Ala Ala Thr Val Ser Ala Ser
20 25 30
Ile Pro Glu Leu Ile Glu Leu Val Asp Ser Asn Thr Ile Phe Thr Asn
35 40 45
Glu Ala Glu Leu Leu Glu Lys Glu Lys Leu Ser Ile Asn Tyr Ala Asn
50 55 60
Cys Arg Ser Trp His Leu Gly Val Glu Thr Ser Asn Ile Ile Asp Phe
65 70 75 80
Asp Thr Val Pro Ala Asn Cys Lys Asp Tyr Val Glu Asp Tyr Leu Ile
85 90 95
Thr Ser Lys Gln Tyr Gln Tyr Asp Ser Lys Thr Val Cys Lys Glu Ala
100 105 110
Tyr Phe Tyr Ala Lys Gly Leu Ala Leu Lys Asn Asp Thr Val Asn Val
115 120 125
Trp Ile Phe Asp Leu Asp Asp Thr Leu Leu Ser Ser Ile Pro Tyr Tyr
130 135 140
Ala Lys Tyr Gly Tyr Gly Thr Glu Lys Thr Asp Pro Gly Ala Tyr Trp
145 150 155 160
Leu Trp Leu Gly Thr Gly Ala Ser Thr Pro Gly Leu Pro Glu Ala Leu
165 170 175
His Leu Tyr Gln Asn Ile Ile Glu Leu Gly Ile Glu Pro Ile Ile Leu
180 185 190
Ser Asp Arg Trp Lys Leu Trp Lys Asn Val Thr Leu Asp Asn Leu Glu
195 200 205
Ala Ala Gly Val Ala Tyr Trp Lys His Leu Ile Leu Lys Pro Asn Gly
210 215 220
Ser Asn Leu Arg Gln Val Val Tyr Lys Ser Lys Val Arg Lys Ser Leu
225 230 235 240
Val Lys Lys Gly Tyr Asn Ile Val Gly Asn Ile Gly Asp Gln Trp Ala
245 250 255
Asp Leu Val Glu Asp Thr Pro Gly Arg Val Phe Lys Leu Pro Asn Pro
260 265 270
Leu Tyr Tyr Val Pro Ser
```

275

(2) INFORMATION FOR SEQ ID NO:2394:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 265 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..265

(D) OTHER INFORMATION: / Ceres Seq. ID 1572828

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2394:

Met	Lys	Ile	Leu	Ser	Leu	Ser	Leu	Leu	Leu	Ala	Ala	Thr	Val
1			5					10				15	
Ser	Ala	Ser	Ile	Pro	Glu	Leu	Ile	Glu	Leu	Val	Asp	Ser	Asn
			20					25				30	Thr
Phe	Thr	Asn	Glu	Ala	Glu	Leu	Leu	Glu	Lys	Glu	Lys	Leu	Ser
			35					40				45	Ile
Tyr	Ala	Asn	Cys	Arg	Ser	Trp	His	Leu	Gly	Val	Glu	Thr	Ser
			50					55				60	Asn
Ile	Asp	Phe	Asp	Thr	Val	Pro	Ala	Asn	Cys	Lys	Asp	Tyr	Val
			65					70				75	Glu
Tyr	Leu	Ile	Thr	Ser	Lys	Gln	Tyr	Gln	Tyr	Asp	Ser	Lys	Thr
			85					90				95	Val
Lys	Glu	Ala	Tyr	Phe	Tyr	Ala	Lys	Gly	Leu	Ala	Leu	Lys	Asn
			100					105				110	Asp
Val	Asn	Val	Trp	Ile	Phe	Asp	Leu	Asp	Asp	Thr	Leu	Leu	Ser
			115					120				125	Ile
Pro	Tyr	Tyr	Ala	Lys	Tyr	Gly	Tyr	Gly	Thr	Glu	Lys	Thr	Asp
			130					135				140	Pro
Ala	Tyr	Trp	Leu	Trp	Leu	Gly	Thr	Gly	Ala	Ser	Thr	Pro	Gly
			145					150				155	Leu
Glu	Ala	Leu	His	Leu	Tyr	Gln	Asn	Ile	Ile	Glu	Leu	Gly	Ile
			165					170				175	Pro
Ile	Ile	Leu	Ser	Asp	Arg	Trp	Lys	Leu	Trp	Lys	Asn	Val	Thr
			180					185				190	Leu
Asn	Leu	Glu	Ala	Ala	Gly	Val	Ala	Tyr	Trp	Lys	His	Leu	Ile
			195					200				205	Leu
Pro	Asn	Gly	Ser	Asn	Leu	Arg	Gln	Val	Val	Tyr	Lys	Ser	Lys
			210					215				220	Val
Lys	Ser	Leu	Val	Lys	Lys	Gly	Tyr	Asn	Ile	Val	Gly	Asn	Ile
			225					230				235	Gly
Gln	Trp	Ala	Asp	Leu	Val	Glu	Asp	Thr	Pro	Gly	Arg	Val	Phe
			245					250				255	Lys
Pro	Asn	Pro	Leu	Tyr	Tyr	Val	Pro	Ser					Leu
			260					265					

(2) INFORMATION FOR SEQ ID NO:2395:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1005 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1005

(D) OTHER INFORMATION: / Ceres Seq. ID 1572833

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2395:

ctaccactta	agaagcacag	atggacataa	tctcagggca	agctctgtta	ctctcttttt	60
gctttatctt	atcatgtttt	cttatcttca	ccaccacaag	atctggagca	atctcccgcg	120


```

ggggccacgc gctgcctcca ggacctccac gggtaccgat catcggaat attcacctcg 180
tcggaaaaca tccacatcgc tcattcgccg agctctcaaa aacttatgga ccagtcgatga 240
gtcttaagct tggaaagttta aatacagtggt ttatagcttc accagaagct gcgagagagg 300
ttttacgaac acatgaccag attttgtctg cccgtagctc cactaacgcg gtacgggtcca 360
tcaatcacca agacgcttct ctgtctgggc ttctctgtc gtccgctcgt tggagggctgt 420
tgagaaggct gtcgggtgact cagctcttgt caccacagcg tatcgaagcc acgaaagcct 480
tgaggatgaa caagggtgaag gaacttgatg gcttcataag tgaagcagc gataggggaag 540
aatctGgttg atatttctcg tgtagccttc atcacaaact ttaatatcat atcgaaacatt 600
ctgttttccg tcgactctcg tagctacaac gcgaaagctt ctattaatgg ggttcaagac 660
acgggtgatta gtgttatgga gtctgcccgg actccagacg ctgctaatta ctttccattt 720
ctgagggtttc ttgacttcga aggtaatgtg aagactttta aggtttgcac ggagaggctg 780
gtaagggtttt tccgtgggtt cattgatgct aagattgocg aaaaatcatc gcagaataac 840
cctaaagatg tttaaaaaaa cgattttcgtt gacaaccttc tcgattacaa aggagatgaa 900
tcagaactct ccattagcga tattgaacac ctctcttgg taagtctgac ctactgcag 960
ataatcatga ttataagat aatggaataa tcaattttgt ggatg

```

(2) INFORMATION FOR SEQ ID NO:2396:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 176 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..176

(D) OTHER INFORMATION: / Ceres Seq. ID 1572834

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2396:

```

Met Asp Ile Ile Ser Gly Gln Ala Leu Leu Leu Phe Cys Phe Ile
1      5      10      15
Leu Ser Cys Phe Leu Ile Phe Thr Thr Thr Arg Ser Gly Arg Ile Ser
20      25      30
Arg Gly Ala Thr Ala Leu Pro Pro Gly Pro Pro Arg Leu Pro Ile Ile
35      40      45
Gly Asn Ile His Leu Val Gly Lys His Pro His Arg Ser Phe Ala Glu
50      55      60
Leu Ser Lys Thr Tyr Gly Pro Val Met Ser Leu Lys Leu Gly Ser Leu
65      70      75      80
Asn Thr Val Val Ile Ala Ser Pro Glu Ala Ala Arg Glu Val Leu Arg
85      90      95
Thr His Asp Gln Ile Leu Ser Ala Arg Ser Pro Thr Asn Ala Val Arg
100     105     110
Ser Ile Asn His Gln Asp Ala Ser Leu Val Trp Leu Pro Ser Ser Ser
115     120     125
Ala Arg Trp Arg Leu Leu Arg Arg Leu Ser Val Thr Gln Leu Leu Ser
130     135     140
Pro Gln Arg Ile Glu Ala Thr Lys Ala Leu Arg Met Asn Lys Val Lys
145     150     155     160
Glu Leu Val Ser Phe Ile Ser Glu Ser Ser Asp Arg Glu Glu Ser Gly
165     170     175

```

(2) INFORMATION FOR SEQ ID NO:2397:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 104 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..104

[illegible][illegible]

aacacacata	cataaaagta	gtagaaactaa	aaataggcaa	acctcttggg	ctctactttc	160
aatattttccg	cactttttgct	ctactccaac	gcacacggcg	caacattgcg	aatctctaac	170
caattgtagt	acacgctgtg	ggctgccgca	agccctggag	gtggccgacg	tctagatgct	180
gggcaatcgt	ggaggctaga	tctcgccgct	ggcactaaaa	tggccagatt	tgggggtagg	190
accaatgtga	actttgactc	gtgcgcatgc	ggcgcgatgc	aaactgtgtg	ctgcagtggt	200
ggactccaat	gacttgctgt	ggcacaccca	cacaacacgt	tggctgagta	cgattctgaac	210
caattcaaca	ctactgaact	ctgcqatcac	ctacttgtcg	atggaattta	caactctatg	220

gagtttagcc	caactagttc	gaactgccat	cggatactat	gtaccgcaga	cataaacgga	480
caatgtccaa	acgtgttgag	agccccaggt	ggatgcaaca	accggtgtac	tgatattcag	540
acgaaccaat	actgtttgtac	gaacgggtcag	ggatcatgta	gcgatactga	ctactcaaga	600
ttctttaagc	agagatgccc	tgNacgctta	cagctatcca	caagatgacc	cgactagcac	660
tttcacttgc	accaacacta	actacagggt	cgtgttttgt	ccaaggtcta	ggctcgggtgc	720
tactggatcc	caccagctcc	cgatcaagat	ggtaaccgag	gagaattaat	agactcgtat	780
ctactgtatg	tgtgtgtgtg	tgaggggtga	cgtagatatg	cgtacgtgtg	acgtgatcat	840
atatacgtta	ccataaacac	ttaattggatt	ataataaggc	atgcaataat	aattacgtta	900
gtcgacc						

(2) INFORMATION FOR SEQ ID NO:2400:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 204 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..204

(D) OTHER INFORMATION: / Ceres Seq. ID 1572838

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2400:

Met	Ala	Asn	Leu	Leu	Val	Ser	Thr	Phe	Ile	Phe	Ser	Ala	Leu	Leu	Leu
1		5						10					15		
Ile	Ser	Thr	Ala	Thr	Ala	Ala	Thr	Phe	Glu	Ile	Leu	Asn	Gln	Cys	Ser
		20						25					30		
Tyr	Thr	Val	Trp	Ala	Ala	Ala	Ser	Pro	Gly	Gly	Gly	Arg	Arg	Leu	Asp
		35					40					45			
Ala	Gly	Gln	Ser	Trp	Arg	Leu	Asp	Val	Ala	Ala	Gly	Thr	Lys	Met	Ala
	50				55				60						
Arg	Ile	Trp	Gly	Arg	Thr	Asn	Cys	Asn	Phe	Asp	Ser	Ser	Gly	Arg	Gly
	65			70					75					80	
Arg	Cys	Gln	Thr	Gly	Asp	Cys	Ser	Gly	Gly	Leu	Gln	Cys	Thr	Gly	Trp
		85						90					95		
Gly	His	Pro	Pro	Asn	Thr	Leu	Ala	Glu	Tyr	Ala	Leu	Asn	Gln	Phe	Asn
	100							105					110		
Asn	Leu	Asp	Phe	Tyr	Asp	Ile	Ser	Leu	Val	Asp	Gly	Phe	Asn	Ile	Pro
	115						120					125			
Met	Glu	Phe	Ser	Pro	Thr	Ser	Ser	Asn	Cys	His	Arg	Ile	Leu	Cys	Thr
	130						135					140			
Ala	Asp	Ile	Asn	Gly	Gln	Cys	Pro	Asn	Val	Leu	Arg	Ala	Pro	Gly	Gly
	145			150					155					160	
Cys	Asn	Asn	Pro	Cys	Thr	Val	Phe	Gln	Thr	Asn	Gln	Tyr	Cys	Cys	Thr
		165						170					175		
Asn	Gly	Gln	Gly	Ser	Cys	Ser	Asp	Thr	Asp	Tyr	Ser	Arg	Phe	Phe	Lys
	180							185					190		
Gln	Arg	Cys	Pro	Xaa	Arg	Leu	Gln	Leu	Ser	Thr	Arg				
	195							200							

(2) INFORMATION FOR SEQ ID NO:2401:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 142 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..142

(D) OTHER INFORMATION: / Ceres Seq. ID 1572839

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2401:

Met	Ala	Arg	Ile	Trp	Gly	Arg	Thr	Asn	Cys	Asn	Phe	Asp	Ser	Ser	Gly
1		5						10					15		

Arg Gly Arg Cys Gln Thr Gly Asp Cys Ser Gly Gly Leu Gln Cys Thr
20 25 30
Gly Trp Gly His Pro Pro Asn Thr Leu Ala Glu Tyr Ala Leu Asn Gln
35 40 45
Phe Asn Asn Leu Asp Phe Tyr Asp Ile Ser Leu Val Asp Gly Phe Asn
50 55 60
Ile Pro Met Glu Phe Ser Pro Thr Ser Ser Asn Cys His Arg Ile Leu
65 70 75 80
Cys Thr Ala Asp Ile Asn Gly Gln Cys Pro Asn Val Leu Arg Ala Pro
85 90 95
Gly Gly Cys Asn Asn Pro Cys Thr Val Phe Gln Thr Asn Gln Tyr Cys
100 105 110
Cys Thr Asn Gly Gln Gly Ser Cys Ser Asp Thr Asp Tyr Ser Arg Phe
115 120 125
Phe Lys Gln Arg Cys Pro Xaa Arg Leu Gln Leu Ser Thr Arg
130 135 140

(2) INFORMATION FOR SEQ ID NO:2402:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 703 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..703
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572840

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2402:

aaaaagagat	ggtctctgcta	gagaagcctt	gggatgatgt	tgtggctgga	cctcagcctg	60
accgtggcct	tggccgcctc	cgtaagatca	ccaccacaac	cattaatatc	cgagatatag	120
gagaagggag	cagcagtaag	gtggtgatgc	ataggtcggt	gaccatgccg	gcggcagtgga	180
gccctgggaa	cccaacgact	ccaaccactc	cgacgacgcc	acgtaaggat	aacgtgttga	240
ggagcgtctt	taatccggga	agcaacccct	ccactagagc	catcggtccc	aacatctttg	300
ataaacccac	ccatccaaat	tctccctccg	tctacgactg	gtgttacagc	ggtgactcaa	360
ggagtcagca	cogttaGgga	tggctccgat	gagtgtagca	tgcgggtgat	gtaaatatgg	420
tgacctgac	ttccgccacc	ttacttttgt	ttttttatat	tgtttttgtg	tactttatca	480
gagtggtata	agtgaacggg	aatgtttttc	ttttgtacaa	aaaactgtct	tcccaccctaa	540
gcaatgtgtg	ttagtttctg	ttttggcgct	tgttttgcaa	gttttttgat	ttcagagttg	600
tagtgtagtt	gcaagtggcg	gttggatctt	tcactatctt	gttggatttt	gatgatgggt	660
gatgcttttg	ctttaaatgt	aaataataaa	gcatactttt	gct		

(2) INFORMATION FOR SEQ ID NO:2403:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 124 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..124
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572841

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2403:

Lys	Glu	Met	Val	Leu	Leu	Glu	Lys	Leu	Trp	Asp	Asp	Val	Val	Ala	Gly
1		5						10					15		
Pro	Gln	Pro	Asp	Arg	Gly	Leu	Gly	Arg	Leu	Arg	Lys	Ile	Thr	Thr	Gln
		20						25					30		
Pro	Ile	Asn	Ile	Arg	Asp	Ile	Gly	Glu	Gly	Ser	Ser	Ser	Lys	Val	Val
		35						40					45		
Met	His	Arg	Ser	Leu	Thr	Met	Pro	Ala	Ala	Val	Ser	Pro	Gly	Thr	Pro
		50						55					60		
Thr	Thr	Pro	Thr	Thr	Pro	Thr	Thr	Pro	Arg	Lys	Asp	Asn	Val	Trp	Arg

65 70 75 80
Ser Val Phe Asn Pro Gly Ser Asn Leu Ala Thr Arg Ala Ile Gly Ser
85 90 95
Asn Ile Phe Asp Lys Pro Thr His Pro Asn Ser Pro Ser Val Tyr Asp
100 105 110
Trp Leu Tyr Ser Gly Asp Ser Arg Ser Gln His Arg
115 120

(2) INFORMATION FOR SEQ ID NO:2404:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 122 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..122

(D) OTHER INFORMATION: / Ceres Seq. ID 1572842

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2404:

Met Val Leu Leu Glu Lys Leu Trp Asp Asp Val Val Ala Gly Pro Gln
1 5 10 15
Pro Asp Arg Gly Leu Gly Arg Leu Arg Lys Ile Thr Thr Gln Pro Ile
20 25 30
Asn Ile Arg Asp Ile Gly Glu Gly Ser Ser Ser Lys Val Val Met His
35 40 45
Arg Ser Leu Thr Met Pro Ala Ala Val Ser Pro Gly Thr Pro Thr Thr
50 55 60
Pro Thr Thr Pro Thr Thr Pro Arg Lys Asp Asn Val Trp Arg Ser Val
65 70 75 80
Phe Asn Pro Gly Ser Asn Leu Ala Thr Arg Ala Ile Gly Ser Asn Ile
85 90 95
Phe Asp Lys Pro Thr His Pro Asn Ser Pro Ser Val Tyr Asp Trp Leu
100 105 110
Tyr Ser Gly Asp Ser Arg Ser Gln His Arg
115 120

(2) INFORMATION FOR SEQ ID NO:2405:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 76 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..76

(D) OTHER INFORMATION: / Ceres Seq. ID 1572843

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2405:

Met His Arg Ser Leu Thr Met Pro Ala Ala Val Ser Pro Gly Thr Pro
1 5 10 15
Thr Thr Pro Thr Thr Pro Thr Thr Pro Arg Lys Asp Asn Val Trp Arg
20 25 30
Ser Val Phe Asn Pro Gly Ser Asn Leu Ala Thr Arg Ala Ile Gly Ser
35 40 45
Asn Ile Phe Asp Lys Pro Thr His Pro Asn Ser Pro Ser Val Tyr Asp
50 55 60
Trp Leu Tyr Ser Gly Asp Ser Arg Ser Gln His Arg
65 70 75

(2) INFORMATION FOR SEQ ID NO:2406:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 597 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
 (A) NAME/KEY: -
 (B) LOCATION: 1.597
 (D) OTHER INFORMATION: / Ceres Seq. ID 1572844
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2406:
tccttatata attaatgttc accctctctc ttaatatgctc ttcaaaacac tttgtgtcaa 60
actctctctt aNttaaaatga aggtctctcc tegtgttgag tcagcccttc tcctattgtt 120
catgatcctt gccacagtga tgggtccggt cagggttagag gcacggagct gtgaaacgag 180
tagcaacttg ttcaatggac catgtctgag tccaagcaat tgcgctaag tttgccacaa 240
tgaaggtttt tcaatgtgtg actgccgtgg attccgtctg cgtctgtttg gcaccagacc 300
ctgttgatag atgatctatt tatataatat gaatatatat tatcaaaaac taaatgatct 360
ttctatgtt ttctatctct ttgatcattt tctgactttt atcctatctg ttgaccttga 420
aacaacgata aggagatcta aaatctttta gtctcttttg cttagagctt ctattatcta 480
ccaaggttaa acaataatac cttttatagt taccatttcc aaatcttatg accttttatg 540
tatcaaaata gattggactt acacatccaa tctaaataaa acatgattat ccaatct
(2) INFORMATION FOR SEQ ID NO:2407:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 76 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1.76
 (D) OTHER INFORMATION: / Ceres Seq. ID 1572845
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2407:
Met Lys Val Ser Pro Arg Leu Lys Ser Ala Leu Leu Leu Leu Phe Met
1 5 10 15
Ile Leu Ala Thr Val Met Gly Pro Val Arg Val Glu Ala Arg Thr Cys
20 25 30
Glu Thr Ser Ser Asn Leu Phe Asn Gly Pro Cys Leu Ser Ser Ser Asn
35 40 45
Cys Ala Asn Val Cys His Asn Glu Gly Phe Ser Asp Gly Asp Cys Arg
50 55 60
Gly Phe Arg Arg Arg Cys Leu Cys Thr Arg Pro Cys
65 70 75
(2) INFORMATION FOR SEQ ID NO:2408:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 61 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1.61
 (D) OTHER INFORMATION: / Ceres Seq. ID 1572846
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2408:
Met Ile Leu Ala Thr Val Met Gly Pro Val Arg Val Glu Ala Arg Thr
1 5 10 15
Cys Glu Thr Ser Ser Asn Leu Phe Asn Gly Pro Cys Leu Ser Ser Ser
20 25 30
Asn Cys Ala Asn Val Cys His Asn Glu Gly Phe Ser Asp Gly Asp Cys
35 40 45
Arg Gly Phe Arg Arg Arg Cys Leu Cys Thr Arg Pro Cys
50 55 60
(2) INFORMATION FOR SEQ ID NO:2409:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 59 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..59
 (D) OTHER INFORMATION: / Ceres Seq. ID 1572847
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2409:
Met Ile Tyr Leu Tyr Ile Met Asn Ile Tyr Tyr Gln Lys Leu Asn Asp
1 5 10 15
Leu Phe Tyr Val Phe Tyr Leu Phe Asp His Phe Leu Thr Phe Ile Leu
 20 25 30
Ser Phe Ala Phe Glu Thr Thr Ile Arg Arg Ser Lys Ile Phe Lys Ser
 35 40 45
Phe Trp Leu Glu Leu Ser Ile Ile Tyr Gln Gly
 50 55

(2) INFORMATION FOR SEQ ID NO:2410:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1145 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: DNA (genomic)
 (ix) FEATURE:
 (A) NAME/KEY: -
 (B) LOCATION: 1..1145
 (D) OTHER INFORMATION: / Ceres Seq. ID 1572852
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2410:
aaattttccc cattaaacaa aaaaaaatca aatctctctc ttctctctc taatggcggc 60
gacatttaggc agagaccagt atgtgtacat ggccaagCtc gccgagcagg cggaagcggtta 120
cgaagagatg gttcaattca tggaacagct cgttacagcc gctactccag cggaagagct 180
cacogttgaa gagaggaatc tctctctctg tgcttacaaa aacgtgatcg gatctctacg 240
cgccgcctgg aggatcttgt ctctgatgga gcagaaggaa gagagttaga agaacgcagca 300
gcacgtgtcg ctgtccaagg attacatata taaagttaga tctgagcttt ctctgtgttg 360
ctctggaatc cttaagctcc ttgactcgca tctgatccca tctgctggag cgagtgaagt 420
taaggtcttt tacttgaaga tgaagggtga ttatcatcgg tacatggctg agtttaagtc 480
tggtgatgag aggaaaactg ctgctgaaga taccatgctc gcttacaaag cagctcaggga 540
tatcgacgct gcgatatagg cacctactca tccgataaag ctggtctcgg cctgaatttt 600
ctcagtggtc tactatgaga ttctcaatc ttacagacaa gcttgtaaca tggccaaaca 660
ggcttttgag gaggccatag ctgagcttga cactctggga gaggaatcct acaagacagc 720
cactctcata atgcagttgc tgagggacaa tttaacctct tggacctccg atatgcagga 780
gcagatggag gaggcctgag gatctagatg aaggggggga ggggtgttac gcgatgtttc 840
tgccaccaaa tggatctcaa aatccccata accttctcgc aaaaactgtg aaaaagatt 900
gaagtgttta tgatgattat gattgtgcac agcttgatga ttatctact ctactaaacc 960
ctgtgtctct taatatattat tgtctcagct ctgctcaagc cttaaaaaaca tctttctcct 1020
taaggtcctc ctggttaaat tatgatcctt ctactgtatc gtcaaaatca agttgggaacc 1080
caaaattcgt ggattttttg tcggtgtgaa actgtgaata ataaaaaccg tcaattgtgt 1140
tactg

(2) INFORMATION FOR SEQ ID NO:2411:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 248 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..248

(D) OTHER INFORMATION: / Ceres Seq. ID 1572853

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2411:

Met Ala Ala Thr Leu Gly Arg Asp Gln Tyr Val Tyr Met Ala Lys Leu
1 5 10 15
Ala Glu Gln Ala Glu Arg Tyr Glu Glu Met Val Gln Phe Met Glu Gln
20 25 30
Leu Val Thr Gly Ala Thr Pro Ala Glu Glu Leu Thr Val Glu Glu Arg
35 40 45
Asn Leu Leu Ser Val Ala Tyr Lys Asn Val Ile Gly Ser Leu Arg Ala
50 55 60
Ala Trp Arg Ile Leu Ser Ser Ile Glu Gln Lys Glu Glu Ser Arg Lys
65 70 75 80
Asn Asp Glu His Val Ser Leu Val Lys Asp Tyr Ile Ser Lys Val Glu
85 90 95
Ser Glu Leu Ser Ser Val Cys Ser Gly Ile Leu Lys Leu Leu Asp Ser
100 105 110
His Leu Ile Pro Ser Ala Gly Ala Ser Glu Ser Lys Val Phe Tyr Leu
115 120 125
Lys Met Lys Gly Asp Tyr His Arg Tyr Met Ala Glu Phe Lys Ser Gly
130 135 140
Asp Glu Arg Lys Thr Ala Ala Glu Asp Thr Met Leu Ala Tyr Lys Ala
145 150 155 160
Ala Gln Asp Ile Ala Ala Ala Asp Met Ala Pro Thr His Pro Ile Arg
165 170 175
Leu Gly Leu Ala Leu Asn Phe Ser Val Phe Tyr Tyr Glu Ile Leu Asn
180 185 190
Ser Ser Asp Lys Ala Cys Asn Met Ala Lys Gln Ala Phe Glu Glu Ala
195 200 205
Ile Ala Glu Leu Asp Thr Leu Gly Glu Glu Ser Tyr Lys Asp Ser Thr
210 215 220
Leu Ile Met Gln Leu Leu Arg Asp Asn Leu Thr Leu Trp Thr Ser Asp
225 230 235 240
Met Gln Glu Gln Met Asp Glu Ala
245

(2) INFORMATION FOR SEQ ID NO:2412:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 236 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..236

(D) OTHER INFORMATION: / Ceres Seq. ID 1572854

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2412:

Met Ala Lys Leu Ala Glu Gln Ala Glu Arg Tyr Glu Glu Met Val Gln
1 5 10 15
Phe Met Glu Gln Leu Val Thr Gly Ala Thr Pro Ala Glu Glu Leu Thr
20 25 30
Val Glu Glu Arg Asn Leu Leu Ser Val Ala Tyr Lys Asn Val Ile Gly
35 40 45
Ser Leu Arg Ala Ala Trp Arg Ile Leu Ser Ser Ile Glu Gln Lys Glu
50 55 60
Glu Ser Arg Lys Asn Asp Glu His Val Ser Leu Val Lys Asp Tyr Ile
65 70 75 80
Ser Lys Val Glu Ser Glu Leu Ser Ser Val Cys Ser Gly Ile Leu Lys
85 90 95
Leu Leu Asp Ser His Leu Ile Pro Ser Ala Gly Ala Ser Glu Ser Lys
100 105 110
Val Phe Tyr Leu Lys Met Lys Gly Asp Tyr His Arg Tyr Met Ala Glu

115 120 125
Phe Lys Ser Gly Asp Glu Arg Lys Thr Ala Ala Glu Asp Thr Met Leu
130 135 140
Ala Tyr Lys Ala Ala Gln Asp Ile Ala Ala Asp Met Ala Pro Thr
145 150 155
His Pro Ile Arg Leu Gly Leu Ala Leu Asn Phe Ser Val Phe Tyr Tyr
165 170 175
Glu Ile Leu Asn Ser Ser Asp Lys Ala Cys Asn Met Ala Lys Gln Ala
180 185 190
Phe Glu Glu Ala Ile Ala Glu Leu Asp Thr Leu Gly Glu Glu Ser Tyr
195 200 205
Lys Asp Ser Thr Leu Ile Met Gln Leu Leu Arg Asp Asn Leu Thr Leu
210 215 220
Trp Thr Ser Asp Met Gln Glu Gln Met Asp Glu Ala
225 230 235

(2) INFORMATION FOR SEQ ID NO:2413:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 223 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..223

(D) OTHER INFORMATION: / Ceres Seq. ID 1572855

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2413:

Met Val Gln Phe Met Glu Gln Leu Val Thr Gly Ala Thr Pro Ala Glu
1 5 10 15
Glu Leu Thr Val Glu Glu Arg Asn Leu Leu Ser Val Ala Tyr Lys Asn
20 25 30
Val Ile Gly Ser Leu Arg Ala Ala Trp Arg Ile Leu Ser Ser Ile Glu
35 40 45
Gln Lys Glu Glu Ser Arg Lys Asn Asp Glu His Val Ser Leu Val Lys
50 55 60
Asp Tyr Ile Ser Lys Val Glu Ser Glu Leu Ser Ser Val Cys Ser Gly
65 70 75 80
Ile Leu Lys Leu Leu Asp Ser His Leu Ile Pro Ser Ala Gly Ala Ser
85 90 95
Glu Ser Lys Val Phe Tyr Leu Lys Met Lys Gly Asp Tyr His Arg Tyr
100 105 110
Met Ala Glu Phe Lys Ser Gly Asp Glu Arg Lys Thr Ala Ala Glu Asp
115 120 125
Thr Met Leu Ala Tyr Lys Ala Ala Gln Asp Ile Ala Ala Ala Asp Met
130 135 140
Ala Pro Thr His Pro Ile Arg Leu Gly Leu Ala Leu Asn Phe Ser Val
145 150 155
Phe Tyr Tyr Glu Ile Leu Asn Ser Ser Asp Lys Ala Cys Asn Met Ala
165 170 175
Lys Gln Ala Phe Glu Glu Ala Ile Ala Glu Leu Asp Thr Leu Gly Glu
180 185 190
Glu Ser Tyr Lys Asp Ser Thr Leu Ile Met Gln Leu Leu Arg Asp Asn
195 200 205
Leu Thr Leu Trp Thr Ser Asp Met Gln Glu Gln Met Asp Glu Ala
210 215 220

(2) INFORMATION FOR SEQ ID NO:2414:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1208 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1208

(D) OTHER INFORMATION: / Ceres Seq. ID 1572858

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2414:

```

acaagcaaaa aaaattcaact ttttgtttt gttaacactc acgtgaaagc ttcgtttctt 60
ttcaaacctt ttgaacaatt ttcctgatgc cggtaaatac cgggtttacg tttagctacc 120
ggttactctt cctcatcttc ctttttgagt tcgaaacggc acagcggttg gtcaccgggtg 180
accacaacga cgaagcatgc ttgacgaatc tccgtcggag tttagaagat cccgcgaata 240
attctcgtaa ctggacaaaa tcttttcttc taaatccttg ctcocggctt tctttttatc 300
ttcatggagt catttgcac aaatggcagaa tttaaaaaa ctcttaaga aaatctcttc 360
tccgtggctc aatctctcog tttctctcta attgcacaaa tctccaatcc ctagatctat 420
cttccaacca gatctccggc gagatccgcg cgcaattaca gtttctcgtt aacctagccg 480
ttcttaactc ctcttctaata cgtctctcgc gtcaaatctc accaacaatc gctctctgcg 540
cttacttaaa cgtcatcgat ctccacgata accaactctc cgggtcaaat ccgtttcagt 600
tcgggtttct cgttagatta acggcggttg atgtctctaa taacaaatta tccggtcaga 660
ttccctcgaa tctggcgcgt cgtaacggaa acttgcgcgag atttaacgcg agctcgttta 720
tagggaacaa gaaattgttc gggatatccg tggaggagat gaagaacaaa ggattgtcga 780
taattggcgt tgttgggttg ggacttggaa gtggaaatcg gagcttagtg attagcttca 840
ctggagtttg tataagggtg aagattacag agaagaagat ggaggaagaa gaaggaaata 900
taagtcaact catgcctgtt tactaaacac aaacatttgc ttttttttct tcttaagtat 960
aattaacggg ttcttttttc acataattag tttttttttt ccattttgat caaaagcata 1020
cagcaaatag gagggttcaa ttaagcgaat ttagggttaa ttaatgcttt gatcataat 1080
acatgtttct ttggttatct ttggatacat attacaacaaa atcacaaagt ttaagcatga 1140
ggactaagt tattgttgta tagtttttgt agttatgaaa gtgtaattta tagtgacatc 1200
atttatgc

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(2) INFORMATION FOR SEQ ID NO:2415:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 279 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..279

(D) OTHER INFORMATION: / Ceres Seq. ID 1572859

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2415:

```

Met Pro Val Asn His Arg Phe Thr Phe Ser Tyr Arg Leu Leu Phe Leu
1      5      10      15
Ile Phe Leu Leu Ser Phe Glu Thr Ala Gln Arg Leu Val Thr Gly Asp
20      25      30
Pro Asn Asp Glu Ala Cys Leu Thr Asn Leu Arg Arg Ser Leu Glu Asp
35      40      45
Pro Ala Asn Asn Leu Arg Asn Trp Thr Lys Ser Phe Phe Ile Asn Pro
50      55      60
Cys Ser Gly Phe Ser Ser Tyr Leu His Gly Val Ile Cys Asn Asn Gly
65      70      75      80
Arg Ile Tyr Lys Leu Ser Leu Thr Asn Leu Ser Leu Arg Gly Ser Ile
85      90      95
Ser Pro Phe Leu Ser Asn Cys Thr Asn Leu Gln Ser Leu Asp Leu Ser
100      105      110
Ser Asn Gln Ile Ser Gly Glu Ile Pro Pro Gln Leu Gln Phe Leu Val
115      120      125
Asn Leu Ala Val Leu Asn Leu Ser Ser Asn Arg Leu Ser Gly Gln Ile
130      135      140
Ser Pro Gln Ile Ala Leu Cys Ala Tyr Leu Asn Val Ile Asp Leu His
145      150      155      160
Asp Asn Gln Leu Ser Gly Gln Ile Pro Phe Gln Phe Gly Leu Leu Ala
165      170      175

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Arg Leu Thr Ala Phe Asp Val Ser Asn Asn Lys Leu Ser Gly Gln Ile
180 185 190
Pro Ser Asn Leu Ala Met Arg Asn Gly Asn Leu Pro Arg Phe Asn Ala
195 200 205
Ser Ser Phe Ile Gly Asn Lys Lys Leu Phe Gly Tyr Pro Leu Glu Glu
210 215 220
Met Lys Asn Lys Gly Leu Ser Ile Met Ala Ile Val Gly Ile Gly Leu
225 230 235 240
Gly Ser Gly Ile Ala Ser Leu Val Ile Ser Phe Thr Gly Val Cys Ile
245 250 255
Trp Leu Lys Ile Thr Glu Lys Lys Met Glu Glu Glu Glu Gly Lys Ile
260 265 270
Ser His Ser Met Pro Val Tyr
275

(2) INFORMATION FOR SEQ ID NO:2416:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 989 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..989
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572860

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2416:

aagttgaagt	tactgatcaa	gataacaaat	ttatcaaaaa	taaatacatc	atactggttt	60
atgagcaaga	aacattgtct	agaattatta	ccaaataaga	tgtttagaaa	ccaagactcg	120
aaatacttga	tcccggtgca	gaaagaagcg	ccaccggtga	caactttacc	gatgaaagct	180
tcaacggtga	aatctccaca	caactgtgag	gccattctca	gagacgcaga	tcctccgatc	240
ctctctctct	ctgttaactc	ctctgaacag	ctacggtctg	gtgttttctt	gaaacccaag	300
aaacagatca	aatatgtggg	ggacgagaga	aacagcaact	gcttcatgct	ctttgcaaa	360
aacctctcta	taacttgggt	tgatgacgtc	aactattgga	cttggtttac	cgaaaaagag	420
tcaccaaacg	agaatgtgga	agctgtggga	ttgaaaaacg	ttgttgggt	cgacatcacg	480
ggaaaattcg	acacgaggaa	cctcactccg	gggattgttt	acgaggtggt	cttcaagggt	540
aagctagagg	atccggccta	tggatgggac	acgccggtga	acctaaaagt	agtccttgc	600
aacggtgaag	agacgccaca	agagcaaaag	ttgagtttga	gggaacttcc	aagggtataaa	660
tgggtgcgat	tcagagtgtg	cgagttcgta	cctgagaaaat	ccgctgcgcg	agagatcaat	720
ttctcaatgt	atgagcatgt	ggctggtggt	tggaaagaaa	ggctctccct	caaaagtggt	780
gcaattcgct	ccaaacagta	ataattgtta	tggcatagaa	aaacataaat	ctccatatgc	840
accaatggac	cttctcaaca	tataattcac	atcatgtcat	gtgtgtataa	taaggttggt	900
ctatcgattt	tttagtttta	ataataaact	taatgttggt	gttgaataaa	ctcaaaaacga	960
gtgttttgaa	ggtgtgtata	ttcgaatcg				

(2) INFORMATION FOR SEQ ID NO:2417:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 266 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..266
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572861

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2417:

Lys	Leu	Asn	Val	Leu	Ile	Lys	Ile	Thr	Asn	Leu	Ser	Lys	Ile	Asn	Thr
1					5			10						15	
Ser	Tyr	Trp	Phe	Met	Ser	Lys	Lys	His	Cys	Ser	Glu	Leu	Leu	Pro	Asn
					20			25						30	
Lys	Met	Phe	Arg	Asn	Gln	Asp	Ser	Lys	Tyr	Leu	Ile	Pro	Val	Gln	Lys
					35			40						45	

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Glu	Ala	Pro	Pro	Val	Thr	Thr	Leu	Pro	Met	Lys	Ala	Ser	Thr	Val	Lys
	50					55					60				
Ser	Pro	His	Asn	Cys	Glu	Ala	Ile	Leu	Arg	Asp	Ala	Asp	Pro	Pro	Ile
65					70				75					80	
Ser	Leu	Ser	Ser	Val	Asn	Leu	Ser	Glu	Gln	Leu	Arg	Ser	Gly	Val	Phe
				85				90					95		
Leu	Lys	Pro	Lys	Lys	Gln	Ile	Lys	Tyr	Trp	Val	Asp	Glu	Arg	Asn	Ser
			100				105						110		
Asn	Cys	Phe	Met	Leu	Phe	Ala	Lys	Asn	Leu	Ser	Ile	Thr	Trp	Ser	Asp
		115					120					125			
Asp	Val	Asn	Tyr	Trp	Thr	Trp	Phe	Thr	Glu	Lys	Glu	Ser	Pro	Asn	Glu
	130					135					140				
Asn	Val	Glu	Ala	Val	Gly	Leu	Lys	Asn	Val	Cys	Trp	Leu	Asp	Ile	Thr
145					150					155				160	
Gly	Lys	Phe	Asp	Thr	Arg	Asn	Leu	Thr	Pro	Gly	Ile	Val	Tyr	Glu	Val
			165					170						175	
Val	Phe	Lys	Val	Lys	Leu	Glu	Asp	Pro	Ala	Tyr	Gly	Trp	Asp	Thr	Pro
			180					185					190		
Val	Asn	Leu	Lys	Leu	Val	Leu	Pro	Asn	Gly	Lys	Glu	Thr	Pro	Gln	Glu
		195					200					205			
Gln	Lys	Leu	Ser	Leu	Arg	Glu	Leu	Pro	Arg	Tyr	Lys	Trp	Val	Asp	Val
	210					215					220				
Arg	Val	Gly	Glu	Phe	Val	Pro	Glu	Lys	Ser	Ala	Ala	Gly	Glu	Ile	Thr
225					230					235				240	
Phe	Ser	Met	Tyr	Glu	His	Val	Ala	Gly	Val	Trp	Lys	Lys	Gly	Leu	Ser
			245					250						255	
Leu	Lys	Gly	Val	Ala	Ile	Arg	Pro	Lys	Gln						
		260					265								

(2) INFORMATION FOR SEQ ID NO:2418:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 246 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..246

(D) OTHER INFORMATION: / Ceres Seq. ID 1572862

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2418:

Met	Ser	Lys	Lys	His	Cys	Ser	Glu	Leu	Leu	Pro	Asn	Lys	Met	Phe	Arg
1			5						10					15	
Asn	Gln	Asp	Ser	Lys	Tyr	Leu	Ile	Pro	Val	Gln	Lys	Glu	Ala	Pro	Pro
		20					25					30			
Val	Thr	Thr	Leu	Pro	Met	Lys	Ala	Ser	Thr	Val	Lys	Ser	Pro	His	Asn
	35					40					45				
Cys	Glu	Ala	Ile	Leu	Arg	Asp	Ala	Asp	Pro	Pro	Ile	Ser	Leu	Ser	Ser
	50				55					60					
Val	Asn	Leu	Ser	Glu	Gln	Leu	Arg	Ser	Gly	Val	Phe	Leu	Lys	Pro	Lys
65				70					75					80	
Lys	Gln	Ile	Lys	Tyr	Trp	Val	Asp	Glu	Arg	Asn	Ser	Asn	Cys	Phe	Met
		85						90					95		
Leu	Phe	Ala	Lys	Asn	Leu	Ser	Ile	Thr	Trp	Ser	Asp	Asp	Val	Asn	Tyr
		100					105						110		
Trp	Thr	Trp	Phe	Thr	Glu	Lys	Glu	Ser	Pro	Asn	Glu	Asn	Val	Glu	Ala
	115						120					125			
Val	Gly	Leu	Lys	Asn	Val	Cys	Trp	Leu	Asp	Ile	Thr	Gly	Lys	Phe	Asp
	130				135						140				
Thr	Arg	Asn	Leu	Thr	Pro	Gly	Ile	Val	Tyr	Glu	Val	Val	Phe	Lys	Val
145				150					155					160	
Lys	Leu	Glu	Asp	Pro	Ala	Tyr	Gly	Trp	Asp	Thr	Pro	Val	Asn	Leu	Lys

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..516

(D) OTHER INFORMATION: / Ceres Seq. ID 1572868

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2420:

aaaccctaga	cctaatactt	tagcgaaatt	aagcagagca	acattttcgt	aatccgatct	60
ccgtcgtcgt	cgtcgaatca	gataaaaaatg	gcgaaGcggt	tgatcccgac	tctcaaccgt	120
gtattggtgg	agaagattct	cccaccgtca	aagaccgtct	ccggcattct	cctaccggag	180
aaatcatctc	agttgaattc	cgggagaggtt	atagcagttg	gtcctgggag	tagagacaga	240
cgagggaatc	taattccggt	ttcggttaag	gaaggagaca	atgtttcttt	gcctgaattt	300
ggtgtgtact	aagtttaagct	tggagagaaa	gagttcctat	tgtataggga	tgaagataac	360
atggctaac	ttcacgagtg	atgtgttaaa	gagatagaat	ttagtattcc	tctttgtttt	420
gttgctctga	attgtctgac	atttggatca	attgttatga	ttgttcttca	ctgttgccaa	480
caagtcttta	taattcaata	atctcttttg	tttgcc			

(2) INFORMATION FOR SEQ ID NO:2421:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 97 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..97

(D) OTHER INFORMATION: / Ceres Seq. ID 1572869

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2421:

Met	Ala	Lys	Arg	Leu	Ile	Pro	Thr	Leu	Asn	Arg	Val	Leu	Val	Glu	Lys
1		5					10					15			
Ile	Leu	Pro	Pro	Ser	Lys	Thr	Val	Ser	Gly	Ile	Leu	Leu	Pro	Glu	Lys
		20					25					30			
Ser	Ser	Gln	Leu	Asn	Ser	Gly	Arg	Val	Ile	Ala	Val	Gly	Pro	Gly	Ala
		35					40					45			
Arg	Asp	Arg	Ala	Gly	Asn	Leu	Ile	Pro	Val	Ser	Val	Lys	Glu	Gly	Asp
		50					55					60			
Asn	Val	Leu	Leu	Pro	Glu	Phe	Gly	Gly	Thr	Gln	Val	Lys	Leu	Gly	Glu
		65					70					75			
Lys	Glu	Phe	Leu	Leu	Tyr	Arg	Asp	Glu	Asp	Ile	Met	Ala	Thr	Leu	His
		85					90					95			
Glu															

(2) INFORMATION FOR SEQ ID NO:2422:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 691 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..691

(D) OTHER INFORMATION: / Ceres Seq. ID 1572878

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2422:

atcagaaatc	gaaaaatcaa	agttctcaag	aagatatcaa	caaaaaaaa	gtaaattctt	60
taaaatgtcg	atgatctcaa	gtttcttcaa	caacaacaga	cgaagcaaca	tctttgatcc	120
attctctctt	gacgtatggg	atccattcaa	ggaactaaca	tcatcatcac	tttctcgtga	180
gaactcagcg	atcgtgaacg	cacgtgtgga	ctggagagag	acgcctgagg	cgcacgtggt	240
taaaagctgc	tgtcctggat	tgaagaagga	ggaagttaaa	gttgagattg	aggagggatg	300
tgtttttgag	atcagtgag	agagacacgt	ggagaaagaa	gataagaatg	acacgtggca	360
ccgtgtggag	agatcagatg	gacagtttac	gaggagggtt	aggttgcggc	agaattgtga	420
gatgatcag	gttaagcgtg	cagtgagaga	tggtgtgtgt	actgttacgg	tgccataaggc	480
tgagRactaa	gaagcgtgat	gttaagtcta	ttcagatctc	tggttgagta	atggggttgc	540
gttttatcat	cggagtgtct	tgtgtttttg	tcatggttat	ggttcatggt	ttacttgagt	600

gtgtgagtcc tctatctctaaa ttataataat ctccgattga gctatgaatt atgatgtatc 660
ggatacatatt gatcctaagt aagtatggaa t

(2) INFORMATION FOR SEQ ID NO:2423:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 162 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..162
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572879

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2423:

Ser	Glu	Ile	Glu	Lys	Ser	Lys	Phe	Ser	Arg	Arg	Tyr	Gln	Gln	Lys	Lys
1			5					10					15		
Ser	Lys	Phe	Phe	Lys	Met	Ser	Met	Ile	Pro	Ser	Phe	Phe	Asn	Asn	Asn
		20						25					30		
Arg	Arg	Ser	Asn	Ile	Phe	Asp	Pro	Phe	Ser	Leu	Asp	Val	Trp	Asp	Pro
		35					40					45			
Phe	Lys	Glu	Leu	Thr	Ser	Ser	Ser	Leu	Ser	Arg	Glu	Asn	Ser	Ala	Ile
		50				55					60				
Val	Asn	Ala	Arg	Val	Asp	Trp	Arg	Glu	Thr	Pro	Glu	Ala	His	Val	Phe
65					70					75				80	
Lys	Ala	Asp	Leu	Pro	Gly	Leu	Lys	Lys	Glu	Glu	Val	Lys	Val	Glu	Ile
			85					90					95		
Glu	Glu	Asp	Ser	Val	Leu	Lys	Ile	Ser	Gly	Glu	Arg	His	Val	Glu	Lys
		100						105					110		
Glu	Asp	Lys	Asn	Asp	Thr	Trp	His	Arg	Val	Glu	Arg	Ser	Ser	Gly	Gln
		115					120					125			
Phe	Thr	Arg	Arg	Phe	Arg	Leu	Pro	Glu	Asn	Val	Lys	Met	Asp	Gln	Val
130						135					140				
Lys	Ala	Ala	Met	Glu	Asn	Gly	Val	Leu	Thr	Val	Thr	Val	Pro	Lys	Ala
145					150					155				160	
Glu	Xaa														

(2) INFORMATION FOR SEQ ID NO:2424:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 141 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..141
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572880

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2424:

Met	Ser	Met	Ile	Pro	Ser	Phe	Phe	Asn	Asn	Asn	Arg	Arg	Ser	Asn	Ile
1			5					10					15		
Phe	Asp	Pro	Phe	Ser	Leu	Asp	Val	Trp	Asp	Pro	Phe	Lys	Glu	Leu	Thr
		20						25					30		
Ser	Ser	Ser	Leu	Ser	Arg	Glu	Asn	Ser	Ala	Ile	Val	Asn	Ala	Arg	Val
		35					40					45			
Asp	Trp	Arg	Glu	Thr	Pro	Glu	Ala	His	Val	Phe	Lys	Ala	Asp	Leu	Pro
		50				55					60				
Gly	Leu	Lys	Lys	Glu	Glu	Val	Lys	Val	Glu	Ile	Glu	Glu	Asp	Ser	Val
65					70					75				80	
Leu	Lys	Ile	Ser	Gly	Glu	Arg	His	Val	Glu	Lys	Glu	Asp	Lys	Asn	Asp
			85					90				95			
Thr	Trp	His	Arg	Val	Glu	Arg	Ser	Ser	Gly	Gln	Phe	Thr	Arg	Arg	Phe

100 105 110
Arg Leu Pro Glu Asn Val Lys Met Asp Gln Val Lys Ala Ala Met Glu
115 120 125
Asn Gly Val Leu Thr Val Thr Val Pro Lys Ala Glu Xaa
130 135 140

(2) INFORMATION FOR SEQ ID NO:2425:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 139 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..139

(D) OTHER INFORMATION: / Ceres Seq. ID 1572661

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2425:

Met	Ile	Pro	Ser	Phe	Phe	Asn	Asn	Asn	Arg	Ser	Asn	Ile	Phe	Asp
1			5					10				15		
Pro	Phe	Ser	Leu	Asp	Val	Trp	Asp	Pro	Phe	Lys	Glu	Leu	Thr	Ser
			20				25					30		
Ser	Leu	Ser	Arg	Glu	Asn	Ser	Ala	Ile	Val	Asn	Ala	Arg	Val	Asp
		35				40					45			
Arg	Glu	Thr	Pro	Glu	Ala	His	Val	Phe	Lys	Ala	Asp	Leu	Pro	Gly
	50				55						60			
Lys	Lys	Glu	Glu	Val	Lys	Val	Glu	Ile	Glu	Glu	Asp	Ser	Val	Leu
	65			70				75				80		
Ile	Ser	Gly	Glu	Arg	His	Val	Glu	Lys	Glu	Asp	Lys	Asn	Asp	Thr
			85					90				95		
His	Arg	Val	Glu	Arg	Ser	Ser	Gly	Gln	Phe	Thr	Arg	Arg	Phe	Arg
		100					105					110		
Pro	Glu	Asn	Val	Lys	Met	Asp	Gln	Val	Lys	Ala	Ala	Met	Glu	Asn
		115					120					125		
Val	Leu	Thr	Val	Thr	Val	Pro	Lys	Ala	Glu	Xaa				
	130					135								

(2) INFORMATION FOR SEQ ID NO:2426:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1524 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1524

(D) OTHER INFORMATION: / Ceres Seq. ID 1572666

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2426:

ttttttctttc	ttttttcttc	tgggagtttg	ggattttctt	gagggtcttt	ttcaattttc	60
gtctcaatttt	gtacgcatag	aactgggttt	gtgtttacac	acataaagct	cttatctttt	120
ttctctcttc	aatcgagaag	attatagagc	tgagtgaact	attggtggtt	tcttgaggatt	180
ttaattgggag	gttggtttcag	caatcggatt	aaaacagata	ttgcttcacg	tacatggcta	240
agttcgaaat	tcttgagtag	agatgggagc	aagggtctcg	cgaccgcttc	ctctcttatt	300
atgctctgaa	cagaaggcga	gatcttgcaa	aatgctaact	tcaagaactt	tagtctcagt	360
gaactgaaat	ctgcaactag	gaatttcagg	cctgatagtg	tggttggtga	agggtgattt	420
ggttgctgtt	tcaaaagctg	gatcgatgag	tctctctctg	ctccttctaa	accggggacc	480
Gggattgtca	ttgctgtgaa	aagacttaac	caagaagggt	ttcaagggtca	tcgagagtgg	540
ctggctgaga	tcaattattt	aggccagctg	gatcatccta	acctgtgtaa	actgattgga	600
tactgcttgg	aagaggagca	caggctctct	gtttacgagt	ttaatgactg	tggtagtctt	660
gagaaatcag	tattcagaag	aggaacattc	tatcagccac	tttcaatgaa	cacgcggggt	720
cgtatggctc	ttggtgcagc	tagaggactt	gcttttcttc	acaatgtcta	accgcaagtt	780
atataccgag	acttcaaagc	atctaaacat	ttgctgattt	cgaactacaa	cgcaaaagctt	840

tcggatttcg	gtttggctag	agatgggtcca	atgggtgaca	acagccatgt	ttctaccaga	900
gtcatgggaa	ctcagggata	cgctgtccca	gaatatctag	ctacagggtca	tttatcggtg	960
aagagcgatg	tatacagttt	tggggttgtg	ttactggagt	tgttatcagg	aagacgagca	1020
attgacaaga	atcaaccagt	aggagaacac	aatctcgtg	attgggcaag	accctactta	1080
acaaacaaga	gaagacttct	gcgagtgatg	gatcctcgtc	tccaagggtca	atactacta	1140
accggagctt	tgaaaaattgc	agttcttgc	ctcgattgca	tatctataga	tgccaagagt	1200
agaccggaca	tgaacgaat	cgtaacgaca	atggaagaac	ttcatatcca	gaaggaagca	1260
tcaaaagagc	agcagaatcc	tcaaatcagc	attgacaaca	tcatacaaca	atctccacaa	1320
gctgtgaatt	atcctagggc	ttcaattatg	taacaatcct	aggcgagcta	tttaccgagt	1380
tttagagatg	tatatagactc	ttaccctctg	tctgtttaga	tattatgttg	tttgtagtag	1440
acaaaagagc	tggccaatgta	agggagagaa	ggaaacctac	tagttgtaaa	cttaggttct	1500
cttacaacgt	tcacatgtta	tccc				

(2) INFORMATION FOR SEQ ID NO:2427:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 389 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..389
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572887

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2427:

Met	Gly	Gly	Cys	Phe	Ser	Asn	Arg	Ile	Lys	Thr	Asp	Ile	Ala	Ser	Ser
1			5					10					15		
Thr	Trp	Leu	Ser	Ser	Lys	Phe	Leu	Ser	Arg	Asp	Gly	Ser	Lys	Gly	Ser
			20					25					30		
Ser	Thr	Ala	Ser	Phe	Ser	Tyr	Met	Pro	Arg	Thr	Glu	Gly	Glu	Ile	Leu
			35				40					45			
Gln	Asn	Ala	Asn	Leu	Lys	Asn	Phe	Ser	Leu	Ser	Glu	Leu	Lys	Ser	Ala
			50			55					60				
Thr	Arg	Asn	Phe	Arg	Pro	Asp	Ser	Val	Val	Gly	Glu	Gly	Gly	Phe	Gly
65						70				75				80	
Cys	Val	Phe	Lys	Gly	Trp	Ile	Asp	Glu	Ser	Ser	Leu	Ala	Pro	Ser	Lys
			85						90					95	
Pro	Gly	Thr	Gly	Ile	Val	Ile	Ala	Val	Lys	Arg	Leu	Asn	Gln	Glu	Gly
			100					105					110		
Phe	Gln	Gly	His	Arg	Glu	Trp	Leu	Ala	Glu	Ile	Asn	Tyr	Leu	Gly	Gln
			115				120					125			
Leu	Asp	His	Pro	Asn	Leu	Val	Lys	Leu	Ile	Gly	Tyr	Cys	Leu	Glu	Glu
			130				135				140				
Glu	His	Arg	Leu	Leu	Val	Tyr	Glu	Phe	Met	Thr	Arg	Gly	Ser	Leu	Glu
145					150					155				160	
Asn	His	Leu	Phe	Arg	Arg	Gly	Thr	Phe	Tyr	Gln	Pro	Leu	Ser	Trp	Asn
			165						170					175	
Thr	Arg	Val	Arg	Met	Ala	Leu	Gly	Ala	Ala	Arg	Gly	Leu	Ala	Phe	Leu
			180					185					190		
His	Asn	Ala	Gln	Pro	Gln	Val	Ile	Tyr	Arg	Asp	Phe	Lys	Ala	Ser	Asn
			195					200					205		
Ile	Leu	Leu	Asp	Ser	Asn	Tyr	Asn	Ala	Lys	Leu	Ser	Asp	Phe	Gly	Leu
			210				215					220			
Ala	Arg	Asp	Gly	Pro	Met	Gly	Asp	Asn	Ser	His	Val	Ser	Thr	Arg	Val
225					230						235				
Met	Gly	Thr	Gln	Gly	Tyr	Ala	Ala	Pro	Glu	Tyr	Leu	Ala	Thr	Gly	His
			245						250					255	
Leu	Ser	Val	Lys	Ser	Asp	Val	Tyr	Ser	Phe	Gly	Val	Val	Leu	Leu	Glu
			260					265					270		
Leu	Leu	Ser	Gly	Arg	Arg	Ala	Ile	Asp	Lys	Asn	Gln	Pro	Val	Gly	Glu
			275					280					285		
His	Asn	Leu	Val	Asp	Trp	Ala	Arg	Pro	Tyr	Leu	Thr	Asn	Lys	Arg	Arg

290	295	300
Leu Leu Arg Val Met Asp Pro Arg Leu Gln Gly Gln Tyr Ser Leu Thr		
305	310	315
Arg Ala Leu Lys Ile Ala Val Leu Ala Leu Asp Cys Ile Ser Ile Asp		320
	325	330
Ala Lys Ser Arg Pro Thr Met Asn Glu Ile Val Lys Thr Met Glu Glu		335
	340	345
Leu His Ile Gln Lys Glu Ala Ser Lys Glu Gln Gln Asn Pro Gln Ile		350
	355	360
Ser Ile Asp Asn Ile Ile Asn Lys Ser Pro Gln Ala Val Asn Tyr Pro		365
	370	375
Arg Pro Ser Ile Met		380
385		

(2) INFORMATION FOR SEQ ID NO:2428:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 350 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..350
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572888

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2428:

Met Pro Arg Thr Glu Gly Glu Ile Leu Gln Asn Ala Asn Leu Lys Asn	
1	5
Phe Ser Leu Ser Glu Leu Lys Ser Ala Thr Arg Asn Phe Arg Pro Asp	10
	15
	20
Ser Val Val Gly Glu Gly Gly Phe Gly Cys Val Phe Lys Gly Trp Ile	25
	30
Asp Glu Ser Ser Leu Ala Pro Ser Lys Pro Gly Thr Gly Ile Val Ile	35
	40
Ala Val Lys Arg Leu Asn Gln Glu Gly Phe Gln Gly His Arg Glu Trp	45
65	50
Leu Ala Glu Ile Asn Tyr Leu Gly Gln Leu Asp His Pro Asn Leu Val	55
	60
Lys Leu Ile Gly Tyr Cys Leu Glu Glu His Arg Leu Leu Val Tyr	65
	70
Glu Phe Met Thr Arg Gly Ser Leu Glu Asn His Leu Phe Arg Arg Gly	75
	80
Thr Phe Tyr Gln Pro Leu Ser Trp Asn Thr Arg Val Arg Met Ala Leu	85
	90
Gly Ala Ala Arg Gly Leu Ala Phe Leu His Asn Ala Gln Pro Gln Val	95
145	100
Ile Tyr Arg Asp Phe Lys Ala Ser Asn Ile Leu Leu Asp Ser Asn Tyr	105
	110
Asn Ala Lys Leu Ser Asp Phe Gly Leu Ala Arg Asp Gly Pro Met Gly	115
	120
Asp Asn Ser His Val Ser Thr Arg Val Met Gly Thr Gln Gly Tyr Ala	125
	130
Ala Pro Glu Tyr Leu Ala Thr Gly His Leu Ser Val Lys Ser Asp Val	135
	140
Tyr Ser Phe Gly Val Val Leu Leu Glu Leu Leu Ser Gly Arg Arg Ala	145
	150
Ile Asp Lys Asn Gln Pro Val Gly Glu His Asn Leu Val Asp Trp Ala	155
	160
Arg Pro Tyr Leu Thr Asn Lys Arg Arg Leu Leu Arg Val Met Asp Pro	165
	170
Arg Leu Gln Gly Gln Tyr Ser Leu Thr Arg Ala Leu Lys Ile Ala Val	175
	180
	185
	190
	195
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	270
	275
	280
	285

Leu Ala Leu Asp Cys Ile Ser Ile Asp Ala Lys Ser Arg Pro Thr Met
290 295 300
Asn Glu Ile Val Lys Thr Met Glu Leu His Ile Gln Lys Glu Ala
305 310 315 320
Ser Lys Glu Gln Gln Asn Pro Gln Ile Ser Ile Asp Asn Ile Ile Asn
325 330 335
Lys Ser Pro Gln Ala Val Asn Tyr Pro Arg Pro Ser Ile Met
340 345 350

(2) INFORMATION FOR SEQ ID NO:2429:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 236 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..236

(D) OTHER INFORMATION: / Ceres Seq. ID 1572889

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2429:

Met Thr Arg Gly Ser Leu Glu Asn His Leu Phe Arg Arg Gly Thr Phe
1 5 10 15
Tyr Gln Pro Leu Ser Trp Asn Thr Arg Val Arg Met Ala Leu Gly Ala
20 25 30
Ala Arg Gly Leu Ala Phe Leu His Asn Ala Gln Pro Gln Val Ile Tyr
35 40 45
Arg Asp Phe Lys Ala Ser Asn Ile Leu Leu Asp Ser Asn Tyr Asn Ala
50 55 60
Lys Leu Ser Asp Phe Gly Leu Ala Arg Asp Gly Pro Met Gly Asp Asn
65 70 75 80
Ser His Val Ser Thr Arg Val Met Gly Thr Gln Gly Tyr Ala Ala Pro
85 90 95
Glu Tyr Leu Ala Thr Gly His Leu Ser Val Lys Ser Asp Val Tyr Ser
100 105 110
Phe Gly Val Val Leu Leu Glu Leu Leu Ser Gly Arg Arg Ala Ile Asp
115 120 125
Lys Asn Gln Pro Val Gly Glu His Asn Leu Val Asp Trp Ala Arg Pro
130 135 140
Tyr Leu Thr Asn Lys Arg Arg Leu Leu Arg Val Met Asp Pro Arg Leu
145 150 155 160
Gln Gly Gln Tyr Ser Leu Thr Arg Ala Leu Lys Ile Ala Val Leu Ala
165 170 175
Leu Asp Cys Ile Ser Ile Asp Ala Lys Ser Arg Pro Thr Met Asn Glu
180 185 190
Ile Val Lys Thr Met Glu Glu Leu His Ile Gln Lys Glu Ala Ser Lys
195 200 205
Glu Gln Gln Asn Pro Gln Ile Ser Ile Asp Asn Ile Ile Asn Lys Ser
210 215 220
Pro Gln Ala Val Asn Tyr Pro Arg Pro Ser Ile Met
225 230 235

(2) INFORMATION FOR SEQ ID NO:2430:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 583 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..583

(D) OTHER INFORMATION: / Ceres Seq. ID 1572890

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2430:

aaaaacaaaa	ataaaaaaaa	catgcacaaa	gaaaaataaaa	gattttgtaga	atcaactaag	60
aaaaatggcta	gcaactatgat	gactacattg	cctcagttca	atggtctctcg	agccaccaaa	120
atctctgcag	ctcctgtaca	aggcctggca	agtgttcagc	ccatgagacg	caagggaagt	180
ggagctttgg	gtgcaaaagt	tgacttcctc	gggttcacaa	caaattctgat	aatggtaacg	240
tcgacgaccc	tgattttggt	cgcggggaga	ttcggacttg	cgccatcagc	caataggaag	300
gcgacagctg	gacttagggt	ggaggcacgt	gactcaggtc	tacaaacggg	tgaccocggc	360
gggttcacgc	ttgcggacac	tttggtctgt	ggcaccgttg	gtcatatcat	cgggtgtagga	420
gttgcctctg	gccttaaaaa	cattggtgct	atttgagtt	cctaaagctc	ttttatttgt	480
attttgaaaa	Atttgtagat	ttttataaca	atattctcat	gcacctgaac	gagatcctaat	540
ggattttaca	agtttttatg	tttatcttat	aatgttgat	cgc		

(2) INFORMATION FOR SEQ ID NO:2431:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 151 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..151
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572891

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2431:

Lys	Asn	Lys	Asn	Lys	Lys	Asn	Ile	Ala	Gln	Glu	Asn	Lys	Arg	Phe	Val	
1				5					10					15		
Glu	Ser	Thr	Lys	Lys	Met	Ala	Ser	Thr	Met	Met	Thr	Thr	Leu	Pro	Gln	
			20					25					30			
Phe	Asn	Gly	Leu	Arg	Ala	Thr	Lys	Ile	Ser	Ala	Ala	Pro	Val	Gln	Gly	
		35					40				45					
Leu	Ala	Ser	Val	Gln	Pro	Met	Arg	Arg	Lys	Gly	Asn	Gly	Ala	Leu	Gly	
		50				55					60					
Ala	Lys	Cys	Asp	Phe	Ile	Gly	Ser	Ser	Thr	Asn	Leu	Ile	Met	Val	Thr	
		65			70					75				80		
Ser	Thr	Thr	Leu	Ile	Leu	Phe	Ala	Gly	Arg	Phe	Gly	Leu	Ala	Pro	Ser	
			85						90					95		
Ala	Asn	Arg	Lys	Ala	Thr	Ala	Gly	Leu	Arg	Leu	Glu	Ala	Arg	Asp	Ser	
			100					105					110			
Gly	Leu	Gln	Thr	Gly	Asp	Pro	Ala	Gly	Phe	Thr	Leu	Ala	Asp	Thr	Leu	
		115					120					125				
Ala	Cys	Gly	Thr	Val	Gly	His	Ile	Ile	Gly	Val	Gly	Val	Val	Leu	Gly	
		130				135					140					
Leu	Lys	Asn	Ile	Gly	Ala	Ile										
		145			150											

(2) INFORMATION FOR SEQ ID NO:2432:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 130 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..130
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572892

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2432:

Met	Ala	Ser	Thr	Met	Met	Thr	Thr	Leu	Pro	Gln	Phe	Asn	Gly	Leu	Arg	
1				5					10					15		
Ala	Thr	Lys	Ile	Ser	Ala	Ala	Pro	Val	Gln	Gly	Leu	Ala	Ser	Val	Gln	
		20						25					30			
Pro	Met	Arg	Arg	Lys	Gly	Asn	Gly	Ala	Leu	Gly	Ala	Lys	Cys	Asp	Phe	
		35				40						45				

Ile Gly Ser Ser Thr Asn Leu Ile Met Val Thr Ser Thr Thr Leu Ile
50 55 60
Leu Phe Ala Gly Arg Phe Gly Leu Ala Pro Ser Ala Asn Arg Lys Ala
65 70 75 80
Thr Ala Gly Leu Arg Leu Glu Ala Arg Asp Ser Gly Leu Gln Thr Gly
85 90 95
Asp Pro Ala Gly Phe Thr Leu Ala Asp Thr Leu Ala Cys Gly Thr Val
100 105 110
Gly His Ile Ile Gly Val Gly Val Leu Gly Leu Lys Asn Ile Gly
115 120 125
Ala Ile
130

(2) INFORMATION FOR SEQ ID NO:2433:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 126 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide
(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..126
(D) OTHER INFORMATION: / Ceres Seq. ID 1572893

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2433:

Met Met Thr Thr Leu Pro Gln Phe Asn Gly Leu Arg Ala Thr Lys Ile
1 5 10 15
Ser Ala Ala Pro Val Gln Gly Leu Ala Ser Val Gln Pro Met Arg Arg
20 25 30
Lys Gly Asn Gly Ala Leu Gly Ala Lys Cys Asp Phe Ile Gly Ser Ser
35 40 45
Thr Asn Leu Ile Met Val Thr Ser Thr Thr Leu Ile Leu Phe Ala Gly
50 55 60
Arg Phe Gly Leu Ala Pro Ser Ala Asn Arg Lys Ala Thr Ala Gly Leu
65 70 75 80
Arg Leu Glu Ala Arg Asp Ser Gly Leu Gln Thr Gly Asp Pro Ala Gly
85 90 95
Phe Thr Leu Ala Asp Thr Leu Ala Cys Gly Thr Val Gly His Ile Ile
100 105 110
Gly Val Gly Val Val Leu Gly Leu Lys Asn Ile Gly Ala Ile
115 120 125

(2) INFORMATION FOR SEQ ID NO:2434:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 661 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)

- (ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..661
(D) OTHER INFORMATION: / Ceres Seq. ID 1572894

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2434:

attttccag tgagaaatgg cgacgaagga accagaatct gtttacgagt taagcatcga 60
ggatgcaaaa gggaacaact tagcactcag tcaatacaaa gacaaagttc ttittaattgt 120
caatgttgct tccaaatgtg ggatgacaaa ctcaaaactac actgaattga atgagcttta 180
caacaggatg aaagataaag gctctggagat tctagcattt ccttgtaacc agtttggtga 240
cgaggaaccc ggaactaatg accaaattac tgactttgtt tgtactcgct tcaaaactga 300
attccccatt ttcaacaaga ttgaagttaa cggagagaat gctctctcct tgtataaagt 360
cctgaagaaa ggcaaatggg gaactctcgg cgtatgacatt caatggaaat ttgctaagtt 420
tcttgttgac aaaaacggct aagctgtaca acgttattat ccaactactt cccctcttac 480
acttgagcat gacataaaga atctctctgaa tatctctcga atgatgaagc ttgtttgctg 540

(2) INFORMATION FOR SEO ID NO:2435:

(A) LENGTH: 167 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..167

(D) OTHER INFORMATION: / Ceres Seq. ID 1572895

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2435:

[illegible]

(2) INFORMATION FOR SEQ ID NO:2436:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 125 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..125

(D) OTHER INFORMATION: / Ceres Seq. ID 1572896

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2436:

Met	Thr	Asn	Ser	Asn	Tyr	Thr	Glu	Leu	Asn	Glu	Leu	Tyr	Asn	Arg	Tyr
1				5					10					15	
Lys	Asp	Lys	Gly	Leu	Glu	Ile	Leu	Ala	Phe	Pro	Cys	Asn	Gln	Phe	Gly
			20				25						30		
Asp	Glu	Glu	Pro	Gly	Thr	Asn	Asp	Gln	Ile	Thr	Asp	Phe	Val	Cys	Thr
		35					40					45			
Arg	Phe	Lys	Ser	Glu	Phe	Pro	Ile	Phe	Asn	Lys	Ile	Glu	Val	Asn	Gly
	50					55				60					
Glu	Asn	Ala	Ser	Pro	Leu	Tyr	Lys	Phe	Leu	Lys	Lys	Gly	Lys	Trp	Gly
					70					75				80	
Ile	Phe	Gly	Asp	Asp	Ile	Gln	Trp	Asn	Phe	Ala	Lys	Phe	Leu	Val	Asp
			85						90				95		

Lys Asn Gly Gln Ala Val Gln Arg Tyr Tyr Pro Thr Thr Ser Pro Leu
100 105 110
Thr Leu Glu His Asp Ile Lys Asn Leu Leu Asn Ile Ser
115 120 125

(2) INFORMATION FOR SEQ ID NO:2437:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 879 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..879
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572897

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2437:

```
gcaaacgcta gttaccggaa gacacgtctt gagtttcgca gcatctctct cctctcctct 60
gttcatactt ctcttttagaa atttctcaat gaacatactc aacagattgg gtttgggagc 120
aagtggggcaa accaatatgg atcctctctc gatcgctcag ggaaatgacg atgacacacc 180
ggcgccgggg aatcagtttg cccaattogg agctggatgt ttctgggggtg tcgagctggc 240
gtttcacaga gtcccagggg tgactcagac cgaggctgga tacaccaag ggaccgtaca 300
caatccttca tacggagatg ttgttcttgg taccacagcg cattcggagg ttgttagggt 360
tcaatatgat cttaacgatt gcacotatga gtctctgctt gatttgttct ggtctaggca 420
tgatccacc accottgaat gccaggggaaa tgacgtggga aCccaataca gatctggaat 480
atacttctac acaccggagc aggagaaact agcccgtgag tcacttgaac gtcaccagca 540
acaaatggag agaaagatga gactgaaat ctgtccagct aagaaattct acagagctga 600
agagcatcat caacagatgc tgtcaaaagg tgggcggttt ggccaaggcg aatccaactgc 660
caaggctgc aacgaccocaa tccgctgtta cggtttaataa cgtgttttcc tctgtccctc 720
tcgaaaaaca gaggacttag catcaaaagga cttgtgtgtc aaatagattg tgtaaaactt 780
tgactaagtt gtccacacgc tatgtacta cttcttggga atttcattcg caatgttgta 840
atattgatgt tatactctat aaacataaac caaataatc
```

(2) INFORMATION FOR SEQ ID NO:2438:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 231 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..231
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572898

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2438:

```
Gln Thr Leu Val Thr Gly Arg His Val Leu Ser Phe Ala Ala Ser Leu
1 5 10 15
Ser Ser Pro Leu Phe Ile Ser Leu Phe Arg Asn Phe Ser Met Asn Ile
20 25 30
Leu Asn Arg Leu Gly Leu Gly Ser Ser Gly Gln Thr Asn Met Asp Pro
35 40 45
Ser Pro Ile Ala Gln Gly Asn Asp Asp Asp Thr Pro Ala Pro Gly Asn
50 55 60
Gln Phe Ala Gln Phe Gly Ala Gly Cys Phe Trp Gly Val Glu Leu Ala
65 70 75 80
Phe Gln Arg Val Pro Gly Val Thr Gln Thr Glu Ala Gly Tyr Thr Gln
85 90 95
Gly Thr Val His Asn Pro Ser Tyr Gly Asp Val Cys Ser Gly Thr Thr
100 105 110
Gly His Ser Glu Val Val Arg Val Gln Tyr Asp Leu Asn Asp Cys Thr
115 120 125
Tyr Glu Ser Leu Leu Asp Leu Phe Trp Ser Arg His Asp Pro Thr Thr
130 135 140
```

Leu Asn Arg Gln Gly Asn Asp Val Gly Thr Gln Tyr Arg Ser Gly Ile
145 150 155 160
Tyr Phe Tyr Thr Pro Glu Gln Glu Lys Leu Ala Arg Glu Ser Leu Glu
165 170 175
Arg His Gln Gln Gln Met Glu Arg Lys Ile Met Thr Glu Ile Leu Pro
180 185 190
Ala Lys Lys Phe Tyr Arg Ala Glu His His Gln Gln Tyr Leu Ser
195 200 205
Lys Gly Gly Arg Phe Gly Gln Gly Gln Ser Thr Ala Lys Gly Cys Asn
210 215 220
Asp Pro Ile Arg Cys Tyr Gly
225 230

(2) INFORMATION FOR SEQ ID NO:2439:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 202 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..202

(D) OTHER INFORMATION: / Ceres Seq. ID 1572899

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2439:

Met Asn Ile Leu Asn Arg Leu Gly Leu Gly Ser Ser Gly Gln Thr Asn
1 5 10
Met Asp Pro Ser Pro Ile Ala Gln Gly Asn Asp Asp Asp Thr Pro Ala
20 25 30
Pro Gly Asn Gln Phe Ala Gln Phe Gly Ala Gly Cys Phe Trp Gly Val
35 40 45
Glu Leu Ala Phe Gln Arg Val Pro Gly Val Thr Gln Thr Glu Ala Gly
50 55 60
Tyr Thr Gln Gly Thr Val His Asn Pro Ser Tyr Gly Asp Val Cys Ser
65 70 75 80
Gly Thr Thr Gly His Ser Glu Val Val Arg Val Gln Tyr Asp Leu Asn
85 90 95
Asp Cys Thr Tyr Glu Ser Leu Leu Asp Leu Phe Trp Ser Arg His Asp
100 105 110
Pro Thr Thr Leu Asn Arg Gln Gly Asn Asp Val Gly Thr Gln Tyr Arg
115 120 125
Ser Gly Ile Tyr Phe Tyr Thr Pro Glu Gln Glu Lys Leu Ala Arg Glu
130 135 140
Ser Leu Glu Arg His Gln Gln Gln Met Glu Arg Lys Ile Met Thr Glu
145 150 155 160
Ile Leu Pro Ala Lys Lys Phe Tyr Arg Ala Glu Glu His His Gln Gln
165 170 175
Tyr Leu Ser Lys Gly Gly Arg Phe Gly Gln Gly Gln Ser Thr Ala Lys
180 185 190
Gly Cys Asn Asp Pro Ile Arg Cys Tyr Gly
195 200

(2) INFORMATION FOR SEQ ID NO:2440:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 186 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..186

(D) OTHER INFORMATION: / Ceres Seq. ID 1572900

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2440:

Met Asp Pro Ser Pro Ile Ala Gln Gly Asn Asp Asp Asp Thr Pro Ala
1 5 10 15
Pro Gly Asn Gln Phe Ala Gln Phe Gly Ala Gly Cys Phe Trp Gly Val
20 25 30
Glu Leu Ala Phe Gln Arg Val Pro Gly Val Thr Gln Thr Glu Ala Gly
35 40 45
Tyr Thr Gln Gly Thr Val His Asn Pro Ser Tyr Gly Asp Val Cys Ser
50 55 60
Gly Thr Thr Gly His Ser Glu Val Val Arg Val Gln Tyr Asp Leu Asn
65 70 75 80
Asp Cys Thr Tyr Glu Ser Leu Leu Asp Leu Phe Trp Ser Arg His Asp
85 90 95
Pro Thr Thr Leu Asn Arg Gln Gly Asn Asp Val Gly Thr Gln Tyr Arg
100 105 110
Ser Gly Ile Tyr Phe Tyr Thr Pro Glu Gln Glu Lys Leu Ala Arg Glu
115 120 125
Ser Leu Glu Arg His Gln Gln Gln Met Glu Arg Lys Ile Met Thr Glu
130 135 140
Ile Leu Pro Ala Lys Lys Phe Tyr Arg Ala Glu His His Gln Gln
145 150 155 160
Tyr Leu Ser Lys Gly Gly Arg Phe Gly Gln Gly Gln Ser Thr Ala Lys
165 170 175
Gly Cys Asn Asp Pro Ile Arg Cys Tyr Gly
180 185

(2) INFORMATION FOR SEQ ID NO:2441:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1443 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1443
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572905

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2441:

acatgtttttg	ctctgtcttct	ctctttatct	tctttcttcac	cttttgtcac	tctttttctc	60
tgctctaaac	tttttctttt	cgctgcaaaa	aatttttccca	ggaatatttc	ttaaaagaaa	120
tttctacctc	aaataagaaa	aaagcatctc	cttcttttagt	gtcctctcttc	accctaaactc	180
tgattccata	agcatatatt	aaaaaagctc	ctctgtttctt	tcaacttttcc	cgggaaaaatc	240
ttctgtttac	aaagcatcaa	tctctgtttt	taccagtttt	ctctctttat	tctcttttttg	300
ccctttactt	ttcttaactt	tggtctttat	atataaacac	acgacacaaa	gaagaacaca	360
cataagttaa	aactattaca	acagttttta	agagagagat	ttaaaaaatg	gagacagaga	420
agaaagtttc	tctcccaaga	atcttacgaa	tctctgttac	tgatctctac	gcaacagatt	480
cgctcaagca	cgaagaagaa	gaagttgatt	ttgatgcatt	atctacaaaa	cgacgtcgtg	540
ttaaagaagta	cgtgaaggaa	gtggtgcttg	atccgttggt	ttctgataaa	gagaagccga	600
tgaagaagaa	gagaaagaag	cgcgttggtta	ctgttccagt	ggttggttac	acagcgacga	660
ggaagtgttc	tgagtgagtg	caaagaccgt	ggggaaaatg	ggcggcgagg	attagagatc	720
cgagtagacg	tggttagggt	tggttaggta	cttttgacac	ggcgaggagg	gctgccattc	780
tttaacataa	cgcagctatt	cagctacgtg	gtctaacacg	agagcttaac	ttccctctctg	840
ctccggtgac	ggagaatgtg	gagaagaact	cgacggaggt	gaaaggagtt	tccgatttta	900
tcattggcgg	tgagagaatat	cttcgttcgc	cggtttctgt	tctcgaatct	ccgttctccg	960
cgagctctac	tgccgtwaaa	gaggagtttg	tcggtgtatc	gacggcgagg	attgttggtta	1020
aaaaagagcc	gtcttttaac	gggttcagatt	tctcgccgac	gtgtgtctcg	gacgacgacg	1080
tttttggttt	ctcgcagctg	atgagtgaag	gtttcggcgg	cgattatttt	ggagataatt	1140
tttttgcgga	tatgagtttt	ggatccgggt	ttggtattcg	gtctggtctct	ggatctccca	1200
gctgcgcagct	tgaggaccat	tcttcaagat	attggggatt	tattcgaatc	ggatcctgtc	1260
ttaactgttt	aagaaaataa	tgccggttta	acggcgattt	gtgaagtttt	gttacccggcg	1320
acggcgagga	ttaaaaaaaa	acggcgattt	attttttgaa	tgaagatttg	ttaaatatat	1380
ttaaactttt	tgtaacttaa	ttaatggtga	ttttattttt	aaataaaact	aatggttaaa	1440

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(2) INFORMATION FOR SEQ ID NO:2442:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 297 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..297

(D) OTHER INFORMATION: / Ceres Seq. ID 1572906

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2442:

Met	Glu	Thr	Glu	Lys	Val	Ser	Leu	Pro	Arg	Ile	Leu	Arg	Ile	Ser
1				5				10					15	
Val	Thr	Asp	Pro	Tyr	Ala	Thr	Asp	Ser	Ser	Asp	Glu	Glu	Glu	
			20				25					30		
Val	Asp	Phe	Asp	Ala	Leu	Ser	Thr	Lys	Arg	Arg	Arg	Val	Lys	Tyr
			35				40					45		
Val	Lys	Glu	Val	Val	Leu	Asp	Ser	Val	Val	Ser	Asp	Lys	Glu	Pro
			50			55				60				
Met	Lys	Lys	Lys	Arg	Lys	Lys	Arg	Val	Val	Thr	Val	Pro	Val	Val
65				70				75					80	
Thr	Thr	Ala	Thr	Arg	Lys	Phe	Arg	Gly	Val	Arg	Gln	Arg	Pro	Trp
				85				90					95	
Lys	Trp	Ala	Ala	Glu	Ile	Arg	Asp	Pro	Ser	Arg	Arg	Val	Arg	Val
			100				105					110		
Leu	Gly	Thr	Phe	Asp	Thr	Ala	Glu	Glu	Ala	Ala	Ile	Val	Tyr	Asp
			115				120					125		
Ala	Ala	Ile	Gln	Leu	Arg	Gly	Pro	Asn	Ala	Glu	Leu	Asn	Phe	Pro
			130			135				140				
Ala	Pro	Val	Thr	Glu	Asn	Val	Glu	Glu	Ala	Ser	Thr	Glu	Val	Lys
145				150					155				160	
Val	Ser	Asp	Phe	Ile	Gly	Gly	Gly	Glu	Tyr	Leu	Arg	Ser	Pro	Val
			165					170					175	
Ser	Val	Leu	Glu	Ser	Pro	Phe	Ser	Gly	Glu	Ser	Thr	Ala	Xaa	Lys
			180				185						190	
Glu	Phe	Val	Gly	Val	Ser	Thr	Ala	Glu	Ile	Val	Val	Lys	Lys	Glu
			195				200					205		
Ser	Phe	Asn	Gly	Ser	Asp	Phe	Ser	Ala	Pro	Leu	Phe	Ser	Asp	Asp
			210			215					220			
Val	Phe	Gly	Phe	Ser	Thr	Ser	Met	Ser	Glu	Ser	Phe	Gly	Gly	Asp
225				230					235					240
Phe	Gly	Asp	Asn	Leu	Phe	Ala	Asp	Met	Ser	Phe	Gly	Ser	Gly	Phe
			245					250					255	
Phe	Gly	Ser	Gly	Ser	Gly	Phe	Ser	Ser	Trp	His	Val	Glu	Asp	His
			260				265					270		
Ser	Arg	Tyr	Trp	Gly	Phe	Ile	Arg	Val	Gly	Ser	Cys	Leu	Asn	Cys
			275				280					285		
Arg	Asn	Asn	Trp	Pro	Phe	Asn	Gly	Val						
			290			295								

(2) INFORMATION FOR SEQ ID NO:2443:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 233 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..233

(D) OTHER INFORMATION: / Ceres Seq. ID 1572907

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2443:

Met	Lys	Lys	Lys	Arg	Lys	Lys	Arg	Val	Val	Thr	Val	Pro	Val	Val	Val
1				5				10					15		
Thr	Thr	Ala	Thr	Arg	Lys	Phe	Arg	Gly	Val	Arg	Gln	Arg	Pro	Trp	Gly
			20					25					30		
Lys	Trp	Ala	Ala	Glu	Ile	Arg	Asp	Pro	Ser	Arg	Arg	Val	Arg	Val	Trp
			35				40					45			
Leu	Gly	Thr	Phe	Asp	Thr	Ala	Glu	Glu	Ala	Ala	Ile	Val	Tyr	Asp	Asn
	50						55					60			
Ala	Ala	Ile	Gln	Leu	Arg	Gly	Pro	Asn	Ala	Glu	Leu	Asn	Phe	Pro	Pro
	65				70				75					80	
Ala	Pro	Val	Thr	Glu	Asn	Val	Glu	Glu	Ala	Ser	Thr	Glu	Val	Lys	Gly
				85				90					95		
Val	Ser	Asp	Phe	Ile	Ile	Gly	Gly	Gly	Glu	Tyr	Leu	Arg	Ser	Pro	Val
			100					105					110		
Ser	Val	Leu	Glu	Ser	Pro	Phe	Ser	Gly	Glu	Ser	Thr	Ala	Xaa	Lys	Glu
			115					120					125		
Glu	Phe	Val	Gly	Val	Ser	Thr	Ala	Glu	Ile	Val	Val	Lys	Lys	Glu	Pro
			130				135					140			
Ser	Phe	Asn	Gly	Ser	Asp	Phe	Ser	Ala	Pro	Leu	Phe	Ser	Asp	Asp	Asp
				150					155					160	
Val	Phe	Gly	Phe	Ser	Thr	Ser	Met	Ser	Glu	Ser	Phe	Gly	Gly	Asp	Leu
			165					170						175	
Phe	Gly	Asp	Asn	Leu	Phe	Ala	Asp	Met	Ser	Phe	Gly	Ser	Gly	Phe	Gly
			180				185						190		
Phe	Gly	Ser	Gly	Ser	Gly	Phe	Ser	Ser	Trp	His	Val	Glu	Asp	His	Xaa
			195				200					205			
Ser	Arg	Tyr	Trp	Gly	Phe	Ile	Arg	Val	Gly	Ser	Cys	Leu	Asn	Cys	Leu
			210			215					220				
Arg	Asn	Asn	Trp	Pro	Phe	Asn	Gly	Val							
	225				230										

(2) INFORMATION FOR SEQ ID NO:2444:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1284 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1284

(D) OTHER INFORMATION: / Ceres Seq. ID 1572912

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2444:

caagatgac	aagattctgt	tagattattg	gcggttgagg	gttggtgctgc	tcttggggaaa	60
ttgttgaggc	ctcaggattg	tgtccaacac	attcttcccg	tgattgttaa	ttcttcgcag	120
gataagctct	ggcgtgtgag	ctatatgggt	gcaaatcaac	tctacgagct	ttgtgaagcc	180
gtgggacctg	agcctactag	gacggagctg	gtgcctgcac	atgtgcgcct	acttcgtgat	240
aatgaagctg	aagtacgcat	agcagctgcc	ggaaaaagta	caaaagtttg	tcggattcta	300
aacctgaaa	tgtctatcca	gcacattctc	cctgtgtgta	aggagctatc	atcagactct	360
tctcagcatg	tcagatctgc	attggcctca	gttataatgg	gaatggctcc	agctctgggt	420
aaggatgcaa	caattgagca	tctccttoca	atctttcttt	ctctattgaa	agatgagttc	480
cCgagtgatc	gcttgaacat	tatcagcaaa	cttgaccaag	tgaatcaggt	tattgggatt	540
gatctactat	cacaatcctt	gttgccagct	attgtagaAc	ttgctgaaga	tagacactgg	600
agagtgaagc	ttgtcataat	caggtatatc	cctttgttgg	caagtcagtt	aggtgttgGc	660
ttctttGagc	ataagcttgg	tgctcttTgc	atgcaatgg	Tacaagacaa	ggttcactca	720
atcCgcgatg	ctgctgctaa	caatctcaag	cggtcttgctg	aggaatttgg	tcttgaattg	780
gcaatgcaac	atatagtttc	tcaggttctt	gagatgggta	acaaccctca	ctatctctac	840
cgaatgacca	ttttgctgtc	gggtgtctct	cttgcaacctg	taatggggctg	agagattaca	900
tgctctaaag	tcttacctgt	agtaatgact	gcactctaaag	acagagttcc	aaacatcaca	960
ttcaacgtcg	ctaaagactc	tcaatccctc	attccaatag	ttgatcaatc	ggttgtggag	1020

aagacgattc gtccctgggct tgtggagcta agcgaggatc cagatgttga tgcagggttt	1080
ttcgaaaacc aagctctaca atctattgac aatgtgatga tgtctagcta aaaacattag	1140
atcttgctc tctgtgtata atcgttttct atttgattga aaaaaaaaaa aaatctcaag	1200
acttttgtaa cgttagtagtg gattctcgtc ttgtgttttt tattacacgc aaactactag	1260
agtgccctgg tacgggtttt gtcc	

(2) INFORMATION FOR SEQ ID NO:2445:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 376 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..376

(D) OTHER INFORMATION: / Ceres Seq. ID 1572913

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2445:

Gln	Asp	Asp	Gln	Asp	Ser	Val	Arg	Leu	Leu	Ala	Val	Glu	Gly	Cys	Ala	
1			5						10					15		
Ala	Leu	Gly	Lys	Leu	Leu	Glu	Pro	Gln	Asp	Cys	Val	Gln	His	Ile	Leu	
		20						25					30			
Pro	Val	Ile	Val	Asn	Phe	Ser	Gln	Asp	Lys	Ser	Trp	Arg	Val	Arg	Tyr	
		35						40				45				
Met	Val	Ala	Asn	Gln	Leu	Tyr	Glu	Leu	Cys	Glu	Ala	Val	Gly	Pro	Glu	
		50				55					60					
Pro	Thr	Arg	Thr	Glu	Leu	Val	Pro	Ala	Tyr	Val	Arg	Leu	Leu	Arg	Asp	
		65			70				75					80		
Asn	Glu	Ala	Glu	Val	Arg	Ile	Ala	Ala	Ala	Gly	Lys	Val	Thr	Lys	Phe	
			85						90					95		
Cys	Arg	Ile	Leu	Asn	Pro	Glu	Ile	Ala	Ile	Gln	His	Ile	Leu	Pro	Cys	
			100					105					110			
Val	Lys	Glu	Leu	Ser	Ser	Asp	Ser	Ser	Gln	His	Val	Arg	Ser	Ala	Leu	
			115					120				125				
Ala	Ser	Val	Ile	Met	Gly	Met	Ala	Pro	Val	Leu	Gly	Lys	Asp	Ala	Thr	
		130			135						140					
Ile	Glu	His	Leu	Leu	Pro	Ile	Phe	Leu	Ser	Leu	Lys	Asp	Glu	Phe		
		145			150					155				160		
Pro	Asp	Val	Arg	Leu	Asn	Ile	Ile	Ser	Lys	Leu	Asp	Gln	Val	Asn	Gln	
			165						170					175		
Val	Ile	Gly	Ile	Asp	Leu	Leu	Ser	Gln	Ser	Leu	Leu	Pro	Ala	Ile	Val	
			180					185					190			
Glu	Leu	Ala	Glu	Asp	Arg	His	Trp	Arg	Val	Arg	Leu	Ala	Ile	Ile	Glu	
		195					200					205				
Tyr	Ile	Pro	Leu	Leu	Ala	Ser	Gln	Leu	Gly	Val	Gly	Phe	Phe	Asp	Asp	
		210				215						220				
Lys	Leu	Gly	Ala	Leu	Cys	Met	Gln	Trp	Leu	Gln	Asp	Lys	Val	His	Ser	
		225			230					235				240		
Ile	Arg	Asp	Ala	Ala	Ala	Asn	Asn	Leu	Lys	Arg	Leu	Ala	Glu	Glu	Phe	
			245						250					255		
Gly	Pro	Glu	Trp	Ala	Met	Gln	His	Ile	Val	Pro	Gln	Val	Leu	Glu	Met	
			260				265						270			
Val	Asn	Asn	Pro	His	Tyr	Leu	Tyr	Arg	Met	Thr	Ile	Leu	Arg	Ala	Val	
		275					280					285				
Ser	Leu	Leu	Ala	Pro	Val	Met	Gly	Ser	Glu	Ile	Thr	Cys	Ser	Lys	Leu	
		290				295					300					
Leu	Pro	Val	Val	Met	Thr	Ala	Ser	Lys	Asp	Arg	Val	Pro	Asn	Ile	Lys	
		305			310				315					320		
Phe	Asn	Val	Ala	Lys	Val	Leu	Gln	Ser	Leu	Ile	Pro	Ile	Val	Asp	Gln	
			325						330					335		
Ser	Val	Val	Glu	Lys	Thr	Ile	Arg	Pro	Gly	Leu	Val	Glu	Leu	Ser	Glu	
			340				345						350			

Asp Pro Asp Val Asp Val Arg Phe Phe Ala Asn Gln Ala Leu Gln Ser
355 360 365
Ile Asp Asn Val Met Met Ser Ser
370 375

(2) INFORMATION FOR SEQ ID NO:2446:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 328 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..328

(D) OTHER INFORMATION: / Ceres Seq. ID 1572914

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2446:

Met	Val	Ala	Asn	Gln	Leu	Tyr	Glu	Leu	Cys	Glu	Ala	Val	Gly	Pro	Glu
1			5						10					15	
Pro	Thr	Arg	Thr	Glu	Leu	Val	Pro	Ala	Tyr	Val	Arg	Leu	Leu	Arg	Asp
			20					25					30		
Asn	Glu	Ala	Glu	Val	Arg	Ile	Ala	Ala	Ala	Gly	Lys	Val	Thr	Lys	Phe
		35					40					45			
Cys	Arg	Ile	Leu	Asn	Pro	Glu	Ile	Ala	Ile	Gln	His	Ile	Leu	Pro	Cys
		50				55					60				
Val	Lys	Glu	Leu	Ser	Ser	Asp	Ser	Ser	Gln	His	Val	Arg	Ser	Ala	Leu
				70						75				80	
Ala	Ser	Val	Ile	Met	Gly	Met	Ala	Pro	Val	Leu	Gly	Lys	Asp	Ala	Thr
				85					90					95	
Ile	Glu	His	Leu	Leu	Pro	Ile	Phe	Leu	Ser	Leu	Leu	Lys	Asp	Glu	Phe
			100					105					110		
Pro	Asp	Val	Arg	Leu	Asn	Ile	Ile	Ser	Lys	Leu	Asp	Gln	Val	Asn	Gln
			115				120						125		
Val	Ile	Gly	Ile	Asp	Leu	Leu	Ser	Gln	Ser	Leu	Leu	Pro	Ala	Ile	Val
		130				135						140			
Glu	Leu	Ala	Glu	Asp	Arg	His	Trp	Arg	Val	Arg	Leu	Ala	Ile	Ile	Glu
				150						155				160	
Tyr	Ile	Pro	Leu	Leu	Ala	Ser	Gln	Leu	Gly	Val	Gly	Phe	Phe	Asp	Asp
				165					170					175	
Lys	Leu	Gly	Ala	Leu	Cys	Met	Gln	Trp	Leu	Gln	Asp	Lys	Val	His	Ser
			180					185					190		
Ile	Arg	Asp	Ala	Ala	Ala	Asn	Asn	Leu	Lys	Arg	Leu	Ala	Glu	Glu	Phe
			195				200					205			
Gly	Pro	Glu	Trp	Ala	Met	Gln	His	Ile	Val	Pro	Gln	Val	Leu	Glu	Met
						215					220				
Val	Asn	Asn	Pro	His	Tyr	Leu	Tyr	Arg	Met	Thr	Ile	Leu	Arg	Ala	Val
				230					235					240	
Ser	Leu	Leu	Ala	Pro	Val	Met	Gly	Ser	Glu	Ile	Thr	Cys	Ser	Lys	Leu
				245					250					255	
Leu	Pro	Val	Val	Met	Thr	Ala	Ser	Lys	Asp	Arg	Val	Pro	Asn	Ile	Lys
			260					265					270		
Phe	Asn	Val	Ala	Lys	Val	Leu	Gln	Ser	Leu	Ile	Pro	Ile	Val	Asp	Gln
			275				280						285		
Ser	Val	Val	Glu	Lys	Thr	Ile	Arg	Pro	Gly	Leu	Val	Glu	Leu	Ser	Glu
			290				295				300				
Asp	Pro	Asp	Val	Asp	Val	Arg	Phe	Phe	Ala	Asn	Gln	Ala	Leu	Gln	Ser
				310					315					320	
Ile	Asp	Asn	Val	Met	Met	Ser	Ser								
				325											

(2) INFORMATION FOR SEQ ID NO:2447:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 244 amino acids

(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1.244
(D) OTHER INFORMATION: / Ceres Seq. ID 1572915
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2447:

Met	Gly	Met	Ala	Pro	Val	Leu	Gly	Lys	Asp	Ala	Thr	Ile	Glu	His	Leu
1				5				10					15		
Leu	Pro	Ile	Phe	Leu	Ser	Leu	Leu	Lys	Asp	Glu	Phe	Pro	Asp	Val	Arg
		20					25					30			
Leu	Asn	Ile	Ile	Ser	Lys	Leu	Asp	Gln	Val	Asn	Gln	Val	Ile	Gly	Ile
	35						40					45			
Asp	Leu	Leu	Ser	Gln	Ser	Leu	Leu	Pro	Ala	Ile	Val	Glu	Leu	Ala	Glu
	50				55				60						
Asp	Arg	His	Trp	Arg	Val	Arg	Leu	Ala	Ile	Ile	Glu	Tyr	Ile	Pro	Leu
65				70					75					80	
Leu	Ala	Ser	Gln	Leu	Gly	Val	Gly	Phe	Phe	Asp	Asp	Lys	Leu	Gly	Ala
			85					90					95		
Leu	Cys	Met	Gln	Trp	Leu	Gln	Asp	Lys	Val	His	Ser	Ile	Arg	Asp	Ala
		100					105						110		
Ala	Ala	Asn	Asn	Leu	Lys	Arg	Leu	Ala	Glu	Glu	Phe	Gly	Pro	Glu	Trp
	115					120					125				
Ala	Met	Gln	His	Ile	Val	Pro	Gln	Val	Leu	Glu	Met	Val	Asn	Asn	Pro
	130				135						140				
His	Tyr	Leu	Tyr	Arg	Met	Thr	Ile	Leu	Arg	Ala	Val	Ser	Leu	Leu	Ala
145				150					155					160	
Pro	Val	Met	Gly	Ser	Glu	Ile	Thr	Cys	Ser	Lys	Leu	Leu	Pro	Val	Val
			165					170					175		
Met	Thr	Ala	Ser	Lys	Asp	Arg	Val	Pro	Asn	Ile	Lys	Phe	Asn	Val	Ala
	180						185						190		
Lys	Val	Leu	Gln	Ser	Leu	Ile	Pro	Ile	Val	Asp	Gln	Ser	Val	Val	Glu
	195						200					205			
Lys	Thr	Ile	Arg	Pro	Gly	Leu	Val	Glu	Leu	Ser	Glu	Asp	Pro	Asp	Val
	210					215					220				
Asp	Val	Arg	Phe	Phe	Ala	Asn	Gln	Ala	Leu	Gln	Ser	Ile	Asp	Asn	Val
225					230					235				240	
Met	Met	Ser	Ser												

(2) INFORMATION FOR SEQ ID NO:2448:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 578 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1.578
(D) OTHER INFORMATION: / Ceres Seq. ID 1572916
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2448:

aaaaagaaaa	aggttccttt	ttttgacttt	gtatccgtag	atcatctctt	Atctctctct	60
tccagagttt	tatccttatt	cggtccatca	aattctctct	ctaagcaaaag	atgaataaaag	120
gaagcatctt	taagatggac	aacgattttc	aaaaagagaaa	aggaagaaga	agaaggagaa	180
gaagaagcca	actactgaag	ttgaggtaaa	ggaggaagag	aagaaaggtt	ttatggagaa	240
gttgaagag	aagcttctct	gacacaagaa	acctgaagac	gggtcagccg	tcgctgcggc	300
accggtggtt	gttctctctc	ctgtgagaga	agcgcatcca	gtggagaaga	aagggtattc	360
tgagaagatt	aaggagaagc	ttccaggata	ccaccctaag	accacogtag	aggaggagaa	420
gaaagataaa	gaataaaga	attatcatta	aagatattaa	gaataatgat	ggttgatttg	480

ctttgtttttt atttttttta ttgtgatgat tgatcatcct ttgcttttgt gatgtgtaag 540

tttgttggtt tttttgttga ttacaatttc ttattttc

(2) INFORMATION FOR SEQ ID NO:2449:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 37 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..37

(D) OTHER INFORMATION: / Ceres Seq. ID 1572917

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2449:

Lys Lys Lys Lys Val Pro Phe Phe Asp Phe Val Ser Val Asp His Leu

1 5 10 15

Leu Ser Ser Ser Ser Arg Val Leu Ser Leu Ser Val Pro Ser Asn Ser

20 25 30

Leu Ser Lys Gln Arg

35

(2) INFORMATION FOR SEQ ID NO:2450:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 67 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..67

(D) OTHER INFORMATION: / Ceres Seq. ID 1572918

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2450:

Met Glu Lys Leu Lys Glu Lys Leu Pro Gly His Lys Lys Pro Glu Asp

1 5 10 15

Gly Ser Ala Val Ala Ala Ala Pro Val Val Val Pro Pro Pro Val Arg

20 25 30

Glu Ala His Pro Val Glu Lys Lys Gly Ile Leu Glu Lys Ile Lys Glu

35 40 45

Lys Leu Pro Gly Tyr His Pro Lys Thr Thr Val Glu Glu Glu Lys Lys

50 55 60

Asp Lys Glu

65

(2) INFORMATION FOR SEQ ID NO:2451:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 406 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..406

(D) OTHER INFORMATION: / Ceres Seq. ID 1572927

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2451:

avaGWacaac aacaacaaac aagaactcaa acacttcata actaaaaacat cctttaaaagc 60

cttttcaaaa actcaatcat gtcaagcaac tgcggaagct ggcactgtgc tgacaagacc 120

cagtgcgtaa agaagggaac cagctacacac ttcgacatcg tgcagactca ggagagctac 180

aaggaggcca tgatcatgga cgttggtgcc gaggagaaca acgcaaatgt caagtgcagg 240

tgccgctcct cttgcagctg cgtcaactgc acttgctgac ccaactaatg aagctctcttt 300

aatcaaaatg taatatgaat aaaagttgat gtttgtattg ttgtttgttt ctgtatgatt 360

agtgtgcttg taacaaaata atccaatcta aatgtgttgc ttgagc

(2) INFORMATION FOR SEQ ID NO:2452:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 42 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..42
(D) OTHER INFORMATION: / Ceres Seq. ID 1572928

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2452:

Xaa Xaa Asn Asn Asn Lys Gln Glu Leu Lys His Phe Ile Thr Lys Thr
1 5 10 15
Ser Phe Lys Ala Phe Ser Lys Thr Gln Ser Cys Gln Ala Thr Ala Glu
20 25 30
Ala Ala Thr Val Leu Thr Arg Pro Ser Ala
35 40

(2) INFORMATION FOR SEQ ID NO:2453:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 69 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..69
(D) OTHER INFORMATION: / Ceres Seq. ID 1572929

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2453:

Met Ser Ser Asn Cys Gly Ser Cys Asp Cys Ala Asp Lys Thr Gln Cys
1 5 10 15
Val Lys Lys Gly Thr Ser Tyr Thr Phe Asp Ile Val Glu Thr Gln Glu
20 25 30
Ser Tyr Lys Glu Ala Met Ile Met Asp Val Gly Ala Glu Glu Asn Asn
35 40 45
Ala Asn Cys Lys Cys Lys Cys Gly Ser Ser Cys Ser Cys Val Asn Cys
50 55 60
Thr Cys Cys Pro Asn
65

(2) INFORMATION FOR SEQ ID NO:2454:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 615 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..615
(D) OTHER INFORMATION: / Ceres Seq. ID 1572934

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2454:

aacgaaagct	agggtttttt	ctctgtgaaa	tcgctcgccg	gcataaaaga	gagtcagaag	60
aggaagaaga	gagttacaag	gattgaaaat	gaagggacgt	caaggagaga	gagttagatt	120
gtatgttcgt	ggaacagtc	tcggttacaa	gaggtccaag	tcgaaccaat	accctaacac	180
ttctctcgct	cagattgaag	gtgtgaacac	tcaagaggag	gttaattggt	acaagggtaa	240
gcgtttggct	tacatctaca	aggcaaaagc	aaagaagaac	ggttctcact	accgttgcat	300
ttggggcaaa	gtcactaggg	ctcatggtaa	cagtggtgtt	gtccgtttcta	agttcacttc	360
aaacctacca	cccaagtcaa	tgggagctag	agtcagagtc	ttcatgtacc	ctagacaact	420
atgaggaggc	tgattttcaa	caagtatcgg	aaggaatcgc	cattatcatt	tctcaggagc	480
tgtagtttta	tctattcact	tttattctag	actctctggt	gggttttgatt	ttactcttgag	540

acgaagTaaa acatTTTTTT tcttgagatc atatactatc gagtattaat ggaacttgag 600
aaaagctatg atccc

(2) INFORMATION FOR SEQ ID NO:2455:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..111
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572935

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2455:

Met	Lys	Gly	Arg	Gln	Gly	Glu	Arg	Val	Arg	Leu	Tyr	Val	Arg	Gly	Thr
1		5					10			15					
Val	Leu	Gly	Tyr	Lys	Arg	Ser	Lys	Ser	Asn	Gln	Tyr	Pro	Asn	Thr	Ser
		20					25			30					
Leu	Val	Gln	Ile	Glu	Gly	Val	Asn	Thr	Gln	Glu	Glu	Val	Asn	Trp	Tyr
		35					40			45					
Lys	Gly	Lys	Arg	Leu	Ala	Tyr	Ile	Tyr	Lys	Ala	Lys	Thr	Lys	Lys	Asn
		50					55			60					
Gly	Ser	His	Tyr	Arg	Cys	Ile	Trp	Gly	Lys	Val	Thr	Arg	Pro	His	Gly
		65					70			75				80	
Asn	Ser	Gly	Val	Val	Arg	Ser	Lys	Phe	Thr	Ser	Asn	Leu	Pro	Pro	Lys
		85					90							95	
Ser	Met	Gly	Ala	Arg	Val	Arg	Val	Phe	Met	Tyr	Pro	Ser	Asn	Ile	
		100					105						110		

(2) INFORMATION FOR SEQ ID NO:2456:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1803 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1803
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572936

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2456:

acacacatt	ttcacacat	cgtacttate	gccttctctc	ctctctcaat	acctctctca	60
atttttggt	ccaccatgca	agctcttcaa	tcttcatctc	tccgtgcttc	tctctccaaa	120
ccaactcgct	taccatcaaa	ctcgtcaatca	catcagctaa	ttaccaatgc	gagacotttg	180
cgaaagacaac	aacgttctct	catctccgca	tcagcatcca	ctgtctccgc	tcttaaacgc	240
gaaaacagatc	cgaaagaaacg	agttgtcatt	actggtatgg	gtctcgtctc	tgtgtttggt	300
aacgatgttg	atgcttacta	cgagaaaattg	ttgtctgggtg	agagtggaa	cagtttgatt	360
gatcgtttcg	atgcttccaa	gttccctact	cgattcgggtg	gtcagatccg	tggtgtttage	420
tctgaaggtt	atattgatgg	caagaatagag	cgtaggcttg	atgattgttt	gaactattgc	480
attgttgctg	gtaaaaaagc	tcttgaaaag	gccaatcttg	gtggtgataa	gccttaacacg	540
attgataaga	ggaaagctgg	agtaactagt	gggaactggaa	tgggaggttt	aactgtgttt	600
tcagaaggtg	ttcagaattt	gattgagaag	ggctcatagga	ggattatgcc	attttttata	660
ctttatgcta	taacaaatat	gggttctgct	ttgttggcga	ttgatcttgg	tcttatgggt	720
cttaactatt	cgatttcaac	gtctgtgctc	acttogaatt	actgotttta	cgctgctgcg	780
aatcacattc	gtcgtgggtga	agctgatgatg	atgattgctg	gtgggactga	ggctgctatt	840
attcctattg	ggttgggagg	ttttgttgct	tgtagggaat	tgtccacagag	aaatgatgac	900
ctccaaaactg	cttcaggggc	gtgggataaaa	gcaagagatg	ggtttgttat	gggtgaagga	960
gctggtgttc	tggtgatgga	aagcttggaa	catgcAaatg	aaacgtggtg	ctccaatgtg	1020
agcagaatat	cttggagggtg	ctgttaattg	tgatgctcac	catatgactg	atccaaagagc	1080
tgatgtgtct	gggtgttctt	catgcattga	aagatgtctc	gaagatgactg	gtgtatcacc	1140
tgaggaggtg	aattacatca	atgcacatgc	aacttccact	cttgctggtg	atcttgctga	1200
gattaatgac	atttaaaaag	tattcaagag	cacttcaggg	atcaaaaatca	acgccaccaa	1260

gtctatgata	ggtcactgcc	tgggtgcagc	tggaggtcta	gaagccatcg	ccaccgtgaa	1320
ggctatcaac	actgcatggc	tgcatccttc	catcaaccaa	ttaaacccag	aacaagctgt	1380
ggactttgac	acggtcccaa	acgagagaagaa	gcaacacgag	gttgatgttg	ccatatcaaa	1440
ctcgctcggg	ttcggtagac	acaactcgtg	agtcgccttc	tctgccttca	aacctcgatt	1500
tottcatacc	ttttagattc	tctgccttat	cggttactat	catcatccat	catccatcac	1560
caccacttgc	agctctcttg	ttcacaaagt	ggagctcttc	ctctggcctt	ttgcagttct	1620
ttcattcccc	gtttcttacg	gttgctgaga	tttcagattt	tgtttgttct	ctctcttgtc	1680
tgcggaatgt	tgtgtatctt	agttcgttcc	atatttcggt	aatttataaa	aacagaaact	1740
gagagaatct	tgtagttaac	gtgttattgt	cagaataatc	caattagggg	attctcatct	1800
ttt						

(2) INFORMATION FOR SEQ ID NO:2457:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 348 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..348

(D) OTHER INFORMATION: / Ceres Seq. ID 1572937

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2457:

Thr	His	His	Phe	His	Asn	Ile	Val	Leu	Ile	Ala	Phe	Leu	Ser	Leu	Ser
1			5					10						15	
Ile	Pro	Leu	Ser	Ile	Ser	Gly	Ser	Thr	Met	Gln	Ala	Leu	Gln	Ser	Ser
			20					25						30	
Ser	Leu	Arg	Ala	Ser	Pro	Pro	Asn	Pro	Leu	Arg	Leu	Pro	Ser	Asn	Arg
			35					40						45	
Gln	Ser	His	Gln	Leu	Ile	Thr	Asn	Ala	Arg	Pro	Leu	Arg	Arg	Gln	Gln
			50					55						60	
Arg	Ser	Phe	Ile	Ser	Ala	Ser	Ala	Ser	Thr	Val	Ser	Ala	Pro	Lys	Arg
65								70						80	
Glu	Thr	Asp	Pro	Lys	Lys	Arg	Val	Val	Ile	Thr	Gly	Met	Gly	Leu	Val
								85						95	
Ser	Val	Phe	Gly	Asn	Asp	Val	Asp	Ala	Tyr	Tyr	Glu	Lys	Leu	Leu	Ser
								105						110	
Gly	Glu	Ser	Gly	Ile	Ser	Leu	Ile	Asp	Arg	Phe	Asp	Ala	Ser	Lys	Phe
								120						125	
Pro	Thr	Arg	Phe	Gly	Gly	Gln	Ile	Arg	Gly	Phe	Ser	Ser	Glu	Gly	Tyr
								135						140	
Ile	Asp	Gly	Lys	Asn	Glu	Arg	Arg	Leu	Asp	Asp	Cys	Leu	Lys	Tyr	Cys
145								150						155	
Ile	Val	Ala	Gly	Lys	Lys	Ala	Leu	Glu	Ser	Ala	Asn	Leu	Gly	Gly	Asp
								165						170	
Lys	Leu	Asn	Thr	Ile	Asp	Lys	Arg	Lys	Ala	Gly	Val	Leu	Val	Gly	Thr
								185						190	
Gly	Met	Gly	Gly	Leu	Thr	Val	Phe	Ser	Glu	Gly	Val	Gln	Asn	Leu	Ile
								200						205	
Glu	Lys	Gly	His	Arg	Arg	Ile	Ser	Pro	Phe	Phe	Ile	Pro	Tyr	Ala	Ile
								215						220	
Thr	Asn	Met	Gly	Ser	Ala	Leu	Leu	Ala	Ile	Asp	Leu	Gly	Leu	Met	Gly
225								230						235	
Pro	Asn	Tyr	Ser	Ile	Ser	Thr	Ala	Cys	Ala	Thr	Ser	Asn	Tyr	Cys	Phe
								245						250	
Tyr	Ala	Ala	Ala	Asn	His	Ile	Arg	Arg	Gly	Glu	Ala	Asp	Met	Met	Ile
								265						270	
Ala	Gly	Gly	Thr	Glu	Ala	Ala	Ile	Ile	Pro	Ile	Gly	Leu	Gly	Gly	Phe
								280						285	
Val	Ala	Cys	Arg	Ala	Leu	Ser	Gln	Arg	Asn	Asp	Asp	Pro	Gln	Thr	Ala
								295						300	
Ser	Arg	Pro	Trp	Asp	Lys	Ala	Arg	Asp	Gly	Phe	Val	Met	Gly	Glu	Gly

305 310 315 320
Ala Gly Val Leu Val Met Glu Ser Leu Glu His Ala Asn Glu Thr Trp
325 330 335
Cys Ser Asn Cys Ser Arg Ile Ser Trp Arg Cys Cys
340 345

(2) INFORMATION FOR SEQ ID NO:2458:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 323 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide

- (B) LOCATION: 1..323

- (D) OTHER INFORMATION: / Ceres Seq. ID 1572938

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2458:

Met Gln Ala Leu Gln Ser Ser Ser Leu Arg Ala Ser Pro Pro Asn Pro
1 5 10 15
Leu Arg Leu Pro Ser Asn Arg Gln Ser His Gln Leu Ile Thr Asn Ala
20 25 30
Arg Pro Leu Arg Arg Gln Gln Arg Ser Phe Ile Ser Ala Ser Ala Ser
35 40 45
Thr Val Ser Ala Pro Lys Arg Glu Thr Asp Pro Lys Lys Arg Val Val
50 55 60
Ile Thr Gly Met Gly Leu Val Ser Val Phe Gly Asn Asp Val Asp Ala
65 70 75 80
Tyr Tyr Glu Lys Leu Leu Ser Gly Glu Ser Gly Ile Ser Leu Ile Asp
85 90 95
Arg Phe Asp Ala Ser Lys Phe Pro Thr Arg Phe Gly Gly Gln Ile Arg
100 105 110
Gly Phe Ser Ser Glu Gly Tyr Ile Asp Gly Lys Asn Glu Arg Arg Leu
115 120 125
Asp Asp Cys Leu Lys Tyr Cys Ile Val Ala Gly Lys Lys Ala Leu Glu
130 135 140
Ser Ala Asn Leu Gly Gly Asp Lys Leu Asn Thr Ile Asp Lys Arg Lys
145 150 155 160
Ala Gly Val Leu Val Gly Thr Gly Met Gly Gly Leu Thr Val Phe Ser
165 170 175
Glu Gly Val Gln Asn Leu Ile Glu Lys Gly His Arg Arg Ile Ser Pro
180 185 190
Phe Phe Ile Pro Tyr Ala Ile Thr Asn Met Gly Ser Ala Leu Leu Ala
195 200 205
Ile Asp Leu Gly Leu Met Gly Pro Asn Tyr Ser Ile Ser Thr Ala Cys
210 215 220
Ala Thr Ser Asn Tyr Cys Phe Tyr Ala Ala Ala Asn His Ile Arg Arg
225 230 235 240
Gly Glu Ala Asp Met Met Ile Ala Gly Gly Thr Glu Ala Ala Ile Ile
245 250 255
Pro Ile Gly Leu Gly Gly Phe Val Ala Cys Arg Ala Leu Ser Gln Arg
260 265 270
Asn Asp Asp Pro Gln Thr Ala Ser Arg Pro Trp Asp Lys Ala Arg Asp
275 280 285
Gly Phe Val Met Gly Glu Gly Ala Gly Val Leu Val Met Glu Ser Leu
290 295 300
Glu His Ala Asn Glu Thr Trp Cys Ser Asn Cys Ser Arg Ile Ser Trp
305 310 315 320
Arg Cys Cys

(2) INFORMATION FOR SEQ ID NO:2459:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 256 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..256
(D) OTHER INFORMATION: / Ceres Seq. ID 1572939
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2459:

Met	Gly	Leu	Val	Ser	Val	Phe	Gly	Asn	Asp	Val	Asp	Ala	Tyr	Tyr	Glu
1			5						10					15	
Lys	Leu	Leu	Ser	Gly	Glu	Ser	Gly	Ile	Ser	Leu	Ile	Asp	Arg	Phe	Asp
			20					25					30		
Ala	Ser	Lys	Phe	Pro	Thr	Arg	Phe	Gly	Gly	Gln	Ile	Arg	Gly	Phe	Ser
			35					40					45		
Ser	Glu	Gly	Tyr	Ile	Asp	Gly	Lys	Asn	Glu	Arg	Arg	Leu	Asp	Asp	Cys
			50					55				60			
Leu	Lys	Tyr	Cys	Ile	Val	Ala	Gly	Lys	Lys	Ala	Leu	Glu	Ser	Ala	Asn
			65					70				75			80
Leu	Gly	Gly	Asp	Lys	Leu	Asn	Thr	Ile	Asp	Lys	Arg	Lys	Ala	Gly	Val
			85					90						95	
Leu	Val	Gly	Thr	Gly	Met	Gly	Gly	Leu	Thr	Val	Phe	Ser	Glu	Gly	Val
			100					105					110		
Gln	Asn	Leu	Ile	Glu	Lys	Gly	His	Arg	Arg	Ile	Ser	Pro	Phe	Phe	Ile
			115					120					125		
Pro	Tyr	Ala	Ile	Thr	Asn	Met	Gly	Ser	Ala	Leu	Leu	Ala	Ile	Asp	Leu
			130					135					140		
Gly	Leu	Met	Gly	Pro	Asn	Tyr	Ser	Ile	Ser	Thr	Ala	Cys	Ala	Thr	Ser
			145					150					155		160
Asn	Tyr	Cys	Phe	Tyr	Ala	Ala	Ala	Asn	His	Ile	Arg	Arg	Gly	Glu	Ala
			165					170						175	
Asp	Met	Met	Ile	Ala	Gly	Gly	Thr	Glu	Ala	Ala	Ile	Ile	Pro	Ile	Gly
			180					185					190		
Leu	Gly	Gly	Phe	Val	Ala	Cys	Arg	Ala	Leu	Ser	Gln	Arg	Asn	Asp	Asp
			195					200					205		
Pro	Gln	Thr	Ala	Ser	Arg	Pro	Trp	Asp	Lys	Ala	Arg	Asp	Gly	Phe	Val
			210					215					220		
Met	Gly	Glu	Gly	Ala	Gly	Val	Leu	Val	Met	Glu	Ser	Leu	Glu	His	Ala
			225					230					235		240
Asn	Glu	Thr	Trp	Cys	Ser	Asn	Cys	Ser	Arg	Ile	Ser	Trp	Arg	Cys	Cys
			245					250						255	

(2) INFORMATION FOR SEQ ID NO:2460:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1719 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -
(B) LOCATION: 1..1719
(D) OTHER INFORMATION: / Ceres Seq. ID 1572944

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2460:

attttttctca	gccaaacaac	actagtctct	tctgatttgt	accctaacgt	ttaactcgact	60
tatctaaagc	cgtgaacctc	gcgcgaattc	ttaaagtgcg	gatttttccct	taacgcgcgtt	120
tgattccctt	acggcctttg	aggtccaggga	gatatgcaaat	ttgttggtga	gtactgaaaa	180
atggaggaaag	agaacgaagt	agtgaagacg	tttcagagac	ttggtgtgcg	tgaggagctt	240
gttaaagcctt	gcgagagatt	gggatggaag	aacccttcca	aaattcaagc	cgaagaccctt	300

ccttttgcgc	ttgaagggaa	agatgtaatt	ggacttgogc	aaacccgggtc	tggtaaaacc	360
ggagcttttg	caattctcat	attgcaagca	ctacttgagt	atgtttatga	tctcgagcct	420
aagaaaaggac	gtagaccgga	tcctgctttc	ttcgcttggt	ttttatctcc	aactcgagaa	480
cttgcaattc	agatttgctg	acagtttgaa	gctcttggtg	ctgatataac	tcttagggtg	540
gctgtgcttt	ttggagggtat	agacagggatg	caacaaaacta	ttgctcttgg	gaaacggcct	600
catgtttattg	ttgcaacacc	tggctgctct	tgggatacata	tgtctgatac	aaaaggcctt	660
tctctgaaat	cattgaaata	tcTggtttct	tgatgaagca	gatagactgt	tgaatgaaga	720
ttttgagaaa	tcctttaacc	agatttttga	agagatccct	cgtgagcgga	aaacatttct	780
tttttcagcg	actatgacta	aaaagggtcg	aaaacttcaa	aggggcatgtt	tgagggaatcc	840
tgtgaagatt	gaagctgcct	ccaaatattc	cactgtcgat	actcttaagc	agcagtatcg	900
gtttgttgcc	gctaataata	aggattgcta	tctggtatac	attctgagtg	aaatgctctga	960
atcaacatct	atgattttca	cocgaacatg	tgatggtact	cgctttcttg	ctttggtgct	1020
tcggagccct	ggtttttagag	ctattctcat	cagtggctcaa	atgactcagt	caaagagact	1080
gggagcttta	aataagttca	aagcaggggga	atgtaataatc	ttggtttgta	cogatgtggc	1140
tagtagaggg	ctcgatatcc	catcagttga	tgtggttatc	aattatgata	ttcccaacaa	1200
ttcaaggagt	tacatccata	gagtaggaag	aaacgctcgt	ctgggacgtt	ctgggtgttg	1260
gatacaact	gtaaaccagt	atgagctcga	atggtatata	caaatagaaa	aactcattgg	1320
caagaaaata	cctgaatatc	ccgctgagga	agatgaagtc	ttgtcattgt	tgagagagtg	1380
tgcagaagcg	aaaaagctat	ctgcaatgaa	tatgaagaag	tcaggaggta	ggaagagaa	1440
gggagaagat	gatgaagaaa	gtgagaggtt	cttggggagt	aacaaggaca	gaggcaacaa	1500
ggaaagaggt	ggtaaacaa	acaagaagtc	ttctaagaag	ttcaaacgat	aaaatagctc	1560
tgtttttact	gttttccgat	aactcaccaa	agttttgaat	tgaagttttc	catatgaact	1620
agggaaaatt	aatccatttt	gtactcgtaa	tttgtatggt	cttttctttt	tgctttgttt	1680
ctcaatgaca	gattatacaa	tttaagttga	aagatgttt			

(2) INFORMATION FOR SEQ ID NO:2461:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 252 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..252

(D) OTHER INFORMATION: / Ceres Seq. ID 1572945

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2461:

Met	Thr	Lys	Lys	Val	Arg	Lys	Leu	Gln	Arg	Ala	Cys	Leu	Arg	Asn	Pro
1				5				10						15	
Val	Lys	Ile	Glu	Ala	Ala	Ser	Lys	Tyr	Ser	Thr	Val	Asp	Thr	Leu	Lys
			20					25					30		
Gln	Gln	Tyr	Arg	Phe	Val	Ala	Ala	Lys	Tyr	Lys	Asp	Cys	Tyr	Leu	Val
			35					40				45			
Tyr	Ile	Leu	Ser	Glu	Met	Pro	Glu	Ser	Thr	Ser	Met	Ile	Phe	Thr	Arg
			50					55				60			
Thr	Cys	Asp	Gly	Thr	Arg	Phe	Leu	Ala	Leu	Val	Leu	Arg	Ser	Leu	Gly
			65					70				75			80
Phe	Arg	Ala	Ile	Pro	Ile	Ser	Gly	Gln	Met	Thr	Gln	Ser	Lys	Arg	Leu
			85					90						95	
Gly	Ala	Leu	Asn	Lys	Phe	Lys	Ala	Gly	Glu	Cys	Asn	Ile	Leu	Val	Cys
			100					105					110		
Thr	Asp	Val	Ala	Ser	Arg	Gly	Leu	Asp	Ile	Pro	Ser	Val	Asp	Val	Val
			115					120				125			
Ile	Asn	Tyr	Asp	Ile	Pro	Thr	Asn	Ser	Lys	Asp	Tyr	Ile	His	Arg	Val
			130					135				140			
Gly	Arg	Thr	Ala	Arg	Ala	Gly	Arg	Ser	Gly	Val	Gly	Ile	Ser	Leu	Val
			145					150				155			160
Asn	Gln	Tyr	Glu	Leu	Glu	Trp	Tyr	Ile	Gln	Ile	Glu	Lys	Leu	Ile	Gly
			165					170						175	
Lys	Lys	Leu	Pro	Glu	Tyr	Pro	Ala	Glu	Glu	Asp	Glu	Val	Leu	Ser	Leu
			180					185					190		
Leu	Glu	Arg	Val	Ala	Glu	Ala	Lys	Lys	Leu	Ser	Ala	Met	Asn	Met	Lys

195 200 205
Glu Ser Gly Gly Arg Lys Arg Arg Gly Glu Asp Asp Glu Glu Ser Glu
210 215 220
Arg Phe Leu Gly Gly Asn Lys Asp Arg Gly Asn Lys Glu Arg Gly Gly
225 230 235 240
Asn Lys Asp Lys Lys Ser Ser Lys Lys Phe Lys Arg
245 250

(2) INFORMATION FOR SEQ ID NO:2462:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 199 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..199

(D) OTHER INFORMATION: / Ceres Seq. ID 1572946

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2462:

Met Pro Glu Ser Thr Ser Met Ile Phe Thr Arg Thr Cys Asp Gly Thr
1 5 10 15
Arg Phe Leu Ala Leu Val Leu Arg Ser Leu Gly Phe Arg Ala Ile Pro
20 25 30
Ile Ser Gly Gln Met Thr Gln Ser Lys Arg Leu Gly Ala Leu Asn Lys
35 40 45
Phe Lys Ala Gly Glu Cys Asn Ile Leu Val Cys Thr Asp Val Ala Ser
50 55 60
Arg Gly Leu Asp Ile Pro Ser Val Asp Val Val Ile Asn Tyr Asp Ile
65 70 75 80
Pro Thr Asn Ser Lys Asp Tyr Ile His Arg Val Gly Arg Thr Ala Arg
85 90 95
Ala Gly Arg Ser Gly Val Gly Ile Ser Leu Val Asn Gln Tyr Glu Leu
100 105 110
Glu Trp Tyr Ile Gln Ile Glu Lys Leu Ile Gly Lys Lys Leu Pro Glu
115 120 125
Tyr Pro Ala Glu Glu Asp Glu Val Leu Ser Leu Leu Glu Arg Val Ala
130 135 140
Glu Ala Lys Lys Leu Ser Ala Met Asn Met Lys Glu Ser Gly Gly Arg
145 150 155 160
Lys Arg Arg Gly Glu Asp Asp Glu Glu Ser Glu Arg Phe Leu Gly Gly
165 170 175
Asn Lys Asp Arg Gly Asn Lys Glu Arg Gly Gly Asn Lys Asp Lys Lys
180 185 190
Ser Ser Lys Lys Phe Lys Arg
195

(2) INFORMATION FOR SEQ ID NO:2463:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 193 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..193

(D) OTHER INFORMATION: / Ceres Seq. ID 1572947

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2463:

Met Ile Phe Thr Arg Thr Cys Asp Gly Thr Arg Phe Leu Ala Leu Val
1 5 10 15
Leu Arg Ser Leu Gly Phe Arg Ala Ile Pro Ile Ser Gly Gln Met Thr
20 25 30

```

Gln Ser Lys Arg Leu Gly Ala Leu Asn Lys Phe Lys Ala Gly Glu Cys
      35                40                45
Asn Ile Leu Val Cys Thr Asp Val Ala Ser Arg Gly Leu Asp Ile Pro
      50                55                60
Ser Val Asp Val Val Ile Asn Tyr Asp Ile Pro Thr Asn Ser Lys Asp
      65                70                75                80
Tyr Ile His Arg Val Gly Arg Thr Ala Arg Ala Gly Arg Ser Gly Val
      85                90                95
Gly Ile Ser Leu Val Asn Gln Tyr Glu Leu Glu Trp Tyr Ile Gln Ile
      100               105               110
Glu Lys Leu Ile Gly Lys Lys Leu Pro Glu Tyr Pro Ala Glu Glu Asp
      115               120               125
Glu Val Leu Ser Leu Leu Glu Arg Val Ala Glu Ala Lys Lys Leu Ser
      130               135               140
Ala Met Asn Met Lys Glu Ser Gly Gly Arg Lys Arg Arg Gly Glu Asp
      145               150               155               160
Asp Glu Glu Ser Glu Arg Phe Leu Gly Gly Asn Lys Asp Arg Gly Asn
      165               170               175
Lys Glu Arg Gly Gly Asn Lys Asp Lys Lys Ser Ser Lys Lys Phe Lys
      180               185               190
Arg

```

(2) INFORMATION FOR SEQ ID NO:2464:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 592 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..592
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572960

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2464:

```

gaagattaat tgaatcacac aaagtcgaat ccaaagtttt tgatcttaac caagtcgcac      60
aatccagaga ggaatcaaaa gaagatgagt aacgtcagct tcaggcagga tcagtatttc      120
gagaagagga aagctgaggg tttaaggatc agagagaagt attctgcaga agtcccggtt      180
attgtggaga agtcagagaa aagtgatatc ccaaaccattg acaagaagaa ataccttgtc      240
ccagctgatac taacggtagg ccagtttggt tatgtgattc gtaagagaa ccaacttagt      300
gcagagaaag ctatcttcac ctttgttgat aatgtttctc ctcccaccgg agcgatgatg      360
tcaaccattt acgatgagaa taaggagaaga gacggcttct tgtatgttac ctacagtggg      420
gaaaacattt ttggatcgtc aatgacttaa tttggtgttc ttgcttttaa ttgaatgtaa      480
atatccattt ttcttttctt gtccgtgaac ttgcttagat gcgatatga ttattatggc      540
ttatgtaggg acaaccAatc ggtttgcaaa caaagtggtg gtttttttat cc

```

(2) INFORMATION FOR SEQ ID NO:2465:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 121 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..121
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572961

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2465:

```

Met Ser Asn Val Ser Phe Arg Gln Asp His Asp Phe Glu Lys Arg Lys
1          5          10          15
Ala Glu Ala Leu Arg Ile Arg Glu Lys Tyr Ser Asp Arg Val Pro Val
20          25          30
Ile Val Glu Lys Ser Glu Lys Ser Asp Ile Pro Asn Ile Asp Lys Lys

```

35	40	45
Lys Tyr Leu Val Pro Ala Asp	Leu Thr Val Gly	Gln Phe Val Tyr Val
50	55	60
Ile Arg Lys Arg Ile Gln Leu Ser Ala Glu Lys	Ala Ile Phe Ile Phe	
65	70	75
Val Asp Asn Val Leu Pro Pro Thr Gly Ala Met	Ser Thr Ile Tyr	
85	90	95
Asp Glu Asn Lys Glu Glu Asp Gly Phe	Leu Tyr Val Thr Tyr Ser Gly	
100	105	110
Glu Asn Thr Phe Gly Ser Ser Met Thr		
115	120	

(2) INFORMATION FOR SEQ ID NO:2466:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1112 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1112
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572962

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2466:

gtttcatctg ttgttccctg tgacctggc tactccactc tcaatctcat caaatctctt	60
cacctccgcg cattgttacc gtctccactt atcttctact tcaatcaagg taatctctca	120
ttctttctaca aatgtcaatt ttgaatgaat ccataaaaatt ggaatttgaa atgtgtacag	180
ggaatgttaa gtgttttggg gccaacacca agtcagattc tatctctgaa actcaaccaa	240
acccttaaaa cgagaaacca acagcaattt gcgagacccc ttgttgggtg tagccaaacg	300
gcggctacgt cgtcggcagt tgtagctccg gagagattcc gtttggataa tcttggacca	360
cgccaggtt cgaggaaaga gcagaaagaga aaaggtagag gtatctctgc aggacaagga	420
gcaagttgtg gttttggtat gagaggtcag aaatcaagat cgggtctcgg gattatgaga	480
ggctttgaag gtggtcaaac tgccttttat cgtcgtcttc ccaaaacttag aggaactcgt	540
ggaggtatgc gtctcaggatt acctaaatac ttacoggtta atatcaaaaga catagaacc	600
gctgggtttc aagagggaga tgaagtgtca ttggagacat tgaagcaaaa gggtttgatt	660
aatccttcag ggagagaaaag gaaactccct cttaagattc tgggtacagg agaactaagc	720
atgaagctca ccttcaaaagc tctgtccttc tcaacacaag caaaagagaa gcttgaagct	780
tcagggttga cactcactgt gttgccggga agaaagaaat ggggttaagcc atctgttgca	840
aagaaccaag cagcagcaga tgaatacttt gccaaagaaga gagctgcagc agcagaagca	900
gcaacttcag agccagcagc cctcgtctaa attacttcag ttccaagctc ttttagtgt	960
tgtaaaagctg cagagaagat aattgtctat gacaaatgtt aattacaatt ccttctctt	1020
ttgttatggt gaagagattt acattttggt gtttgaagag tcattatcaa aaagatatgt	1080
aaacggtaat gaaatattga acattttggt Tc	

(2) INFORMATION FOR SEQ ID NO:2467:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 163 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..163
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572963

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2467:

Met Arg Gly Gln Lys Ser Arg Ser Gly Pro Gly Ile Met Arg Gly Phe	
1	15
Glu Gly Gly Gln Thr Ala Leu Tyr Arg Arg Leu Pro Lys Leu Arg Gly	
20	30
Ile Ala Gly Gly Met Arg Ser Gly Leu Pro Lys Tyr Leu Pro Val Asn	
35	45
Ile Lys Asp Ile Glu Thr Ala Gly Phe Gln Glu Gly Asp Glu Val Ser	

50	55	60
Leu Glu Thr Leu Lys Gln Lys Gly Leu Ile Asn Pro Ser Gly Arg Glu		
65	70	75
Arg Lys Leu Pro Leu Lys Ile Leu Gly Thr Gly Glu Leu Ser Met Lys		80
	85	90
Leu Thr Phe Lys Ala Arg Ala Phe Ser Thr Gln Ala Lys Glu Lys Leu		95
	100	105
Glu Ala Ser Gly Cys Thr Leu Thr Val Leu Pro Gly Arg Lys Lys Trp		110
	115	120
Val Lys Pro Ser Val Ala Lys Asn Gln Ala Arg Ala Asp Glu Tyr Phe		125
	130	135
Ala Lys Lys Arg Ala Ala Ala Glu Ala Ala Thr Ser Glu Pro Ala		140
	145	150
Ala Ser Ala		155
		160

(2) INFORMATION FOR SEQ ID NO:2468:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 151 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..151

(D) OTHER INFORMATION: / Ceres Seq. ID 1572964

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2468:

Met Arg Gly Phe Glu Gly Gln Thr Ala Leu Tyr Arg Arg Leu Pro		
1	5	10
Lys Leu Arg Gly Ile Ala Gly Gly Met Arg Ser Gly Leu Pro Lys Tyr		15
	20	25
Leu Pro Val Asn Ile Lys Asp Ile Glu Thr Ala Gly Phe Gln Glu Gly		30
	35	40
Asp Glu Val Ser Leu Glu Thr Leu Lys Gln Lys Gly Leu Ile Asn Pro		45
	50	55
Ser Gly Arg Glu Arg Lys Leu Pro Leu Lys Ile Leu Gly Thr Gly Glu		60
	65	70
Leu Ser Met Lys Leu Thr Phe Lys Ala Arg Ala Phe Ser Thr Gln Ala		75
	85	90
Lys Glu Lys Leu Glu Ala Ser Gly Cys Thr Leu Thr Val Leu Pro Gly		95
	100	105
Arg Lys Lys Trp Val Lys Pro Ser Val Ala Lys Asn Gln Ala Arg Ala		110
	115	120
Asp Glu Tyr Phe Ala Lys Lys Arg Ala Ala Ala Ala Glu Ala Ala Thr		125
	130	135
Ser Glu Pro Ala Ala Ser Ala		140
	145	150

(2) INFORMATION FOR SEQ ID NO:2469:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 127 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..127

(D) OTHER INFORMATION: / Ceres Seq. ID 1572965

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2469:

Met Arg Ser Gly Leu Pro Lys Tyr Leu Pro Val Asn Ile Lys Asp Ile		
1	5	10
		15

(2) INFORMATION FOR SEQ ID NO:2470:

(A) LENGTH: 740 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

```
(ix) FEATURE:
```

- (A) NAME/KEY: -
(B) LOCATION: 1..740
(D) OTHER INFORMATION: / Ceres Seq. ID 1572966

gaattttttt	aaagaaaata	aaaatcaagt	ctttctcttc	gtctatctct	ctctctgtct	60
agactctctg	gtgtgcgaaga	ctaactcact	aagcagatct	attatccgga	gcacgaagaa	120
gagtgtatcg	cagcagcaaga	atttcattga	tttgcaaaagc	gactctgggt	ttTgggacga	180
tagctctcgg	ctgcgcggcg	atgcagatct	tgtctctctc	ctctcaacat	ctgcgcggcg	240
tcaagactcc	gcgcatagga	attcagatct	tgtctctctc	aaagactctg	ttgagatggt	300
tccccattac	gagcattaca	tggcaataaa	agaaaagcagt	tgtttaaagc	ggcgctggctc	360
catgatctac	actaaagatc	ctcaaaaaga	attcttgtct	cgaattggGaa	gaaatgcttc	420
ctaaacagtc	ccaggagaag	acgaagaagc	ccaagagggg	aatgacgagt	ttatgaacaa	480
ttctagggaa	gagtgcagaa	acgcaaaagg	tttgctggtg	ggagaaaagg	agaagaatgag	540
tagctaaaga	gcaagtgaat	gaactgcaga	caaaattatc	ggagaaaagc	gaggttttaa	600
actgaatgag	gaagtcaaa	aattcaggtta	cagaatgata	cgaaaagctt	gaagcaacaa	660
atagatttgt	tgtctgaaag	gatattgtta	tcaagctctat	cgagttacaa	ttatcgcaga	720
caagatatac	actctctgac					

(i) SEQUENCE CHARACTERISTICS:

(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ix) FEATURE:

- ```
(A) NAME/KEY: peptide
(B) LOCATION: 1..146
(D) OTHER INFORMATION: / Ceres Seq. ID 1572967
```

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Tyr | Glu | Gln | Gln | Gln | His | Phe | Met | Asp | Leu | Gln | Ser | Asp | Ser | Gly |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     | 15  |     |     |
| Phe | Xaa | Asp | Asp | Ser | Ser | Trp | Leu | Ala | Gly | Asp | Asp | Asp | Leu | Arg | Leu |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ser | Pro | His | Gln | Ser | Ala | Ala | Gly | Thr | Asn | Ser | Gly | Asn | Glu | Asn | Leu |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Asp | Arg | Arg | Leu | Leu | Lys | Asp | Leu | Val | Glu | Met | Val | Pro | Leu | Ile | Glu |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| His | Tyr | Met | Glu | His | Lys | Glu | Arg | Ser | Ser | Phe | Lys | Arg | Arg | Gly | Ser |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |

Met Ile Tyr Thr Lys Met Pro Ser Lys Glu Ser Leu Ser Arg Arg Gly  
85 90 95  
Arg Asn Ala Ser Gln Thr Val Pro Gly Arg Lys Lys Arg Asp Gln Glu  
100 105 110  
Gly Asn Asp Asp Val Met Asn Asn Ser Arg Glu Asp Asp Glu Asn Ala  
115 120 125  
Lys Ala Leu Ala Gly Ala Glu Lys Glu Glu Met Ser Arg Leu Arg Ala  
130 135 140  
Ser Glu  
145

(2) INFORMATION FOR SEQ ID NO:2472:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 138 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..138  
(D) OTHER INFORMATION: / Ceres Seq. ID 1572968

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2472:

Met Asp Leu Gln Ser Asp Ser Gly Phe Xaa Asp Asp Ser Ser Trp Leu  
1 5 10 15  
Ala Gly Asp Asp Asp Leu Arg Leu Ser Pro His Gln Ser Ala Ala Gly  
20 25 30  
Thr Asn Ser Ser Gly Asn Glu Asn Leu Asp Arg Arg Leu Leu Lys Asp Leu  
35 40 45  
Val Glu Met Val Pro Leu Ile Glu His Tyr Met Glu His Lys Glu Arg  
50 55 60  
Ser Ser Phe Lys Arg Arg Gly Ser Met Ile Tyr Thr Lys Met Pro Ser  
65 70 75 80  
Lys Glu Ser Leu Ser Arg Arg Gly Arg Asn Ala Ser Gln Thr Val Pro  
85 90 95  
Gly Arg Lys Lys Arg Asp Gln Glu Gly Asn Asp Asp Val Met Asn Asn  
100 105 110  
Ser Arg Glu Asp Asp Glu Asn Ala Lys Ala Leu Ala Gly Ala Glu Lys  
115 120 125  
Glu Glu Met Ser Arg Leu Arg Ala Ser Glu  
130 135

(2) INFORMATION FOR SEQ ID NO:2473:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 88 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..88  
(D) OTHER INFORMATION: / Ceres Seq. ID 1572969

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2473:

Met Val Pro Leu Ile Glu His Tyr Met Glu His Lys Glu Arg Ser Ser  
1 5 10 15  
Phe Lys Arg Arg Gly Ser Met Ile Tyr Thr Lys Met Pro Ser Lys Glu  
20 25 30  
Ser Leu Ser Arg Arg Gly Arg Asn Ala Ser Gln Thr Val Pro Gly Arg  
35 40 45  
Lys Lys Arg Asp Gln Glu Gly Asn Asp Asp Val Met Asn Asn Ser Arg  
50 55 60  
Glu Asp Asp Glu Asn Ala Lys Ala Leu Ala Gly Ala Glu Lys Glu Glu

65 70 75 80  
Met Ser Arg Leu Arg Ala Ser Glu  
85

(2) INFORMATION FOR SEQ ID NO:2474:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1450 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1450
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572970

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2474:

```

agggggcctt tgtgttgacg gtgggtggaa caaaggaaca tcgtatccat tctgtccggg 60
aaaRcaccagc aatgttccatt tccgacaaat ctgctcctac tgattttctac aaagacgac 120
atcacaaattc ctccaccacc agcaccacac gcgatgatgat gatcgatgta ctccaccacta 180
ccaacgaatc agtagatctc caatctcacc accaccacaa tcacaatcac cacaatcatc 240
atctccacca atctccagca caacaacaga ttctcctcgg agaaagcagt ggagaagatc 300
acgaagttaa agcaccaaag aacgagcggg agacatgggt tcaagacgaa actcgtagct 360
taatcatgtt ccgtagaggt atggatgggt tattcaatc atccaaatct aataaacatc 420
tctgggaaca gatttcgtct aagatgaqag aaaaagggtt tgatcgatct ccgactatgt 480
gtactgataa atggaggaat ctgttgaaag agttaaagaa agctaagcat catgatagag 540
gaaatggatc ggcgagaagt tcgtattaca aagagattga agatatctct agagagagga 600
gcacaaaggt gacaccacca cagtataata agagccctaa tacaccacct acatcagcca 660
aagttgattc ctttatgcaa ttactgata aaggttttga tgatacagac atttctcttt 720
gatccgttga agctaatggc aggccagcct taacccctga aaggcgctct gatcatgatg 780
gtcatcctct tgcaatcact acagcagttg atgctgttgc agcaaatgga gttactcctt 840
ggaattggag agagaactct gaaacgggt atgatagtc tggtcagcct ttgttggtga 900
gggtcataac agtgaaattt ggtgactata caagaagaat cgggtgtgat ggtagtgcag 960
aagcaatcaa agaggtaatt agatctgctt ttgggttaa aactcgaagg gcttttttgt 1020
tagaagatga agatcagatt attcgtctc ttgaccgaga catgccctta gggaactact 1080
tactccgtct ggatgatgga ctggccatta gggtttgcc ttatgatgaa tccaaccaat 1140
taccagtcca ttcagaagag aaaattctt acactgaaga agactaccgc gagtttctg 1200
ctcgacgggg atggtcagtc ctgcaagtt atggtttag gaacatagaa aacatggatg 1260
attctcaacc tgggtcgtg tatcgaggt tgagatgagg aaatgagatc acaaaacttc 1320
ttctccaatt ctatcaacag ttatctgac agaaaacagt ccctgtgata tatgatctca 1380
ttctcttatt acatttcttc ttttttctc gtacttgctc aaatatgaaa tatcataact 1440
ggcatttacc

```

(2) INFORMATION FOR SEQ ID NO:2475:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 431 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..431
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572971

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2475:

```

Gly Ala Phe Val Leu Thr Val Val Gly Thr Lys Glu His Arg Ile His
1 5 10 15
Ser Val Arg Glu Xaa Thr Ala Met Phe Ile Ser Asp Lys Ser Arg Pro
20 25 30
Thr Asp Phe Tyr Lys Asp Asp His His Asn Ser Ser Thr Thr Ser Thr
35 40 45
Thr Arg Asp Met Met Ile Asp Val Leu Thr Thr Thr Asn Glu Ser Val
50 55 60
Asp Leu Gln Ser Ser His His His Asn His Asn His His Asn His His

```

|                 |                         |                         |     |
|-----------------|-------------------------|-------------------------|-----|
| 65              | 70                      | 75                      | 80  |
| Leu His Gln Ser | Gln Pro Gln Gln Gln Ile | Leu Leu Gly Glu Ser Ser |     |
|                 | 85                      | 90                      | 95  |
| Gly Glu Asp His | Glu Val Lys Ala Pro Lys | Lys Arg Ala Glu Thr Trp |     |
|                 | 100                     | 105                     | 110 |
| Val Gln Asp Glu | Thr Arg Ser Leu Ile Met | Phe Arg Arg Gly Met Asp |     |
|                 | 115                     | 120                     | 125 |
| Gly Leu Phe Asn | Thr Ser Lys Ser Asn Lys | His Leu Trp Glu Gln Ile |     |
|                 | 130                     | 135                     | 140 |
| Ser Ser Lys Met | Arg Glu Lys Gly Phe Asp | Arg Ser Pro Thr Met Cys |     |
|                 | 145                     | 150                     | 155 |
| Thr Asp Lys Trp | Arg Asn Leu Leu Lys Glu | Phe Lys Lys Ala Lys His |     |
|                 | 165                     | 170                     | 175 |
| His Asp Arg Gly | Asn Gly Ser Ala Lys Met | Ser Tyr Tyr Lys Glu Ile |     |
|                 | 180                     | 185                     | 190 |
| Glu Asp Ile Leu | Arg Glu Arg Ser Lys Lys | Val Thr Pro Pro Gln Tyr |     |
|                 | 195                     | 200                     | 205 |
| Asn Lys Ser Pro | Asn Thr Pro Pro Thr Ser | Ala Lys Val Asp Ser Phe |     |
|                 | 210                     | 215                     | 220 |
| Met Gln Phe Thr | Asp Lys Gly Phe Asp Asp | Thr Ser Ile Ser Phe Gly |     |
|                 | 225                     | 230                     | 235 |
| Ser Val Glu Ala | Asn Gly Arg Pro Ala Leu | Asn Leu Glu Arg Arg Leu |     |
|                 | 245                     | 250                     | 255 |
| Asp His Asp Gly | His Pro Leu Ala Ile Thr | Thr Ala Val Asp Ala Val |     |
|                 | 260                     | 265                     | 270 |
| Ala Ala Asn Gly | Val Thr Pro Trp Asn Trp | Arg Glu Thr Pro Gly Asn |     |
|                 | 275                     | 280                     | 285 |
| Gly Asp Asp Ser | His Gly Gln Pro Phe Gly | Gly Arg Val Ile Thr Val |     |
|                 | 290                     | 295                     | 300 |
| Lys Phe Gly Asp | Tyr Thr Arg Arg Ile Gly | Val Asp Gly Ser Ala Glu |     |
|                 | 305                     | 310                     | 315 |
| Ala Ile Lys Glu | Val Ile Arg Ser Ala Phe | Gly Leu Arg Thr Arg Arg |     |
|                 | 325                     | 330                     | 335 |
| Ala Phe Trp Leu | Glu Asp Glu Asp Gln Ile | Ile Arg Cys Leu Asp Arg |     |
|                 | 340                     | 345                     | 350 |
| Asp Met Pro Leu | Gly Asn Tyr Leu Leu Arg | Leu Asp Asp Gly Leu Ala |     |
|                 | 355                     | 360                     | 365 |
| Ile Arg Val Cys | His Tyr Asp Glu Ser Asn | Gln Leu Pro Val His Ser |     |
|                 | 370                     | 375                     | 380 |
| Glu Glu Lys Ile | Phe Tyr Thr Glu Glu Asp | Tyr Arg Glu Phe Leu Ala |     |
|                 | 385                     | 390                     | 395 |
| Arg Arg Gly Trp | Ser Cys Leu Gln Val Asp | Gly Phe Arg Asn Ile Glu |     |
|                 | 405                     | 410                     | 415 |
| Asn Met Asp Asp | Leu Gln Pro Gly Ala Val | Tyr Arg Gly Val Arg     |     |
|                 | 420                     | 425                     | 430 |

(2) INFORMATION FOR SEQ ID NO:2476:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 408 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..408
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572972

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2476:

|                 |                     |                         |         |
|-----------------|---------------------|-------------------------|---------|
| Met Phe Ile Ser | Asp Lys Ser Arg Pro | Thr Asp Phe Tyr Lys Asp | Asp     |
| 1               | 5                   | 10                      | 15      |
| His His Asn Ser | Ser Thr Thr Ser Thr | Thr Arg Asp Met Met     | Ile Asp |
|                 | 20                  | 25                      | 30      |

Val Leu Thr Thr Thr Asn Glu Ser Val Asp Leu Gln Ser His His His  
35 40 45  
His Asn His Asn His His Asn His His Leu His Gln Ser Gln Pro Gln  
50 55 60  
Gln Gln Ile Leu Leu Gly Glu Ser Ser Gly Glu Asp His Glu Val Lys  
65 70 75 80  
Ala Pro Lys Lys Arg Ala Glu Thr Trp Val Gln Asp Glu Thr Arg Ser  
85 90 95  
Leu Ile Met Phe Arg Arg Gly Met Asp Gly Leu Phe Asn Thr Ser Lys  
100 105 110  
Ser Asn Lys His Leu Trp Glu Gln Ile Ser Ser Lys Met Arg Glu Lys  
115 120 125  
Gly Phe Asp Arg Ser Pro Thr Met Cys Thr Asp Lys Trp Arg Asn Leu  
130 135 140  
Leu Lys Glu Phe Lys Lys Ala Lys His His Asp Arg Gly Asn Gly Ser  
145 150 155 160  
Ala Lys Met Ser Tyr Tyr Lys Glu Ile Glu Asp Ile Leu Arg Glu Arg  
165 170 175  
Ser Lys Lys Val Thr Pro Pro Gln Tyr Asn Lys Ser Pro Asn Thr Pro  
180 185 190  
Pro Thr Ser Ala Lys Val Asp Ser Phe Met Gln Phe Thr Asp Lys Gly  
195 200 205  
Phe Asp Asp Thr Ser Ile Ser Phe Gly Ser Val Glu Ala Asn Gly Arg  
210 215 220  
Pro Ala Leu Asn Leu Glu Arg Arg Leu Asp His Asp Gly His Pro Leu  
225 230 235 240  
Ala Ile Thr Thr Ala Val Asp Ala Val Ala Ala Asn Gly Val Thr Pro  
245 250 255  
Trp Asn Trp Arg Glu Thr Pro Gly Asn Gly Asp Asp Ser His Gly Gln  
260 265 270  
Pro Phe Gly Gly Arg Val Ile Thr Val Lys Phe Gly Asp Tyr Thr Arg  
275 280 285  
Arg Ile Gly Val Asp Gly Ser Ala Glu Ala Ile Lys Glu Val Ile Arg  
290 295 300  
Ser Ala Phe Gly Leu Arg Thr Arg Arg Ala Phe Trp Leu Glu Asp Glu  
305 310 315 320  
Asp Gln Ile Ile Arg Cys Leu Asp Arg Asp Met Pro Leu Gly Asn Tyr  
325 330 335  
Leu Leu Arg Leu Asp Asp Gly Leu Ala Ile Arg Val Cys His Tyr Asp  
340 345 350  
Glu Ser Asn Gln Leu Pro Val His Ser Glu Glu Lys Ile Phe Tyr Thr  
355 360 365  
Glu Glu Asp Tyr Arg Glu Phe Leu Ala Arg Arg Gly Trp Ser Cys Leu  
370 375 380  
Gln Val Asp Gly Phe Arg Asn Ile Glu Asn Met Asp Asp Leu Gln Pro  
385 390 395 400  
Gly Ala Val Tyr Arg Gly Val Arg  
405

(2) INFORMATION FOR SEQ ID NO:2477:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 380 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..380

(D) OTHER INFORMATION: / Ceres Seq. ID 1572973

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2477:

Met Met Ile Asp Val Leu Thr Thr Thr Asn Glu Ser Val Asp Leu Gln

|                                                                 |     |     |     |
|-----------------------------------------------------------------|-----|-----|-----|
| 1                                                               | 5   | 10  | 15  |
| Ser His His His His Asn His Asn His His His Leu His Gln         | 20  | 25  | 30  |
| Ser Gln Pro Gln Gln Gln Ile Leu Leu Gly Glu Ser Ser Gly Glu Asp | 35  | 40  | 45  |
| His Glu Val Lys Ala Pro Lys Lys Arg Ala Glu Thr Trp Val Gln Asp | 50  | 55  | 60  |
| Glu Thr Arg Ser Leu Ile Met Phe Arg Arg Gly Met Asp Gly Leu Phe | 65  | 70  | 75  |
| Asn Thr Ser Lys Ser Asn Lys His Leu Trp Glu Gln Ile Ser Ser Lys | 85  | 90  | 95  |
| Met Arg Glu Lys Gly Phe Asp Arg Ser Pro Thr Met Cys Thr Asp Lys | 100 | 105 | 110 |
| Trp Arg Asn Leu Leu Lys Glu Phe Lys Lys Ala Lys His Asp Arg     | 115 | 120 | 125 |
| Gly Asn Gly Ser Ala Lys Met Ser Tyr Tyr Lys Glu Ile Glu Asp Ile | 130 | 135 | 140 |
| Leu Arg Glu Arg Ser Lys Lys Val Thr Pro Pro Gln Tyr Asn Lys Ser | 145 | 150 | 155 |
| Pro Asn Thr Pro Pro Thr Ser Ala Lys Val Asp Ser Phe Met Gln Phe | 165 | 170 | 175 |
| Thr Asp Lys Gly Phe Asp Asp Thr Ser Ile Ser Phe Gly Ser Val Glu | 180 | 185 | 190 |
| Ala Asn Gly Arg Pro Ala Leu Asn Leu Glu Arg Arg Leu Asp His Asp | 195 | 200 | 205 |
| Gly His Pro Leu Ala Ile Thr Thr Ala Val Asp Ala Val Ala Ala Asn | 210 | 215 | 220 |
| Gly Val Thr Pro Trp Asn Trp Arg Glu Thr Pro Gly Asn Gly Asp Asp | 225 | 230 | 235 |
| Ser His Gly Gln Pro Phe Gly Gly Arg Val Ile Thr Val Lys Phe Gly | 245 | 250 | 255 |
| Asp Tyr Thr Arg Arg Ile Gly Val Asp Gly Ser Ala Glu Ala Ile Lys | 260 | 265 | 270 |
| Glu Val Ile Arg Ser Ala Phe Gly Leu Arg Thr Arg Arg Ala Phe Trp | 275 | 280 | 285 |
| Leu Glu Asp Glu Asp Gln Ile Ile Arg Cys Leu Asp Arg Asp Met Pro | 290 | 295 | 300 |
| Leu Gly Asn Tyr Leu Leu Arg Leu Asp Asp Gly Leu Ala Ile Arg Val | 305 | 310 | 315 |
| Cys His Tyr Asp Glu Ser Asn Gln Leu Pro Val His Ser Glu Glu Lys | 325 | 330 | 335 |
| Ile Phe Tyr Thr Glu Glu Asp Tyr Arg Glu Phe Leu Ala Arg Arg Gly | 340 | 345 | 350 |
| Trp Ser Cys Leu Gln Val Asp Gly Phe Arg Asn Ile Glu Asn Met Asp | 355 | 360 | 365 |
| Asp Leu Gln Pro Gly Ala Val Tyr Arg Gly Val Arg                 | 370 | 375 | 380 |

(2) INFORMATION FOR SEQ ID NO:2478:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2262 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..2262
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572974

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2478:

gtttcttctt caacctcttt gtcagagaag tttaaaacc cccacacac actttacaca  
ctcttcacat tcttctctt cttcatcggt ttgcgattgt tgctccgata atgctggttc

60  
120

|             |             |             |             |             |             |      |
|-------------|-------------|-------------|-------------|-------------|-------------|------|
| tataaccgga  | agatcatcaa  | cgaagaaagc  | gaaataaacc  | tcaaaaaatca | cagagattat  | 180  |
| tacaataggc  | ggctactgat  | ttttttcttc  | ctttctgtct  | ctcttttacc  | cttatctctg  | 240  |
| gcttctcttt  | cgcttggtgat | ctttacgtct  | cttacgattt  | cactctctcc  | tacatcactg  | 300  |
| ctttctctct  | cggtgtttct  | caacaggtca  | tagcagtcac  | tgggaaatct  | ccaggctcgt  | 360  |
| tgattaaagc  | tacgacaaac  | tacaatgttc  | atgttaaact  | actcaatcat  | tggatgagc   | 420  |
| ctcttttact  | tacttggcct  | ggtgttcaga  | tgaggcgtaa  | ctcgtggcaa  | gacggtgttc  | 480  |
| ttggaaacaa  | ctgttccaatt | ccaccgaatt  | ggaacttcac  | ttatgatttt  | cagttgaaag  | 540  |
| atcagatttg  | aagtattttc  | tactctcttc  | cacttaactt  | tcagagagcc  | ttcgttggtt  | 600  |
| ttggtgcact  | cataatcaat  | aacagagacc  | ttgttccat   | tcggttcact  | gagcctgatg  | 660  |
| gtgaaattat  | ctttattatt  | gttgatttgg  | atactcagaa  | ccatacagct  | ttagggagga  | 720  |
| tacttgactc  | tggttaaaag  | cttgggatgc  | ccgatggagt  | actcatcaat  | gggaaaggct  | 780  |
| ctttcaagta  | caatagcagt  | gcactgatg   | gaattgaaca  | tgaacccgtt  | aatgtgtatc  | 840  |
| cagggaaaac  | atacaggatc  | cgtgttccaa  | atgttggtat  | ctcgacaagc  | ttgaacttca  | 900  |
| ggattcagaa  | ccacaaattg  | ctcttgattg  | agactgaggg  | tcgctacacc  | tcocaaatga  | 960  |
| acttccacga  | ttttgatatt  | catgtgggac  | agtccttatt  | tttctcgtga  | accatggacc  | 1020 |
| aaaacgccac  | aagtgactac  | tacattgttg  | cgagtgtcag  | atttgttaat  | gaacactgtg  | 1080 |
| ggcaaaagag  | tacaggtgtt  | ggcattctcc  | attattccaa  | ttccaaagga  | ctcgtctctg  | 1140 |
| gtcctttggc  | agtttcagca  | actgatgtta  | atcacccctg  | gtctgcaatg  | aaccaaccca  | 1200 |
| gagccataaa  | gcacaaacaca | tctgcaagtg  | gagctcgtcc  | aaatcccgag  | ggatcatttc  | 1260 |
| actacggata  | gatcaacatt  | acaagaacat  | acatcttgag  | gagtttgctc  | ccaacaaaaa  | 1320 |
| tcaatgggaa  | actctgtgct  | acacttaagt  | gaatttcatt  | tgtcaatcca  | agcaccctcca | 1380 |
| tgaggcttcc  | ggatgaccat  | aaagtgaag   | gagattatat  | gttagatttc  | ccagacagac  | 1440 |
| cacttgatga  | aaaaacttcca | cgtttgtcca  | gctctatcat  | caacccaaca  | tacaagggct  | 1500 |
| ttatacaagt  | tatcttccag  | aacaatgaca  | ccaaaatcca  | gagcttccat  | attgatggat  | 1560 |
| atgcatttta  | cgttggttgcg | atggactttg  | gtatatggtc  | agaagacaga  | aacggttcat  | 1620 |
| atacaacactg | ggatgcagta  | gcacgaagca  | cggtggagtg  | ctatccagga  | gcattggactg | 1680 |
| ctgtacttat  | ttctctcgtc  | gaatgttggg  | gtttggaata  | tcgggttgta  | gaattcttgc  | 1740 |
| agatggtatc  | ttggcccaaga | aacatacatg  | cgaattataa  | aacctgagga  | aacgggaagt  | 1800 |
| acggaaatgg  | atccgcctga  | aaatgttatg  | tactgtgggtg | ctcttcagggc | catgcaaaag  | 1860 |
| gaacacatc   | acagctcgcc  | cacaaaaatca | atgacaaatg  | gcagcttgat  | actaattttc  | 1920 |
| agcatgatga  | tggttttgct  | ctctctgttt  | tgtctctttt  | gctgagctcg  | ttccatcaat  | 1980 |
| tacgaatcta  | ctctggtttg  | gtattctgat  | ctccatttag  | ggctgttagat | ggagaatgta  | 2040 |
| taactacaaa  | cagctgtttg  | gttcgtttct  | tttctctcat  | atttcattga  | ttgttaggta  | 2100 |
| ctcatatctt  | ctatctcatc  | gattcctaac  | aacgttagtt  | cgtgaggggt  | tgtgtttaga  | 2160 |
| gctttgtctt  | togtagttct  | aggtcatttg  | gagttcaaaa  | cttggccaac  | gactgtaact  | 2220 |
| aaagtctcca  | tttgttggtc  | ttctacatta  | atttctacta  | tt          |             |      |

(2) INFORMATION FOR SEQ ID NO:2479:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 514 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..514
- (D) OTHER INFORMATION: / Ceres Seq. ID 1572975

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2479:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Ala | Thr | Asp | Phe | Phe | Phe | Ala | Phe | Val | Phe | Ser | Phe | Thr | Leu |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Ile | Phe | Gly | Phe | Ser | Phe | Ala | Gly | Asp | Pro | Tyr | Val | Ser | Tyr | Asp | Phe |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Thr | Leu | Ser | Tyr | Ile | Thr | Ala | Ser | Pro | Leu | Gly | Val | Pro | Gln | Gln | Val |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |
| Ile | Ala | Val | Asn | Gly | Lys | Phe | Pro | Gly | Pro | Val | Ile | Asn | Ala | Thr | Thr |
|     |     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |
| Asn | Tyr | Asn | Val | His | Val | Asn | Val | Leu | Asn | His | Leu | Asp | Glu | Pro | Leu |
|     |     |     | 65  |     |     |     | 70  |     |     |     | 75  |     |     | 80  |     |
| Leu | Leu | Thr | Trp | Pro | Gly | Val | Gln | Met | Arg | Arg | Asn | Ser | Trp | Gln | Asp |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Gly | Val | Leu | Gly | Thr | Asn | Cys | Pro | Ile | Pro | Pro | Asn | Trp | Asn | Phe | Thr |



|     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|
|     | 100 |     | 105 |     | 110 |
| Tyr | Asp | Phe | Gln | Leu | Lys |
|     | 115 |     | 120 |     | 125 |
| Ser | Leu | Asn | Phe | Gln | Arg |
|     | 130 |     | 135 |     | 140 |
| Asn | Asn | Arg | Asp | Leu | Val |
|     | 145 |     | 150 |     | 155 |
| Ile | Ile | Phe | Ile | Ile | Gly |
|     | 165 |     | 170 |     | 175 |
| Arg | Arg | Ile | Leu | Asp | Ser |
|     | 180 |     | 185 |     | 190 |
| Leu | Ile | Asn | Gly | Lys | Pro |
|     | 195 |     | 200 |     | 205 |
| Gly | Ile | Glu | His | Glu | Thr |
|     | 210 |     | 215 |     | 220 |
| Ile | Arg | Val | His | Asn | Val |
|     | 225 |     | 230 |     | 235 |
| Gln | Asn | His | Lys | Leu | Leu |
|     | 245 |     | 250 |     | 255 |
| Gln | Met | Asn | Phe | Thr | Asp |
|     | 260 |     | 265 |     | 270 |
| Phe | Leu | Val | Thr | Met | Asp |
|     | 275 |     | 280 |     | 285 |
| Ala | Ser | Ala | Arg | Phe | Val |
|     | 290 |     | 295 |     | 300 |
| Val | Gly | Ile | Leu | His | Tyr |
|     | 305 |     | 310 |     | 315 |
| Leu | Pro | Val | Ser | Ala | Thr |
|     | 325 |     | 330 |     | 335 |
| Gln | Pro | Arg | Ala | Ile | Lys |
|     | 340 |     | 345 |     | 350 |
| Asn | Pro | Gln | Gly | Ser | Phe |
|     | 355 |     | 360 |     | 365 |
| Tyr | Ile | Leu | Arg | Ser | Leu |
|     | 370 |     | 375 |     | 380 |
| Ala | Thr | Leu | Asn | Gly | Ile |
|     | 385 |     | 390 |     | 395 |
| Leu | Pro | Asp | Asp | His | Lys |
|     | 405 |     | 410 |     | 415 |
| Asp | Arg | Pro | Leu | Asp | Glu |
|     | 420 |     | 425 |     | 430 |
| Asn | Ala | Thr | Tyr | Lys | Gly |
|     | 435 |     | 440 |     | 445 |
| Thr | Lys | Ile | Gln | Ser | Phe |
|     | 450 |     | 455 |     | 460 |
| Ala | Met | Asp | Phe | Gly | Ile |
|     | 465 |     | 470 |     | 475 |
| Asn | Trp | Asp | Ala | Val | Ala |
|     | 485 |     | 490 |     | 495 |
| Trp | Thr | Ala | Val | Leu | Ile |
|     | 500 |     | 505 |     | 510 |
| Pro | Gly |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2480:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 426 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide  
(B) LOCATION: 1..426  
(D) OTHER INFORMATION: / Ceres Seq. ID 1572976

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2480:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Arg | Arg | Asn | Ser | Trp | Gln | Asp | Gly | Val | Leu | Gly | Thr | Asn | Cys | Pro |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ile | Pro | Pro | Asn | Trp | Asn | Phe | Thr | Tyr | Asp | Phe | Gln | Leu | Lys | Asp | Gln |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ile | Gly | Ser | Tyr | Phe | Tyr | Ser | Pro | Ser | Leu | Asn | Phe | Gln | Arg | Ala | Ser |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Gly | Gly | Phe | Gly | Ala | Leu | Ile | Ile | Asn | Asn | Arg | Asp | Leu | Val | Pro | Ile |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Pro | Phe | Thr | Glu | Pro | Asp | Gly | Glu | Ile | Ile | Phe | Ile | Ile | Gly | Asp | Trp |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     |     | 80  |
| Tyr | Thr | Gln | Asn | His | Thr | Ala | Leu | Arg | Arg | Ile | Leu | Asp | Ser | Gly | Lys |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Glu | Leu | Gly | Met | Pro | Asp | Gly | Val | Leu | Ile | Asn | Gly | Lys | Gly | Pro | Phe |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Lys | Tyr | Asn | Ser | Ser | Val | Pro | Asp | Gly | Ile | Glu | His | Glu | Thr | Val | Asn |
|     |     | 115 |     |     |     | 120 |     |     |     |     |     | 125 |     |     |     |
| Val | Asp | Pro | Gly | Lys | Thr | Tyr | Arg | Ile | Arg | Val | His | Asn | Val | Gly | Ile |
|     | 130 |     |     |     |     | 135 |     |     |     |     |     | 140 |     |     |     |
| Ser | Thr | Ser | Leu | Asn | Phe | Arg | Ile | Gln | Asn | His | Lys | Leu | Leu | Ile |     |
| 145 |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |     |
| Glu | Thr | Glu | Gly | Arg | Tyr | Thr | Ser | Gln | Met | Asn | Phe | Thr | Asp | Phe | Asp |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Ile | His | Val | Gly | Gln | Ser | Tyr | Ser | Phe | Leu | Val | Thr | Met | Asp | Gln | Asn |
|     |     | 180 |     |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Ala | Thr | Ser | Asp | Tyr | Tyr | Ile | Val | Ala | Ser | Ala | Arg | Phe | Val | Asn | Glu |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Thr | Val | Trp | Gln | Arg | Val | Thr | Gly | Val | Gly | Ile | Leu | His | Tyr | Ser | Asn |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Ser | Lys | Gly | Pro | Ala | Ser | Gly | Pro | Leu | Pro | Val | Ser | Ala | Thr | Asp | Val |
| 225 |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |     |
| Asn | His | Pro | Trp | Ser | Ala | Met | Asn | Gln | Pro | Arg | Ala | Ile | Lys | Gln | Asn |
|     |     |     | 245 |     |     |     |     |     | 250 |     |     |     | 255 |     |     |
| Thr | Ser | Ala | Ser | Gly | Ala | Arg | Pro | Asn | Pro | Gln | Gly | Ser | Phe | His | Tyr |
|     |     | 260 |     |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Gly | Gln | Ile | Asn | Ile | Thr | Arg | Thr | Tyr | Ile | Leu | Arg | Ser | Leu | Pro | Pro |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Thr | Lys | Ile | Asn | Gly | Lys | Leu | Arg | Ala | Thr | Leu | Asn | Gly | Ile | Ser | Phe |
|     |     | 290 |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Val | Asn | Pro | Ser | Thr | Pro | Met | Arg | Leu | Pro | Asp | Asp | His | Lys | Val | Lys |
| 305 |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |     |
| Gly | Asp | Tyr | Met | Leu | Asp | Phe | Pro | Asp | Arg | Pro | Leu | Asp | Glu | Lys | Leu |
|     |     |     | 325 |     |     |     |     |     | 330 |     |     |     | 335 |     |     |
| Pro | Arg | Leu | Ser | Ser | Ser | Ile | Ile | Asn | Ala | Thr | Tyr | Lys | Gly | Phe | Ile |
|     |     | 340 |     |     |     |     |     | 345 |     |     |     |     | 350 |     |     |
| Gln | Val | Ile | Phe | Gln | Asn | Asn | Asp | Thr | Lys | Ile | Gln | Ser | Phe | His | Ile |
|     |     | 355 |     |     |     |     | 360 |     |     |     |     | 365 |     |     |     |
| Asp | Gly | Tyr | Ala | Phe | Tyr | Val | Val | Ala | Met | Asp | Phe | Gly | Ile | Trp | Ser |
|     |     | 370 |     |     |     | 375 |     |     |     |     | 380 |     |     |     |     |
| Glu | Asp | Arg | Asn | Gly | Ser | Tyr | Asn | Asn | Trp | Asp | Ala | Val | Ala | Arg | Ser |
| 385 |     |     |     | 390 |     |     |     |     | 395 |     |     |     |     | 400 |     |
| Thr | Val | Glu | Val | Tyr | Pro | Gly | Ala | Trp | Thr | Ala | Val | Leu | Ile | Ser | Leu |
|     |     |     | 405 |     |     |     |     |     | 410 |     |     |     | 415 |     |     |
| Asp | Glu | Cys | Trp | Ser | Leu | Glu | Tyr | Pro | Gly |     |     |     |     |     |     |
|     |     | 420 |     |     |     |     |     | 425 |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2481:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 327 amino acids

SEQUENCE LISTING

(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..327  
(D) OTHER INFORMATION: / Ceres Seq. ID 1572977  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2481:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Pro | Asp | Gly | Val | Leu | Ile | Asn | Gly | Lys | Gly | Pro | Phe | Lys | Tyr | Asn |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Ser | Ser | Val | Pro | Asp | Gly | Ile | Glu | His | Glu | Thr | Val | Asn | Val | Asp | Pro |
|     |     |     | 20  |     |     |     | 25  |     |     |     |     | 30  |     |     |     |
| Gly | Lys | Thr | Tyr | Arg | Ile | Arg | Val | His | Asn | Val | Gly | Ile | Ser | Thr | Ser |
|     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| Leu | Asn | Phe | Arg | Ile | Gln | Asn | His | Lys | Leu | Leu | Ile | Glu | Thr | Glu |     |
|     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |     |
| Gly | Arg | Tyr | Thr | Ser | Gln | Met | Asn | Phe | Thr | Asp | Phe | Asp | Ile | His | Val |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Gly | Gln | Ser | Tyr | Ser | Phe | Leu | Val | Thr | Met | Asp | Gln | Asn | Ala | Thr | Ser |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Asp | Tyr | Tyr | Ile | Val | Ala | Ser | Ala | Arg | Phe | Val | Asn | Glu | Thr | Val | Trp |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Gln | Arg | Val | Thr | Gly | Val | Gly | Ile | Leu | His | Tyr | Ser | Asn | Ser | Lys | Gly |
|     |     | 115 |     |     |     | 120 |     |     |     |     |     | 125 |     |     |     |
| Pro | Ala | Ser | Gly | Pro | Leu | Pro | Val | Ser | Ala | Thr | Asp | Val | Asn | His | Pro |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Trp | Ser | Ala | Met | Asn | Gln | Pro | Arg | Ala | Ile | Lys | Gln | Asn | Thr | Ser | Ala |
| 145 |     |     |     | 150 |     |     |     |     |     | 155 |     |     |     | 160 |     |
| Ser | Gly | Ala | Arg | Pro | Asn | Pro | Gln | Gly | Ser | Phe | His | Tyr | Gly | Gln | Ile |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |     |
| Asn | Ile | Thr | Arg | Thr | Tyr | Ile | Leu | Arg | Ser | Leu | Pro | Pro | Thr | Lys | Ile |
|     |     | 180 |     |     |     |     | 185 |     |     |     |     |     | 190 |     |     |
| Asn | Gly | Lys | Leu | Arg | Ala | Thr | Leu | Asn | Gly | Ile | Ser | Phe | Val | Asn | Pro |
|     | 195 |     |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Ser | Thr | Pro | Met | Arg | Leu | Pro | Asp | Asp | His | Lys | Val | Lys | Gly | Asp | Tyr |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Met | Leu | Asp | Phe | Pro | Asp | Arg | Pro | Leu | Asp | Gly | Lys | Leu | Pro | Arg | Leu |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     | 240 |     |
| Ser | Ser | Ser | Ile | Ile | Asn | Ala | Thr | Tyr | Lys | Gly | Phe | Ile | Gln | Val | Ile |
|     |     |     | 245 |     |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Phe | Gln | Asn | Asn | Asp | Thr | Lys | Ile | Gln | Ser | Phe | His | Ile | Asp | Gly | Tyr |
|     |     | 260 |     |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Ala | Phe | Tyr | Val | Val | Ala | Met | Asp | Phe | Gly | Ile | Trp | Ser | Glu | Asp | Arg |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Asn | Gly | Ser | Tyr | Asn | Asn | Trp | Asp | Ala | Val | Ala | Arg | Ser | Thr | Val | Glu |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Val | Tyr | Pro | Gly | Ala | Trp | Thr | Ala | Val | Leu | Ile | Ser | Leu | Asp | Glu | Cys |
|     | 305 |     |     |     |     | 310 |     |     |     | 315 |     |     |     | 320 |     |
| Trp | Ser | Leu | Glu | Tyr | Pro | Gly |     |     |     |     |     |     |     |     |     |
|     |     |     |     | 325 |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2482:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 737 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
(A) NAME/KEY: -  
(B) LOCATION: 1..737

(D) OTHER INFORMATION: / Ceres Seq. ID 1573108

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2482:

|            |             |             |            |             |             |     |
|------------|-------------|-------------|------------|-------------|-------------|-----|
| agaaaaatcg | caagtgtgaat | gaccttcttg  | atgcgttgga | cttcaatcaa  | gttgtcattt  | 60  |
| ttgtgaagag | cgtagCagg   | gctgcgggaGc | tgaacaagtt | actggtggaa  | tgcaatttcc  | 120 |
| cctcaatatg | catacactct  | ggcatgtctc  | aagaagagag | gttgactcga  | tacaaaagtt  | 180 |
| tcaaggaagg | gcacaagagg  | atccttgtgg  | cgactgactt | ggtaggaaga  | gggattgaca  | 240 |
| tagagcgtgt | caacatttgt  | atcaactatg  | acatgccaga | ttctgcggat  | acctatcttc  | 300 |
| atagggttgg | gagagctggg  | agatttgga   | ccaagggtct | tgcaatcaca  | tttgttgcat  | 360 |
| ctgcttcaga | ttcagaggtc  | cttaaatcagg | ttcaagagag | gtttgagggtc | gatataaagg  | 420 |
| agcttctcga | gcagattgat  | acatcgactt  | acatgccgtc | ttaacaagt   | agcatcatct  | 480 |
| ctgaggaaac | aaacctcttca | gatttcaacc  | ttttagggtg | tcaaaaggggt | catggaggctc | 540 |
| cacaactatc | tctcacacgc  | tttgttgctt  | cgtatttita | gacttttctc  | tgaggacaag  | 600 |
| tttttccata | tatttagacc  | gttttgtaac  | tcttgaaaaa | tgagattgag  | ctaactccca  | 660 |
| aatcgcgcac | agttgagagc  | tctcctgttt  | ttgtactag  | tgatggttat  | ctttaaaaaa  | 720 |
| taaagatttc | aggatct     |             |            |             |             |     |

(2) INFORMATION FOR SEQ ID NO:2483:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 153 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..153

(D) OTHER INFORMATION: / Ceres Seq. ID 1573109

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2483:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Lys | Asn | Arg | Lys | Leu | Asn | Asp | Leu | Leu | Asp | Ala | Leu | Asp | Phe | Asn | Gln |
| 1   |     |     |     | 5   |     |     |     |     |     | 10  |     |     |     | 15  |     |
| Val | Val | Ile | Phe | Val | Lys | Ser | Val | Ser | Arg | Ala | Ala | Glu | Leu | Asn | Lys |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     | 30  |     |     |     |
| Leu | Leu | Val | Glu | Cys | Asn | Phe | Pro | Ser | Ile | Cys | Ile | His | Ser | Gly | Met |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ser | Gln | Glu | Glu | Arg | Leu | Thr | Arg | Tyr | Lys | Ser | Phe | Lys | Glu | Gly | His |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Lys | Arg | Ile | Leu | Val | Ala | Thr | Asp | Leu | Val | Gly | Arg | Gly | Ile | Asp | Ile |
|     | 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Glu | Arg | Val | Asn | Ile | Val | Ile | Asn | Tyr | Asp | Met | Pro | Asp | Ser | Ala | Asp |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Thr | Tyr | Leu | His | Arg | Val | Gly | Arg | Ala | Gly | Arg | Phe | Gly | Thr | Lys | Gly |
|     |     |     | 100 |     |     |     | 105 |     |     |     |     | 110 |     |     |     |
| Leu | Ala | Ile | Thr | Phe | Val | Ala | Ser | Ala | Ser | Asp | Ser | Glu | Val | Leu | Asn |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Gln | Val | Gln | Glu | Arg | Phe | Glu | Val | Asp | Ile | Lys | Glu | Leu | Pro | Glu | Gln |
|     | 130 |     |     |     |     |     | 135 |     |     |     | 140 |     |     |     |     |
| Ile | Asp | Thr | Ser | Thr | Tyr | Met | Pro | Ser |     |     |     |     |     |     |     |
|     | 145 |     |     |     |     | 150 |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2484:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 106 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..106
- (D) OTHER INFORMATION: / Ceres Seq. ID 1573110

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2484:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ser | Gln | Glu | Glu | Arg | Leu | Thr | Arg | Tyr | Lys | Ser | Phe | Lys | Glu | Gly |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     | 15  |     |     |

His Lys Arg Ile Leu Val Ala Thr Asp Leu Val Gly Arg Gly Ile Asp  
20 25 30  
Ile Glu Arg Val Asn Ile Val Ile Asn Tyr Asp Met Pro Asp Ser Ala  
35 40 45  
Asp Thr Tyr Leu His Arg Val Gly Arg Ala Gly Arg Phe Gly Thr Lys  
50 55 60  
Gly Leu Ala Ile Thr Phe Val Ala Ser Ala Ser Asp Ser Glu Val Leu  
65 70 75 80  
Asn Gln Val Gln Glu Arg Phe Glu Val Asp Ile Lys Glu Leu Pro Glu  
85 90 95  
Gln Ile Asp Thr Ser Thr Tyr Met Pro Ser  
100 105

(2) INFORMATION FOR SEQ ID NO:2485:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2412 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..2412
- (D) OTHER INFORMATION: / Ceres Seq. ID 1573151

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2485:

|             |             |             |             |             |             |      |
|-------------|-------------|-------------|-------------|-------------|-------------|------|
| atgcaatatt  | acggagacct  | acaagtgtat  | cttggtact   | taaaataacca | atggtcactt  | 60   |
| ggagaggaac  | gtaagcgcaa  | agaggcattt  | accaagctgc  | agattctaac  | gagagagctc  | 120  |
| ccaagtgtgc  | caacattctc  | atctgacata  | ctggctagaca | tgttatctag  | caagggcgca  | 180  |
| aatgttccac  | ttctgtcacg  | tgtaaatctc  | aaactgggaa  | cggtggcagt  | ggcactttct  | 240  |
| tcgggtttga  | atgatgggtc  | tattcaagaa  | attcgtgatg  | cggttgacaa  | atctactctg  | 300  |
| tatgtctcta  | aatgggctaa  | agcatggcac  | acatgggcac  | tattcaatca  | acgagtgtat  | 360  |
| tcgcattaca  | tttcaagagg  | tcaaatgtct  | tcccagtagc  | ttgtttctgc  | agtcactgga  | 420  |
| tatttttatt  | ctatagcatg  | tgccagcaaat | gccaaaggag  | ttgatgatag  | tttacaggac  | 480  |
| atactcggtc  | ttctgacatt  | gtggttcaac  | catggagcta  | caagctgatg  | ccaaaccgca  | 540  |
| ttgaagacag  | gattcagcta  | tgtaaacatt  | aacacatggc  | ttgttggctc  | acctcaaatc  | 600  |
| attgtcagga  | tacattctaa  | taatcgtgct  | gtcagggaac  | tgattcagtc  | tccttctcatc | 660  |
| cgcataaggc  | aaaaccaccc  | acaggctctg  | atgtatcccc  | ttctcgttgc  | cttcaaatca  | 720  |
| ataagcaaat  | ttcggagagc  | tgccggctcaa | gaggtgggtg  | ataaaagtgc  | ccagcacagt  | 780  |
| gggtcactcg  | tggatcagcc  | gcaacttgta  | tcacatgaac  | ttatcagggt  | tgccatactt  | 840  |
| tgccatgaaa  | tgtggcatga  | agcactagaa  | gaagctagtc  | gcttgatttt  | tggtgaacat  | 900  |
| aaacttgaa   | gcattgcgaa  | agtacttgaa  | cccttacatg  | acatgctgca  | cgaaaggtgta | 960  |
| aaaaaggaca  | gtacgcgatac | acaggaagaa  | gcatttatag  | agggcatccg  | tacagaaacta | 1020 |
| aaagaggcac  | atgaatcgct  | ttgcaattac  | aagataactg  | ggaagaatgc  | tgaacttata  | 1080 |
| cagggttcgg  | atcttttact  | tacagttttc  | aaacgggattg | acaaacagct  | agccactctc  | 1140 |
| acgacattgg  | atttggaaatc | tggtttctct  | gagttgctgc  | tggtgccgtga | cttgagagcta | 1200 |
| gcagttccgc  | gaacatattg  | tgccagatgc  | cccgctgtga  | ctatatctac  | tttttcaagc  | 1260 |
| caacttgggt  | ttataacctc  | taaacaaaga  | ccaaggaaat  | tgactattca  | cggaagtgtc  | 1320 |
| ggtaggagat  | acgccttctt  | gttgaaggga  | catgaagatt  | taaggcaaga  | tgagcgtggt  | 1380 |
| atgcagcttt  | ttggtttggt  | gaacactttg  | cttgagaatt  | ccagaaaaaa  | agccgaaaaa  | 1440 |
| gattctttcca | ttcaacgcga  | ttctgttaata | ccactatctc  | ccaatagtgg  | actcatcgga  | 1500 |
| tggtttccga  | actgcgatac  | ccctcaccat  | cttattcgag  | agcraagaga  | tgaagaaag   | 1560 |
| atcattctta  | atcaagaaaa  | taagcatatg  | ttgagttttg  | ctccagacta  | tgaacttata  | 1620 |
| ccgctttatg  | caaaggttga  | agttatttga  | tatgctctag  | aaaaacacga  | gggaatgat   | 1680 |
| ctatcccaag  | ttctctgggt  | aaaaagtcgc  | tcgtcagaag  | tttggtctga  | aagaagaaca  | 1740 |
| aactatacta  | gaagtttagc  | agttatgagt  | atggtttggt  | atattctgtg  | gttaggtgat  | 1800 |
| cgacacccaa  | gtaaccttat  | gcttcataga  | tacagaatgc  | ttgtcaaaag  | aatggaagtc  | 1860 |
| agtggtcatt  | aaggaaactt  | ccgctcaacc  | tgcgaaaaag  | ttatgcaagt  | ttcgaagacc  | 1920 |
| aataaagata  | gtgtaatggc  | aatgatggaa  | gcgtttgtac  | atgatccttt  | aatcaattgg  | 1980 |
| cgctctttca  | atttcaatga  | agtcctccaa  | ttagcactgc  | tcggtataca  | caactcttct  | 2040 |
| gctcctgtgc  | atgttgagcc  | tgacgaagaa  | gatgaagatc  | ccgctgatat  | agactcttct  | 2100 |
| cagcctcaaa  | ggagtactcg  | agagaaggag  | attcttcagg  | ctgtaaatat  | gcttgagagt  | 2160 |
| gctaataag   | tttaaatga   | gcgtgcgcga  | gttggtatgg  | cagctatgag  | tcaataagct  | 2220 |

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acaggcgctg attttttctt gctcgcaatt ccgagcaatc ccattgctga tcataataac 2280  
ttgctcgag gagattctca tgaagtcgaa catggtttgt ctgtgaaagt tcagggttcaa 2340  
aaactaatca atcaagccac ttcccatgag aatctctgtc aaaactatgt tgggtggtgc 2400  
cctttctggt ga

(2) INFORMATION FOR SEQ ID NO:2486:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 803 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..803
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1573152

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2486:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Gln | Tyr | His | Gly | Pro | Pro | Gln | Val | Met | Leu | Gly | Tyr | Leu | Lys | Tyr |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Gln | Trp | Ser | Leu | Gly | Glu | Glu | Arg | Lys | Arg | Lys | Glu | Ala | Phe | Thr | Lys |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Leu | Gln | Ile | Leu | Thr | Arg | Glu | Leu | Ser | Ser | Val | Pro | His | Ser | Gln | Ser |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Asp | Ile | Leu | Ala | Ser | Met | Val | Ser | Ser | Lys | Gly | Ala | Asn | Val | Pro | Leu |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Leu | Ala | Arg | Val | Asn | Leu | Lys | Leu | Gly | Thr | Trp | Gln | Trp | Ala | Leu | Ser |
|     | 65  |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Ser | Gly | Leu | Asn | Asp | Gly | Ser | Ile | Gln | Glu | Ile | Arg | Asp | Ala | Phe | Asp |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Lys | Ser | Thr | Cys | Tyr | Ala | Pro | Lys | Trp | Ala | Lys | Ala | Trp | His | Thr | Trp |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Ala | Leu | Phe | Asn | Thr | Ala | Val | Met | Ser | His | Tyr | Ile | Ser | Arg | Gly | Gln |
|     |     | 115 |     |     |     | 120 |     |     |     |     |     | 125 |     |     |     |
| Ile | Ala | Ser | Gln | Tyr | Val | Val | Ser | Ala | Val | Thr | Gly | Tyr | Phe | Tyr | Ser |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Ile | Ala | Cys | Ala | Ala | Asn | Ala | Lys | Gly | Val | Asp | Asp | Ser | Leu | Gln | Asp |
|     | 145 |     |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |     |
| Ile | Leu | Arg | Leu | Leu | Thr | Leu | Trp | Phe | Asn | His | Gly | Ala | Thr | Ala | Asp |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | 175 |     |
| Val | Gln | Thr | Ala | Leu | Lys | Thr | Gly | Phe | Ser | His | Val | Asn | Ile | Asn | Thr |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Trp | Leu | Val | Val | Leu | Pro | Gln | Ile | Ile | Ala | Arg | Ile | His | Ser | Asn | Asn |
|     |     | 195 |     |     |     | 200 |     |     |     |     |     | 205 |     |     |     |
| Arg | Ala | Val | Arg | Glu | Leu | Ile | Gln | Ser | Leu | Leu | Ile | Arg | Ile | Gly | Glu |
|     |     | 210 |     |     |     | 215 |     |     |     |     |     | 220 |     |     |     |
| Asn | His | Pro | Gln | Ala | Leu | Met | Tyr | Pro | Leu | Leu | Val | Ala | Cys | Lys | Ser |
|     | 225 |     |     |     | 230 |     |     |     |     |     | 235 |     |     | 240 |     |
| Ile | Ser | Asn | Leu | Arg | Arg | Ala | Ala | Ala | Gln | Glu | Val | Val | Asp | Lys | Val |
|     |     |     | 245 |     |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Arg | Gln | His | Ser | Gly | Ala | Leu | Val | Asp | Gln | Ala | Gln | Leu | Val | Ser | His |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Glu | Leu | Ile | Arg | Val | Ala | Ile | Leu | Trp | His | Glu | Met | Trp | His | Glu | Ala |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Leu | Glu | Glu | Ala | Ser | Arg | Leu | Tyr | Phe | Gly | Glu | His | Asn | Ile | Glu | Gly |
|     |     | 290 |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Met | Leu | Lys | Val | Leu | Glu | Pro | Leu | His | Asp | Met | Leu | Asp | Glu | Gly | Val |
|     | 305 |     |     |     | 310 |     |     |     |     | 315 |     |     |     | 320 |     |
| Lys | Lys | Asp | Ser | Thr | Thr | Ile | Gln | Glu | Arg | Ala | Phe | Ile | Glu | Ala | Tyr |
|     |     |     | 325 |     |     |     |     |     | 330 |     |     |     |     | 335 |     |
| Arg | His | Glu | Leu | Lys | Glu | Ala | His | Glu | Cys | Cys | Asn | Tyr | Lys | Ile |     |
|     |     |     | 340 |     |     |     |     | 345 |     |     |     | 350 |     |     |     |
| Thr | Gly | Lys | Asp | Ala | Glu | Leu | Thr | Gln | Ala | Trp | Asp | Leu | Tyr | Tyr | His |

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 794 amino acids  
 (B) TYPE: amino acid

(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..794  
(D) OTHER INFORMATION: / Ceres Seq. ID 1573154  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2487:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Leu | Gly | Tyr | Leu | Lys | Tyr | Gln | Trp | Ser | Leu | Gly | Glu | Glu | Arg | Lys |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Arg | Lys | Glu | Ala | Phe | Thr | Lys | Leu | Gln | Ile | Leu | Thr | Arg | Glu | Leu | Ser |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     |     | 30  |     |
| Ser | Val | Pro | His | Ser | Gln | Ser | Asp | Ile | Leu | Ala | Ser | Met | Val | Ser | Ser |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     |     |     |     |     |
| Lys | Gly | Ala | Asn | Val | Pro | Leu | Leu | Ala | Arg | Val | Asn | Leu | Lys | Leu | Gly |
|     |     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |
| Thr | Trp | Gln | Trp | Ala | Leu | Ser | Ser | Gly | Leu | Asn | Asp | Gly | Ser | Ile | Gln |
|     |     | 65  |     |     |     | 70  |     |     |     | 75  |     |     |     | 80  |     |
| Glu | Ile | Arg | Asp | Ala | Phe | Asp | Lys | Ser | Thr | Cys | Tyr | Ala | Pro | Lys | Trp |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Ala | Lys | Ala | Trp | His | Thr | Trp | Ala | Leu | Phe | Asn | Thr | Ala | Val | Met | Ser |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| His | Tyr | Ile | Ser | Arg | Gly | Gln | Ile | Ala | Ser | Gln | Tyr | Val | Val | Ser | Ala |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Val | Thr | Gly | Tyr | Phe | Tyr | Ser | Ile | Ala | Cys | Ala | Ala | Asn | Ala | Lys | Gly |
|     |     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |
| Val | Asp | Asp | Ser | Leu | Gln | Asp | Ile | Leu | Arg | Leu | Leu | Thr | Leu | Trp | Phe |
|     |     | 145 |     |     |     | 150 |     |     |     | 155 |     |     |     | 160 |     |
| Asn | His | Gly | Ala | Thr | Ala | Asp | Val | Gln | Thr | Ala | Leu | Lys | Thr | Gly | Phe |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Ser | His | Val | Asn | Ile | Asn | Thr | Trp | Leu | Val | Val | Leu | Pro | Gln | Ile | Ile |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Ala | Arg | Ile | His | Ser | Asn | Asn | Arg | Ala | Val | Arg | Glu | Leu | Ile | Gln | Ser |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Leu | Leu | Ile | Arg | Ile | Gly | Glu | Asn | His | Pro | Gln | Ala | Leu | Met | Tyr | Pro |
|     |     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |
| Leu | Leu | Val | Ala | Cys | Lys | Ser | Ile | Ser | Asn | Leu | Arg | Arg | Ala | Ala | Ala |
|     |     | 225 |     |     |     | 230 |     |     |     | 235 |     |     |     | 240 |     |
| Gln | Glu | Val | Val | Asp | Lys | Val | Arg | Gln | His | Ser | Gly | Ala | Leu | Val | Asp |
|     |     |     | 245 |     |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Gln | Ala | Gln | Leu | Val | Ser | His | Glu | Leu | Ile | Arg | Val | Ala | Ile | Leu | Trp |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| His | Glu | Met | Trp | His | Glu | Ala | Leu | Glu | Glu | Ala | Ser | Arg | Leu | Tyr | Phe |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Gly | Glu | His | Asn | Ile | Glu | Gly | Met | Leu | Lys | Val | Leu | Glu | Pro | Leu | His |
|     |     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |
| Asp | Met | Leu | Asp | Glu | Gly | Val | Lys | Lys | Asp | Ser | Thr | Thr | Ile | Gln | Glu |
|     |     | 305 |     |     |     | 310 |     |     |     | 315 |     |     |     | 320 |     |
| Arg | Ala | Phe | Ile | Glu | Ala | Tyr | Arg | His | Glu | Leu | Lys | Glu | Ala | His | Glu |
|     |     |     | 325 |     |     |     |     |     | 330 |     |     |     |     | 335 |     |
| Cys | Cys | Cys | Asn | Tyr | Lys | Ile | Thr | Gly | Lys | Asp | Ala | Glu | Leu | Thr | Gln |
|     |     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |
| Ala | Trp | Asp | Leu | Tyr | Tyr | His | Val | Phe | Lys | Arg | Ile | Asp | Lys | Gln | Leu |
|     |     | 355 |     |     |     |     | 360 |     |     |     |     | 365 |     |     |     |
| Ala | Ser | Leu | Thr | Thr | Leu | Asp | Leu | Glu | Ser | Val | Ser | Pro | Glu | Leu | Leu |
|     |     | 370 |     |     |     | 375 |     |     |     |     |     | 380 |     |     |     |
| Leu | Cys | Arg | Asp | Leu | Glu | Leu | Ala | Val | Pro | Gly | Thr | Tyr | Arg | Ala | Asp |
|     |     | 385 |     |     |     | 390 |     |     |     | 395 |     |     |     | 400 |     |
| Ala | Pro | Val | Val | Thr | Ile | Ser | Ser | Phe | Ser | Arg | Gln | Leu | Val | Val | Ile |
|     |     |     | 405 |     |     |     |     |     | 410 |     |     |     | 415 |     |     |
| Thr | Ser | Lys | Gln | Arg | Pro | Arg | Lys | Leu | Thr | Ile | His | Gly | Asn | Asp | Gly |



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420 425 430
Glu Asp Tyr Ala Phe Leu Leu Lys Gly His Glu Asp Leu Arg Gln Asp
435 440 445
Glu Arg Val Met Gln Leu Phe Gly Leu Val Asn Thr Leu Leu Glu Asn
450 455 460
Ser Arg Lys Thr Ala Glu Lys Asp Leu Ser Ile Gln Arg Tyr Ser Val
465 470 475
Ile Pro Leu Ser Pro Asn Ser Gly Leu Ile Gly Trp Val Pro Asn Cys
485 490 495
Asp Thr Leu His His Leu Ile Arg Glu Xaa Arg Asp Ala Arg Lys Ile
500 505 510
Ile Leu Asn Gln Glu Asn Lys His Met Leu Ser Phe Ala Pro Asp Tyr
515 520 525
Asp Asn Leu Pro Leu Ile Ala Lys Val Glu Val Phe Glu Tyr Ala Leu
530 535 540
Glu Asn Thr Glu Gly Asn Asp Leu Ser Arg Val Leu Trp Leu Lys Ser
545 550 555
Arg Ser Ser Glu Val Trp Leu Glu Arg Arg Thr Asn Tyr Thr Arg Ser
565 570 575
Leu Ala Val Met Ser Met Val Gly Tyr Ile Leu Gly Leu Gly Asp Arg
580 585 590
His Pro Ser Asn Leu Met Leu His Arg Tyr Arg Met Leu Val Lys Ala
595 600 605
Met Glu Val Ser Gly Ile Glu Gly Asn Phe Arg Ser Thr Cys Glu Asn
610 615 620
Val Met Gln Val Leu Arg Thr Asn Lys Asp Ser Val Met Ala Met Met
625 630 635
Glu Ala Phe Val His Asp Pro Leu Ile Asn Trp Arg Leu Phe Asn Phe
645 650 655
Asn Glu Val Pro Gln Leu Ala Leu Leu Gly Asn Asn Asn Pro Asn Ala
660 665 670
Pro Ala Asp Val Glu Pro Asp Glu Glu Asp Glu Asp Pro Ala Asp Ile
675 680 685
Asp Leu Pro Gln Pro Gln Arg Ser Thr Arg Glu Lys Glu Ile Leu Gln
690 695 700
Ala Val Asn Met Leu Gly Asp Ala Asn Glu Val Leu Asn Glu Arg Ala
705 710 715
Val Val Val Met Ala Arg Met Ser His Lys Leu Thr Gly Arg Asp Phe
725 730 735
Ser Ser Ser Ala Ile Pro Ser Asn Pro Ile Ala Asp His Asn Asn Leu
740 745 750
Leu Gly Gly Asp Ser His Glu Val Glu His Gly Leu Ser Val Lys Val
755 760 765
Gln Val Gln Lys Leu Ile Asn Gln Ala Thr Ser His Glu Asn Leu Cys
770 775 780
Gln Asn Tyr Val Gly Trp Cys Pro Phe Trp
785 790

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(2) INFORMATION FOR SEQ ID NO:2488:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 837 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..837

(D) OTHER INFORMATION: / Ceres Seq. ID 1573308

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2488:

```

atggcggaag aagcaaaatc caaaggaaac gcagctttct cttccggcga ttacgccacc 60
gcaataaacc atttcacaga agcaatcaac ctttcatcaa ccaatcacat cctctactca 120

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|            |            |            |            |             |             |     |
|------------|------------|------------|------------|-------------|-------------|-----|
| aacagatccg | cttcttaccg | tctctccac  | cgttacgaag | aagctttatc  | agacgcgaag  | 180 |
| aagactatag | agcttaaac  | tgatttgtct | aaaggatata | gccgattagg  | tgctgcgttt  | 240 |
| attggattgt | ccaagtttga | tgaagcgggt | gattcgtata | agaaaaggatt | agagattgat  | 300 |
| ccgagtaagt | agatgcttaa | atcgggatta | gctgatgctt | cgagatctag  | ggtttcgtca  | 360 |
| aagtcgaatc | cttttgttga | tgcttttcaa | gggaaggaga | tgtggggagaa | gttgacggcg  | 420 |
| gacccgggga | ctaggggtta | tttggagcag | gatgatattg | ttaagacgat  | gaaggagatt  | 480 |
| cagaggaacc | ctaataatct | taatttgtat | atgaaggata | agagagttat  | gaaggcttta  | 540 |
| ggggttttgt | tgaatgtgaa | gtttgttgga | tctagtgtgt | aagatactga  | gatgaaggag  | 600 |
| gctgatgaga | ggaaagagcc | tgaaccggag | atggaacctc | tggagtgtac  | ggagggaggag | 660 |
| aggcagaaga | aggagagaaa | ggagaaggct | ttgaaggaga | aaggggaagg  | aaatgttgct  | 720 |
| tataagaaga | aggattttga | gagagctgtt | gaacattata | ctaaggccat  | ggagctcgat  | 780 |
| gatgcagata | tttcttattt | gacgaatcgt | gtgctgtttt | atcttgagat  | gggggaag    |     |

(2) INFORMATION FOR SEQ ID NO:2489:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 279 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..279
- (D) OTHER INFORMATION: / Ceres Seq. ID 1573309

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2489:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Glu | Glu | Ala | Lys | Ser | Lys | Gly | Asn | Ala | Ala | Phe | Ser | Ser | Gly |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Asp | Tyr | Ala | Thr | Ala | Ile | Thr | His | Phe | Thr | Glu | Ala | Ile | Asn | Leu | Ser |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ser | Thr | Asn | His | Ile | Leu | Tyr | Ser | Asn | Arg | Ser | Ala | Ser | Tyr | Ala | Ser |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Leu | His | Arg | Tyr | Glu | Glu | Ala | Leu | Ser | Asp | Ala | Lys | Lys | Thr | Ile | Glu |
|     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Leu | Lys | Pro | Asp | Trp | Ser | Lys | Gly | Tyr | Ser | Arg | Leu | Gly | Ala | Ala | Phe |
| 65  |     |     |     | 70  |     |     |     | 75  |     |     |     |     |     |     | 80  |
| Ile | Gly | Leu | Ser | Lys | Phe | Asp | Glu | Ala | Val | Asp | Ser | Tyr | Lys | Lys | Gly |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Leu | Glu | Ile | Asp | Pro | Ser | Asn | Glu | Met | Leu | Lys | Ser | Gly | Leu | Ala | Asp |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Ala | Ser | Arg | Ser | Arg | Val | Ser | Ser | Lys | Ser | Asn | Pro | Phe | Val | Asp | Ala |
|     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |     |
| Phe | Gln | Gly | Lys | Glu | Met | Trp | Glu | Lys | Leu | Thr | Ala | Asp | Pro | Gly | Thr |
|     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Arg | Val | Tyr | Leu | Glu | Gln | Asp | Asp | Phe | Val | Lys | Thr | Met | Lys | Glu | Ile |
| 145 |     |     |     | 150 |     |     |     | 155 |     |     |     |     |     |     | 160 |
| Gln | Arg | Asn | Pro | Asn | Asn | Leu | Asn | Leu | Tyr | Met | Lys | Asp | Lys | Arg | Val |
|     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |     |
| Met | Lys | Ala | Leu | Gly | Val | Leu | Leu | Asn | Val | Lys | Phe | Gly | Gly | Ser | Ser |
|     |     | 180 |     |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Gly | Glu | Asp | Thr | Glu | Met | Lys | Glu | Ala | Asp | Glu | Arg | Lys | Glu | Pro | Glu |
|     |     | 195 |     |     |     |     |     | 200 |     |     |     | 205 |     |     |     |
| Pro | Glu | Met | Glu | Pro | Met | Glu | Leu | Thr | Glu | Glu | Glu | Arg | Gln | Lys | Lys |
|     |     | 210 |     |     |     | 215 |     |     |     |     |     | 220 |     |     |     |
| Glu | Arg | Lys | Glu | Lys | Ala | Leu | Lys | Glu | Lys | Gly | Glu | Gly | Asn | Val | Ala |
| 225 |     |     |     | 230 |     |     |     |     |     |     | 235 |     |     |     | 240 |
| Tyr | Lys | Lys | Lys | Asp | Phe | Glu | Arg | Ala | Val | Glu | His | Tyr | Thr | Lys | Ala |
|     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |     |
| Met | Glu | Leu | Asp | Asp | Glu | Asp | Ile | Ser | Tyr | Leu | Thr | Asn | Arg | Ala | Ala |
|     |     | 260 |     |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Val | Tyr | Leu | Glu | Met | Gly | Lys |     |     |     |     |     |     |     |     |     |
|     |     | 275 |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2490:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 175 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..175  
(D) OTHER INFORMATION: / Ceres Seq. ID 1573311  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2490:  
Met Leu Lys Ser Gly Leu Ala Asp Ala Ser Arg Ser Arg Val Ser Ser  
1 5 10 15  
Lys Ser Asn Pro Phe Val Asp Ala Phe Gln Gly Lys Glu Met Trp Glu  
20 25 30  
Lys Leu Thr Ala Asp Pro Gly Thr Arg Val Tyr Leu Glu Gln Asp Asp  
35 40 45  
Phe Val Lys Thr Met Lys Glu Ile Gln Arg Asn Pro Asn Asn Leu Asn  
50 55 60  
Leu Tyr Met Lys Asp Lys Arg Val Met Lys Ala Leu Gly Val Leu Leu  
65 70 75  
Asn Val Lys Phe Gly Gly Ser Ser Gly Glu Asp Thr Glu Met Lys Glu  
85 90 95  
Ala Asp Glu Arg Lys Glu Pro Glu Pro Glu Met Glu Pro Met Glu Leu  
100 105 110  
Thr Glu Glu Glu Arg Gln Lys Lys Glu Arg Lys Glu Lys Ala Leu Lys  
115 120 125  
Glu Lys Gly Glu Gly Asn Val Ala Tyr Lys Lys Lys Asp Phe Glu Arg  
130 135 140  
Ala Val Glu His Tyr Thr Lys Ala Met Glu Leu Asp Asp Glu Asp Ile  
145 150 155 160  
Ser Tyr Leu Thr Asn Arg Ala Ala Val Tyr Leu Glu Met Gly Lys  
165 170 175

(2) INFORMATION FOR SEQ ID NO:2491:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 137 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..137  
(D) OTHER INFORMATION: / Ceres Seq. ID 1573315

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2491:

acttacacca cgacaaaaag ggaatgtgtt cacgtgtgtc ttctgttttt tgatcgctat 60  
cggattcgct cgagttatcg ttatgtctg ctttgcatca gcacgagaaa cacgtgaaaa 120  
acggcgtgaa gaacaac

(2) INFORMATION FOR SEQ ID NO:2492:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 38 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..38  
(D) OTHER INFORMATION: / Ceres Seq. ID 1573316

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2492:

Thr Tyr Thr Thr Lys Arg Glu Cys Val His Val Cys Leu Arg Phe

1 5 10 15  
Phe Asp Arg Tyr Arg Ile Arg Cys Ser Tyr Arg Leu Cys Leu Leu Cys  
20 25 30  
Ile Ser Thr Arg Asn Thr  
35

(2) INFORMATION FOR SEQ ID NO:2493:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..45
- (D) OTHER INFORMATION: / Ceres Seq. ID 1573317

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2493:

Leu Thr Pro Arg Gln Lys Gly Asn Val Phe Thr Cys Val Phe Val Phe  
1 5 10 15  
Leu Ile Ala Ile Gly Phe Ala Ala Val Ile Val Tyr Val Cys Phe Ala  
20 25 30  
Ser Ala Arg Glu Thr Arg Glu Lys Arg Arg Glu Glu Gln  
35 40 45

(2) INFORMATION FOR SEQ ID NO:2494:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..117
- (D) OTHER INFORMATION: / Ceres Seq. ID 1573351

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2494:

atggaaaaaa acttgaagaa gattcaggct aaggaagagg agctctctat gatgagaagt 60  
gaatttggtg ctgccgtgac gaatgtgtg tcaagcaaga caacgcattct tattcct

(2) INFORMATION FOR SEQ ID NO:2495:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..39
- (D) OTHER INFORMATION: / Ceres Seq. ID 1573352

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2495:

Met Glu Lys Asn Leu Lys Lys Ile Gln Ala Lys Glu Glu Leu Ser  
1 5 10 15  
Met Met Arg Ser Glu Phe Val Ala Ala Val Thr Asn Val Leu Ser Ser  
20 25 30  
Lys Thr Thr His Leu Ile Pro  
35

(2) INFORMATION FOR SEQ ID NO:2496:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 114 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
    (A) NAME/KEY: -  
    (B) LOCATION: 1..114  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1573401  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2496:  
atggatgaag aaggtcacat tatacacatt gatttcggct ttatgctttc aaattctcct 60  
ggtagcggtga actttgagag tgccccattt aagctaactc gggaactctt tgag  
(2) INFORMATION FOR SEQ ID NO:2497:  
    (i) SEQUENCE CHARACTERISTICS:  
        (A) LENGTH: 38 amino acids  
        (B) TYPE: amino acid  
        (C) STRANDEDNESS:  
        (D) TOPOLOGY: linear  
    (ii) MOLECULE TYPE: peptide  
    (ix) FEATURE:  
        (A) NAME/KEY: peptide  
        (B) LOCATION: 1..38  
        (D) OTHER INFORMATION: / Ceres Seq. ID 1573402  
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2497:  
Met Asp Glu Gly His Ile Ile His Ile Asp Phe Gly Phe Met Leu  
1                  5                  10                  15  
Ser Asn Ser Pro Gly Gly Val Asn Phe Glu Ser Ala Pro Phe Lys Leu  
                  20                  25                  30  
Thr Arg Glu Leu Leu Glu  
                  35  
(2) INFORMATION FOR SEQ ID NO:2498:  
    (i) SEQUENCE CHARACTERISTICS:  
        (A) LENGTH: 178 base pairs  
        (B) TYPE: nucleic acid  
        (C) STRANDEDNESS: single  
        (D) TOPOLOGY: linear  
    (ii) MOLECULE TYPE: DNA (genomic)  
    (ix) FEATURE:  
        (A) NAME/KEY: -  
        (B) LOCATION: 1..178  
        (D) OTHER INFORMATION: / Ceres Seq. ID 1573446  
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2498:  
atgtatgaaa acaagagtga tgggccaaagc tggcgagtac caacggggtcg taaagacggg 60  
agactctcgt tggcaactaa agcatcgaat ctaccttctc cacttgactc tgttgcgtgt 120  
caaaagcaaa agtttcaaga taaaggattg gatactcatg atcttggttac tctactag  
(2) INFORMATION FOR SEQ ID NO:2499:  
    (i) SEQUENCE CHARACTERISTICS:  
        (A) LENGTH: 59 amino acids  
        (B) TYPE: amino acid  
        (C) STRANDEDNESS:  
        (D) TOPOLOGY: linear  
    (ii) MOLECULE TYPE: peptide  
    (ix) FEATURE:  
        (A) NAME/KEY: peptide  
        (B) LOCATION: 1..59  
        (D) OTHER INFORMATION: / Ceres Seq. ID 1573447  
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2499:  
Met Tyr Glu Asn Lys Ser Asp Gly Pro Ser Trp Arg Val Pro Thr Gly  
1                  5                  10                  15  
Arg Lys Asp Gly Arg Leu Ser Leu Ala Thr Lys Ala Ser Asn Leu Pro  
                  20                  25                  30  
Ser Pro Leu Asp Ser Val Ala Val Gln Lys Gln Lys Phe Gln Asp Lys  
                  35                  40                  45  
Gly Leu Asp Thr His Asp Leu Val Thr Leu Leu  
                  50                  55

(2) INFORMATION FOR SEQ ID NO:2500:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..58
- (D) OTHER INFORMATION: / Ceres Seq. ID 1573449

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2500:

Cys Met Lys Thr Arg Val Met Gly Gln Ala Gly Glu Tyr Gln Arg Val  
1 5 10 15  
Val Lys Thr Gly Asp Ser Arg Trp Gln Leu Lys His Arg Ile Tyr Leu  
20 25 30  
Leu His Leu Thr Leu Leu Leu Phe Lys Ser Lys Ser Phe Lys Ile Lys  
35 40 45  
Asp Trp Ile Leu Met Ile Leu Leu Tyr  
50 55

(2) INFORMATION FOR SEQ ID NO:2501:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 759 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..759
- (D) OTHER INFORMATION: / Ceres Seq. ID 1573532

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2501:

|             |             |             |            |            |            |     |
|-------------|-------------|-------------|------------|------------|------------|-----|
| atgcaaaactc | gatccaaagg  | ttctgcacac  | ctactaccat | tcagagacgg | aatagataga | 60  |
| atagctcgtg  | agttacaaga  | aaccaaaagca | aaggcaacct | gtgatcagca | aagaccagct | 120 |
| gctatggatc  | aacagaacat  | accagttgat  | gttcaagacc | cacctaatgt | tgatcaacca | 180 |
| agaaacattg  | gtgctgggtg  | tgccccaagg  | aatcatcacc | aaagacaagg | gatagtgcct | 240 |
| ccaccagttc  | agaacaacaa  | ctttgaaatc  | aagagtggtc | tcactccat  | gatccaagga | 300 |
| aacaagtttc  | atggtttacc  | tatggaagat  | cccctggacc | atcttgacag | ctttgatagg | 360 |
| ctctgtggcc  | ttaccaagat  | caatggtgtc  | actgaagata | tgtttaagct | cagactattt | 420 |
| ccctctctct  | tgggaaacaa  | ggcacaccac  | tgggagaaga | ctctgcccc  | agaactccat | 480 |
| aactcatggg  | acgattataa  | gaaagctttt  | cttgtcaagt | ctactcttaa | cgctcgcaac | 540 |
| gctagattga  | ggaacagagat | cccaggcttc  | acacagaaaa | acaatgaaac | tttctgtgaa | 600 |
| gcttgggaaa  | ggtttcaaga  | aggcttcatt  | attgagcaca | ctctaccaag | gagctttacc | 660 |
| aaatatcaga  | attgctactcg | acacgcgctc  | caatggaac  | ttctggaact | aggatgtaga | 720 |
| agaaggctag  | gagttagtcg  | aaaatctagc  | acaatctaa  |            |            |     |

(2) INFORMATION FOR SEQ ID NO:2502:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 252 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..252
- (D) OTHER INFORMATION: / Ceres Seq. ID 1573533

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2502:

Met Gln Thr Arg Ser Lys Gly Ser Ala His Leu Leu Pro Phe Arg Asp  
1 5 10 15  
Gly Ile Asp Arg Ile Ala Arg Glu Leu Gln Glu Thr Lys Ala Lys Ala  
20 25 30

Thr Cys Asp Gln Gln Arg Pro Ala Ala Met Asp Gln Gln Asn Ile Pro  
35 40 45  
Val Asp Val Gln Asp Pro Pro Asn Val Asp Gln Pro Arg Asn Ile Gly  
50 55 60  
Ala Gly Asp Ala Pro Arg Asn His His Gln Arg Gln Gly Ile Val Pro  
65 70 75 80  
Pro Pro Val Gln Asn Asn Asn Phe Glu Ile Lys Ser Gly Leu Ile Ser  
85 90 95  
Met Ile Gln Gly Asn Lys Phe His Gly Leu Pro Met Glu Asp Pro Leu  
100 105 110  
Asp His Leu Asp Ser Phe Asp Arg Leu Cys Gly Leu Thr Lys Ile Asn  
115 120 125  
Gly Val Thr Glu Asp Met Phe Lys Leu Arg Leu Phe Pro Phe Ser Leu  
130 135 140  
Gly Asn Lys Ala His His Trp Glu Lys Thr Leu Pro Pro Asp Ser Ile  
145 150 155 160  
Asn Ser Trp Asp Asp Tyr Lys Lys Ala Phe Leu Val Lys Phe Tyr Ser  
165 170 175  
Asn Ala Arg Thr Ala Arg Leu Arg Asn Glu Ile Pro Gly Phe Thr Gln  
180 185 190  
Lys Asn Asn Glu Thr Phe Cys Glu Ala Trp Glu Arg Phe Gln Glu Gly  
195 200 205  
Phe Ile Glu His Thr Leu Pro Arg Ser Phe Thr Lys Tyr Gln Asn  
210 215 220  
Ala Thr Arg His Arg Val Gln Trp Lys Leu Pro Glu Leu Gly Cys Arg  
225 230 235 240  
Arg Arg Leu Gly Val Ser Arg Lys Ser Ser Thr Ile  
245 250

(2) INFORMATION FOR SEQ ID NO:2503:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 211 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..211

(D) OTHER INFORMATION: / Ceres Seq. ID 1573535

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2503:

Met Asp Gln Gln Asn Ile Pro Val Asp Val Gln Asp Pro Pro Asn Val  
1 5 10 15  
Asp Gln Pro Arg Asn Ile Gly Ala Gly Asp Ala Pro Arg Asn His His  
20 25 30  
Gln Arg Gln Gly Ile Val Pro Pro Val Gln Asn Asn Asn Phe Glu  
35 40 45  
Ile Lys Ser Gly Leu Ile Ser Met Ile Gln Gly Asn Lys Phe His Gly  
50 55 60  
Leu Pro Met Glu Asp Pro Leu Asp His Leu Asp Ser Phe Asp Arg Leu  
65 70 75 80  
Cys Gly Leu Thr Lys Ile Asn Gly Val Thr Glu Asp Met Phe Lys Leu  
85 90 95  
Arg Leu Phe Pro Phe Ser Leu Gly Asn Lys Ala His His Trp Glu Lys  
100 105 110  
Thr Leu Pro Pro Asp Ser Ile Asn Ser Trp Asp Asp Tyr Lys Lys Ala  
115 120 125  
Phe Leu Val Lys Phe Tyr Ser Asn Ala Arg Thr Ala Arg Leu Arg Asn  
130 135 140  
Glu Ile Pro Gly Phe Thr Gln Lys Asn Asn Glu Thr Phe Cys Glu Ala  
145 150 155 160  
Trp Glu Arg Phe Gln Glu Gly Phe Ile Glu His Thr Leu Pro Arg

(2) INFORMATION FOR SEQ ID NO:2504:

(A) LENGTH: 566 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(A) NAME/KEY: -

(B) LOCATION: 1..566

(D) OTHER INFORMATION: / Ceres Seq. ID 1573558

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2504:

|            |             |             |             |            |             |     |
|------------|-------------|-------------|-------------|------------|-------------|-----|
| atgctcaaa  | caaccaaca   | cataaaagag  | agattttaa   | caaaagtag  | agaaaanaa   | 60  |
| aagatcaga  | aggactcac   | acaagaatg   | gagacgact   | ccacattga  | ggaggcaaca  | 120 |
| aggaaggtga | gcacaagaag  | gaagaagaac  | acaagaaaa   | cggtgcagag | caacaagatg  | 180 |
| gttgacacaa | agaaggttat  | gttgacacaa  | tcaaaagaca  | gtatccagg  | ggtgaaggtta | 240 |
| aaagccacga | cgggagaaggc | aaaagccacg  | acgctgagaa  | gaaaaaagaa | aaggacaaga  | 300 |
| agggaaagaa | acatcatgat  | gatgtgtcac  | acagcagcag  | cagtgcagc  | gcagcatttt  | 360 |
| aaggtggagg | agtgaggagg  | atcgcttgga  | taaaaacagat | gtctgtcttc | ctattattaa  | 420 |
| ttaagtgttg | tgtatgtgtt  | tatcatcttta | gagagagaggt | aaagacaagg | gaaccgtgca  | 480 |
| tctatcttgg | YYtgttatgt  | tgtgtgttttc | ttgtcatgaa  | aattatgctc | atgtattctta | 540 |
| tctaaatcag | aaaaataaat  | ttctatg     |             |            |             |     |

(2) INFORMATION FOR SEQ ID NO:2505:

(A) LENGTH: 124 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(A) NAME/KEY: peptide

(B) LOCATION: 1..124

(D) OTHER INFORMATION

SEQUENCE DESCRIPTION: SEQ ID NO:2505:

## Val Lys Ala Thr Lys His Ile Lys Glu Arg Ph

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Arg | Glu | Lys | Arg | Lys | Ile | Trp | Gln | Asp | Ser | Ser | Thr | Arg | Ser | Glu | Thr |
| His | Ser | Thr | Leu | Glu | Glu | Ala | Thr | Arg | Lys | Val | Ser | Thr | Arg | Arg | Lys |
| Arg | Asn | Thr | Arg | Asn | Thr | Leu | Thr | Ser | Thr | Arg | Val | Val | Ser | Thr | Lys |
| Lys | Val | Leu | Leu | Thr | Arg | Ser | Lys | Thr | Arg | Ser | Thr | Val | Val | Lys | Val |
| Lys | Ala | Thr | Thr | Glu | Lys | Ala | Lys | Ala | Thr | Thr | Val | Arg | Arg | Lys | Arg |
| Arg | Arg | Thr | Arg | Arg | Arg | Asn | Ile | Met | Met | Met | Val | Thr | Thr | Ala |     |
| Ala | Ala | Val | Thr | Ala | Thr | Ala | Phe | Lys | Val | Arg | Lys |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2506:

## (1) SEQUENCE CHARACTERISTICS

(A) LENGTH: 98 amino acids

(B) TYPE: amino acid



(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..98  
(D) OTHER INFORMATION: / Ceres Seq. ID 1573560  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2506:  
Met Ala Gly Leu Ile Asn Lys Ile Gly Asp Ala Leu His Ile Gly Gly  
1 5 10 15  
Gly Asn Lys Glu Gly Glu His Lys Lys Glu Glu Glu His Lys Lys His  
20 25 30  
Val Asp Glu His Lys Ser Gly Glu His Lys Glu Gly Ile Val Asp Lys  
35 40 45  
Ile Lys Asp Lys Ile His Gly Gly Glu Glu Lys Ser His Asp Gly Glu  
50 55 60  
Gly Lys Ser His Asp Gly Glu Lys Lys Lys Lys Lys Asp Lys Lys Glu  
65 70 75 80  
Lys Lys His His Asp Asp Gly His His Ser Ser Ser Asp Ser Asp  
85 90 95  
Ser Ile

(2) INFORMATION FOR SEQ ID NO:2507:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1363 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..1363  
(D) OTHER INFORMATION: / Ceres Seq. ID 1573561

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2507:

|             |             |             |             |             |             |      |
|-------------|-------------|-------------|-------------|-------------|-------------|------|
| acaatctatc  | gagctaaaa   | actgaagcag  | acattagcgt  | tgagaaaaaW  | aaaaaaaaag  | 60   |
| aagaacgaga  | gagagaaagc  | catgtctcgc  | aaaacaatcc  | tatcatcagt  | agtttttggtg | 120  |
| gttctcgtcg  | cgcgatcagc  | agcggctaata | atcggattcg  | atgagtcaaa  | cccgatccga  | 180  |
| atggtctccg  | atggtctccg  | ggaggtagaa  | gaatctgttt  | cccagatcct  | aggtcaatct  | 240  |
| cgtcacgttc  | tctctttcgc  | tgccttcaact | caccgatatg  | gtaaaaagta  | tcagaaacgtg | 300  |
| gaggagatga  | agcttcgatt  | ctcgtatttc  | aaggagaatc  | ttgatttgat  | cagatccacc  | 360  |
| aacaagaaga  | gcttatctta  | caaaactcgt  | gttaatacaat | ttgctgattt  | gacatggcaa  | 420  |
| gagtttcaaa  | ggaccaagct  | tggtgtcgtc  | cagaactgct  | ctgccacttt  | aaaggggcagc | 480  |
| cacaaggcca  | cagaagcagc  | tcttctctgaa | acaaaagact  | ggagagaaga  | tggtatcggt  | 540  |
| agtcgggtca  | aagatcaggg  | agggttggtga | tcttgctgga  | cattcagcac  | aaactggagct | 600  |
| cttgaggcag  | cttaccatca  | ggcatttgga  | aaaggaaatc  | ctctctctga  | gcaacagcgt  | 660  |
| gtggttggtg  | ctggagcttt  | caataactat  | ggttgcaatg  | gtggccctcc  | ttctcaagcc  | 720  |
| tttgaataca  | taaaatccaa  | cggtgggcctc | gacacagaga  | aagcttatcc  | ttataccggt  | 780  |
| aagcatagca  | ctgcgaatt   | ttcagctgaa  | aacgttggtg  | tacaagtcct  | caactcagtc  | 840  |
| aatcattact  | tgggtgctga  | agatgaactg  | aagcatgcgg  | ttgBgattgg  | tacggccaagt | 900  |
| aagcatagca  | tttgagttta  | tacactcggt  | cggcttttac  | aagagtgagg  | tttcaactga  | 960  |
| tagtcaactg  | ggaagtactc  | caatggatgt  | gaaccaacgc  | gttttggccg  | ttgggttatgg | 1020 |
| agttgaagac  | ggtgtaccat  | attggcttat  | taagaactca  | tggggagcgg  | attggggcga  | 1080 |
| caaaaggttac | ttcaagatgg  | agatggggaa  | gaacatgtgt  | ggtatttgcta | catgtgcac   | 1140 |
| ataccocggt  | tggtcttgag  | atgatcagcg  | aatctgggtg  | gcgaatttat  | aaattacgaa  | 1200 |
| attgttcacgt | attttatgga  | tttaagacatt | acgtaaaaagt | tgggacttgg  | gaatgcata   | 1260 |
| ggtttatgct  | tgttgttaaca | taaaaaggct  | tgtttaatatg | tacaaaataa  | agccaaaact  | 1320 |
| atagacgaca  | aatttataat  | attttcatgt  | taaatattatg | aac         |             |      |

(2) INFORMATION FOR SEQ ID NO:2508:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 304 amino acids  
(B) TYPE: amino acid

| Thr | (X1) | Ala | Leu | Arg | Ala | Lys | Thr | Leu | Lys | Gln | Thr | Leu | Ala | Leu | Arg | Lys |
|-----|------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Xaa | Ile  | Ser | Val | Asn | Lys | Glu | Arg | Glu | Lys | Gln | Thr | Leu | Ala | Leu | Arg | Lys |
| 1   |      |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Xaa | Lys  | Lys | Ser | Ser | Val | Val | Leu | Val | Val | Leu | Val | Ala | Ala | Ser | Aia | Ala |
|     |      |     | 20  |     |     |     |     | 25  |     |     |     |     | 45  |     | 30  |     |
| Ile | Leu  | Ser | Ser | Val | Val | Leu | Val | Val | Val | Leu | Val | Ala | Ala | Ser | Aia | Ala |
|     |      |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ala | Asn  | Ile | Gly | Phe | Asp | Glu | Ser | Asn | Pro | Ile | Arg | Met | Val | Ser | Ser | Asp |
|     |      |     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |
| Gly | Leu  | Arg | Glu | Val | Glu | Glu | Ser | Val | Ser | Gln | Ile | Leu | Gly | Gln | Ser |     |
| 65  |      |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Arg | His  | Val | Leu | Ser | Phe | Ala | Arg | Phe | Thr | His | Arg | Tyr | Gly | Lys | Lys |     |
|     |      |     |     |     | 85  |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Tyr | Gln  | Asn | Val | Glu | Glu | Met | Lys | Leu | Arg | Phe | Ser | Ile | Phe | Phy | Glu |     |
|     |      |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |     |
| Asn | Leu  | Asp | Leu | Ile | Arg | Ser | Thr | Asn | Lys | Lys | Gly | Leu | Ser | Tyr | Lys |     |
|     |      |     | 115 |     |     |     |     | 120 |     |     |     | 125 |     |     |     |     |
| Leu | Gly  | Val | Asn | Gln | Phe | Ala | Asp | Leu | Thr | Trp | Gln | Glu | Phe | Gln | Arg |     |
|     |      |     | 130 |     |     |     | 135 |     |     |     | 140 |     |     |     |     |     |
| Thr | Lys  | Leu | Gly | Ala | Ala | Gln | Asn | Cys | Ser | Ala | Thr | Leu | Lys | Gly | Ser |     |
| 145 |      |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |     |
| His | Lys  | Val | Thr | Glu | Ala | Ala | Leu | Pro | Glu | Thr | Lys | Asp | Trp | Arg | Glu |     |
|     |      |     |     |     | 165 |     |     |     | 170 |     |     |     |     | 175 |     |     |
| Asp | Gly  | Ile | Val | Ser | Pro | Val | Lys | Asp | Gln | Gly | Gly | Cys | Gly | Ser | Cys |     |
|     |      |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |     |
| Trp | Thr  | Phe | Ser | Ser | Thr | Thr | Gly | Ala | Leu | Glu | Ala | Ala | Tyr | His | Gln | Ala |
|     |      |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Phe | Gly  | Lys | Gly | Ile | Ser | Leu | Ser | Glu | Gln | Gln | Leu | Val | Asp | Cys | Ala |     |
|     |      |     | 210 |     |     |     | 215 |     |     |     | 220 |     |     |     |     |     |
| Gly | Ala  | Phe | Asn | Asn | Tyr | Gly | Cys | Asn | Gly | Gly | Leu | Pro | Ser | Gln | Ala |     |
| 225 |      |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |     |
| Phe | Glu  | Tyr | Ile | Lys | Ser | Asn | Gly | Gly | Leu | Asp | Thr | Glu | Lys | Ala | Tyr |     |
|     |      |     |     |     | 245 |     |     |     | 250 |     |     |     |     | 255 |     |     |
| Pro | Tyr  | Thr | Gly | Lys | Asp | Glu | Thr | Cys | Lys | Phe | Ser | Ala | Glu | Asn | Val |     |
|     |      |     |     |     | 260 |     |     | 265 |     |     |     |     | 270 |     |     |     |
| Gly | Val  | Gln | Val | Leu | Asn | Ser | Val | Asn | Ile | Thr | Leu | Gly | Ala | Glu | Asp |     |
|     |      |     | 275 |     |     |     |     | 280 |     |     |     | 285 |     |     |     |     |
| Glu | Leu  | Lys | His | Ala | Val | Xaa | Ile | Gly | Thr | Ala | Ser | Lys | His | Ser | Ile |     |
|     |      |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |     |

Met Ser Ala Lys Thr Ile Leu Ser Ser Val Val Leu Val Val Leu Val

1 5 10 15  
Ala Ala Ser Ala Ala Asn Ile Gly Phe Asp Glu Ser Asn Pro Ile  
20 25 30  
Arg Met Val Ser Asp Gly Leu Arg Glu Val Glu Glu Ser Val Ser Gln  
35 40 45  
Ile Leu Gly Gln Ser Arg His Val Leu Ser Phe Ala Arg Phe Thr His  
50 55 60  
Arg Tyr Gly Lys Lys Tyr Gln Asn Val Glu Glu Met Lys Leu Arg Phe  
65 70 75 80  
Ser Ile Phe Lys Glu Asn Leu Asp Leu Ile Arg Ser Thr Asn Lys Lys  
85 90 95  
Gly Leu Ser Tyr Lys Leu Gly Val Asn Gln Phe Ala Asp Leu Thr Trp  
100 105 110  
Gln Glu Phe Gln Arg Thr Lys Leu Gly Ala Ala Gln Asn Cys Ser Ala  
115 120 125  
Thr Leu Lys Gly Ser His Lys Val Thr Glu Ala Ala Leu Pro Glu Thr  
130 135 140  
Lys Asp Trp Arg Glu Asp Gly Ile Val Ser Pro Val Lys Asp Gln Gly  
145 150 155 160  
Gly Cys Gly Ser Cys Trp Thr Phe Ser Thr Thr Gly Ala Leu Glu Ala  
165 170 175  
Ala Tyr His Gln Ala Phe Gly Lys Gly Ile Ser Leu Ser Glu Gln Gln  
180 185 190  
Leu Val Asp Cys Ala Gly Ala Phe Asn Asn Tyr Gly Cys Asn Gly Gly  
195 200 205  
Leu Pro Ser Gln Ala Phe Glu Tyr Ile Lys Ser Asn Gly Gly Leu Asp  
210 215 220  
Thr Glu Lys Ala Tyr Pro Tyr Thr Gly Lys Asp Glu Thr Cys Lys Phe  
225 230 235 240  
Ser Ala Glu Asn Val Gly Val Gln Val Leu Asn Ser Val Asn Ile Thr  
245 250 255  
Leu Gly Ala Glu Asp Glu Leu Lys His Ala Val Xaa Ile Gly Thr Ala  
260 265 270  
Ser Lys His Ser Ile  
275

(2) INFORMATION FOR SEQ ID NO:2510:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 244 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..244

(D) OTHER INFORMATION: / Ceres Seq. ID 1573564

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2510:

Met Val Ser Asp Gly Leu Arg Glu Val Glu Glu Ser Val Ser Gln Ile  
1 5 10 15  
Leu Gly Gln Ser Arg His Val Leu Ser Phe Ala Arg Phe Thr His Arg  
20 25 30  
Tyr Gly Lys Lys Tyr Gln Asn Val Glu Met Lys Leu Arg Phe Ser  
35 40 45  
Ile Phe Lys Glu Asn Leu Asp Leu Ile Arg Ser Thr Asn Lys Lys Gly  
50 55 60  
Leu Ser Tyr Lys Leu Gly Val Asn Gln Phe Ala Asp Leu Thr Trp Gln  
65 70 75 80  
Glu Phe Gln Arg Thr Lys Leu Gly Ala Ala Gln Asn Cys Ser Ala Thr  
85 90 95  
Leu Lys Gly Ser His Lys Val Thr Glu Ala Ala Leu Pro Glu Thr Lys  
100 105 110

Asp Trp Arg Glu Asp Gly Ile Val Ser Pro Val Lys Asp Gln Gly Gly  
115 120 125  
Cys Gly Ser Cys Trp Thr Phe Ser Thr Thr Gly Ala Leu Glu Ala Ala  
130 135 140  
Tyr His Gln Ala Phe Gly Lys Gly Ile Ser Leu Ser Glu Gln Gln Leu  
145 150 155 160  
Val Asp Cys Ala Gly Ala Phe Asn Asn Tyr Gly Cys Asn Gly Gly Leu  
165 170 175  
Pro Ser Gln Ala Phe Glu Tyr Ile Lys Ser Asn Gly Gly Leu Asp Thr  
180 185 190  
Glu Lys Ala Tyr Pro Tyr Thr Gly Lys Asp Glu Thr Cys Lys Phe Ser  
195 200 205  
Ala Glu Asn Val Gly Val Gln Val Leu Asn Ser Val Asn Ile Thr Leu  
210 215 220  
Gly Ala Glu Asp Glu Leu Lys His Ala Val Xaa Ile Gly Thr Ala Ser  
225 230 235 240  
Lys His Ser Ile

(2) INFORMATION FOR SEQ ID NO:2511:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 545 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..545
- (D) OTHER INFORMATION: / Ceres Seq. ID 1573565

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2511:

|             |             |            |            |             |            |     |
|-------------|-------------|------------|------------|-------------|------------|-----|
| ttttctttga  | gtcgtctcac  | ttctcttgca | tccttcaaac | tcattccacag | gaatggcgac | 60  |
| agCagcagca  | ccagcagtg   | tttcatggac | aagatcaggc | attgtgtcca  | aatccggaca | 120 |
| aaaccagaag  | aaatctgaga  | tgaagtgttc | ttacataact | ggacttaact  | catatgggtg | 180 |
| tctcaaggca  | cagaacaaca  | aggttgtctc | aatgggatca | ccactctgca  | cagaacagt  | 240 |
| ttttgtctaac | gttgtgatgt  | ctctcaaagg | aagaagaggt | aatggaggag  | ccttatccac | 300 |
| cacgtgtaac  | ctgtccggaga | gattttcaag | attgcagcaa | tcattgaacg  | tcttactctt | 360 |
| gttggtgttg  | cagttggatt  | cgttcttctt | cgaatcgaaa | cttctgttga  | agaagctgaa | 420 |
| gcagagtaaa  | tagagtaaat  | tgtgtctctt | ataattatat | atttttggtt  | attgttgttg | 480 |
| tcaagctttg  | gtaaaaactt  | atggatacat | gttacatttg | tttatgaaga  | agctcttttc | 540 |
| ttggc       |             |            |            |             |            |     |

(2) INFORMATION FOR SEQ ID NO:2512:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 97 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..97
- (D) OTHER INFORMATION: / Ceres Seq. ID 1573566

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2512:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Thr | Ala | Ala | Ala | Pro | Ala | Val | Ile | Ser | Trp | Thr | Arg | Ser | Gly |
| 1   |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| Ile | Val | Ser | Lys | Ser | Gly | Gln | Thr | Gln | Lys | Lys | Ser | Glu | Met | Lys | Val |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| Ser | Tyr | Ile | Thr | Gly | Leu | Asn | Ser | Tyr | Gly | Gly | Leu | Lys | Ala | Gln | Asn |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| Asn | Lys | Val | Val | Ser | Met | Gly | Ser | Pro | Leu | Cys | Thr | Glu | Gln | Cys | Phe |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| Ala | Asn | Val | Val | Met | Ser | Leu | Lys | Gly | Arg | Arg | Gly | Asn | Gly | Gly | Ala |

|                                                                 |    |    |    |
|-----------------------------------------------------------------|----|----|----|
| 65                                                              | 70 | 75 | 80 |
| Leu Ser Thr Thr Cys Asn Leu Ser Glu Arg Phe Ser Arg Leu Gln Gln |    |    |    |
|                                                                 | 85 | 90 | 95 |
| Ser                                                             |    |    |    |

(2) INFORMATION FOR SEQ ID NO:2513:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..68
- (D) OTHER INFORMATION: / Ceres Seq. ID 1573567

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2513:

|                                                                 |          |
|-----------------------------------------------------------------|----------|
| Met Lys Val Ser Tyr Ile Thr Gly Leu Asn Ser Tyr Gly Gly Leu Lys |          |
| 1                                                               | 5 10 15  |
| Ala Gln Asn Asn Lys Val Val Ser Met Gly Ser Pro Leu Cys Thr Glu |          |
|                                                                 | 20 25 30 |
| Gln Cys Phe Ala Asn Val Val Met Ser Leu Lys Gly Arg Arg Gly Asn |          |
|                                                                 | 35 40 45 |
| Gly Gly Ala Leu Ser Thr Thr Cys Asn Leu Ser Glu Arg Phe Ser Arg |          |
|                                                                 | 50 55 60 |
| Leu Gln Gln Ser                                                 |          |

(2) INFORMATION FOR SEQ ID NO:2514:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1357 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1357
- (D) OTHER INFORMATION: / Ceres Seq. ID 1573568

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2514:

|            |             |            |             |             |             |      |
|------------|-------------|------------|-------------|-------------|-------------|------|
| aaaacctccc | tcaggagcct  | cgccttatt  | cagagaggag  | gatccaaaag  | aaaagaggaa  | 60   |
| aaaatggact | atatgtatgk  | gaccagggag | acaccatctg  | tttgtaccag  | gaccagtga   | 120  |
| cataccggaa | ccggtaatcc  | ggcgatgaa  | ccggaacaac  | gaggattacc  | ggtcaccagc  | 180  |
| cattccggcg | cttacgaaaa  | cattgttgga | ggatgttaag  | aagatattca  | agaccacatc  | 240  |
| agggacacct | tttctgtttc  | ccacgaccgg | gactgtgtct  | tgggagagtg  | ccttgaccaa  | 300  |
| cacgttatct | cctggagaca  | ggattgtttc | gtttctgatt  | ggacaattta  | gcttgctctg  | 360  |
| gattgaccag | cagaagagggc | ttaatttcaa | tgttgatgtg  | gttgagagtg  | attggggaca  | 420  |
| aggtgcta   | ctccaagtct  | tggcctcaaa | gctctcacia  | acacgaagt   | ataccatcaa  | 480  |
| agccatttgc | attgtccaca  | acgagacgcg | gaccggagtt  | accaatgaca  | tctctgtcgt  | 540  |
| ccgcacacac | ctcgatcaat  | acaagcatcc | ggctttgtct  | ctagtggagc  | gtgtttogtc  | 600  |
| catctgcgcg | cttgatttcc  | gaatggatga | gtggggagtg  | gacgtggcct  | tgactgggctc | 660  |
| tcagaaagcc | ttatctcttc  | caacaggact | tgttattgtc  | tgccgacgtc  | ctaaagcttt  | 720  |
| ggaagctacc | aaaactttcta | aattctctaa | agtattcttt  | gactggaatg  | actaccttaa  | 780  |
| gttttacaa  | ctaggaaacct | attggccata | cacacottcc  | attcaacttc  | tctacgggtc  | 840  |
| tagagctcgt | cttgatcttta | tctttgagga | aggacttgag  | aacatcatcg  | cccgccatgc  | 900  |
| tgcgttgagg | aaggccaccca | ggccttcggt | ggaagcatgg  | gggctgaaaa  | actgcacaca  | 960  |
| gaaggaggaa | tgataaagta  | acacagtgac | agcagttatg  | gtgcctccgc  | atatagacgg  | 1020 |
| ttcggagatt | gtgagaaagg  | catggcagag | gtacaaactta | agtccttgct  | ttgggtctcaa | 1080 |
| caaatggcgt | ggaagggttt  | tcagaattgg | acatctagga  | aattgtgaatg | agttgcaact  | 1140 |
| tctcgggtgt | cttcggcgag  | ttggagatga | ctggaagagt  | ttgggaacc   | cagttgtaat  | 1200 |
| gggaagtggg | gttgacagtg  | cctctactta | tcttcagcac  | cacattctct  | tcattctcct  | 1260 |
| tagaatctaa | tccatgtggt  | ctttctcttt | ctttctctct  | ctctcaatgt  | aaacaaactc  | 1320 |

tcactgtttttc tctttttcttc atctatatatt ttactgc

(2) INFORMATION FOR SEQ ID NO:2515:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 422 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..422

(D) OTHER INFORMATION: / Ceres Seq. ID 1573569

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2515:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Lys | Pro | Pro | Ser | Gly | Ala | Ser | Ala | Leu | Phe | Arg | Glu | Glu | Asp | Pro | Lys |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Glu | Lys | Arg | Lys | Lys | Trp | Thr | Ile | Cys | Met | Xaa | Pro | Gly | Arg | His | His |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Leu | Phe | Val | Pro | Gly | Pro | Val | Asn | Ile | Pro | Glu | Pro | Val | Ile | Arg | Ala |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Met | Asn | Arg | Asn | Asn | Glu | Asp | Tyr | Arg | Ser | Pro | Ala | Ile | Pro | Ala | Leu |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Thr | Lys | Thr | Leu | Leu | Glu | Asp | Val | Lys | Lys | Ile | Phe | Lys | Thr | Thr | Ser |
|     | 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Gly | Thr | Pro | Phe | Leu | Phe | Pro | Thr | Thr | Gly | Thr | Gly | Ala | Trp | Glu | Ser |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Ala | Leu | Thr | Asn | Thr | Leu | Ser | Pro | Gly | Asp | Arg | Ile | Val | Ser | Phe | Leu |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Ile | Gly | Gln | Phe | Ser | Leu | Leu | Trp | Ile | Asp | Gln | Gln | Lys | Arg | Leu | Asn |
|     | 115 |     |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Phe | Asn | Val | Asp | Val | Val | Glu | Ser | Asp | Trp | Gly | Gln | Gly | Ala | Asn | Leu |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Gln | Val | Leu | Ala | Ser | Lys | Leu | Ser | Gln | Asp | Glu | Asn | His | Thr | Ile | Lys |
|     | 145 |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Ala | Ile | Cys | Ile | Val | His | Asn | Glu | Thr | Ala | Thr | Gly | Val | Thr | Asn | Asp |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Ile | Ser | Ala | Val | Arg | Thr | Leu | Leu | Asp | His | Tyr | Lys | His | Pro | Ala | Leu |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Leu | Leu | Val | Asp | Gly | Val | Ser | Ser | Ile | Cys | Ala | Leu | Asp | Phe | Arg | Met |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Asp | Glu | Trp | Gly | Val | Asp | Val | Ala | Leu | Thr | Gly | Ser | Gln | Lys | Ala | Leu |
|     | 210 |     |     |     |     |     | 215 |     |     |     | 220 |     |     |     |     |
| Ser | Leu | Pro | Thr | Gly | Leu | Gly | Ile | Val | Cys | Ala | Ser | Pro | Lys | Ala | Leu |
|     | 225 |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Glu | Ala | Thr | Lys | Thr | Ser | Lys | Ser | Leu | Lys | Val | Phe | Phe | Asp | Trp | Asn |
|     |     |     | 245 |     |     |     |     |     |     | 250 |     |     |     | 255 |     |
| Asp | Tyr | Leu | Lys | Phe | Tyr | Lys | Leu | Gly | Thr | Tyr | Trp | Pro | Tyr | Thr | Pro |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Ser | Ile | Gln | Leu | Leu | Tyr | Gly | Leu | Arg | Ala | Ala | Leu | Asp | Leu | Ile | Phe |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Glu | Glu | Gly | Leu | Glu | Asn | Ile | Ile | Ala | Arg | His | Ala | Arg | Leu | Gly | Lys |
|     |     |     |     |     | 295 |     |     |     |     |     | 300 |     |     |     |     |
| Ala | Thr | Arg | Leu | Ala | Val | Glu | Ala | Trp | Gly | Leu | Lys | Asn | Cys | Thr | Gln |
|     | 305 |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |
| Lys | Glu | Glu | Trp | Ile | Ser | Asn | Thr | Val | Thr | Ala | Val | Met | Val | Pro | Pro |
|     |     |     | 325 |     |     |     |     |     |     | 330 |     |     |     | 335 |     |
| His | Ile | Asp | Gly | Ser | Glu | Ile | Val | Arg | Arg | Ala | Trp | Gln | Arg | Tyr | Asn |
|     |     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |
| Leu | Ser | Leu | Gly | Leu | Gly | Leu | Asn | Lys | Val | Ala | Gly | Lys | Val | Phe | Arg |
|     |     | 355 |     |     |     |     | 360 |     |     |     |     | 365 |     |     |     |
| Ile | Gly | His | Leu | Gly | Asn | Val | Asn | Glu | Leu | Gln | Leu | Leu | Gly | Cys | Leu |
|     | 370 |     |     |     |     | 375 |     |     |     |     |     | 380 |     |     |     |

Ala Gly Val Glu Met Ile Leu Lys Asp Val Gly Tyr Pro Val Val Met  
385 390 395 400  
Gly Ser Gly Val Ala Ala Ser Thr Tyr Leu Gln His His Ile Pro  
405 410 415  
Leu Ile Pro Ser Arg Ile  
420

(2) INFORMATION FOR SEQ ID NO:2516:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 397 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..397

(D) OTHER INFORMATION: / Ceres Seq. ID 1573570

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2516:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Xaa | Pro | Gly | Arg | His | His | Leu | Phe | Val | Pro | Gly | Pro | Val | Asn | Ile |
| 1   |     |     |     |     |     |     |     |     |     |     |     |     |     | 15  |     |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| Pro | Glu | Pro | Val | Ile | Arg | Ala | Met | Asn | Arg | Asn | Asn | Glu | Asp | Tyr | Arg |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| Ser | Pro | Ala | Ile | Pro | Ala | Leu | Thr | Lys | Thr | Leu | Leu | Glu | Asp | Val | Lys |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| Lys | Ile | Phe | Lys | Thr | Thr | Ser | Gly | Thr | Pro | Phe | Leu | Phe | Pro | Thr | Thr |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| Gly | Thr | Gly | Ala | Trp | Glu | Ser | Ala | Leu | Thr | Asn | Thr | Leu | Ser | Pro | Gly |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| Asp | Arg | Ile | Val | Ser | Phe | Leu | Ile | Gly | Gln | Phe | Ser | Leu | Leu | Trp | Ile |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| Asp | Gln | Gln | Lys | Arg | Leu | Asn | Phe | Asn | Val | Asp | Val | Val | Glu | Ser | Asp |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| Trp | Gly | Gln | Gly | Ala | Asn | Leu | Gln | Val | Leu | Ala | Ser | Lys | Leu | Ser | Gln |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| Asp | Glu | Asn | His | Thr | Ile | Lys | Ala | Ile | Cys | Ile | Val | His | Asn | Glu | Thr |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| Ala | Thr | Gly | Val | Thr | Asn | Asp | Ile | Ser | Ala | Val | Arg | Thr | Leu | Leu | Asp |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| His | Tyr | Lys | His | Pro | Ala | Leu | Leu | Leu | Val | Asp | Gly | Val | Ser | Ser | Ile |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| Cys | Ala | Leu | Asp | Phe | Arg | Met | Asp | Glu | Trp | Gly | Val | Asp | Val | Ala | Leu |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| Thr | Gly | Ser | Gln | Lys | Ala | Leu | Ser | Leu | Pro | Thr | Gly | Leu | Gly | Ile | Val |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| Cys | Ala | Ser | Pro | Lys | Ala | Leu | Glu | Ala | Thr | Lys | Thr | Ser | Lys | Ser | Leu |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| Lys | Val | Phe | Phe | Asp | Trp | Asn | Asp | Tyr | Leu | Lys | Phe | Tyr | Lys | Leu | Gly |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| Thr | Tyr | Trp | Pro | Tyr | Thr | Pro | Ser | Ile | Gln | Leu | Leu | Tyr | Gly | Leu | Arg |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| Ala | Ala | Leu | Asp | Leu | Ile | Phe | Glu | Glu | Gly | Leu | Glu | Asn | Ile | Ile | Ala |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| Arg | His | Ala | Arg | Leu | Gly | Lys | Ala | Thr | Arg | Leu | Ala | Val | Glu | Ala | Trp |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| Gly | Leu | Lys | Asn | Cys | Thr | Gln | Lys | Glu | Glu | Trp | Ile | Ser | Asn | Thr | Val |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| Thr | Ala | Val | Met | Val | Pro | His | Ile | Asp | Gly | Ser | Glu | Ile | Val | Arg |     |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| Arg | Ala | Trp | Gln | Arg | Tyr | Asn | Leu | Ser | Leu | Gly | Leu | Gly | Leu | Asn | Lys |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| Val | Ala | Gly | Lys | Val | Phe | Arg | Ile | Gly | His | Leu | Gly | Asn | Val | Asn | Glu |

340 345 350  
Leu Gln Leu Leu Gly Cys Leu Ala Gly Val Glu Met Ile Leu Lys Asp  
355 360 365  
Val Gly Tyr Pro Val Val Met Gly Ser Gly Val Ala Ala Ala Ser Thr  
370 375 380  
Tyr Leu Gln His His Ile Pro Leu Ile Pro Ser Arg Ile  
385 390 395

(2) INFORMATION FOR SEQ ID NO:2517:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 374 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..374

(D) OTHER INFORMATION: / Ceres Seq. ID 1573571

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2517:

Met Asn Arg Asn Asn Glu Asp Tyr Arg Ser Pro Ala Ile Pro Ala Leu  
1 5 10 15  
Thr Lys Thr Leu Leu Glu Asp Val Lys Lys Ile Phe Lys Thr Thr Ser  
20 25 30  
Gly Thr Pro Phe Leu Phe Pro Thr Thr Gly Thr Gly Ala Trp Glu Ser  
35 40 45  
Ala Leu Thr Asn Thr Leu Ser Pro Gly Asp Arg Ile Val Ser Phe Leu  
50 55 60  
Ile Gly Gln Phe Ser Leu Leu Trp Ile Asp Gln Gln Lys Arg Leu Asn  
65 70 75 80  
Phe Asn Val Asp Val Val Glu Ser Asp Trp Gly Gln Gly Ala Asn Leu  
85 90 95  
Gln Val Leu Ala Ser Lys Leu Ser Gln Asp Glu Asn His Thr Ile Lys  
100 105 110  
Ala Ile Cys Ile Val His Asn Glu Thr Ala Thr Gly Val Thr Asn Asp  
115 120 125  
Ile Ser Ala Val Arg Thr Leu Leu Asp His Tyr Lys His Pro Ala Leu  
130 135 140  
Leu Leu Val Asp Gly Val Ser Ser Ile Cys Ala Leu Asp Phe Arg Met  
145 150 155 160  
Asp Glu Trp Gly Val Asp Val Ala Leu Thr Gly Ser Gln Lys Ala Leu  
165 170 175  
Ser Leu Pro Thr Gly Leu Gly Ile Val Cys Ala Ser Pro Lys Ala Leu  
180 185 190  
Glu Ala Thr Lys Thr Ser Lys Ser Leu Lys Val Phe Phe Asp Trp Asn  
195 200 205  
Asp Tyr Leu Lys Phe Tyr Lys Leu Gly Thr Tyr Trp Pro Tyr Thr Pro  
210 215 220  
Ser Ile Gln Leu Leu Tyr Gly Leu Arg Ala Ala Leu Asp Leu Ile Phe  
225 230 235 240  
Glu Glu Gly Leu Glu Asn Ile Ile Ala Arg His Ala Arg Leu Gly Lys  
245 250 255  
Ala Thr Arg Leu Ala Val Glu Ala Trp Gly Leu Lys Asn Cys Thr Gln  
260 265 270  
Lys Glu Glu Trp Ile Ser Asn Thr Val Thr Ala Val Met Val Pro Pro  
275 280 285  
His Ile Asp Gly Ser Glu Ile Val Arg Arg Ala Trp Gln Arg Tyr Asn  
290 295 300  
Leu Ser Leu Gly Leu Gly Leu Asn Lys Val Ala Gly Lys Val Phe Arg  
305 310 315 320  
Ile Gly His Leu Gly Asn Val Asn Glu Leu Gln Leu Leu Gly Cys Leu  
325 330 335

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Ala Gly Val Glu Met Ile Leu Lys Asp Val Gly Tyr Pro Val Val Met  
340 345 350  
Gly Ser Gly Val Ala Ala Ala Ser Thr Tyr Leu Gln His His Ile Pro  
355 360 365  
Leu Ile Pro Ser Arg Ile  
370

(2) INFORMATION FOR SEQ ID NO:2518:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1449 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1449

(D) OTHER INFORMATION: / Ceres Seq. ID 1573572

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2518:

caaaacctcc ctcaggagct tccgccttat tcagagtgtg gaggaggatc caaaagaaaa 60  
gaggaaaaaa tggactatat gtatggacca gggagacacc atctgtttgt accaggacca 120  
gtgaacatac cggaaccggt aatccggggc atgaaccgga taccgggtca 180  
cgagccattc cggcgcttac gaaaacattg ttggaggatg ttaagaagat attcaagacc 240  
acatcaaggga cacctttttc gtttccacg accgggactg gtgcttggga gagtgccttg 300  
accaacacgt tatctcctcg agacaggatt gtttcgtttc tgattggaca atttagcctg 360  
ctctggattg accagcagaa gaggcttaat ttcaatgttg atgtggttga gagtgttGg 420  
gggacaaggt gctaattctc aagtcttggc ctcaaagctc tcacaagacg agaatcatac 480  
catcaagcgc atttgcatgt tccacaacga gaccgcgacc ggagttacca atgacatctc 540  
tgctgtccgc acactctctg atcaactaca gcatcggctt ttgctgctag tggacgggtg 600  
tcgttcattc tgcgcgcttg atttccgaat ggaatgagtg ggagtggaag tggccttgac 660  
tgggtctcag aagagccttat ctcttccaac aggaacttgg attgtctgag ccagtctctaa 720  
agctttggaa gctacaaaaa cttctaaatc tctcaaaagta ttctttgact ggaatgacta 780  
ccttaagtgt ttacaagctag gaacctattg gccatacaca ccttccattc aacttctcta 840  
cggtcttaga gctgctcttg atcttatctt tgaggaaagga cttgagaaca tcatcgcccg 900  
ccatgctcgt ttgggaaaag ccaccaggct tgcggtggaa gcatgggggc tgaaaaaactg 960  
cacacagaag gaggaaatga taagtaacac agtgacagca gttattgtgc ctccgcatat 1020  
agacgggttg gagattgtga gaagggcatg gcagaggtag aacttaagtc ttggtcttgg 1080  
tctcaacaaa tgggctggaa aggttttcag aattggacat ctaggaaatg tgaatgagtt 1140  
gcaactcttc ggggtgcttg cgaggagtga gatgatactg aaggatgttg gataccagat 1200  
tgtaatggga agtggagttg cagctgcctc tacttatctt cagcaccaca ttctctctat 1260  
tccctctaga atctaatacca tgtgttcctt ctctttcttt ctcttctctc caatgtaaac 1320  
aaactctcat gttttctctt tttctcatct atatttttac tactattctt atgtttttat 1380  
ttgctatctc caacaaactt attgaacaaa agatcaaaata tgtttattac tcactataaa 1440  
ctttgtctc

(2) INFORMATION FOR SEQ ID NO:2519:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 293 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..293

(D) OTHER INFORMATION: / Ceres Seq. ID 1573573

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2519:

Met Leu Met Trp Leu Arg Val Ile Gly Gly Gln Gly Ala Asn Leu Gln  
1 5 10 15  
Val Leu Ala Ser Lys Leu Ser Gln Asp Glu Asn His Thr Ile Lys Ala  
20 25 30  
Ile Cys Ile Val His Asn Glu Thr Ala Thr Gly Val Thr Asn Asp Ile  
35 40 45

Ser Ala Val Arg Thr Leu Leu Asp His Tyr Lys His Pro Ala Leu Leu  
50 55 60  
Leu Val Asp Gly Val Ser Ser Ile Cys Ala Leu Asp Phe Arg Met Asp  
65 70 75 80  
Glu Trp Gly Val Asp Val Ala Leu Thr Gly Ser Gln Lys Ala Leu Ser  
85 90 95  
Leu Pro Thr Gly Leu Gly Ile Val Cys Ala Ser Pro Lys Ala Leu Glu  
100 105 110  
Ala Thr Lys Thr Ser Lys Ser Leu Lys Val Phe Phe Asp Trp Asn Asp  
115 120 125  
Tyr Leu Lys Phe Tyr Lys Leu Gly Thr Tyr Trp Pro Tyr Thr Pro Ser  
130 135 140  
Ile Gln Leu Leu Tyr Gly Leu Arg Ala Ala Leu Asp Leu Ile Phe Glu  
145 150 155 160  
Glu Gly Leu Glu Asn Ile Ile Ala Arg His Ala Arg Leu Gly Lys Ala  
165 170 175  
Thr Arg Leu Ala Val Glu Ala Trp Gly Leu Lys Asn Cys Thr Gln Lys  
180 185 190  
Glu Glu Trp Ile Ser Asn Thr Val Thr Ala Val Met Val Pro Pro His  
195 200 205  
Ile Asp Gly Ser Glu Ile Val Arg Arg Ala Trp Gln Arg Tyr Asn Leu  
210 215 220  
Ser Leu Gly Leu Gly Leu Asn Lys Val Ala Gly Lys Val Phe Arg Ile  
225 230 235 240  
Gly His Leu Gly Asn Val Asn Glu Leu Gln Leu Leu Gly Cys Leu Ala  
245 250 255  
Gly Val Glu Met Ile Leu Lys Asp Val Gly Tyr Pro Val Val Met Gly  
260 265 270  
Ser Gly Val Ala Ala Ala Ser Thr Tyr Leu Gln His His Ile Pro Leu  
275 280 285  
Ile Pro Ser Arg Ile  
290

(2) INFORMATION FOR SEQ ID NO:2520:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 291 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..291
- (D) OTHER INFORMATION: / Ceres Seq. ID 1573574

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2520:

Met Trp Leu Arg Val Ile Gly Gly Gln Gly Ala Asn Leu Gln Val Leu  
1 5 10 15  
Ala Ser Lys Leu Ser Gln Asp Glu Asn His Thr Ile Lys Ala Ile Cys  
20 25 30  
Ile Val His Asn Glu Thr Ala Thr Gly Val Thr Asn Asp Ile Ser Ala  
35 40 45  
Val Arg Thr Leu Leu Asp His Tyr Lys His Pro Ala Leu Leu Leu Val  
50 55 60  
Asp Gly Val Ser Ser Ile Cys Ala Leu Asp Phe Arg Met Asp Glu Trp  
65 70 75 80  
Gly Val Asp Val Ala Leu Thr Gly Ser Gln Lys Ala Leu Ser Leu Pro  
85 90 95  
Thr Gly Leu Gly Ile Val Cys Ala Ser Pro Lys Ala Leu Glu Ala Thr  
100 105 110  
Lys Thr Ser Lys Ser Leu Lys Val Phe Phe Asp Trp Asn Asp Tyr Leu  
115 120 125  
Lys Phe Tyr Lys Leu Gly Thr Tyr Trp Pro Tyr Thr Pro Ser Ile Gln



(2) INFORMATION FOR SEQ ID NO:2522:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 581 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..581
- (D) OTHER INFORMATION: / Ceres Seq. ID 1573580

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2522:

|            |             |             |            |            |             |     |
|------------|-------------|-------------|------------|------------|-------------|-----|
| aagaattatt | gtttttggat  | cggaaaagag  | atctagaatc | accaaaaggt | tttattttat  | 60  |
| acaatgggtc | gtggaaacag  | ctgtgggtgga | ggccaaagct | cattggatta | tctctttggt  | 120 |
| ggtgacgttc | ctgctctctaa | gccagttcca  | gctctcgtc  | ccgtccctac | tgagttctaac | 180 |
| aacggacctg | caccaccagt  | aacagctgtg  | actgcaaccg | cactcaagac | tgctactact  | 240 |
| tctgttgagc | ctgcagagct  | taacaagcag  | attcctgctg | gtatcaaaac | tcctgttaac  | 300 |
| aactatgcca | gagctgaagg  | acagaacacc  | ggcaacttcc | tcactgaccg | tccttcgacc  | 360 |
| aaagttcacg | cagctccggg  | aggaggatca  | tccttggtat | atctcttcac | tggtggcgaag | 420 |
| taaaaataat | gcaaagacct  | ttaactatcc  | attgtctttg | ctgcgttatc | tcactatgaa  | 480 |
| actgtttgat | gtgagccttt  | aaatgataag  | aagtcggttt | cttgtctcaa | ctcttatctg  | 540 |
| taatatattg | ctgaaaaaAt  | gtttgaatca  | aaaccttccc | t          |             |     |

(2) INFORMATION FOR SEQ ID NO:2523:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..66
- (D) OTHER INFORMATION: / Ceres Seq. ID 1573581

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2523:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Arg | Ile | Ile | Val | Phe | Gly | Ser | Glu | Lys | Arg | Ser | Arg | Ile | Thr | Lys | Arg |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Phe | Tyr | Phe | Ile | Gln | Trp | Val | Val | Glu | Thr | Ala | Val | Val | Glu | Val | Lys |
|     |     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |
| Ala | His | Trp | Ile | Ile | Ser | Leu | Val | Val | Thr | Leu | Leu | Leu | Ser | Gln |     |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Phe | Gln | Leu | Leu | Val | Pro | Leu | Leu | Ser | Leu | Thr | Thr | Asp | Leu | His |     |
|     |     |     | 50  |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| His | Gln |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| 65  |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2524:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..119
- (D) OTHER INFORMATION: / Ceres Seq. ID 1573582

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2524:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Gly | Arg | Gly | Asn | Ser | Cys | Gly | Gly | Gly | Gln | Ser | Ser | Leu | Asp | Tyr |
| 1   |     |     |     | 5   |     |     |     |     |     | 10  |     |     |     | 15  |     |
| Leu | Phe | Gly | Gly | Asp | Ala | Pro | Ala | Pro | Lys | Pro | Val | Pro | Ala | Pro | Arg |
|     |     |     |     | 20  |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Pro | Ala | Pro | Thr | Glu | Ser | Asn | Asn | Gly | Pro | Ala | Pro | Pro | Val | Thr | Ala |

35 40 45  
Val Thr Ala Thr Ala Leu Thr Thr Thr Val Glu Pro Ala  
50 55 60  
Glu Leu Asn Lys Gln Ile Pro Ala Gly Ile Lys Thr Pro Val Asn Asn  
65 70 75  
Tyr Ala Arg Ala Glu Gly Gln Asn Thr Gly Asn Phe Leu Thr Asp Arg  
85 90 95  
Pro Ser Thr Lys Val His Ala Ala Pro Gly Gly Ser Ser Leu Asp  
100 105 110  
Tyr Leu Phe Thr Gly Gly Lys  
115

(2) INFORMATION FOR SEQ ID NO:2525:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 65 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..65

(D) OTHER INFORMATION: / Ceres Seq. ID 1573583

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2525:

Met Pro Glu Leu Lys Asp Arg Thr Pro Ala Thr Ser Ser Leu Thr Val  
1 5 10 15  
Leu Arg Pro Lys Phe Thr Gln Leu Arg Glu Glu Asp His Pro Trp Ile  
20 25 30  
Ile Ser Ser Leu Val Ala Ser Lys Ile Ile Ala Lys Thr Phe Ile Tyr  
35 40 45  
Pro Leu Ser Leu Leu Arg Tyr Leu Thr Met Lys Leu Phe Asp Val Ser  
50 55 60  
Leu  
65

(2) INFORMATION FOR SEQ ID NO:2526:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 982 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..982

(D) OTHER INFORMATION: / Ceres Seq. ID 1573584

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2526:

aatttttttt tttgacgac tttgtctctt ttctctcttt ttctctcttt ttctctcttt  
aactcgttac catcaacgct caaatcctgt atacaatctt ttctcagctg taattcttat  
aatctcgtca attatcatct attcagggtt aagctatggg atgtgctct ttctctccag  
ataggaaact tggaaacttta agtggcttta gcaattcaga gaatgctgtt ccagctgatg  
ccaaaaatct acgtgtgaag ttagtcttat taggagaact tgggtgtgtt aaaagtgtga  
ttgtctctgc atttgtacgt ggtcagtttg acgctacatc taaggtaact gttggagcct  
cgttctgttc ccaactata gcaTtgcaag actctaccac agtgaagttt gaaatatggt  
atacagcagg acaggagagg tattctgctc ttgcaccact atactaccgt ggagctggag  
ttgctgttat tgtttatgat ataacaagcc ctgaatcgtt caagaaagca cagtattggg  
ttaaggaact gcaaaagcat ggaagcccaag atattgttat ggctctggtt ggtaacaaag  
ctgatctaca tgaaaaaaga gaagtacctt ctgaggatgg aatggagctt gcagagaaga  
acggcatgtt cttcattgag acgtcagcca agacagccga taacataaat caactgtttg  
aggaaaatgg caagaggcta cctcgtcctg ctcctctgtc atgattggag tgttgaatca  
ttcatctctc agccatgtct tcagactact aatctttcca tacttttttaa tgaatttttt  
caaaacaata ttctctatc tgttaagtca agtgtgttgt ataagtgaag gatttgagtt  
tgaaactggg gatattacga acctcaaaag tggaaaccca agttatatca agcaatggat

catcagtaca tatatttagtg gg

(2) INFORMATION FOR SEQ ID NO:2527:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 202 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..202
- (D) OTHER INFORMATION: / Ceres Seq. ID 1573585

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2527:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Gly | Cys | Ala | Ser | Ser | Leu | Pro | Asp | Arg | Asn | Ser | Gly | Thr | Leu | Ser |  |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |  |
| Gly | Leu | Ser | Asn | Ser | Glu | Asn | Ala | Val | Pro | Ala | Asp | Ala | Lys | Asn | Leu |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Arg | Val | Lys | Leu | Val | Leu | Leu | Gly | Asp | Ser | Gly | Val | Gly | Lys | Ser | Cys |  |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Ile | Val | Leu | Arg | Phe | Val | Arg | Gly | Gln | Phe | Asp | Ala | Thr | Ser | Lys | Val |  |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |  |
| Thr | Val | Gly | Ala | Ser | Phe | Leu | Ser | Gln | Thr | Ile | Ala | Leu | Gln | Asp | Ser |  |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |  |
| Thr | Thr | Val | Lys | Phe | Glu | Ile | Trp | Asp | Thr | Ala | Gly | Gln | Glu | Arg | Tyr |  |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |  |
| Ser | Ala | Leu | Ala | Pro | Leu | Tyr | Tyr | Arg | Gly | Ala | Gly | Val | Ala | Val | Ile |  |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |
| Val | Tyr | Asp | Ile | Thr | Ser | Pro | Glu | Ser | Phe | Lys | Lys | Ala | Gln | Tyr | Trp |  |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |  |
| Val | Lys | Glu | Leu | Gln | Lys | His | Gly | Ser | Pro | Asp | Ile | Val | Met | Ala | Leu |  |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |  |
| Val | Gly | Asn | Lys | Ala | Asp | Leu | His | Glu | Lys | Arg | Glu | Val | Pro | Thr | Glu |  |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |     |  |
| Asp | Gly | Met | Glu | Leu | Ala | Glu | Lys | Asn | Gly | Met | Phe | Phe | Ile | Glu | Thr |  |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | 175 |     |  |
| Ser | Ala | Lys | Thr | Ala | Asp | Asn | Ile | Asn | Gln | Leu | Phe | Glu | Glu | Ile | Gly |  |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |  |
| Lys | Arg | Leu | Pro | Arg | Pro | Ala | Pro | Ser | Ser |     |     |     |     |     |     |  |
|     |     | 195 |     |     |     | 200 |     |     |     |     |     |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:2528:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 619 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..619
- (D) OTHER INFORMATION: / Ceres Seq. ID 1573586

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2528:

|             |            |            |            |             |             |     |
|-------------|------------|------------|------------|-------------|-------------|-----|
| ctctctgctgt | cgctcgtcta | caTttacact | cggagottag | accttccaat  | ctaccggcgg  | 60  |
| cgaaaatggg  | tttcaagagg | tacgttgaga | tccggagagt | agcaacttgtg | aactaccggag | 120 |
| aaagtcatgg  | aaagctcgtc | gttatcgtcg | acgttgttga | ccagaacaga  | gctttggtgg  | 180 |
| atgccctcga  | tatggagagg | atccagatga | acttoaagag | gttgtctctt  | accgatattg  | 240 |
| tcaattgacat | caacogtgtg | ccaaagaaga | aggctttgat | cgaggcaatg  | gaaaaggctg  | 300 |
| atgtgaagaa  | caagtggagg | aaaagctcat | ggggtaggaa | gcttatcgtg  | cagaaacgta  | 360 |
| gggctaaact  | taacgacttt | gatatgttca | agatcatgtt | ggccaagatc  | aagaaagctg  | 420 |
| gtgtttgcag  | gcaagagctt | gcaaaactca | agaaggagat | cactgcctca  | tcaaatatta  | 480 |
| tctacaattc  | tgttgtcttt | cttttttgat | tttgatttcg | gaaattagtg  | tttttggaac  | 540 |
| tatcaaatatc | agtatgtgtc | caattatcag | acattattca | agtttgaaac  | cttggttgca  | 600 |

aaactcaaaag tttttgtgc

(2) INFORMATION FOR SEQ ID NO:2529:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 155 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..155

(D) OTHER INFORMATION: / Ceres Seq. ID 1573587

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2529:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Ser | Ala | Val | Ala | Arg | Leu | His | Leu | His | Ser | Glu | Leu | Arg | Pro | Ser | Asn |  |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Leu | Pro | Ala | Ala | Lys | Met | Gly | Phe | Lys | Arg | Tyr | Val | Glu | Ile | Arg | Arg |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Val | Ala | Leu | Val | Asn | Tyr | Gly | Glu | Asp | His | Gly | Lys | Leu | Val | Val | Ile |  |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Val | Asp | Val | Val | Asp | Gln | Asn | Arg | Ala | Leu | Val | Asp | Ala | Pro | Asp | Met |  |
|     |     |     | 50  |     |     | 55  |     |     |     | 60  |     |     |     |     |     |  |
| Glu | Arg | Ile | Gln | Met | Asn | Phe | Lys | Arg | Leu | Ser | Leu | Thr | Asp | Ile | Val |  |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |  |
| Ile | Asp | Ile | Asn | Arg | Val | Pro | Lys | Lys | Lys | Ala | Leu | Ile | Glu | Ala | Met |  |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |  |
| Glu | Lys | Ala | Asp | Val | Lys | Asn | Lys | Trp | Glu | Lys | Ser | Ser | Trp | Gly | Arg |  |
|     |     |     | 100 |     |     |     | 105 |     |     |     |     |     | 110 |     |     |  |
| Lys | Leu | Ile | Val | Gln | Lys | Arg | Arg | Ala | Asn | Leu | Asn | Asp | Phe | Asp | Arg |  |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |  |
| Phe | Lys | Ile | Met | Leu | Ala | Lys | Ile | Lys | Lys | Ala | Gly | Val | Val | Arg | Gln |  |
|     |     |     | 130 |     |     | 135 |     |     |     |     | 140 |     |     |     |     |  |
| Glu | Leu | Ala | Lys | Leu | Lys | Lys | Glu | Ile | Thr | Ala |     |     |     |     |     |  |
| 145 |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:2530:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 134 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..134

(D) OTHER INFORMATION: / Ceres Seq. ID 1573588

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2530:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Gly | Phe | Lys | Arg | Tyr | Val | Glu | Ile | Arg | Arg | Val | Ala | Leu | Val | Asn |  |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Tyr | Gly | Glu | Asp | His | Gly | Lys | Leu | Val | Val | Ile | Val | Asp | Val | Val | Asp |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Gln | Asn | Arg | Ala | Leu | Val | Asp | Ala | Pro | Asp | Met | Glu | Arg | Ile | Gln | Met |  |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Asn | Phe | Lys | Arg | Leu | Ser | Leu | Thr | Asp | Ile | Val | Ile | Asp | Ile | Asn | Arg |  |
|     |     |     | 50  |     |     | 55  |     |     |     | 60  |     |     |     |     |     |  |
| Val | Pro | Lys | Lys | Lys | Ala | Leu | Ile | Glu | Ala | Met | Glu | Lys | Ala | Asp | Val |  |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |  |
| Lys | Asn | Lys | Trp | Glu | Lys | Ser | Ser | Trp | Gly | Arg | Lys | Leu | Ile | Val | Gln |  |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     | 95  |     |     |  |
| Lys | Arg | Arg | Ala | Asn | Leu | Asn | Asp | Phe | Asp | Arg | Phe | Lys | Ile | Met | Leu |  |
|     |     |     | 100 |     |     |     | 105 |     |     |     |     | 110 |     |     |     |  |
| Ala | Lys | Ile | Lys | Lys | Ala | Gly | Val | Val | Arg | Gln | Glu | Leu | Ala | Lys | Leu |  |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |  |

Lys Lys Glu Ile Thr Ala  
130

(2) INFORMATION FOR SEQ ID NO:2531:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 92 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..92
- (D) OTHER INFORMATION: / Ceres Seq. ID 1573589

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2531:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Glu | Arg | Ile | Gln | Met | Asn | Phe | Lys | Arg | Leu | Ser | Leu | Thr | Asp | Ile |
| 1   |     |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |
| Val | Ile | Asp | Ile | Asn | Arg | Val | Pro | Lys | Lys | Lys | Ala | Leu | Ile | Glu | Ala |
|     |     |     | 20  |     |     |     | 25  |     |     |     |     | 30  |     |     |     |
| Met | Glu | Lys | Ala | Asp | Val | Lys | Asn | Lys | Trp | Glu | Lys | Ser | Ser | Trp | Gly |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Arg | Lys | Leu | Ile | Val | Gln | Lys | Arg | Arg | Ala | Asn | Leu | Asn | Asp | Phe | Asp |
|     |     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |
| Arg | Phe | Lys | Ile | Met | Leu | Ala | Lys | Ile | Lys | Lys | Ala | Gly | Val | Val | Arg |
|     |     |     | 65  |     |     |     | 70  |     |     |     | 75  |     |     | 80  |     |
| Gln | Glu | Leu | Ala | Lys | Leu | Lys | Lys | Glu | Ile | Thr | Ala |     |     |     |     |
|     |     |     |     |     | 85  |     |     |     | 90  |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2532:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 748 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..748
- (D) OTHER INFORMATION: / Ceres Seq. ID 1573606

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2532:

|             |             |            |            |            |             |     |
|-------------|-------------|------------|------------|------------|-------------|-----|
| ccttctcact  | tcaaattcat  | aatctctcta | cttctctctc | tctctaaaat | caaaaatggc  | 60  |
| gaaactcgtg  | atgtgtgttg  | ttctttgtat | cttaccggcg | ataGccatgg | cggcaaggag  | 120 |
| gagtaataat  | ggaaagaata  | caatggtggt | tcaaggtagc | acttaactgt | acatttgcga  | 180 |
| attcggcttc  | gagactcctg  | aatcctccta | cttcatcccc | ggtgcaacgg | tgaagctatc  | 240 |
| atgcaaaagc  | aggaagacaa  | tggaagaggt | ttacacagac | aaagctgtat | cggacaaaaga | 300 |
| aggaagatat  | aagttcattg  | tccacgacga | tcacagagac | cagatgtgcg | atgttttgct  | 360 |
| tgtgaaaagc  | tccgataaaa  | cctgctctaa | aatctccgtt | ggacgtgaga | agctctogtt  | 420 |
| gatcttgaac  | cattacagtg  | gcattgcctc | gcagatcaga | catgctaaca | acatgggatt  | 480 |
| cgagaaagaa  | gtgagtgatg  | tgtttctgct | tgctttgttt | cagaagtata | tggttgatga  | 540 |
| agatgaggat  | gatatttaaaa | accatctcta | atctctctgt | ttaattattt | gatctgctgt  | 600 |
| ttcttctcatt | aatgagtttc  | gagttatgga | agagatatat | ttgtattttg | ttgattactt  | 660 |
| atttgtgtgc  | tttagagatg  | ttgactctgg | tgactcgata | actatctggt | tgtgtaaagct | 720 |
| tcttatatat  | tgatgtgtca  | ttctcttg   |            |            |             |     |

(2) INFORMATION FOR SEQ ID NO:2533:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 171 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..171



(D) OTHER INFORMATION: / Ceres Seq. ID 1573607

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2533:

```
Met Ala Lys Leu Val Met Leu Leu Val Leu Cys Ile Leu Pro Ala Ile
1 5 10 15
Ala Met Ala Ala Arg Arg Ser Asn Ile Gly Lys Asn Thr Met Val Val
20 25 30
Gln Gly Ser Thr Tyr Cys Asp Ile Cys Lys Phe Gly Phe Glu Thr Pro
35 40 45
Glu Ser Ser Tyr Phe Ile Pro Gly Ala Thr Val Lys Leu Ser Cys Lys
50 55 60
Asp Arg Lys Thr Met Glu Glu Val Tyr Thr Asp Lys Ala Val Ser Asp
65 70 75 80
Lys Glu Gly Lys Tyr Lys Phe Ile Val His Asp Asp His Arg Asp Gln
85 90 95
Met Cys Asp Val Leu Leu Val Lys Ser Ser Asp Lys Thr Cys Ser Lys
100 105 110
Ile Ser Val Gly Arg Glu Lys Ser Arg Val Ile Leu Asn His Tyr Ser
115 120 125
Gly Ile Ala Ser Gln Ile Arg His Ala Asn Asn Met Gly Phe Glu Lys
130 135 140
Glu Val Ser Asp Val Phe Cys Ser Ala Leu Phe Gln Lys Tyr Met Val
145 150 155 160
Asp Glu Asp Glu Asp Asp Ile Lys Asn His Leu
165 170
```

(2) INFORMATION FOR SEQ ID NO:2534:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 166 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..166

(D) OTHER INFORMATION: / Ceres Seq. ID 1573608

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2534:

```
Met Leu Leu Val Leu Cys Ile Leu Pro Ala Ile Ala Met Ala Ala Arg
1 5 10 15
Arg Ser Asn Ile Gly Lys Asn Thr Met Val Val Gln Gly Ser Thr Tyr
20 25 30
Cys Asp Ile Cys Lys Phe Gly Phe Glu Thr Pro Glu Ser Ser Tyr Phe
35 40 45
Ile Pro Gly Ala Thr Val Lys Leu Ser Cys Lys Asp Arg Lys Thr Met
50 55 60
Glu Glu Val Tyr Thr Asp Lys Ala Val Ser Asp Lys Glu Gly Lys Tyr
65 70 75 80
Lys Phe Ile Val His Asp Asp His Arg Asp Gln Met Cys Asp Val Leu
85 90 95
Leu Val Lys Ser Ser Asp Lys Thr Cys Ser Lys Ile Ser Val Gly Arg
100 105 110
Glu Lys Ser Arg Val Ile Leu Asn His Tyr Ser Gly Ile Ala Ser Gln
115 120 125
Ile Arg His Ala Asn Asn Met Gly Phe Glu Lys Glu Val Ser Asp Val
130 135 140
Phe Cys Ser Ala Leu Phe Gln Lys Tyr Met Val Asp Glu Asp Glu Asp
145 150 155 160
Asp Ile Lys Asn His Leu
165
```

(2) INFORMATION FOR SEQ ID NO:2535:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 154 amino acids

(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..154  
(D) OTHER INFORMATION: / Ceres Seq. ID 1573609  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2535:  
Met Ala Ala Arg Arg Ser Asn Ile Gly Lys Asn Thr Met Val Val Gln  
1 5 10 15  
Gly Ser Thr Tyr Cys Asp Ile Cys Lys Phe Gly Phe Glu Thr Pro Glu  
20 25 30  
Ser Ser Tyr Phe Ile Pro Gly Ala Thr Val Lys Leu Ser Cys Lys Asp  
35 40 45  
Arg Lys Thr Met Glu Glu Val Tyr Thr Asp Lys Ala Val Ser Asp Lys  
50 55 60  
Glu Gly Lys Tyr Lys Phe Ile Val His Asp Asp His Arg Asp Gln Met  
65 70 75 80  
Cys Asp Val Leu Leu Val Lys Ser Ser Asp Lys Thr Cys Ser Lys Ile  
85 90 95  
Ser Val Gly Arg Glu Lys Ser Arg Val Ile Leu Asn His Tyr Ser Gly  
100 105 110  
Ile Ala Ser Gln Ile Arg His Ala Asn Asn Met Gly Phe Glu Lys Glu  
115 120 125  
Val Ser Asp Val Phe Cys Ser Ala Leu Phe Gln Lys Tyr Met Val Asp  
130 135 140  
Glu Asp Glu Asp Asp Ile Lys Asn His Leu  
145 150

(2) INFORMATION FOR SEQ ID NO:2536:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1707 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..1707  
(D) OTHER INFORMATION: / Ceres Seq. ID 1573624

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2536:

|             |             |                |             |             |            |      |
|-------------|-------------|----------------|-------------|-------------|------------|------|
| atacacacaa  | ttcaatat    | ttt gacttcacat | agagagagat  | agagagatgg  | cgacggaaac | 60   |
| ggaagtgtga  | gtctccgttaa | cggtaagcaa     | cggcggaagc  | aaaggatgtt  | gcaagtacgg | 120  |
| gtgtcctggg  | tacgcgactc  | ctctcgccgc     | tatgtctgtt  | ccatcgagga  | aacttatcta | 180  |
| cgtaaccgcc  | gtctacacccg | gaactggaa      | agataaaccc  | gattatttgg  | cgacggtgga | 240  |
| tgtagatcca  | agctcgccct  | cgtattcaag     | tggtattcat  | agattaccaa  | tgccctttgt | 300  |
| tggtgatgag  | cttcatcatt  | ctgggtggaa     | ctctttagat  | tcttgccatg  | gtgatgtctc | 360  |
| tggtgataga  | cgtttatctc  | tggtaccgtc     | tcttatatct  | ggtcgattt   | atgccgatga | 420  |
| tactaaggaa  | aacccgaggg  | ctccgtcttt     | gtataagtat  | gttgatccta  | aagagattgc | 480  |
| tgataagMac  | tggtattggcg | tttctcaca      | cggctcattg  | cctcgccacg  | ggcgagatct | 540  |
| tggtgtctcg  | tcttgagagt  | gaagagggga     | atgctaaggg  | gaatgggttt  | cttcttsttg | 600  |
| actctgattt  | taacatcaag  | aataggtggg     | agaaaaccag  | acatagtcc   | ttgatgggt  | 660  |
| atgatgttct  | agatgttttt  | ggtaccaacc     | tcggcaccaag | accatgatca  | gcacatcttg | 720  |
| gggagcacct  | aaagcctctc  | ctaaagggtt     | caatcttca   | cacgttgctg  | atggcttgta | 780  |
| tggaagtcat  | ctacatgttt  | atagttggcc     | aggaggtgaa  | atgaaacaat  | taattgacct | 840  |
| tggaaccgact | ggtctcttcc  | ctttggagat     | tagatttctg  | catgatccat  | ctaaagatac | 900  |
| agggtttgtt  | gggagtgcct  | gtctgagtaa     | tatgataaga  | tttttcaaga  | acagtgtatg | 960  |
| aacatggagc  | catgaggttg  | ttatatcggt     | taaaccgttg  | aaagtgcgaa  | actgggatac | 1020 |
| tcacgaaatg  | ccgggggttaa | tcacccgactt    | cttgatctcc  | ctcgatgacc  | gatttatta  | 1080 |
| ctttgtgaac  | tggtccatg   | gagacattcg     | tcagtacaac  | atagaggacc  | ctaaaaaccc | 1140 |
| tgtaattaaca | gggcaaat    | gggttggagg     | attactacaa  | aaggggcagtc | ctgttaaggc | 1200 |

ggtgtggagaa gacggaacaa ctttccagtt cgaggttctt cagatcaagg ggaatctttt 1260  
acgaggttga cctcaaatga ttcagctgag cctcgatggg aaacgattgt atgcaacaaa 1320  
ctcgcgtttt agcgcatggg atcgtcagtt ttatcctgaa atcatggaga aaggctcaca 1380  
cataattcag attgatgttg atacagaaaa aggtggtctc accataaacc ctgattttctt 1440  
tgtggacttt ggtgatgaac cagacggtcc ttactagccc caccagatga gatattccagg 1500  
tggagactgc acttccgata tctggatttg aatttggctt tgttttagagt gtgttttgtg 1560  
ttaagttaa attgagtttt attattttgt tgtgttttag taCgagttga ataaaaaagg 1620  
gagtaagatg actcagacaa ttaacacttg ttgtacatt ttgactccta tgtgtcttaa 1680  
gtaataaac ttttacaat tcgactg

(2) INFORMATION FOR SEQ ID NO:2537:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 275 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..275
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1573625
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2537:

Met Ile Ser Thr Ser Trp Gly Ala Pro Lys Ala Phe Ser Lys Gly Phe  
1 5 10 15  
Asn Leu Gln His Val Ala Asp Gly Leu Tyr Gly Ser His Leu His Val  
20 25 30  
Tyr Ser Trp Pro Gly Gly Glu Met Lys Gln Leu Ile Asp Leu Gly Pro  
35 40 45  
Thr Gly Leu Leu Pro Leu Glu Ile Arg Phe Leu His Asp Pro Ser Lys  
50 55 60  
Asp Thr Gly Phe Val Gly Ser Ala Leu Ser Ser Asn Met Ile Arg Phe  
65 70 75 80  
Phe Lys Asn Ser Asp Glu Thr Trp Ser His Glu Val Val Ile Ser Val  
85 90 95  
Lys Pro Leu Lys Val Glu Asn Trp Ile Leu Pro Glu Met Pro Gly Leu  
100 105 110  
Ile Thr Asp Phe Leu Ile Ser Leu Asp Asp Arg Phe Ile Tyr Phe Val  
115 120 125  
Asn Trp Leu His Gly Asp Ile Arg Gln Tyr Asn Ile Glu Asp Pro Lys  
130 135 140  
Asn Pro Val Leu Thr Gly Gln Ile Trp Val Gly Gly Leu Leu Gln Lys  
145 150 155 160  
Gly Ser Pro Val Lys Ala Val Gly Glu Asp Gly Asn Thr Phe Gln Phe  
165 170 175  
Glu Val Pro Gln Ile Lys Gly Lys Ser Leu Arg Gly Gly Pro Gln Met  
180 185 190  
Ile Gln Leu Ser Leu Asp Gly Lys Arg Leu Tyr Ala Thr Asn Ser Leu  
195 200 205  
Phe Ser Ala Trp Asp Arg Gln Phe Tyr Pro Glu Ile Met Glu Lys Gly  
210 215 220  
Ser His Ile Ile Gln Ile Asp Val Asp Thr Glu Lys Gly Gly Leu Thr  
225 230 235 240  
Ile Asn Pro Asp Phe Phe Val Asp Phe Gly Asp Glu Pro Asp Gly Pro  
245 250 255  
Ser Leu Ala His Glu Met Arg Tyr Pro Gly Gly Asp Cys Thr Ser Asp  
260 265 270  
Ile Trp Ile  
275

(2) INFORMATION FOR SEQ ID NO:2538:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 236 amino acids
- (B) TYPE: amino acid

SEQUENCE 1573625

- (C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..236  
(D) OTHER INFORMATION: / Ceres Seq. ID 1573626

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2538:

Met Lys Gln Leu Ile Asp Leu Gly Pro Thr Gly Leu Leu Pro Leu Glu  
1 5 10 15  
Ile Arg Phe Leu His Asp Pro Ser Lys Asp Thr Gly Phe Val Gly Ser  
20 25 30  
Ala Leu Ser Ser Asn Met Ile Arg Phe Phe Lys Asn Ser Asp Glu Thr  
35 40 45  
Trp Ser His Glu Val Val Ile Ser Val Lys Pro Leu Lys Val Glu Asn  
50 55 60  
Trp Ile Leu Pro Glu Met Pro Gly Leu Ile Thr Asp Phe Leu Ile Ser  
65 70 75 80  
Leu Asp Asp Arg Phe Ile Tyr Phe Val Asn Trp Leu His Gly Asp Ile  
85 90 95  
Arg Gln Tyr Asn Ile Glu Asp Pro Lys Asn Pro Val Leu Thr Gly Gln  
100 105 110  
Ile Trp Val Gly Gly Leu Leu Gln Lys Gly Ser Pro Val Lys Ala Val  
115 120 125  
Gly Glu Asp Gly Asn Thr Phe Gln Phe Glu Val Pro Gln Ile Lys Gly  
130 135 140  
Lys Ser Leu Arg Gly Gly Pro Gln Met Ile Gln Leu Ser Leu Asp Gly  
145 150 155 160  
Lys Arg Leu Tyr Ala Thr Asn Ser Leu Phe Ser Ala Trp Asp Arg Gln  
165 170 175  
Phe Tyr Pro Glu Ile Met Glu Lys Gly Ser His Ile Ile Gln Ile Asp  
180 185 190  
Val Asp Thr Glu Lys Gly Gly Leu Thr Ile Asn Pro Asp Phe Phe Val  
195 200 205  
Asp Phe Gly Asp Glu Pro Asp Gly Pro Ser Leu Ala His Glu Met Arg  
210 215 220  
Tyr Pro Gly Gly Asp Cys Thr Ser Asp Ile Trp Ile  
225 230 235

(2) INFORMATION FOR SEQ ID NO:2539:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 199 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..199  
(D) OTHER INFORMATION: / Ceres Seq. ID 1573627

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2539:

Met Ile Arg Phe Phe Lys Asn Ser Asp Glu Thr Trp Ser His Glu Val  
1 5 10 15  
Val Ile Ser Val Lys Pro Leu Lys Val Glu Asn Trp Ile Leu Pro Glu  
20 25 30  
Met Pro Gly Leu Ile Thr Asp Phe Leu Ile Ser Leu Asp Asp Arg Phe  
35 40 45  
Ile Tyr Phe Val Asn Trp Leu His Gly Asp Ile Arg Gln Tyr Asn Ile  
50 55 60  
Glu Asp Pro Lys Asn Pro Val Leu Thr Gly Gln Ile Trp Val Gly Gly  
65 70 75 80  
Leu Leu Gln Lys Gly Ser Pro Val Lys Ala Val Gly Glu Asp Gly Asn

85 90 95  
Thr Phe Gln Phe Glu Val Pro Gln Ile Lys Gly Lys Ser Leu Arg Gly  
100 105 110  
Gly Pro Gln Met Ile Gln Leu Ser Leu Asp Gly Lys Arg Leu Tyr Ala  
115 120 125  
Thr Asn Ser Leu Phe Ser Ala Trp Asp Arg Gln Phe Tyr Pro Glu Ile  
130 135 140  
Met Glu Lys Gly Ser His Ile Ile Gln Ile Asp Val Asp Thr Glu Lys  
145 150 155 160  
Gly Gly Leu Thr Ile Asn Pro Asp Phe Phe Val Asp Phe Gly Asp Glu  
165 170 175  
Pro Asp Gly Pro Ser Leu Ala His Glu Met Arg Tyr Pro Gly Gly Asp  
180 185 190  
Cys Thr Ser Asp Ile Trp Ile  
195

(2) INFORMATION FOR SEQ ID NO:2540:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 777 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..777

(D) OTHER INFORMATION: / Ceres Seq. ID 1573628

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2540:

|            |             |            |             |            |             |     |
|------------|-------------|------------|-------------|------------|-------------|-----|
| atcttcacaa | ttttttttcg  | tctctcaaac | caacgcaaaa  | gaacaatgtc | taacgttgtta | 60  |
| gtaatcgccg | ttgtttctcat | cgtagcatcg | ctaacaggac  | atgtgtcagc | acaaatggat  | 120 |
| atgtctccgt | cgtcaggacc  | atcggttgca | ccagactgca  | tgcggaacct | aatgaacatg  | 180 |
| acaggctgtc | tctgtacgt   | tacggtcgga | gaaggtggtg  | gtgcgccaac | gccggacaag  | 240 |
| acgtgtgtgc | cggcgctaGc  | ggggctagtg | gagagctcgc  | cgcaatgctt | atgttacctc  | 300 |
| ctctccgggt | acatggccgc  | gaaacttggg | atcaagattg  | ataaggcaaa | ggctctcaaa  | 360 |
| cttcccgga  | tttgcggcgt  | gatcactccc | gatccctcac  | tttgtctct  | ttttggaatt  | 420 |
| cctgttgga  | caacctgtagc | tatgggagac | gaggagacct  | ccccagccta | tgctccaggt  | 480 |
| tcgatgtcag | aatcaccagg  | aggatttggg | tcgggtCctt  | cggttagtag | aggagcgat   | 540 |
| gcaccaagca | gtgcacctta  | ttctcgtttt | ctcaactctta | taattttccc | attagctttt  | 600 |
| gcattttaca | tctttttgct  | atttcattct | cttccaacca  | ttacaacac  | cattatttgt  | 660 |
| tatgtatttt | cttaaaagag  | tattattgct | ttgttaggtc  | atgttcttga | atttattact  | 720 |
| ttgtgtatcc | acggattatt  | tcttcattca | tcttattgaa  | taaagattgt | ttttttt     |     |

(2) INFORMATION FOR SEQ ID NO:2541:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 206 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..206

(D) OTHER INFORMATION: / Ceres Seq. ID 1573629

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2541:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ile | Phe | Thr | Ile | Phe | Phe | Arg | Leu | Ser | Asn | Gln | Arg | Lys | Arg | Thr | Met |
| 1   |     |     | 5   |     |     |     | 10  |     |     |     | 15  |     |     |     |     |
| Ser | Asn | Val | Val | Val | Ile | Ala | Val | Val | Leu | Ile | Val | Ala | Ser | Leu | Thr |
|     |     |     | 20  |     |     |     | 25  |     |     |     | 30  |     |     |     |     |
| Gly | His | Val | Ser | Ala | Gln | Met | Asp | Met | Ser | Pro | Ser | Ser | Gly | Pro | Ser |
|     |     |     | 35  |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| Gly | Ala | Pro | Asp | Cys | Met | Ala | Asn | Leu | Met | Asn | Met | Thr | Gly | Cys | Leu |
|     |     |     | 50  |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ser | Tyr | Val | Thr | Val | Gly | Glu | Gly | Gly | Ala | Ala | Lys | Pro | Asp | Lys |     |

(2) INFORMATION FOR SEQ ID NO:2542:

(A) LENGTH: 191 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ix) FEATURE:

- ```
(A) NAME/KEY: peptide
(B) LOCATION: 1..191
```

(D) OTHER INFORMATION: / Ceres Seq. ID 1573630

Met	Ser	Asn	Val	Val	Val	Ile	Ala	Val	Val	Leu	Ile	Val	Ala	Ser	Leu
1			5					10						15	
Thr	Gly	His	Val	Ser	Ala	Gln	Met	Asp	Met	Ser	Pro	Ser	Ser	Gly	Pro
			20					25					30		
Ser	Gly	Ala	Pro	Asp	Cys	Met	Ala	Asn	Leu	Met	Asn	Met	Thr	Gly	Cys
		35					40				45				
Leu	Ser	Tyr	Val	Thr	Val	Gly	Glu	Gly	Gly	Gly	Ala	Ala	Lys	Pro	Asp
		50				55					60				
Lys	Thr	Cys	Cys	Pro	Ala	Leu	Ala	Gly	Leu	Val	Glu	Ser	Ser	Pro	Gln
65					70					75				80	
Cys	Leu	Cys	Tyr	Leu	Leu	Ser	Gly	Asp	Met	Ala	Ala	Gln	Leu	Gly	Ile
				85					90					95	
Lys	Ile	Asp	Lys	Ala	Lys	Ala	Leu	Lys	Leu	Pro	Gly	Val	Cys	Gly	Val
		100						105					110		
Ile	Thr	Pro	Asp	Pro	Ser	Leu	Cys	Ser	Leu	Phe	Gly	Ile	Pro	Val	Gly
		115					120					125			
Ala	Pro	Val	Ala	Met	Gly	Asp	Glu	Gly	Ala	Ser	Pro	Ala	Tyr	Ala	Pro
		130					135					140			
Gly	Ser	Met	Ser	Glu	Ser	Pro	Gly	Gly	Phe	Gly	Ser	Gly	Pro	Ser	Ala
145					150					155				160	
Ser	Arg	Gly	Ser	Asp	Ala	Pro	Ser	Ser	Ala	Pro	Tyr	Ser	Arg	Phe	Leu
				165					170					175	
Asn	Leu	Ile	Ile	Phe	Pro	Leu	Ala	Phe	Ala	Phe	Tyr	Ile	Phe	Cys	
			180					185					190		

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 168 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

```
(ix) FEATURE:
```

- (A) NAME/KEY: peptide
(B) LOCATION: 1..168
(D) OTHER INFORMATION: / Ceres Seq. ID 1573631

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2543:

Met	Asp	Met	Ser	Pro	Ser	Ser	Gly	Pro	Ser	Gly	Ala	Pro	Asp	Cys	Met	
1				5				10						15		
Ala	Asn	Leu	Met	Asn	Met	Thr	Gly	Cys	Leu	Ser	Tyr	Val	Thr	Val	Gly	
			20				25						30			
Glu	Gly	Gly	Gly	Ala	Ala	Lys	Pro	Asp	Lys	Thr	Cys	Cys	Pro	Ala	Leu	
			35				40					45				
Ala	Gly	Leu	Val	Glu	Ser	Ser	Pro	Gln	Cys	Leu	Cys	Tyr	Leu	Leu	Ser	
			50			55					60					
Gly	Asp	Met	Ala	Ala	Gln	Leu	Gly	Ile	Lys	Ile	Asp	Lys	Ala	Lys	Ala	
			65			70				75				80		
Leu	Lys	Leu	Pro	Gly	Val	Cys	Gly	Val	Ile	Thr	Pro	Asp	Pro	Ser	Leu	
				85					90					95		
Cys	Ser	Leu	Phe	Gly	Ile	Pro	Val	Gly	Ala	Pro	Val	Ala	Met	Gly	Asp	
			100					105					110			
Glu	Gly	Ala	Ser	Pro	Ala	Tyr	Ala	Pro	Gly	Ser	Met	Ser	Glu	Ser	Pro	
			115				120					125				
Gly	Gly	Phe	Gly	Ser	Gly	Pro	Ser	Ala	Ser	Arg	Gly	Ser	Asp	Ala	Pro	
			130				135				140					
Ser	Ser	Ala	Pro	Tyr	Ser	Arg	Phe	Leu	Asn	Leu	Ile	Ile	Phe	Pro	Leu	
				150						155					160	
Ala	Phe	Ala	Phe	Tyr	Ile	Phe	Cys									
				165												

(2) INFORMATION FOR SEQ ID NO:2544:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 788 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..788
(D) OTHER INFORMATION: / Ceres Seq. ID 1573632

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2544:

atttatcttc	aCaatttttG	tttcgtctct	caaaccaacg	caaaagaaca	atgtctaacg	60
ttgtagtaat	cgccgttgtt	ctcatcgtag	catcgctaac	aggacatgtg	tcagacacaaa	120
tggatattgc	tcgcgtgtca	ggaccatcgg	gtgcaccaga	ctgcgtggcg	aacctaatga	180
acatgacagg	ctgtctctcg	tacgttaacg	tcggagaagg	tggtggtgcG	gcgaagccgg	240
acaagacgtg	ttgtccggcg	ctaGcggggc	tagtgagag	ctgcgcgcaa	tgcttatggt	300
acctctcttc	cggtgacatg	gcggcacaac	ttggaaatcaa	gattgataag	gcaaaggctc	360
tcaaacitcc	cggaagtttg	ggcgtgatca	cttcogatcc	ttcactttgt	tccttttttg	420
gaattctcgt	tggagcacct	gtagctatgg	gagacgaggg	agcctcccca	gcctatgctc	480
cagggttcgat	gtcagggtgca	gaatcaccag	gaggatttgg	gtcgggtCct	tcggctaagta	540
gagggagcga	tgcaaccaagc	agtgcacctt	attctcgttt	tctcaattct	ataattttcc	600
cattagcttt	tgcattttac	atcttttgct	gattttcatc	tcttccaacc	attaaacaac	660
ccattatttg	ttatgtattt	tcttaaaaga	gtattattgc	ttttgtaggc	tatgtctctg	720
aattttattc	tttgtgtatc	cacggattat	ttcttcattc	atcttatgta	ataaagattg	780
tttttttc						

(2) INFORMATION FOR SEQ ID NO:2545:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 209 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide

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(B) LOCATION: 1..209

(D) OTHER INFORMATION: / Ceres Seq. ID 1573633

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2545:

Leu Ser Ser Gln Phe Leu Phe Arg Leu Ser Asn Gln Arg Lys Arg Thr
1 5 10 15
Met Ser Asn Val Val Val Ile Ala Val Val Leu Ile Val Ala Ser Leu
20 25 30
Thr Gly His Val Ser Ala Gln Met Asp Met Ser Pro Ser Ser Gly Pro
35 40 45
Ser Gly Ala Pro Asp Cys Met Ala Asn Leu Met Asn Met Thr Gly Cys
50 55 60
Leu Ser Tyr Val Thr Val Gly Glu Gly Gly Gly Ala Ala Lys Pro Asp
65 70 75 80
Lys Thr Cys Cys Pro Ala Leu Ala Gly Leu Val Glu Ser Ser Pro Gln
85 90 95
Cys Leu Cys Tyr Leu Leu Ser Gly Asp Met Ala Ala Gln Leu Gly Ile
100 105 110
Lys Ile Asp Lys Ala Lys Ala Leu Lys Leu Pro Gly Val Cys Gly Val
115 120 125
Ile Thr Ser Asp Pro Ser Leu Cys Ser Leu Phe Gly Ile Pro Val Gly
130 135 140
Ala Pro Val Ala Met Gly Asp Glu Gly Ala Ser Pro Ala Tyr Ala Pro
145 150 155 160
Gly Ser Met Ser Gly Ala Glu Ser Pro Gly Gly Phe Gly Ser Gly Pro
165 170 175
Ser Ala Ser Arg Gly Ser Asp Ala Pro Ser Ser Ala Pro Tyr Ser Arg
180 185 190
Phe Leu Asn Leu Ile Ile Phe Pro Leu Ala Phe Ala Phe Tyr Ile Phe
195 200 205
Cys

(2) INFORMATION FOR SEQ ID NO:2546:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 193 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..193

(D) OTHER INFORMATION: / Ceres Seq. ID 1573634

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2546:

Met Ser Asn Val Val Val Ile Ala Val Val Leu Ile Val Ala Ser Leu
1 5 10 15
Thr Gly His Val Ser Ala Gln Met Asp Met Ser Pro Ser Ser Gly Pro
20 25 30
Ser Gly Ala Pro Asp Cys Met Ala Asn Leu Met Asn Met Thr Gly Cys
35 40 45
Leu Ser Tyr Val Thr Val Gly Glu Gly Gly Gly Ala Ala Lys Pro Asp
50 55 60
Lys Thr Cys Cys Pro Ala Leu Ala Gly Leu Val Glu Ser Ser Pro Gln
65 70 75 80
Cys Leu Cys Tyr Leu Leu Ser Gly Asp Met Ala Ala Gln Leu Gly Ile
85 90 95
Lys Ile Asp Lys Ala Lys Ala Leu Lys Leu Pro Gly Val Cys Gly Val
100 105 110
Ile Thr Ser Asp Pro Ser Leu Cys Ser Leu Phe Gly Ile Pro Val Gly
115 120 125
Ala Pro Val Ala Met Gly Asp Glu Gly Ala Ser Pro Ala Tyr Ala Pro
130 135 140

Gly Ser Met Ser Gly Ala Glu Ser Pro Gly Gly Phe Gly Ser Gly Pro
145 150 155 160
Ser Ala Ser Arg Gly Ser Asp Ala Pro Ser Ser Ala Pro Tyr Ser Arg
165 170 175
Phe Leu Asn Leu Ile Ile Phe Pro Leu Ala Phe Ala Phe Tyr Ile Phe
180 185 190

Cys

(2) INFORMATION FOR SEQ ID NO:2547:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 170 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..170

(D) OTHER INFORMATION: / Ceres Seq. ID 1573635

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2547:

Met Asp Met Ser Pro Ser Ser Gly Pro Ser Gly Ala Pro Asp Cys Met
1 5 10 15
Ala Asn Leu Met Asn Met Thr Gly Cys Leu Ser Tyr Val Thr Val Gly
20 25 30
Glu Gly Gly Gly Ala Ala Lys Pro Asp Lys Thr Cys Cys Pro Ala Leu
35 40 45
Ala Gly Leu Val Glu Ser Ser Pro Gln Cys Leu Cys Tyr Leu Leu Ser
50 55 60
Gly Asp Met Ala Ala Gln Leu Gly Ile Lys Ile Asp Lys Ala Lys Ala
65 70 75 80
Leu Lys Leu Pro Gly Val Cys Gly Val Ile Thr Ser Asp Pro Ser Leu
85 90 95
Cys Ser Leu Phe Gly Ile Pro Val Gly Ala Pro Val Ala Met Gly Asp
100 105 110
Glu Gly Ala Ser Pro Ala Tyr Ala Pro Gly Ser Met Ser Gly Ala Glu
115 120 125
Ser Pro Gly Gly Phe Gly Ser Gly Pro Ser Ala Ser Arg Gly Ser Asp
130 135 140
Ala Pro Ser Ser Ala Pro Tyr Ser Arg Phe Leu Asn Leu Ile Ile Phe
145 150 155 160
Pro Leu Ala Phe Ala Phe Tyr Ile Phe Cys
165 170

(2) INFORMATION FOR SEQ ID NO:2548:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1403 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1403

(D) OTHER INFORMATION: / Ceres Seq. ID 1573636

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2548:

aaaaatTTTTT aaaggGcaag acctcctctg ttccatatt ctcaccacag aagaactctt 60
gaggctttct ctttctctca coattggcgaa accggtgtgc attgaagtgt ataattctaa 120
tgggaaatcac agagttgtta gcacaaaacc gatgcctgga actcgctgga tcaatctctt 180
ggtagaccocaa ggttgtctcg ttgagatatg tcatttgaag aagacaatct tgctctgtaga 240
agatatcatt gatctgatcg gagacaagtg tgatggagtc atcggtcagt tgacggaaga 300
ttggggagag acctctgtct cagctttgag caaagctgga gggaaagctt tcaagtaacct 360
ggccgttgtt tataacaacg ttgatgttga agctgccaat aagtatggaa ttgctgtcgg 420

taaacactccg	ggagtggtga	ctgagacgac	ggctgaacta	gctgcttctc	ttctcttggc	480
tgctgcgaaga	agaattgttg	aagccgacga	attcatgaga	ggtgctgtgt	acgagggatg	540
gcttctctcat	ctgtttgttg	ggaacttact	taaaaggacag	actgttgagc	ttattggagc	600
tggaacgtatt	ggactctgctt	atgctagaa	gatggtggaa	gggttcaaga	tgaatttgat	660
ctactttgat	ctttaccaat	ccactctgct	tgagaaatct	gtgacagctt	atggacagtt	720
cttgaaaaga	aatggagaa	aaactgtgac	atggaaaacga	gcttctgtcca	tgaggagggt	780
gctgcgtgag	gctgatctga	taagtcttca	cccggtgctg	gacaaaacca	cttaccatct	840
tgtaacaacag	gagaggcttg	ccatgatgaa	aaaggaaagca	atccttgtga	actgcagcag	900
aggtcctgtg	atcgatgagg	cagcttttgt	cgaacatctc	aaagagaacc	cgatgttccg	960
agttgtctc	gatgtgttgc	aggaagagcc	attcatgaaa	ccagggtctg	ctgatatgaa	1020
aaacgctatt	gttgttcttc	acattgcttc	tgcttccaag	tggactctgt	aaggaatggc	1080
tNacgcttgc	agctctcaac	gttctcgaa	gagtcacaag	gtacccgatt	tggcatgacc	1140
cgaaaccgagt	cgaatccatt	ttgaacgaaa	acgcttcacc	gcccactgcc	agtcacaaga	1200
tcgtcaactc	aaagggcctta	ggattgcctg	tttcgaagct	atgagttaa	tatgaagaag	1260
gggagatttg	gaagaatcct	tttagtgaa	atatgatggt	gtcaaagttg	gtttatgtat	1320
tgtatatgaa	acaaccatgt	tggatcatat	aatcactcc	tttaaagtgt	tacattgttg	1380
atgagtctat	tagacgatta	ccc				

(2) INFORMATION FOR SEQ ID NO:2549:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 378 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..378

(D) OTHER INFORMATION: / Ceres Seq. ID 1573637

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2549:

Lys	Phe	Phe	Lys	Arg	Gln	Asp	Leu	Leu	Cys	Phe	His	Ile	Leu	Thr	Thr
1			5					10						15	
Glu	Glu	Leu	Leu	Arg	Leu	Ser	Leu	Phe	Ser	Thr	Met	Ala	Lys	Pro	Val
			20					25					30		
Ser	Ile	Glu	Val	Tyr	Asn	Pro	Asn	Gly	Lys	Tyr	Arg	Val	Val	Ser	Thr
			35				40					45			
Lys	Pro	Met	Pro	Gly	Thr	Arg	Trp	Ile	Asn	Leu	Leu	Val	Asp	Gln	Gly
			50				55					60			
Cys	Arg	Val	Glu	Ile	Cys	His	Leu	Lys	Lys	Thr	Ile	Leu	Ser	Val	Glu
65					70					75				80	
Asp	Ile	Ile	Asp	Leu	Ile	Gly	Asp	Lys	Cys	Asp	Gly	Val	Ile	Gly	Gln
			85						90					95	
Leu	Thr	Glu	Asp	Trp	Gly	Glu	Thr	Leu	Phe	Ser	Ala	Leu	Ser	Lys	Ala
			100					105					110		
Gly	Gly	Lys	Ala	Phe	Ser	Asn	Met	Ala	Val	Gly	Tyr	Asn	Asn	Val	Asp
			115				120						125		
Val	Glu	Ala	Ala	Asn	Lys	Tyr	Gly	Ile	Ala	Val	Gly	Asn	Thr	Pro	Gly
			130				135					140			
Val	Leu	Thr	Glu	Thr	Thr	Ala	Glu	Leu	Ala	Ala	Ser	Leu	Ser	Leu	Ala
145						150				155				160	
Ala	Ala	Arg	Arg	Ile	Val	Glu	Ala	Asp	Glu	Phe	Met	Arg	Gly	Gly	Leu
			165					170					175		
Tyr	Glu	Gly	Trp	Leu	Pro	His	Leu	Phe	Val	Gly	Asn	Leu	Leu	Lys	Gly
			180					185					190		
Gln	Thr	Val	Gly	Val	Ile	Gly	Ala	Gly	Arg	Ile	Gly	Ser	Ala	Tyr	Ala
			195				200					205			
Arg	Met	Met	Val	Glu	Gly	Phe	Lys	Met	Asn	Leu	Ile	Tyr	Phe	Asp	Leu
			210				215					220			
Tyr	Gln	Ser	Thr	Arg	Leu	Glu	Lys	Phe	Val	Thr	Ala	Tyr	Gly	Gln	Phe
225					230					235				240	
Leu	Lys	Ala	Asn	Gly	Glu	Gln	Pro	Val	Thr	Trp	Lys	Arg	Ala	Ser	Ser
			245					250						255	

Met Glu Glu Val Leu Arg Glu Ala Asp Leu Ile Ser Leu His Pro Val
260 265 270
Leu Asp Lys Thr Thr Tyr His Leu Val Asn Lys Glu Arg Leu Ala Met
275 280 285
Met Lys Lys Glu Ala Ile Leu Val Asn Cys Ser Arg Gly Pro Val Ile
290 295 300
Asp Glu Ala Ala Leu Val Glu His Leu Lys Glu Asn Pro Met Phe Arg
305 310 315 320
Val Gly Leu Asp Val Phe Glu Glu Glu Pro Phe Met Lys Pro Gly Leu
325 330 335
Ala Asp Met Lys Asn Ala Ile Val Val Pro His Ile Ala Ser Ala Ser
340 345 350
Lys Trp Thr Arg Glu Gly Met Ala Xaa Ala Cys Ser Ser Gln Arg Pro
355 360 365
Arg Lys Ser Gln Arg Val Pro Asp Leu Ala
370 375

(2) INFORMATION FOR SEQ ID NO:2550:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 351 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..351

(D) OTHER INFORMATION: / Ceres Seq. ID 1573638

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2550:

Met Ala Lys Pro Val Ser Ile Glu Val Tyr Asn Pro Asn Gly Lys Tyr
1 5 10 15
Arg Val Val Ser Thr Lys Pro Met Pro Gly Thr Arg Trp Ile Asn Leu
20 25 30
Leu Val Asp Gln Gly Cys Arg Val Glu Ile Cys His Leu Lys Lys Thr
35 40 45
Ile Leu Ser Val Glu Asp Ile Ile Asp Leu Ile Gly Asp Lys Cys Asp
50 55 60
Gly Val Ile Gly Gln Leu Thr Glu Asp Trp Gly Glu Thr Leu Phe Ser
65 70 75 80
Ala Leu Ser Lys Ala Gly Gly Lys Ala Phe Ser Asn Met Ala Val Gly
85 90 95
Tyr Asn Asn Val Asp Val Glu Ala Ala Asn Lys Tyr Gly Ile Ala Val
100 105 110
Gly Asn Thr Pro Gly Val Leu Thr Glu Thr Thr Ala Glu Leu Ala Ala
115 120 125
Ser Leu Ser Leu Ala Ala Ala Arg Arg Ile Val Glu Ala Asp Glu Phe
130 135 140
Met Arg Gly Gly Leu Tyr Glu Gly Trp Leu Pro His Leu Phe Val Gly
145 150 155 160
Asn Leu Leu Lys Gly Gln Thr Val Gly Val Ile Gly Ala Gly Arg Ile
165 170 175
Gly Ser Ala Tyr Ala Arg Met Met Val Glu Gly Phe Lys Met Asn Leu
180 185 190
Ile Tyr Phe Asp Leu Tyr Gln Ser Thr Arg Leu Glu Lys Phe Val Thr
195 200 205
Ala Tyr Gly Gln Phe Leu Lys Ala Asn Gly Glu Gln Pro Val Thr Trp
210 215 220
Lys Arg Ala Ser Ser Met Glu Glu Val Leu Arg Glu Ala Asp Leu Ile
225 230 235 240
Ser Leu His Pro Val Leu Asp Lys Thr Thr Tyr His Leu Val Asn Lys
245 250 255
Glu Arg Leu Ala Met Lys Lys Glu Ala Ile Leu Val Asn Cys Ser

Arg	Gly	Pro	Val	Ile	Asp	Glu	Ala	Ala	Leu	Val	Glu	His	Leu	Lys	Glu
275							260					285			
Asn	Pro	Met	Phe	Arg	Val	Gly	Leu	Asp	Val	Phe	Glu	Glu	Glu	Pro	Phe
290							295				300				
Met	Lys	Pro	Gly	Leu	Ala	Asp	Met	Lys	Asn	Ala	Ile	Val	Val	Pro	His
305					310					315					320
Ile	Ala	Ser	Ala	Ser	Lys	Trp	Thr	Arg	Glu	Gly	Met	Ala	Xaa	Ala	Cys
					325				330					335	
Ser	Ser	Gln	Arg	Pro	Arg	Lys	Ser	Gln	Arg	Val	Pro	Asp	Leu	Ala	
					340			345					350		

(2) INFORMATION FOR SEQ ID NO:2551:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 328 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..328

(D) OTHER INFORMATION: / Ceres Seq. ID 1573639

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2551:

Met	Pro	Gly	Thr	Arg	Trp	Ile	Asn	Leu	Leu	Val	Asp	Gln	Gly	Cys	Arg
1					5				10					15	
Val	Glu	Ile	Cys	His	Leu	Lys	Lys	Thr	Ile	Leu	Ser	Val	Glu	Asp	Ile
			20					25					30		
Ile	Asp	Leu	Ile	Gly	Asp	Lys	Cys	Asp	Gly	Val	Ile	Gly	Gln	Leu	Thr
		35				40					45				
Glu	Asp	Trp	Gly	Glu	Thr	Leu	Phe	Ser	Ala	Leu	Ser	Lys	Ala	Gly	Gly
	50					55				60					
Lys	Ala	Phe	Ser	Asn	Met	Ala	Val	Gly	Tyr	Asn	Asn	Val	Asp	Val	Glu
65					70				75					80	
Ala	Ala	Asn	Lys	Tyr	Gly	Ile	Ala	Val	Gly	Asn	Thr	Pro	Gly	Val	Leu
			85						90				95		
Thr	Glu	Thr	Thr	Ala	Glu	Leu	Ala	Ala	Ser	Leu	Ser	Leu	Ala	Ala	
		100					105						110		
Arg	Arg	Ile	Val	Glu	Ala	Asp	Glu	Phe	Met	Arg	Gly	Gly	Leu	Tyr	Glu
		115				120						125			
Gly	Trp	Leu	Pro	His	Leu	Phe	Val	Gly	Asn	Leu	Leu	Lys	Gly	Gln	Thr
	130					135					140				
Val	Gly	Val	Ile	Gly	Ala	Gly	Arg	Ile	Gly	Ser	Ala	Tyr	Ala	Arg	Met
145					150				155					160	
Met	Val	Glu	Gly	Phe	Lys	Met	Asn	Leu	Ile	Tyr	Phe	Asp	Leu	Tyr	Gln
				165					170				175		
Ser	Thr	Arg	Leu	Glu	Lys	Phe	Val	Thr	Ala	Tyr	Gly	Gln	Phe	Leu	Lys
			180					185					190		
Ala	Asn	Gly	Glu	Gln	Pro	Val	Thr	Trp	Lys	Arg	Ala	Ser	Ser	Met	Glu
		195				200					205				
Glu	Val	Leu	Arg	Glu	Ala	Asp	Leu	Ile	Ser	Leu	His	Pro	Val	Leu	Asp
		210				215					220				
Lys	Thr	Thr	Tyr	His	Leu	Val	Asn	Lys	Glu	Arg	Leu	Ala	Met	Met	Lys
225					230				235					240	
Lys	Glu	Ala	Ile	Leu	Val	Asn	Cys	Ser	Arg	Gly	Pro	Val	Ile	Asp	Glu
			245					250					255		
Ala	Ala	Leu	Val	Glu	His	Leu	Lys	Glu	Asn	Pro	Met	Phe	Arg	Val	Gly
		260					265						270		
Leu	Asp	Val	Phe	Glu	Glu	Glu	Pro	Phe	Met	Lys	Pro	Gly	Leu	Ala	Asp
		275					280					285			
Met	Lys	Asn	Ala	Ile	Val	Val	Pro	His	Ile	Ala	Ser	Ala	Ser	Lys	Trp
290						295						300			

Thr Arg Glu Gly Met Ala Xaa Ala Cys Ser Ser Gln Arg Pro Arg Lys
305 310 315 320
Ser Gln Arg Val Pro Asp Leu Ala
325

(2) INFORMATION FOR SEQ ID NO:2552:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1318 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1318
- (D) OTHER INFORMATION: / Ceres Seq. ID 1573640

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2552:

```
aaaaccocaaa cccctactca cttttttcac attctttctc tctctcgata tcatctaaat 60
ctctctcttg atctcaattt cgcacaaatgg ctgacaaaga gatcagaatc ggaatcaacg 120
gtttcggaag aatcggtcgt ttggttgcta gagttgtctc tcagagggat gatgttgagc 180
tcgtcgctgt taacgatcct ttcatacaca ccgagtatcat gacatacatg ttttaagtatg 240
acagtgttca cggctcagtg aagcaccatg agcttaagggt gaaggatgac aaaactcttc 300
ctcttcgtga gaagccagtc actgttttgc gcatcaggaa cctcgaggac atccccatggg 360
gtgaggtcgg agctgacttt gttgttgagt ctactggtgt cttcactgac aaagacaagg 420
ctgctgctca cttgaagggt ggtgctaaaa aggttgtcat ctctgcccc aacaaagatg 480
cgccccatgt cgttgttggt gtcAacgagc acgagtacaa gtctgacctt gacattgttt 540
ccaaacgtag ttgaccacct aactgccttg ctctctctgc caaggttatt aatgacaggt 600
ttggcattgt tgagggactc atgaccactg tccactctat cactgctact cagaagacag 660
ttgatgttcc atcaatgaag gactggagag gtggaagagc tgcttctctc aacattatc 720
ctagacgacac tgggtgccgc aaggtcgttg ggaagtggtt gccatccctc aatggaaaat 780
tgacccgaat gctcttccgt gtcccaacgc ttgatgtctc agttgttgat ctcacccgtta 840
gacttgagaa agctgcaaca tacgacgaaa tcaagaaggc catcaaggag gaatctgaag 900
gcacaaatgaa gggaaatttg ggatacaact aggatgatgt ttgtctacc gacttttgtt 960
gtgacaacacg gtcaagcatt ttcatgacca aggtcgggat tgcattgagc gacaaattgt 1020
tgaagtgtgt gtcatggtac gacaaacgaat ggggttacag tctcgtgtc ttgacctta 1080
tcgttccatc gtcaaaagcc taagcttaca ccggcgagag tttgtgtgtg gttgagttc 1140
tactgttctg aataaaaaaa aggagaaaaa aaaactcgag ttgttatgtt ttttactga 1200
ttccatgcgc agtcatgaga ttgttagct tttgtcttt tgctttctct taatgtttcc 1260
ctgctttatt tactgaaacc attggtttgg tttttatgt taattaagtt tttagtcc
```

(2) INFORMATION FOR SEQ ID NO:2553:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 338 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..338
- (D) OTHER INFORMATION: / Ceres Seq. ID 1573641

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2553:

```
Met Ala Asp Lys Lys Ile Arg Ile Gly Ile Asn Gly Phe Gly Arg Ile
1 5 10 15
Gly Arg Leu Val Ala Arg Val Val Leu Gln Arg Asp Asp Val Glu Leu
20 25 30
Val Ala Val Asn Asp Pro Phe Ile Thr Thr Glu Tyr Met Thr Tyr Met
35 40 45
Phe Lys Tyr Asp Ser Val His Gly Gln Trp Lys His His Glu Leu Lys
50 55 60
Val Lys Asp Asp Lys Thr Leu Leu Phe Gly Glu Lys Pro Val Thr Val
65 70 75 80
Phe Gly Ile Arg Asn Pro Glu Asp Ile Pro Trp Gly Glu Ala Gly Ala
```

1. Introduction

(i) SEQUENCE CHARACTERISTICS:

- | (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2554: | | | | | | | | | | | | | | | | | |
|--|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|
| Met | Thr | Tyr | Met | Phe | Lys | Tyr | Asp | Ser | Val | His | Gly | Gln | Trp | Lys | His | | |
| 1 | | | 5 | | | | | | 10 | | | | | 15 | | | |
| His | Glu | Leu | Lys | Val | Lys | Asp | Asp | Lys | Thr | Leu | Leu | Phe | Gly | Glu | Lys | | |
| | | | 20 | | | | | 25 | | | | | | 30 | | | |
| Pro | Val | Thr | Val | Phe | Gly | Ile | Arg | Asn | Pro | Glu | Asp | Ile | Pro | Trp | Gly | | |
| | | | 35 | | | | 40 | | | | | | | 45 | | | |
| Glu | Ala | Gly | Ala | Asp | Phe | Val | Val | Glu | Ser | Thr | Gly | Val | Phe | Thr | Asp | | |
| | | | 50 | | | | 55 | | | | | 60 | | | | | |
| Lys | Asp | Lys | Ala | Ala | Ala | His | Leu | Lys | Gly | Gly | Ala | Lys | Lys | Val | Val | | |
| 65 | | | | | 70 | | | | | | 75 | | | | 80 | | |
| Ile | Ser | Ala | Pro | Ser | Lys | Asp | Ala | Pro | Met | Phe | Val | Val | Gly | Val | Asn | | |
| | | | | 85 | | | | | 90 | | | | | | 95 | | |
| Glu | His | Glu | Tyr | Lys | Ser | Asp | Leu | Asp | Ile | Val | Ser | Asn | Ala | Ser | Cys | | |
| | | | 100 | | | | | 105 | | | | | 110 | | | | |
| Thr | Thr | Asn | Cys | Leu | Ala | Pro | Leu | Ala | Lys | Val | Ile | Asn | Asp | Arg | Phe | | |
| | | | 115 | | | | 120 | | | | | | 125 | | | | |

Gly Ile Val Glu Gly Leu Met Thr Thr Val His Ser Ile Thr Ala Thr
130 135 140
Gln Lys Thr Val Asp Gly Pro Ser Met Lys Asp Trp Arg Gly Gly Arg
145 150 155 160
Ala Ala Ser Phe Asn Ile Ile Pro Ser Ser Thr Gly Ala Ala Lys Ala
165 170 175
Val Gly Lys Val Leu Pro Ser Leu Asn Gly Lys Leu Thr Gly Met Ser
180 185 190
Phe Arg Val Pro Thr Val Asp Val Ser Val Val Asp Leu Thr Val Arg
195 200 205
Leu Glu Lys Ala Ala Thr Tyr Asp Glu Ile Lys Lys Ala Ile Lys Glu
210 215 220
Glu Ser Glu Gly Lys Met Lys Gly Ile Leu Gly Tyr Thr Glu Asp Asp
225 230 235 240
Val Val Ser Thr Asp Phe Val Gly Asp Asn Arg Ser Ser Ile Phe Asp
245 250 255
Ala Lys Ala Gly Ile Ala Leu Ser Asp Lys Phe Val Lys Leu Val Ser
260 265 270
Trp Tyr Asp Asn Glu Trp Gly Tyr Ser Ser Arg Val Val Asp Leu Ile
275 280 285
Val His Met Ser Lys Ala
290

(2) INFORMATION FOR SEQ ID NO:2555:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 291 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..291
- (D) OTHER INFORMATION: / Ceres Seq. ID 1573643

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2555:

Met Phe Lys Tyr Asp Ser Val His Gly Gln Trp Lys His His Glu Leu
1 5 10 15
Lys Val Lys Asp Asp Lys Thr Leu Leu Phe Gly Glu Lys Pro Val Thr
20 25 30
Val Phe Gly Ile Arg Asn Pro Glu Asp Ile Pro Trp Gly Glu Ala Gly
35 40 45
Ala Asp Phe Val Val Glu Ser Thr Gly Val Phe Thr Asp Lys Asp Lys
50 55 60
Ala Ala Ala His Leu Lys Gly Gly Ala Lys Lys Val Val Ile Ser Ala
65 70 75 80
Pro Ser Lys Asp Ala Pro Met Phe Val Val Gly Val Asn Glu His Glu
85 90 95
Tyr Lys Ser Asp Leu Asp Ile Val Ser Asn Ala Ser Cys Thr Thr Asn
100 105 110
Cys Leu Ala Pro Leu Ala Lys Val Ile Asn Asp Arg Phe Gly Ile Val
115 120 125
Glu Gly Leu Met Thr Thr Val His Ser Ile Thr Ala Thr Gln Lys Thr
130 135 140
Val Asp Gly Pro Ser Met Lys Asp Trp Arg Gly Gly Arg Ala Ala Ser
145 150 155 160
Phe Asn Ile Ile Pro Ser Ser Thr Gly Ala Ala Lys Ala Val Gly Lys
165 170 175
Val Leu Pro Ser Leu Asn Gly Lys Leu Thr Gly Met Ser Phe Arg Val
180 185 190
Pro Thr Val Asp Val Ser Val Val Asp Leu Thr Val Arg Leu Glu Lys
195 200 205
Ala Ala Thr Tyr Asp Glu Ile Lys Lys Ala Ile Lys Glu Glu Ser Glu

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(2) INFORMATION FOR SEQ ID NO:2556:

(2) INFORMATION FOR SEQ ID NO:2557:

```
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2557:
```

(2) INFORMATION FOR SEQ ID NO:2558:

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:

(A) NAME/KEY: -
(B) LOCATION: 1.533
(D) OTHER INFORMATION: / Ceres Seq. ID 1573646

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2558:

ataacacaaa	tacacacaaa	aaaaandRaa	Wacagaaagt	aacatgagat	ctctcttatt	60
agccgtgtgc	ctgtgtcttg	ctttacactg	cggtgaagca	gccgtgtctt	gcaacacggt	120
gattgaggat	ctttaccctt	gcttatccta	cggtgactcag	ggcggaacgg	tcccaacctt	180
ctgtctgaac	ggctctcaaa	cactcaagag	tcaggctcaa	acttctgtgg	accgtcaggg	240
gNgtctgtcg	ttgcatcaaa	tctgctattg	gaggactcac	tctctctctt	agaaccatcc	300
aaaatgcttt	ggaattgcct	tctaaatgtg	gtgtcgatct	cccttacaag	ttcagccctt	360
ccactgactg	cgacagtatc	cagtgagaca	agcagaaaaa	cttaaaggaa	gctactacaa	420
gaactataat	aaactaataa	ttaataaagt	agggcattgg	ttgtctagtt	gctaattgat	480
cagtgtatga	ttgtcatttt	gaatgttcta	atacgcag	gcatttatct	ctg	

(2) INFORMATION FOR SEQ ID NO:2559:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 82 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1.82
(D) OTHER INFORMATION: / Ceres Seq. ID 1573647

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2559:

Met	Arg	Ser	Leu	Leu	Ala	Val	Cys	Leu	Val	Leu	Ala	Leu	His	Cys
1		5					10			15				
Gly	Glu	Ala	Ala	Val	Ser	Cys	Asn	Thr	Val	Ile	Ala	Asp	Leu	Tyr
		20					25			30				
Cys	Leu	Ser	Tyr	Val	Thr	Gln	Gly	Pro	Val	Pro	Thr	Leu	Cys	Cys
		35				40				45				
Asn	Gly	Leu	Thr	Thr	Leu	Lys	Ser	Gln	Ala	Gln	Thr	Ser	Val	Asp
		50				55				60				
Gln	Gly	Xaa	Leu	Ser	Leu	His	Gln	Ile	Cys	Tyr	Trp	Arg	Thr	His
		65				70				75				80
Leu	Ser													

(2) INFORMATION FOR SEQ ID NO:2560:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 896 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -
(B) LOCATION: 1..896
(D) OTHER INFORMATION: / Ceres Seq. ID 1573648

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2560:

accattaggg	ctctctctaa	attctcagt	ctcgtgagaa	tgtctatcgt	cttcacggag	60
ctcaatcgaa	gatgttaacg	gcagatatca	caccgaatca	ttcaatctac	atccaGaaac	120
ctcaatgaaa	ggatcaagaa	agaggaaattg	aagagatctc	tttactgttt	gttctctcag	180
tttgggagaa	tacttctgtg	ggttgccttg	aagactccga	agctccgagg	acaagcttgg	240
gttactttta	gtgaagtcac	tgctgctggt	catgctgttc	gtcagatgca	aaattttccc	300
ttvtatgata	aaaccaatgcy	cttacaatat	gcaaaagcaa	agtcagattg	tctagctaaa	360
gctgagggaa	ctttgcttcc	aaaagataag	aagagggaag	aagaagaaaa	agttgaaaga	420
aagcgtgaag	aatcccaacg	accaaacaca	gctaagtgtc	caagtgcata	tggtccaaat	480
gccaaataacg	gagtcacctg	gccttcgttc	cagccgagcg	ggcaagaana	aatgccacca	540

aacaacatac tcttcattca gaatctccca cactgagaaa caagcatgat gctccagctt 600
ctcttcgaac agtaccctgg attcaaaagc ataagaatga tgcacgcaaa accaggaatc 660
gcggttttag agtacgaaga cgaatgttcaa gcttccatag ctatgcaacc tcttcaaggt 720
tccaaaatca ctccccagaa tccaatggct atctctttcg ccaagaaatg ataagatgtc 780
tggttttggt tggtttgtgt cctttaagac gatagtactg gaccaaccaa acctggtgtg 840
tataaccaac caacggttct attggttaac ggattaatcc gggttttggt taateg

(2) INFORMATION FOR SEQ ID NO:2561:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 161 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..161

(D) OTHER INFORMATION: / Ceres Seq. ID 1573649

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2561:

Met	Gln	Asn	Phe	Pro	Xaa	Tyr	Asp	Lys	Pro	Met	Arg	Leu	Gln	Tyr	Ala
1		5						10					15		
Lys	Ala	Lys	Ser	Asp	Cys	Leu	Ala	Lys	Ala	Glu	Gly	Thr	Phe	Val	Pro
		20						25					30		
Lys	Asp	Lys	Lys	Arg	Lys	Gln	Glu	Glu	Lys	Val	Glu	Arg	Lys	Arg	Glu
		35				40					45				
Glu	Ser	Gln	Arg	Pro	Asn	Thr	Ala	Asn	Gly	Pro	Ser	Ala	Asn	Gly	Pro
		50				55					60				
Ser	Ala	Asn	Asn	Gly	Val	Pro	Ala	Pro	Ser	Phe	Gln	Pro	Ser	Gly	Gln
		65			70					75				80	
Glu	Thr	Met	Pro	Pro	Asn	Asn	Ile	Leu	Phe	Ile	Gln	Asn	Leu	Pro	His
			85					90					95		
Glu	Thr	Thr	Ser	Met	Met	Leu	Gln	Leu	Leu	Phe	Glu	Gln	Tyr	Pro	Gly
			100					105					110		
Phe	Lys	Glu	Ile	Arg	Met	Ile	Asp	Ala	Lys	Pro	Gly	Ile	Ala	Phe	Val
			115				120					125			
Glu	Tyr	Glu	Asp	Asp	Val	Gln	Ala	Ser	Ile	Ala	Met	Gln	Pro	Leu	Gln
		130				135					140				
Gly	Phe	Lys	Ile	Thr	Pro	Gln	Asn	Pro	Met	Val	Ile	Ser	Phe	Ala	Lys
				150					155					160	
Lys															

(2) INFORMATION FOR SEQ ID NO:2562:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 151 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..151

(D) OTHER INFORMATION: / Ceres Seq. ID 1573650

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2562:

Met	Arg	Leu	Gln	Tyr	Ala	Lys	Ala	Lys	Ser	Asp	Cys	Leu	Ala	Lys	Ala
1			5					10					15		
Glu	Gly	Thr	Phe	Val	Pro	Lys	Asp	Lys	Lys	Arg	Lys	Gln	Glu	Glu	Lys
			20					25					30		
Val	Glu	Arg	Lys	Arg	Glu	Glu	Ser	Gln	Arg	Pro	Asn	Thr	Ala	Asn	Gly
			35				40					45			
Pro	Ser	Ala	Asn	Gly	Pro	Ser	Ala	Asn	Asn	Gly	Val	Pro	Ala	Pro	Ser
			50				55				60				
Phe	Gln	Pro	Ser	Gly	Gln	Glu	Thr	Met	Pro	Pro	Asn	Asn	Ile	Leu	Phe

65 70 75 80
Ile Gln Asn Leu Pro His Glu Thr Thr Ser Met Met Leu Gln Leu Leu
85 90 95
Phe Glu Gln Tyr Pro Gly Phe Lys Glu Ile Arg Met Ile Asp Ala Lys
100 105 110
Pro Gly Ile Ala Phe Val Glu Tyr Glu Asp Asp Val Gln Ala Ser Ile
115 120 125
Ala Met Gln Pro Leu Gln Gly Phe Lys Ile Thr Pro Gln Asn Pro Met
130 135 140
Val Ile Ser Phe Ala Lys Lys
145 150

(2) INFORMATION FOR SEQ ID NO:2563:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1070 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1070
- (D) OTHER INFORMATION: / Ceres Seq. ID 1573651

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2563:

acatttttca	cgctctcgac	aactctcttc	tctccaaccc	aaattctctt	cttctcaacc	60
tcgtctcttc	cgctctcttc	ctccaacatt	tctccgatca	ttgatgggtt	cgctctcttc	120
ttctctctct	tctctctcga	agcttctctt	tcgtcaacac	tttgagaacg	aatcttccac	180
ctttactatt	cttctcgccg	acgtttctca	tcttgataaa	cctgctttgt	tgattgatcc	240
ggtggacaag	actgtggata	gagacttgaa	actgattgat	gagttaggat	taaagcttat	300
ctatgctatg	aacactcatg	tctatgctga	tcagtcaact	ggctactggc	ttcttaagac	360
gaagctcccg	ggtgtgaaat	ccgttatctc	gaaagcaagt	gggtccaaag	ctgatttggt	420
ctttgaacct	ggtgacaaga	tatctattgg	tgatatatac	cttgaggttc	gtgctacacc	480
tggaacaact	acaggatgtg	ttacatatgt	gactggtgaa	ggagctgac	agccccaacc	540
aagaatggct	tttaccgggg	atgctgtact	catcctgggt	tgtggggagg	ctgacttttc	600
gggagggaagc	tcagatcaac	ctcacgagtc	tgtacattca	cagataattt	cattgccaaa	660
ggacacattg	atctatccag	ctcacgacta	caaaggtttc	gaggtaaagta	cagttggaga	720
agagatgcaa	cacaaccgcc	gtctaaactaa	agataaagaa	acattcaaaa	ccattatgtc	780
aaatctgaat	ctgtcgtatc	ogaagatgat	tgatgttgca	gtaccagcaa	atatgtgtct	840
tgggtttaca	gatgtgcctt	ctcaagccaa	ctaaaaaaaa	ctcttaccata	taatgtttgt	900
ctttttatcg	atgtcattct	atatattacca	aagccaataa	aaactcttga	gagtaatttc	960
tacaataaga	tttgcctccg	tttagataaa	gttcatttaga	aaattgtgta	aattagattg	1020
aaactgttga	attgtttatg	aagatgaaga	cagtatttgc	gtgttcagac		

(2) INFORMATION FOR SEQ ID NO:2564:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 290 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..290
- (D) OTHER INFORMATION: / Ceres Seq. ID 1573652

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2564:

His Phe Ser Arg Leu Arg Gln Leu Leu Leu Leu Gln Pro Lys Phe Leu	
1 5 10 15	
Ser Ser Gln Pro Arg Pro Leu Arg Ser Pro Pro Thr Phe Leu Arg	
20 25 30	
Ser Leu Met Gly Ser Ser Ser Phe Ser Ser Ser Ser Lys Leu	
35 40 45	
Leu Phe Arg Gln Leu Phe Glu Asn Glu Ser Ser Thr Phe Thr Tyr Leu	
50 55 60	

Leu Ala Asp Val Ser His Pro Asp Lys Pro Ala Leu Leu Ile Asp Pro
65 70 75 80
Val Asp Lys Thr Val Asp Arg Asp Leu Lys Leu Ile Asp Glu Leu Gly
85 90 95
Leu Lys Leu Ile Tyr Ala Met Asn Thr His Val His Ala Asp His Val
100 105 110
Thr Gly Thr Gly Leu Leu Lys Thr Lys Leu Pro Gly Val Lys Ser Val
115 120 125
Ile Ser Lys Ala Ser Gly Ser Lys Ala Asp Leu Phe Leu Glu Pro Gly
130 135 140
Asp Lys Val Ser Ile Gly Asp Ile Tyr Leu Glu Val Arg Ala Thr Pro
145 150 155 160
Gly His Thr Thr Gly Cys Val Thr Tyr Val Thr Gly Glu Gly Ala Asp
165 170 175
Gln Pro Gln Pro Arg Met Ala Phe Thr Gly Asp Ala Val Leu Ile Arg
180 185 190
Gly Cys Gly Arg Thr Asp Phe Gln Gly Gly Ser Ser Asp Gln Leu Tyr
195 200 205
Glu Ser Val His Ser Gln Ile Phe Ser Leu Pro Lys Asp Thr Leu Ile
210 215 220
Tyr Pro Ala His Asp Tyr Lys Gly Phe Glu Val Ser Thr Val Gly Glu
225 230 235 240
Glu Met Gln His Asn Pro Arg Leu Thr Lys Asp Lys Glu Thr Phe Lys
245 250 255
Thr Ile Met Ser Asn Leu Asn Leu Ser Tyr Pro Lys Met Ile Asp Val
260 265 270
Ala Val Pro Ala Asn Met Val Cys Gly Leu Gln Asp Val Pro Ser Gln
275 280 285
Ala Asn
290

(2) INFORMATION FOR SEQ ID NO:2565:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 256 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..256

(D) OTHER INFORMATION: / Ceres Seq. ID 1573653

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2565:

Met Gly Ser Ser Ser Phe Ser Ser Ser Ser Lys Leu Leu Phe
1 5 10 15
Arg Gln Leu Phe Glu Asn Glu Ser Ser Thr Phe Thr Tyr Leu Leu Ala
20 25 30
Asp Val Ser His Pro Asp Lys Pro Ala Leu Leu Ile Asp Pro Val Asp
35 40 45
Lys Thr Val Asp Arg Asp Leu Lys Leu Ile Asp Glu Leu Gly Leu Lys
50 55 60
Leu Ile Tyr Ala Met Asn Thr His Val His Ala Asp His Val Thr Gly
65 70 75 80
Thr Gly Leu Leu Lys Thr Lys Leu Pro Gly Val Lys Ser Val Ile Ser
85 90 95
Lys Ala Ser Gly Ser Lys Ala Asp Leu Phe Leu Glu Pro Gly Asp Lys
100 105 110
Val Ser Ile Gly Asp Ile Tyr Leu Glu Val Arg Ala Thr Pro Gly His
115 120 125
Thr Thr Gly Cys Val Thr Tyr Val Thr Gly Glu Gly Ala Asp Gln Pro
130 135 140
Gln Pro Arg Met Ala Phe Thr Gly Asp Ala Val Leu Ile Arg Gly Cys

(2) INFORMATION FOR SEQ ID NO:2566:

(A) LENGTH: 188 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

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(D) TOPOLOGY: lin
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MOLECULE TYPE: peptide

(A) NAM

(B) LOCATION: 1..188

(D) OTHER INFORMATION

SEQUENCE DESCRIPTION: SEQ ID NO:2566:

Asn Thr His Val His Ala Asp His Val Thr Gl

(2) INFORMATION FOR SEQ ID NO:2567:

(A) LENGTH: 1151 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1151

(D) OTHER INFORMATION: / Ceres Seq. ID 1573655

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2567:

acacatcttta	aaaagtaaaa	acacattcat	ctatccaaca	aaaaaaaaaa	aaaaaggag	60
aaatgggaag	aatgatcat	agaatgggtg	gtgtcaatgg	cataactatg	cacattgcgc	120
agaaaggtcc	caaagaagga	cctgtggtgc	ttctctccca	tggtattccct	gatctctggt	180
acacgtggcg	tcaccagatt	agtgggttat	catctctagg	ttaccgcgct	gtatgctcag	240
acctcccgag	ctacggagac	cttgattcgc	cagagtcttt	ctccgagtac	acgtgtctta	300
acgtcggttg	ggacctcgta	gctctctcgg	acagtggtgc	tggaatcaaa	gagaagggtg	360
ttctgttcgg	tcattgattg	ggagccatta	tcggatggtt	ttctgttttg	tttcgacctg	420
aaaagattaa	cggctttgtg	tgtttgagtg	tgccgtatag	atcaagaaac	cctaaagtca	480
agcccgttca	agggttcaag	gctgtatttg	gagatgatta	ctacatttgt	agatttcagg	540
aaccggggaa	gattgaagga	gagattgcaa	gtgcagatcc	aagaatatct	ctgagggaacc	600
ttcttcacag	gaggacactc	ggctccgcga	ttttacctaa	ggataatccc	tttggggaaa	660
aacctaaacc	taatagcgaa	aacattgaa	tgccctgaatg	gttttctaag	aaagatctcg	720
atttctatgt	ctccaaatct	gagaaggcag	gatttaccgg	tggtttgaac	tactacagag	780
ccatggatct	gaattgggag	ctcactgcac	catggaccgg	agctaagatt	caagtctccag	840
tgaagttcat	gacagggtgac	ttcgacatgg	tttacaccac	accagggatg	aaagagtaca	900
ttcacgggtg	tggaattgct	gcagatgttc	caactcttca	agagatagtg	gtgattgaag	960
atgtctggKYM	Ytcgtttaacc	aagagaaacc	taagaggttc	actgctcaca	tcaatgactt	1020
cttcaccaag	cttcggggaca	acaacaaaag	cttttagagt	ttctgttttg	ttctattatg	1080
ttggctctca	aaacaagtgt	gtttcttgcat	gtgtgtgttc	gacaagattt	tgaataagac	1140
ttggcattat	g					

(2) INFORMATION FOR SEQ ID NO:2568:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 356 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..356

(D) OTHER INFORMATION: / Ceres Seq. ID 1573656

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2568:

Met	Glu	Gly	Ile	Asp	His	Arg	Met	Val	Ser	Val	Asn	Gly	Ile	Thr	Met
1				5					10					15	
His	Ile	Ala	Glu	Lys	Gly	Pro	Lys	Glu	Gly	Pro	Val	Val	Leu	Leu	
				20					25					30	
His	Gly	Phe	Pro	Asp	Leu	Trp	Tyr	Thr	Trp	Arg	His	Gln	Ile	Ser	Gly
				35					40					45	
Leu	Ser	Ser	Leu	Gly	Tyr	Arg	Ala	Val	Ala	Pro	Asp	Leu	Arg	Gly	Tyr
				50					55					60	
Gly	Asp	Ser	Asp	Ser	Pro	Glu	Ser	Phe	Ser	Glu	Tyr	Thr	Cys	Leu	Asn
				65					70					75	80
Val	Val	Gly	Asp	Leu	Val	Ala	Leu	Leu	Asp	Ser	Val	Ala	Gly	Asn	Gln
				85					90					95	
Glu	Lys	Val	Phe	Leu	Val	Gly	His	Asp	Trp	Gly	Ala	Ile	Ile	Gly	Trp
				100					105					110	
Phe	Leu	Cys	Leu	Phe	Arg	Pro	Glu	Lys	Ile	Asn	Gly	Phe	Val	Cys	Leu
				115					120					125	
Ser	Val	Pro	Tyr	Arg	Ser	Arg	Asn	Pro	Lys	Val	Lys	Pro	Val	Gln	Gly
				130					135					140	
Phe	Lys	Ala	Val	Phe	Gly	Asp	Asp	Tyr	Tyr	Ile	Cys	Arg	Phe	Gln	Glu
				145					150					155	160
Pro	Gly	Lys	Ile	Glu	Gly	Glu	Ile	Ala	Ser	Ala	Asp	Pro	Arg	Ile	Phe
				165					170					175	
Leu	Arg	Asn	Leu	Phe	Thr	Gly	Arg	Thr	Leu	Gly	Pro	Pro	Ile	Leu	Pro
				180					185					190	
Lys	Asp	Asn	Pro	Phe	Gly	Glu	Lys	Pro	Asn	Pro	Asn	Ser	Glu	Asn	Ile
				195					200					205	
Glu	Leu	Pro	Glu	Trp	Phe	Ser	Lys	Lys	Asp	Leu	Asp	Phe	Tyr	Val	Ser

Met	Val	Ser	Val	Asn	Gly	Ile	Thr	Met	His	Ile	Ala	Glu	Lys	Gly	Pro
1				5				10						15	
Lys	Gly	Gly	Pro	Val	Val	Leu	Leu	Leu	His	Gly	Phe	Pro	Asp	Leu	Trp
			20					25					30		
Tyr	Thr	Trp	Arg	His	Gln	Ile	Ser	Gly	Leu	Ser	Ser	Leu	Gly	Tyr	Arg
		35					40					45			
Ala	Val	Ala	Pro	Asp	Leu	Arg	Gly	Tyr	Gly	Asp	Ser	Asp	Ser	Pro	Glu
		50				55				60					
Ser	Phe	Ser	Glu	Tyr	Thr	Cys	Leu	Asn	Val	Val	Gly	Asp	Leu	Val	Ala
65					70					75					80
Leu	Leu	Asp	Ser	Val	Ala	Gly	Asn	Gln	Glu	Lys	Val	Phe	Leu	Val	Gly
				85					90					95	
His	Asp	Trp	Gly	Ala	Ile	Ile	Gly	Trp	Phe	Leu	Cys	Leu	Phe	Arg	Pro
			100					105					110		
Glu	Lys	Ile	Asn	Gly	Phe	Val	Cys	Leu	Ser	Val	Pro	Tyr	Arg	Ser	Arg
			115				120					125			
Asn	Pro	Lys	Val	Lys	Pro	Val	Gln	Gly	Phe	Lys	Ala	Val	Phe	Gly	Asp
						135					140				
Asp	Tyr	Tyr	Ile	Cys	Arg	Phe	Gln	Glu	Pro	Gly	Lys	Ile	Glu	Gly	Glu
145					150					155					160
Ile	Ala	Ser	Ala	Asp	Pro	Arg	Ile	Phe	Leu	Arg	Asn	Leu	Phe	Thr	Gly
				165					170					175	
Arg	Thr	Leu	Gly	Pro	Pro	Ile	Leu	Pro	Lys	Asp	Asn	Pro	Phe	Gly	Glu
			180					185					190		
Lys	Pro	Asn	Pro	Asn	Ser	Glu	Asn	Ile	Glu	Leu	Pro	Glu	Trp	Phe	Ser
			195				200					205			
Lys	Lys	Asp	Leu	Asp	Phe	Tyr	Val	Ser	Lys	Phe	Glu	Lys	Ala	Gly	Phe
			210				215				220				
Thr	Gly	Gly	Leu	Asn	Tyr	Tyr	Arg	Ala	Met	Asp	Leu	Asn	Trp	Glu	Leu
225					230					235					240

Thr Ala Pro Trp Thr Gly Ala Lys Ile Gln Val Pro Val Lys Phe Met
245 250 255
Thr Gly Asp Phe Asp Met Val Tyr Thr Thr Pro Gly Met Lys Glu Tyr
260 265 270
Ile His Gly Gly Gly Phe Ala Ala Asp Val Pro Thr Leu Gln Glu Ile
275 280 285
Val Val Ile Glu Asp Ala Xaa Xaa Ser Leu Thr Lys Arg Asn Leu Lys
290 295 300
Arg Ser Leu Leu Thr Ser Met Thr Ser Ser Pro Ser Phe Gly Thr Thr
305 310 315 320
Thr Lys Ala Phe Arg Val Leu Val Trp Phe Tyr Tyr Val Gly Ser Gln
325 330 335
Asn Lys Leu Val Leu Ala Cys Val Val Ser Thr Arg Phe
340 345

(2) INFORMATION FOR SEQ ID NO:2570:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 341 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..341
- (D) OTHER INFORMATION: / Ceres Seq. ID 1573658

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2570:

Met His Ile Ala Glu Lys Gly Pro Lys Glu Gly Pro Val Val Leu Leu
1 5 10 15
Leu His Gly Phe Pro Asp Leu Trp Tyr Thr Trp Arg His Gln Ile Ser
20 25 30
Gly Leu Ser Ser Leu Gly Tyr Arg Ala Val Ala Pro Asp Leu Arg Gly
35 40 45
Tyr Gly Asp Ser Asp Ser Pro Glu Ser Phe Ser Glu Tyr Thr Cys Leu
50 55 60
Asn Val Val Gly Asp Leu Val Ala Leu Leu Asp Ser Val Ala Gly Asn
65 70 75 80
Gln Glu Lys Val Phe Leu Val Gly His Asp Trp Gly Ala Ile Ile Gly
85 90 95
Trp Phe Leu Cys Leu Phe Arg Pro Glu Lys Ile Asn Gly Phe Val Cys
100 105 110
Leu Ser Val Pro Tyr Arg Ser Arg Asn Pro Lys Val Lys Pro Val Gln
115 120 125
Gly Phe Lys Ala Val Phe Gly Asp Asp Tyr Tyr Ile Cys Arg Phe Gln
130 135 140
Glu Pro Gly Lys Ile Glu Gly Glu Ile Ala Ser Ala Asp Pro Arg Ile
145 150 155 160
Phe Leu Arg Asn Leu Phe Thr Gly Arg Thr Leu Gly Pro Pro Ile Leu
165 170 175
Pro Lys Asp Asn Pro Phe Gly Glu Lys Pro Asn Pro Asn Ser Glu Asn
180 185 190
Ile Glu Leu Pro Glu Trp Phe Ser Lys Lys Asp Leu Asp Phe Tyr Val
195 200 205
Ser Lys Phe Glu Lys Ala Gly Phe Thr Gly Gly Leu Asn Tyr Tyr Arg
210 215 220
Ala Met Asp Leu Asn Trp Glu Leu Thr Ala Pro Trp Thr Gly Ala Lys
225 230 235 240
Ile Gln Val Pro Val Lys Phe Met Thr Gly Asp Phe Asp Met Val Tyr
245 250 255
Thr Thr Pro Gly Met Lys Glu Tyr Ile His Gly Gly Gly Phe Ala Ala
260 265 270
Asp Val Pro Thr Leu Gln Glu Ile Val Val Ile Glu Asp Ala Xaa Xaa

(2) INFORMATION FOR SEQ ID NO:2571:

(A) LENGTH: 1153 base pairs

(C) STRANDEDNESS: sing

(D) TOPOLOGY: linear

MOLECULE TYPE: DNA (a

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(ix) FEATURE:
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(A) NAME

(B) LOCATION: 1

(D) OTHER INFORMATION

SEQUENCE DESCRIPTION: SEQ ID NO:2571:

taaaaaa gtaaaaaacac attcatctat ccaacaaaaaa aa

ggaaggaatc	gatcataatg	tggtagtggt	caatgcataa	actatgcaca	ttgcgcgaga	120
aggctccaaa	gaatgacctg	tgggtctctt	ctctccatga	ttccctgac	tgtcacagt	180
ggcgtcacca	gattagtggt	ttatcatctc	taggttccg	cgcttgaagt	ccagactctc	240
ggaggtcata	agactctgat	ctggcagaagt	ctttctccga	gtacacagtg	cttaacgtgc	300
ttggggacct	cgtagctctt	ctggacaggt	ttgctgaaa	tcagagaagg	tgtttctggt	360
cggctcatgt	tggggagcca	ttatccgtagt	gtttctctgt	ttgtctcgac	ctgaaaagat	420
taacgttgat	tTgGgttttg	agtgctcogt	atagatacta	gaaacctcaa	agtcagacc	480
tgtcaagggt	tcaaggcgtg	atttggagat	gattactaca	tttgtagatt	tacgagaccg	540
gggaagatg	aagagagagt	tgcaagtgc	gatccaaga	tattcttag	caaacctctc	600
acagggagta	cactcggctc	cgcgatttta	ctcaaggata	atcccttttg	ggaaaacctc	660
aacctcaaga	gcgaacaatc	tgaattgct	gaatggtttt	ctaaagaaagg	ctcgaattc	720
tatgtctcca	gatttcagaa	ggcaggaatt	accgggtgat	tgaactacta	cagagccatg	780
gactcgaatt	ggagagctc	tgcaccatg	accggagata	agattcaagt	tcacgtgaag	840
ttctagacag	tgtacttcca	catggtttac	accacacacg	ggatgaaga	gtacattcac	900
gggtggtgat	ttgcttcaga	tgtttccaat	cttcaagaa	tagtggtgat	tgaagtgcct	960
ggctcacttc	ttaacacaa	gaaacctcaa	gaaggtctct	ctcacataa	tgaactcttc	1020
accaattcgt	gggacaacaa	caaaagcttt	tagatttcgt	gtttggtctt	attatgtgtc	1080
ctctcaaaac	aagttggttc	ttgcatgtgt	tgtttcgaca	agattttgaa	taagactttg	1140
cattataaag	ccc					

(2) INFORMATION FOR SEQ ID NO:2572:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 104 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..104

(D) OTHER INFORMATION: / Ceres Seq. ID 1573660

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2572:

Met	Asp	Ser	Leu	5	le	Ser	Tyr	Thr	Trp	Arg	His	Gln	Ile	Ser	Gly	Leu
1										10					15	
Ser	Ser	Leu	Gly	20	Tyr	Arg	Ala	Val	Ala	Pro	Asp	Leu	Arg	Gly	Tyr	Gly
									25					30		
Asp	Ser	Asp	Ser	35	Pro	Glu	Ser	40	Ser	Glu	Tyr	Thr	Cys	Leu	Asn	Val
													45			
Val	Gly	Asp	Leu	50	Val	Ala	Leu	55	Leu	Asp	Ser	Val	Ala	Gly	Asn	Gln
												60				Arg

Arg Cys Phe Trp Ser Val Met Ile Gly Glu Pro Leu Ser Asp Gly Phe
65 70 75 80
Ser Val Cys Phe Asp Leu Lys Arg Leu Thr Ala Leu Trp Cys Leu Ser
85 90 95
Val Pro Tyr Arg Ser Arg Lys Pro
100

(2) INFORMATION FOR SEQ ID NO:2573:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 91 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..91

(D) OTHER INFORMATION: / Ceres Seq. ID 1573661

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2573:

Met Asp Leu Asn Trp Glu Leu Thr Ala Pro Trp Thr Gly Ala Lys Ile
1 5 10 15
Gln Val Pro Val Lys Phe Met Thr Gly Asp Phe Asn Met Val Tyr Thr
20 25 30
Thr Pro Gly Met Lys Glu Tyr Ile His Gly Gly Phe Ala Ala Asp
35 40 45
Val Pro Thr Leu Gln Glu Ile Val Val Ile Glu Asp Ala Gly His Phe
50 55 60
Val Asn Gln Glu Lys Pro Gln Glu Val Thr Ala His Ile Asn Asp Phe
65 70 75 80
Phe Thr Asn Leu Arg Asp Asn Asn Lys Ser Phe
85 90

(2) INFORMATION FOR SEQ ID NO:2574:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 69 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..69

(D) OTHER INFORMATION: / Ceres Seq. ID 1573662

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2574:

Met Thr Gly Asp Phe Asn Met Val Tyr Thr Thr Pro Gly Met Lys Glu
1 5 10 15
Tyr Ile His Gly Gly Phe Ala Ala Asp Val Pro Thr Leu Gln Glu
20 25 30
Ile Val Val Ile Glu Asp Ala Gly His Phe Val Asn Gln Glu Lys Pro
35 40 45
Gln Glu Val Thr Ala His Ile Asn Asp Phe Phe Thr Asn Leu Arg Asp
50 55 60
Asn Asn Lys Ser Phe
65

(2) INFORMATION FOR SEQ ID NO:2575:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1155 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1155

(D) OTHER INFORMATION: / Ceres Seq. ID 1573663

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2575:

acatcttataa	aagtaaaac	acattcatct	atccaacaaa	aaaaaaaaa	aaaaaggaga	60
aatgggaagga	atcgatcata	gaatgggtgag	tgtaaatggc	ataactatgc	acattgccga	120
gaaaggtccc	aaagaaggac	ctgtggtgct	tctctcccat	ggattcccta	atctctggta	180
cacgtggcgt	caccagatta	gtgggttatc	atctctaggt	taccgcgctg	tagctccaga	240
ctcccgaggc	tacggagact	ctgattcgcc	agagcttttc	tcggagtaca	cgtgtcttaa	300
cgtcgttggg	gacctcgtag	ctcttctgga	cagtggtgct	ggaaatcaag	agaaggtggt	360
ctcgttcggt	catgattggg	gagccattat	cggatgggtt	ctctgtttgt	tccagactga	420
aaagattaac	ggcttttgtg	gtttgagtg	gccgtataga	tcaagaaacc	ctaaagtcaa	480
gccggttcaa	gggttcaagg	ctgtatttgg	agatgattac	tacattttga	gatttccaga	540
accggggaag	attgaaggag	agattgcaag	tgcatatcca	agaattattc	tgaggaaact	600
cttcaacagg	aggacactcg	gtccgcogag	tttaacctaa	gataatccct	ttggggaaaa	660
acctaacctc	aatacgcaaa	acattgaatt	gcctgaatgg	ttttctaaga	aagatctcga	720
ttcttatgtc	tccaaattcg	agaaggcagg	atttaccggt	ggattgaact	actacaagac	780
catggatctg	aattgggagc	tcactgcacc	atggaccgga	gctgaagattc	aagttccagt	840
gaagttcatc	acaggtgact	tcgacatggt	ttacaccaca	ccagggatga	aagatgacat	900
tcacggtggt	ggattttgct	cagatgttcc	aacttttcaa	gagatagttg	tgattgaaga	960
tgctgtTchc	ttcgttaacc	aagagaaacc	tcaagaggtc	actgctcaca	tcaatgacct	1020
cttcaaccaag	cttcgggaca	acaacaaaag	cttttagagt	ttcgttttgg	ttctattatg	1080
ttggctctca	aaacaagttg	gtttcttgc	gtgtgttttc	gacaagattt	tgaataagac	1140
ttggcattat	gaagc					

(2) INFORMATION FOR SEQ ID NO:2576:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 331 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..331

(D) OTHER INFORMATION: / Ceres Seq. ID 1573664

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2576:

Met	Glu	Gly	Ile	Asp	His	Arg	Met	Val	Ser	Val	Asn	Gly	Ile	Thr	Met
1				5				10					15		
His	Ile	Ala	Glu	Lys	Gly	Pro	Lys	Glu	Gly	Pro	Val	Val	Leu	Leu	Leu
			20					25					30		
His	Gly	Phe	Pro	Asn	Leu	Trp	Tyr	Thr	Trp	Arg	His	Gln	Ile	Ser	Gly
			35				40					45			
Leu	Ser	Ser	Leu	Gly	Tyr	Arg	Ala	Val	Ala	Pro	Asp	Leu	Arg	Gly	Tyr
			50				55				60				
Gly	Asp	Ser	Asp	Ser	Pro	Glu	Ser	Phe	Ser	Glu	Tyr	Thr	Cys	Leu	Asn
65				70				75					80		
Val	Val	Gly	Asp	Leu	Val	Ala	Leu	Leu	Asp	Ser	Val	Ala	Gly	Asn	Gln
			85					90					95		
Glu	Lys	Val	Phe	Leu	Val	Gly	His	Asp	Trp	Gly	Ala	Ile	Ile	Gly	Trp
			100					105					110		
Phe	Leu	Cys	Leu	Phe	Arg	Pro	Glu	Lys	Ile	Asn	Gly	Phe	Val	Cys	Leu
			115				120					125			
Ser	Val	Pro	Tyr	Arg	Ser	Arg	Asn	Pro	Lys	Val	Lys	Pro	Val	Gln	Gly
			130				135				140				
Phe	Lys	Ala	Val	Phe	Gly	Asp	Asp	Tyr	Tyr	Ile	Cys	Arg	Phe	Gln	Glu
145				150				155					160		
Pro	Gly	Lys	Ile	Glu	Gly	Glu	Ile	Ala	Ser	Ala	Asp	Pro	Arg	Ile	Phe
			165					170					175		
Leu	Arg	Asn	Leu	Phe	Thr	Gly	Arg	Thr	Leu	Gly	Pro	Pro	Ile	Leu	Pro
			180				185						190		
Lys	Asp	Asn	Pro	Phe	Gly	Glu	Lys	Pro	Asn	Pro	Asn	Ser	Glu	Asn	Ile
			195				200						205		

Glu Leu Pro Glu Trp Phe Ser Lys Lys Asp Leu Asp Phe Tyr Val Ser
210 215 220
Lys Phe Glu Lys Ala Gly Phe Thr Gly Gly Leu Asn Tyr Tyr Arg Ala
225 230 235 240
Met Asp Leu Asn Trp Glu Leu Thr Ala Pro Trp Thr Gly Ala Lys Ile
245 250 255
Gln Val Pro Val Lys Phe Met Thr Gly Asp Phe Asp Met Val Tyr Thr
260 265 270
Thr Pro Gly Met Lys Glu Tyr Ile His Gly Gly Gly Phe Ala Ala Asp
275 280 285
Val Pro Thr Leu Gln Glu Ile Val Val Ile Glu Asp Ala Gly Xaa Phe
290 295 300
Val Asn Gln Glu Lys Pro Gln Glu Val Thr Ala His Ile Asn Asp Phe
305 310 315 320
Phe Thr Lys Leu Arg Asp Asn Asn Lys Ser Phe
325 330

(2) INFORMATION FOR SEQ ID NO:2577:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 324 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..324

(D) OTHER INFORMATION: / Ceres Seq. ID 1573665

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2577:

Met Val Ser Val Asn Gly Ile Thr Met His Ile Ala Glu Lys Gly Pro
1 5 10 15
Lys Glu Gly Pro Val Val Leu Leu Leu His Gly Phe Pro Asn Leu Trp
20 25 30
Tyr Thr Trp Arg His Gln Ile Ser Gly Leu Ser Ser Leu Gly Tyr Arg
35 40 45
Ala Val Ala Pro Asp Leu Arg Gly Tyr Gly Asp Ser Asp Ser Pro Glu
50 55 60
Ser Phe Ser Glu Tyr Thr Cys Leu Asn Val Val Gly Asp Leu Val Ala
65 70 75 80
Leu Leu Asp Ser Val Ala Gly Asn Gln Glu Lys Val Phe Leu Val Gly
85 90 95
His Asp Trp Gly Ala Ile Ile Gly Trp Phe Leu Cys Leu Phe Arg Pro
100 105 110
Glu Lys Ile Asn Gly Phe Val Cys Leu Ser Val Pro Tyr Arg Ser Arg
115 120 125
Asn Pro Lys Val Lys Pro Val Gln Gly Phe Lys Ala Val Phe Gly Asp
130 135 140
Asp Tyr Tyr Ile Cys Arg Phe Gln Glu Pro Gly Lys Ile Glu Gly Glu
145 150 155 160
Ile Ala Ser Ala Asp Pro Arg Ile Phe Leu Arg Asn Leu Phe Thr Gly
165 170 175
Arg Thr Leu Gly Pro Pro Ile Leu Pro Lys Asp Asn Pro Phe Gly Glu
180 185 190
Lys Pro Asn Pro Asn Ser Glu Asn Ile Glu Leu Pro Glu Trp Phe Ser
195 200 205
Lys Lys Asp Leu Asp Phe Tyr Val Ser Lys Phe Glu Lys Ala Gly Phe
210 215 220
Thr Gly Gly Leu Asn Tyr Tyr Arg Ala Met Asp Leu Asn Trp Glu Leu
225 230 235 240
Thr Ala Pro Trp Thr Gly Ala Lys Ile Gln Val Pro Val Lys Phe Met
245 250 255
Thr Gly Asp Phe Asp Met Val Tyr Thr Pro Gly Met Lys Glu Tyr

(2) INFORMATION FOR SEQ ID NO:2578:

(A) LENGTH: 316 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(1x) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..316

(D) OTHER INFORMATION: / Ceres Seq. ID 1573666

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2578:

Met	His	Ile	Ala	Glu	Lys	Gly	Pro	Lys	Glu	Gly	Pro	Val	Val	Leu	Leu
1				5					10					15	
Leu	His	Gly	Phe	20	Pro	Asn	Leu	Trp	Tyr	Thr	Trp	Arg	His	Gln	Ile
									25					30	
Gly	Leu	Ser	Ser	Leu	Gly		Tyr	Arg	Ala	Val	Ala	Pro	Asp	Leu	Arg
			35					40					45		Gly
Tyr	Gly	Asp	Ser	Asp	Ser		Pro	Glu	Ser	Phe	Ser	Glu	Tyr	Thr	Cys
							55						60		Leu
Asn	Val	Val	Gly	Asp	Leu	Val	Ala	Leu	Leu	Asp	Ser	Val	Tyr	Ala	Gly
65					70						75				80
Gln	Glu	Lys	Val	Phe	Leu	Val	Gly	His	Asp	Trp	Gly	Ala	Ile	Ile	Gly
				85					90					95	
Trp	Phe	Leu	Cys	Leu	Phe	Arg	Pro	Glu	Lys	Ile	Asn	Gly	Phe	Val	Cys
				100				105					110		
Leu	Ser	Val	Pro	Tyr	Arg	Ser	Arg	Asn	Pro	Lys	Val	Lys	Pro	Val	Gln
				115				120					125		
Gly	Phe	Lys	Ala	Val	Phe	Gly	Asp	Asp	Tyr	Tyr	Ile	Cys	Arg	Phe	Gln
						135					140				
Glu	Pro	Gly	Lys	Ile	Glu	Gly	Glu	Ile	Ala	Ser	Ala	Asp	Pro	Arg	Ile
145					150					155					160
Phe	Leu	Arg	Asn	Leu	Phe	Thr	Gly	Arg	Thr	Leu	Gly	Pro	Pro	Ile	Leu
				165					170					175	
Pro	Lys	Asp	Asn	Pro	Phe	Gly	Glu	Lys	Pro	Asn	Pro	Asn	Ser	Glu	Asn
				180				185					190		
Ile	Glu	Leu	Pro	Glu	Trp	Phe	Ser	Lys	Lys	Asp	Leu	Asp	Phe	Tyr	Val
							200					205			
Ser	Lys	Phe	Glu	Lys	Ala	Gly	Phe	Thr	Gly	Gly	Leu	Asn	Tyr	Tyr	Arg
						215					220				
Ala	Met	Asp	Leu	Asn	Trp	Glu	Leu	Thr	Ala	Pro	Trp	Thr	Gly	Ala	Lys
225					230					235					240
Ile	Gln	Val	Pro	Val	Lys	Phe	Met	Thr	Gly	Asp	Phe	Asp	Met	Val	Tyr
				245					250					255	
Thr	Thr	Pro	Gly	Met	Lys	Glu	Tyr	Ile	His	Gly	Gly	Gly	Phe	Ala	Ala
			260					265					270		
Asp	Val	Pro	Thr	Leu	Gln	Glu	Ile	Val	Val	Ile	Glu	Asp	Ala	Gly	Xaa
				275			280					285			
Phe	Val	Asn	Gln	Glu	Lys	Pro	Gln	Glu	Val	Thr	Ala	His	Ile	Asn	Asp
				290			295				300				
Phe	Phe	Thr	Lys	Leu	Arg	Asp	Asn	Asn	Lys	Ser	Phe				
305					310					315					

(2) INFORMATION FOR SEQ ID NO:2579:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1213 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1213
- (D) OTHER INFORMATION: / Ceres Seq. ID 1573682

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2579:

aaagagaaMa	acgtatgagt	tgcttaaacc	ataaacctca	agctcaaaat	tttatcaacc	60
ttataaaagt	tcgtEWWtctc	gagattttga	atcttttcag	ctaaaaaaga	tcacagcttt	120
ttgcgttttc	tggatgagtt	tgagataaga	gaagatgaag	attcagtgta	acgtttgtga	180
ggcggcgga	gcgacgggtc	tatgwtgcgc	cgaygaggt	gctctttgt	gggcttgcca	240
tgagaaaatt	cacgccgcta	ataaactcgc	cggaaaaacat	cagagagtcc	ctctctctgc	300
ctctgcctct	tccataccca	aatgtgacat	ttgtcarraa	gcactctgat	tcttcttttg	360
tctgcaagat	agagcttttc	tatgtaggaa	atgtgatgtt	gcaatccaca	ctgtgaatcc	420
tcattgtttc	gctcaccaga	gRdtYcttM	ctcactggaa	tcaaaagtgg	tcttgaatct	480
atagacactg	gtcctcttac	taaaactctc	ctaccacatg	atgataaaaac	catggagacc	540
aaaccttttg	ttaactctat	acctgagcct	caaaagatgg	cttcgatca	tcatcatcac	600
cagcagcagc	aggaacagca	ggaaggagtt	ataccgggaa	ctaaagtcaa	tgatcagaca	660
tcgacaaagc	tctctctcgt	aagtgcggga	tcaactactg	gaagcattcc	tcagtggcaa	720
atagaggaga	ttttcgggct	aaccgacttt	gatcagagct	atgaatacat	ggagaaatat	780
ggatcatcta	agggcgatac	tagtagacga	ggagattcag	acagttcttc	gatgatgaga	840
tctgcagaag	aagatgagga	agataacaat	aactgcttgg	gaggtgagac	atcatggggc	900
gtttcacaga	ttcaggtctc	acctacagcg	tctgttctaa	actggcctaa	gcattttcac	960
caccactctg	tgtttgttcc	ggacataact	tcttcaactc	cttataccgg	ttcatccccc	1020
aatcaaaagg	tgggaaacg	cgccgcaacg	tcttagcatt	tgtaatatc	tttagccgcg	1080
ttgagaaaag	agattggcag	ctttctcagt	agatgtaaga	tcacataaat	gatttggaaa	1140
cttctaatgt	atgtactctg	gagagtccgt	gttctttgtt	agctgaaaaa	acaaaaagat	1200
gtttatttgg	tcg					

(2) INFORMATION FOR SEQ ID NO:2580:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 109 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..109
- (D) OTHER INFORMATION: / Ceres Seq. ID 1573683

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2580:

Met	Lys	Ile	Gln	Cys	Asn	Val	Cys	Glu	Ala	Ala	Glu	Ala	Thr	Val	Leu	
1					5					10				15		
Xaa	Cys	Ala	Xaa	Glu	Ala	Ala	Leu	Cys	Trp	Ala	Cys	Asp	Glu	Lys	Ile	
			20				25					30				
His	Ala	Ala	Asn	Lys	Leu	Ala	Gly	Lys	His	Gln	Arg	Val	Pro	Leu	Ser	
			35				40				45					
Ala	Ser	Ala	Ser	Ser	Ile	Pro	Lys	Cys	Asp	Ile	Cys	Xaa	Xaa	Ala	Ser	
			50				55				60					
Gly	Phe	Phe	Phe	Cys	Leu	Gln	Asp	Arg	Ala	Leu	Cys	Arg	Lys	Cys		
			65			70			75				80			
Asp	Val	Ala	Ile	His	Thr	Val	Asn	Pro	His	Val	Ser	Ala	His	Gln	Xaa	
			85				90						95			
Xaa	Xaa	Xaa	Ser	Leu	Glu	Ser	Lys	Leu	Val	Leu	Asn	Leu				
			100				105									

(2) INFORMATION FOR SEQ ID NO:2581:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 174 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..174
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1573684
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2581:

```
Met Glu Thr Lys Pro Phe Val Gln Ser Ile Pro Glu Pro Gln Lys Met
1      5      10      15
Ala Phe Asp His His His Gln Gln Gln Glu Gln Gln Glu Gly
20     25     30
Val Ile Pro Gly Thr Lys Val Asn Asp Gln Thr Ser Thr Lys Leu Pro
35     40     45
Leu Val Ser Ser Gly Ser Thr Thr Gly Ser Ile Pro Gln Trp Gln Ile
50     55     60
Glu Glu Ile Phe Gly Leu Thr Asp Phe Asp Gln Ser Tyr Glu Tyr Met
65     70     75     80
Glu Asn Asn Gly Ser Ser Lys Ala Asp Thr Ser Arg Arg Gly Asp Ser
85     90     95
Asp Ser Ser Ser Met Met Arg Ser Ala Glu Glu Asp Gly Glu Asp Asn
100    105    110
Asn Asn Cys Leu Gly Gly Glu Thr Ser Trp Ala Val Pro Gln Ile Gln
115    120    125
Ser Pro Pro Thr Ala Ser Gly Leu Asn Trp Pro Lys His Phe His His
130    135    140
His Ser Val Phe Val Pro Asp Ile Thr Ser Ser Thr Pro Tyr Thr Gly
145    150    155    160
Ser Ser Pro Asn Gln Arg Val Gly Lys Arg Arg Arg Arg Phe
165    170
```

- (2) INFORMATION FOR SEQ ID NO:2582:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 159 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..159
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1573685
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2582:

```
Met Ala Phe Asp His His His His Gln Gln Gln Glu Gln Glu
1      5      10      15
Gly Val Ile Pro Gly Thr Lys Val Asn Asp Gln Thr Ser Thr Lys Leu
20     25     30
Pro Leu Val Ser Ser Gly Ser Thr Thr Gly Ser Ile Pro Gln Trp Gln
35     40     45
Ile Glu Glu Ile Phe Gly Leu Thr Asp Phe Asp Gln Ser Tyr Glu Tyr
50     55     60
Met Glu Asn Asn Gly Ser Ser Lys Ala Asp Thr Ser Arg Arg Gly Asp
65     70     75     80
Ser Asp Ser Ser Ser Met Met Arg Ser Ala Glu Glu Asp Gly Glu Asp
85     90     95
Asn Asn Asn Cys Leu Gly Gly Glu Thr Ser Trp Ala Val Pro Gln Ile
100    105    110
Gln Ser Pro Pro Thr Ala Ser Gly Leu Asn Trp Pro Lys His Phe His
115    120    125
His His Ser Val Phe Val Pro Asp Ile Thr Ser Ser Thr Pro Tyr Thr
```

130 135 140
Gly Ser Ser Pro Asn Gln Arg Val Gly Lys Arg Arg Arg Phe
145 150 155

(2) INFORMATION FOR SEQ ID NO:2583:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1583 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..1583
(D) OTHER INFORMATION: / Ceres Seq. ID 1573701

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2583:

```

aaaaaagcta gaaaaacctt tccaaaaaatg gcaaaagaacc gtaacttagt cttcttcttta 60
gggggtattag cgtctttttac actctccagt ttcccggtaa ctgtttccgg cgagccccctt 120
atcttatttca ctttccggcga ctcttctctac gatgtgggca acacgaagtt cttctctgtcg 180
gagttcgaac cagccaccac gtggccttac ggcgattcca tcgatgatcc ctccggctcgt 240
tggtctgacg gccacattgt cccagatttc gtccgtcgat tgattgtgca tcgtgaacgc 300
attctctccg tacttgatcc aaaagctgat ctttctcgtg gagcaagctt tgccattcgt 360
ggagcagttt ttcttggatc tcaatctact actgcatcca tgaatttttg acaacagata 420
tcgaagtttt tagagttaca taagcaatgg actgataaag aacgagcaga agctatatac 480
atggtaaaaca taggagctga ggactacttg aatttcgcaa aggcctcatcc aaatggcaat 540
actgtgggagc agctaaactga agttgcccac gttctccaaa ggataccaa agagctcacg 600
agctgtgggagc agctaaactga agttgcccac gttctccaaa ggataccaa agagctcacg 660
agctgtgggagc agctaaactga agttgcccac gttctccaaa ggataccaa agagctcacg 720
tgttttaccga tagtgagaca agagttaaag accggtgaga attgtatgga gatggtcaac 780
ttcatgttga aaacgcacaa tgaaaggctt agtcgtttgc tcgttgcgat aaccgtaccg 840
atactgtacc gtggcttcgc gtacagcctc ttgtatttca atggtgaaat tctccggagg 900
atcaatgaac catcaactcca ttgatatact gatacaacga cttcttgcgt cggaactgga 960
tcgagaaagt catacgggtg cggttatagt aacgtgcgat ctaagctctg cagctaccag 1020
aaatcatttt tgttcttcga cggcgctcac aacacgcaga aaacgcgata agaaagttgt 1080
aatctgtttt attccggaga caaacatgtc gtctctccga tgaatataaa ggatctcgtg 1140
ggtaaaagcag cgaccgatct tcttgcaaaa gaaatctaga aatcccaact ggtgtctcgtt 1200
ctgtttcttt gaaataagta Ccaatgggtg ttgtgtgaaa ctgtaaaact ctgtattcaa 1260
cttcatatat atatgatgat aaagaaaaaa taacacgttt acattgcaaa aaaaaaaa 1320
aaaaaacgatg acaagaccaa cgtcaaggcc gctggggta aggtcgccgc gcaagctggc 1380
gagataggtg cggaggccct ggagaggatg ttctgtcctt tccccaccac caagacctac 1440
ttcccgcact tcgacctgag ccacggctct gccaggtta agggccacgg caagaaggtg 1500
gccgacgcgc tgaccaacgc cgtggcgcac gtggacgaca tgcccaacgc gctgtccgcg 1560
ctgagcgacc tgcacgcgca agcacttcgg gtggacccGG Tcaacttcaa gctcctaagc
cactgcctgc tggtagcccc atc

```

(2) INFORMATION FOR SEQ ID NO:2584:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 372 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..372
(D) OTHER INFORMATION: / Ceres Seq. ID 1573702

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2584:

```

Lys Lys Ala Arg Lys Thr Phe Pro Lys Met Ala Lys Asn Arg Asn Leu
1 5 10 15
Val Phe Phe Leu Gly Val Leu Ala Ser Phe Thr Leu Ser Ser Phe Pro
20 25 30
Val Thr Val Ser Gly Glu Pro Pro Ile Leu Phe Thr Phe Gly Asp Ser
35 40 45
Ser Tyr Asp Val Gly Asn Thr Lys Phe Phe Ser Ser Glu Phe Asp Pro

```


50	55	60
Ala Thr Thr Trp Pro Tyr Gly Asp Ser Ile Asp Asp Pro Ser Gly Arg		
65	70	75
Trp Ser Asp Gly His Ile Val Pro Asp Phe Val Gly Arg Leu Ile Gly		
	85	90
His Arg Glu Pro Ile Pro Pro Val Leu Asp Pro Lys Ala Asp Leu Ser		
	100	105
Arg Gly Ala Ser Phe Ala Ile Ala Gly Ala Val Val Leu Gly Ser Gln		
	115	120
Ser Thr Thr Ala Ser Met Asn Phe Gly Gln Gln Ile Ser Lys Phe Leu		
	130	135
Glu Leu His Lys Gln Trp Thr Asp Lys Glu Arg Ala Glu Ala Ile Tyr		
	145	150
Met Val Asn Ile Gly Ala Glu Asp Tyr Leu Asn Phe Ala Lys Ala His		
	165	170
Pro Asn Ala Asn Thr Val Glu Gln Leu Thr Gln Val Ala His Val Leu		
	180	185
Gln Arg Ile Pro Arg Glu Leu Thr Ser Leu Tyr Arg Ala Gly Gly Ala		
	195	200
Arg Lys Phe Ala Val Gln Asn Leu Gly Pro Leu Gly Cys Leu Pro Ile		
	210	215
Val Arg Gln Glu Phe Lys Thr Gly Glu Asn Cys Met Glu Met Val Asn		
	225	230
Phe Met Val Lys Thr His Asn Glu Arg Leu Ser Arg Leu Leu Val Ala		
	245	250
Ile Thr Val Pro Ile Leu Tyr Arg Gly Phe Arg Tyr Ser Leu Phe Asp		
	260	265
Phe Asn Gly Glu Ile Leu Arg Arg Ile Asn Glu Pro Ser Leu His Gly		
	275	280
Tyr Thr Asp Thr Thr Thr Ser Cys Cys Gly Thr Gly Ser Arg Asn Ala		
	290	295
Tyr Gly Cys Gly Tyr Ser Asn Val His Ala Lys Leu Cys Ser Tyr Gln		
	305	310
Lys Ser Phe Leu Phe Phe Asp Gly Arg His Asn Thr Glu Lys Thr Asp		
	325	330
Glu Glu Val Ala Asn Leu Phe Tyr Ser Gly Asp Lys His Val Val Ser		
	340	345
Pro Met Asn Ile Lys Asp Leu Val Gly Lys Ala Ala Thr Asp Leu Leu		
	355	360
Ala Gln Glu Ile		
370		

(2) INFORMATION FOR SEQ ID NO:2585:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 363 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..363

(D) OTHER INFORMATION: / Ceres Seq. ID 1573703

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2585:

Met Ala Lys Asn Arg Asn Leu Val Phe Phe Leu Gly Val Leu Ala Ser		
1	5	10
Phe Thr Leu Ser Ser Phe Pro Val Thr Val Ser Gly Glu Pro Pro Ile		
	20	25
Leu Phe Thr Phe Gly Asp Ser Ser Tyr Asp Val Gly Asn Thr Lys Phe		
	35	40
Phe Ser Ser Glu Phe Asp Pro Ala Thr Thr Trp Pro Tyr Gly Asp Ser		
	50	55
		60

```

Ile Asp Asp Pro Ser Gly Arg Trp Ser Asp Gly His Ile Val Pro Asp
65              70              75              80
Phe Val Gly Arg Leu Ile Gly His Arg Glu Pro Ile Pro Pro Val Leu
85
Asp Pro Lys Ala Asp Leu Ser Arg Gly Ala Ser Phe Ala Ile Ala Gly
100              105
Ala Val Val Leu Gly Ser Gln Ser Thr Thr Ala Ser Met Asn Phe Gly
115              120              125
Gln Gln Ile Ser Lys Phe Leu Glu Leu His Lys Gln Trp Thr Asp Lys
130              135
Glu Arg Ala Glu Ala Ile Tyr Met Val Asn Ile Gly Ala Glu Asp Tyr
145              150              155              160
Leu Asn Phe Ala Lys Ala His Pro Asn Ala Asn Thr Val Glu Gln Leu
165              170              175
Thr Gln Val Ala His Val Leu Gln Arg Ile Pro Arg Glu Leu Thr Ser
180              185
Leu Tyr Arg Ala Gly Gly Ala Arg Lys Phe Ala Val Gln Asn Leu Gly
195              200              205
Pro Leu Gly Cys Leu Pro Ile Val Arg Gln Glu Phe Lys Thr Gly Glu
210              215              220
Asn Cys Met Glu Met Val Asn Phe Met Val Lys Thr His Asn Glu Arg
225              230              235              240
Leu Ser Arg Leu Leu Val Ala Ile Thr Val Pro Ile Leu Tyr Arg Gly
245              250              255
Phe Arg Tyr Ser Leu Phe Asp Phe Asn Gly Glu Ile Leu Arg Arg Ile
260              265              270
Asn Glu Pro Ser Leu His Gly Tyr Thr Asp Thr Thr Thr Ser Cys Cys
275              280              285
Gly Thr Gly Ser Arg Asn Ala Tyr Gly Cys Gly Tyr Ser Asn Val His
290              295              300
Ala Lys Leu Cys Ser Tyr Gln Lys Ser Phe Leu Phe Phe Asp Gly Arg
305              310              315              320
His Asn Thr Glu Lys Thr Asp Glu Glu Val Ala Asn Leu Phe Tyr Ser
325              330              335
Gly Asp Lys His Val Val Ser Pro Met Asn Ile Lys Asp Leu Val Gly
340              345              350
Lys Ala Ala Thr Asp Leu Leu Ala Gln Glu Ile
355              360

```

(2) INFORMATION FOR SEQ ID NO:2586:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 239 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..239
- (D) OTHER INFORMATION: / Ceres Seq. ID 1573704

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2586:

```

Met Asn Phe Gly Gln Gln Ile Ser Lys Phe Leu Glu Leu His Lys Gln
1              5              10              15
Trp Thr Asp Lys Glu Arg Ala Glu Ala Ile Tyr Met Val Asn Ile Gly
20              25              30
Ala Glu Asp Tyr Leu Asn Phe Ala Lys Ala His Pro Asn Ala Asn Thr
35              40              45
Val Glu Gln Leu Thr Gln Val Ala His Val Leu Gln Arg Ile Pro Arg
50              55              60
Glu Leu Thr Ser Leu Tyr Arg Ala Gly Gly Ala Arg Lys Phe Ala Val
65              70              75              80
Gln Asn Leu Gly Pro Leu Gly Cys Leu Pro Ile Val Arg Gln Glu Phe

```

(2) INFORMATION FOR SEQ ID NO:2587:

(A) LENGTH: 1188 base pairs

(ii) MOLECULE TYPE: DNA (genomic)

(A) NAME/KEY: -

(B) LOCATION: 1..1188

(D) OTHER INFORMATION: / Ceres Seq. ID 1573705

```
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2587:
```

atcattctcgc	gtttaactaca	aacacataaat	aaaaacaaaga	gaaagagata	taatatgggt	60
gggtggggaca	tcgcagtagca	cgttggtgc	ggtagtcacc	ctaatcttcc	gcgacagaga	120
caagaagaaga	cgaaacagct	cttactcgt	tgctccaacc	tcggcataat	agctttgcgt	180
tcgaattgtt	ccgcacattga	cgtctgttg	ctcgtcata	gagaatttga	gacgcattat	240
ctgttttaatt	caggcccggtg	atctctctt	acggagaaga	gacccgttga	gatggaagct	300
agcaattatgc	acgttgacga	gagcgcgat	gggtgcggtt	cggggataac	acccgctgaa	360
aatctcatac	ctcttgcgtc	tcctgcgtac	gacaaacttc	cccacttcta	octgtgtctc	420
tcaggttgcag	aggaatttcgc	cgccaaacac	ggagttgaaa	tgttggaaca	cgagctatct	480
gtcacggcag	acaacgttag	aatgtctcaag	tggccaagtc	aaagtaactc	catcttgttt	540
atgaccggta	ttccgcgat	gggattgtgc	ggcgacgtc	cgaccgcagc	tccaatccaa	600
atgaacggtc	tctgcatac	catttacgca	cgcggagaca	ctcgggtgag	tttgtgttga	660
cgggaaaagga	cattgtgcgc	cggagacatc	cacgggttgt	tgaatgaaca	agatgactgg	720
aaggatttgt	gactcgcgc	tcgtaggaga	cgggacgtat	cgctcgagct	tttgtgggtg	780
gtcgtgtacc	ggagaaggag	aagcattat	aagagcaacc	ctagctctgt	atgtgtcacg	840
tgttatggag	tataaaggac	ttaacctcca	agagccggt	gattacgca	tcaagcatg	900
acttgacaga	gggttcgctg	gcactcattg	gttcgcgaat	aaacgagagg	ttgtttggcg	960
ttttaactct	aatgggatgt	tcaggggatt	tgcaactgag	gactgattca	tggaactgtc	1020
tattttggag	tgaaaaatat	tttagattaa	gaaaatgtct	tactgattat	ttaatcatga	1080
tcgtctctatt	aattttggtta	ttcatattca	taaaagctga	gtagataatt	tagttctctc	1140
gtctatcacca	gtctataatt	gatttgtgtt	taatcggtt	tcaaatgg		

(2) INFORMATION FOR SEQ ID NO:2588:

SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 219 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

FEATURE:

(A) NAME/KEY: peptid

(B) LOCATION: 1..219

1	Leu	1	Leu	5	Leu	5	Thr	5	Glu	10	Thr	10	His	10	Asn	10	Lys	15	Thr	15	Lys	15	Arg	15	Lys	15	Arg
Tyr	Asn	20	Met	20	Gly	20	Trp	20	Ala	25	Ile	25	Ala	25	Val	25	His	30	Gly	30	Gly	30	Ala	30	Gly	30	Ile
Asp	Pro	35	Asn	35	Leu	35	Pro	35	Ala	40	Glu	40	Arg	40	Gln	40	Glu	45	Ala	45	Lys	45	Gln	45	Leu	45	Leu
Thr	Arg	50	Cys	50	Leu	50	Asn	50	Leu	55	Gly	55	Ile	55	Ile	55	Ala	60	Leu	60	Arg	60	Ser	60	Asn	60	Val
Ala	Ile	65	Asp	65	Val	65	Val	65	Glu	70	Leu	70	Val	70	Ile	70	Arg	75	Glu	75	Leu	75	Glu	75	Thr	75	Asp
Leu	Phe	85	Asn	85	Ser	85	Gly	85	Arg	90	Gly	90	Ser	90	Ser	90	Leu	90	Thr	90	Glu	95	Lys	95	Gly	95	Thr
Glu	Met	100	Glu	100	Ala	100	Ser	100	Ile	105	Met	105	Asp	105	Gly	105	Thr	110	Lys	110	Arg	110	Arg	110	Cys	110	Gly
Val	Ser	115	Gly	115	Ile	115	Thr	115	Thr	120	Thr	120	Val	120	Lys	120	Asn	125	Pro	125	Ile	125	Ser	125	Leu	125	Ala
Val	Met	130	Asp	130	Lys	130	Ser	130	Pro	135	His	135	Ser	135	Tyr	135	Leu	140	Ala	140	Phe	140	Ser	140	Gly	140	Ala
Asp	Phe	145	Ala	145	Arg	145	Lys	145	Gln	150	Gly	150	Val	150	Glu	150	Ile	155	Val	155	Asp	155	Asn	155	Glu	155	Tyr
Val	Thr	165	Asp	165	Asp	165	Asn	165	Val	170	Gly	170	Met	170	Leu	170	Val	175	Leu	175	Ala	175	Lys	175	Glu	175	Ala
Ser	Ile	180	Leu	180	Phe	180	Asp	180	Tyr	185	Arg	185	Ile	185	Pro	185	Pro	190	Met	190	Gly	190	Cys	190	Ala	190	Gly
Ala	Ala	195	Thr	195	Asp	195	Ser	195	Pro	200	Ile	200	Gln	200	Met	200	Asn	205	Gly	205	Leu	205	Pro	205	Ile	205	Ser
Tyr	Ala	210	Pro	210	Gly	210	Asp	210	Ser	215	Arg	215	Val	215	Arg	215	Cys	215	Gly	215							

Met	Gly	Gly	Trp	Ala	Ile	Ala	Val	His	Gly	Gly	Ala	Gly	Ile	Asp	Pro
1			5						10					15	
Asn	Leu	Pro	Ala	Glu	Arg	Gln	Glu	Glu	Ala	Lys	Gln	Leu	Leu	Thr	Arg
			20					25					30		
Cys	Leu	Asn	Leu	Gly	Ile	Ile	Ala	Leu	Arg	Ser	Asn	Val	Ser	Ala	Ile
			35				40				45				
Asp	Val	Val	Glu	Leu	Val	Ile	Arg	Glu	Leu	Glu	Thr	Asp	Pro	Leu	Phe
			50			55					60				
Asn	Ser	Gly	Arg	Gly	Ser	Ser	Leu	Thr	Glu	Lys	Gly	Thr	Val	Glu	Met
65					70					75					80
Glu	Ala	Ser	Ile	Met	Asp	Gly	Thr	Lys	Arg	Arg	Cys	Gly	Ala	Val	Ser
				85				90						95	
Gly	Ile	Thr	Thr	Val	Lys	Asn	Pro	Ile	Ser	Leu	Ala	Arg	Leu	Val	Met
			100					105					110		
Asp	Lys	Ser	Pro	His	Ser	Tyr	Leu	Ala	Phe	Ser	Gly	Ala	Glu	Asp	Phe
			115				120					125			
Ala	Arg	Lys	Gln	Gly	Val	Glu	Ile	Val	Asp	Asn	Glu	Tyr	Phe	Val	Thr
			130			135					140				
Asp	Asp	Asn	Val	Gly	Met	Leu	Lys	Leu	Ala	Lys	Glu	Ala	Asn	Ser	Ile

145 150 155 160
Leu Phe Asp Tyr Arg Ile Pro Pro Met Gly Cys Ala Gly Ala Ala Ala
165 170 175
Thr Asp Ser Pro Ile Gln Met Asn Gly Leu Pro Ile Ser Ile Tyr Ala
180 185 190
Pro Gly Asp Ser Arg Val Arg Cys Gly
195 200

(2) INFORMATION FOR SEQ ID NO:2590:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 122 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..122
- (D) OTHER INFORMATION: / Ceres Seq. ID 1573708

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2590:

Met Glu Ala Ser Ile Met Asp Gly Thr Lys Arg Arg Cys Gly Ala Val
1 5 10 15
Ser Gly Ile Thr Thr Val Lys Asn Pro Ile Ser Leu Ala Arg Leu Val
20 25 30
Met Asp Lys Ser Pro His Ser Tyr Leu Ala Phe Ser Gly Ala Glu Asp
35 40 45
Phe Ala Arg Lys Gln Gly Val Glu Ile Val Asp Asn Glu Tyr Phe Val
50 55 60
Thr Asp Asp Asn Val Gly Met Leu Lys Leu Ala Lys Glu Ala Asn Ser
65 70 75 80
Ile Leu Phe Asp Tyr Arg Ile Pro Pro Met Gly Cys Ala Gly Ala Ala
85 90 95
Ala Thr Asp Ser Pro Ile Gln Met Asn Gly Leu Pro Ile Ser Ile Tyr
100 105 110
Ala Pro Gly Asp Ser Arg Val Arg Cys Gly
115 120

(2) INFORMATION FOR SEQ ID NO:2591:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1048 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1048
- (D) OTHER INFORMATION: / Ceres Seq. ID 1573713

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2591:

aacgcaattta aattaatatt tatggataat atgggtaata aataaggaac ttctatttat 60
atcacaaaaa gtcactgggtc ttcttcgtgt gacttcacca cttttctcgc tccccaaaaa 120
atggctctct cactcttttc agtctttatc tttttccgat tttttaccac ttgtgttttt 180
gtgtgttcaa atgagggaatc caaggcccta gtttttttac caacgccaac acttccatcg 240
ccatctcgcg ctaccacaaac gccgtcgcca gctctcaaac cgccgacgoc tgcgtacaag 300
ccaccacgcg tgccaaactac tctattataa ccaccaccca caaaacctcc ggtcaaaCct 360
ccaactactt cggttacacc agtaaaacct ccggtttcaa ctctccgat caaactaccg 420
ccggttacacc cactctacga caaaccacca acgccaacag ttaaaccacc tgcctgccaa 480
ccactactgt acaaaacccc actccaacg gttaaaccac ccactacatc accggtttaa 540
ccaccacta ccgcaaccagt ccaatcacgc ccggtccaac cactactcga caaaccoccc 600
acgtcacccg ttaaaccacc caccacaact ccaccggta aacccccacc caccgaccca 660
ccggtccaac cactctacga caatccccca actacacgta ttaaaccacc tacagccgcg 720
cctgtcaaac ctccgacacc acctcccgta agaactcgga tagattcggt gcctttatgt 780
gggacgaggt gtgggcaaca ctcgaggaag aacgtatgta tgagagcgctg cgtcacgtgc 840

tgctaccggt gcaagtgtgt tccccaggc acctacggta ataaggagaa gtgtggatct 900
tgttacggca acatgaagac acgtggtgga aaatccaaat gtccttgaac ctttatatga 960
cgatggttgt taaacgaaat aatttaaatac aatggagttt ttataagttt gtaatgcgtt 1020
tgttttttgtt atagtaatat tgagttgg

(2) INFORMATION FOR SEQ ID NO:2592:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 275 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..275

(D) OTHER INFORMATION: / Ceres Seq. ID 1573714

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2592:

Met	Ala	Leu	Ser	Leu	Ser	Val	Phe	Ile	Phe	Phe	His	Val	Phe	Thr
1		5						10					15	
Asn	Val	Val	Phe	Ala	Ala	Ser	Asn	Glu	Glu	Ser	Lys	Ala	Leu	Val
		20						25				30		
Leu	Pro	Thr	Pro	Thr	Leu	Pro	Ser	Pro	Ser	Pro	Ala	Thr	Lys	Pro
		35				40					45			
Ser	Pro	Ala	Leu	Lys	Pro	Pro	Thr	Pro	Ser	Tyr	Lys	Pro	Pro	Thr
		50				55				60				
Pro	Thr	Thr	Pro	Ile	Lys	Pro	Pro	Thr	Thr	Lys	Pro	Pro	Val	Lys
65					70					75				80
Pro	Thr	Thr	Ser	Val	Thr	Pro	Val	Lys	Pro	Pro	Val	Ser	Thr	Pro
				85				90						95
Ile	Lys	Leu	Pro	Pro	Val	Gln	Pro	Pro	Thr	Tyr	Lys	Pro	Pro	Thr
		100				105						110		
Thr	Val	Lys	Pro	Pro	Ser	Val	Gln	Pro	Pro	Thr	Tyr	Lys	Pro	Thr
		115				120						125		
Pro	Thr	Val	Lys	Pro	Pro	Thr	Thr	Ser	Pro	Val	Lys	Pro	Pro	Thr
		130				135					140			
Pro	Pro	Val	Gln	Ser	Pro	Pro	Val	Gln	Pro	Pro	Thr	Tyr	Lys	Pro
145					150					155				160
Thr	Ser	Pro	Val	Lys	Pro	Pro	Thr	Thr	Thr	Pro	Pro	Val	Lys	Pro
				165				170						175
Thr	Thr	Thr	Pro	Pro	Val	Gln	Pro	Pro	Thr	Tyr	Asn	Pro	Pro	Thr
			180					185				190		
Pro	Val	Lys	Pro	Pro	Thr	Ala	Pro	Pro	Val	Lys	Pro	Pro	Thr	Pro
			195			200					205			
Pro	Val	Arg	Thr	Arg	Ile	Asp	Cys	Val	Pro	Leu	Cys	Gly	Thr	Arg
		210				215					220			
Gly	Gln	His	Ser	Arg	Lys	Asn	Val	Cys	Met	Arg	Ala	Cys	Val	Thr
225					230					235				240
Cys	Tyr	Arg	Cys	Lys	Cys	Val	Pro	Pro	Gly	Thr	Tyr	Gly	Asn	Lys
				245				250						255
Lys	Cys	Gly	Ser	Cys	Tyr	Ala	Asn	Met	Lys	Thr	Arg	Gly	Gly	Lys
			260					265						270
Lys	Cys	Pro												
		275												

(2) INFORMATION FOR SEQ ID NO:2593:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 836 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..836

(D) OTHER INFORMATION: / Ceres Seq. ID 1573727

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2593:

cttttttttt	tgtctattat	ttttttgact	ttgatctccc	atcagttcat	cttctcttct	60
ttcttctgat	caacctatgg	tgtgtgtata	agtgtgtcag	tctctttacc	ttcctccaag	120
tcctctctct	ttctcaccaa	aatctctctt	gtatccctct	aaaggatttt	cctcaagaag	180
agcacagtgt	gttacagaag	agttgtgtca	gtgaaggctc	aggtgacaac	agatactacc	240
gaggcaccac	cagttaaagt	agtcaaggag	tctaagaaac	aggaagaagg	gattgtgtgc	300
aacaaatttc	aacctaaaga	cccttacact	ggtcgtgtcc	ttttgaacac	caagatcacc	360
ggtgatgacg	ctcccggtga	gacttggcac	attgtcttca	ccaccgaagg	TGagWgNttc	420
cgtatagaga	aggacaatgc	ataggagtag	ttccagaggg	aatagacaag	aacgggaagc	480
cgcacaagct	cagcgtttac	tctatcgcga	gtagtcccat	tgtgtacttt	ggagactcca	540
agaccgcttc	ttctctgttc	aagagactag	tttacacaaa	tgatggcgga	gagattgtta	600
agggggctgt	ctccaacttc	ttgtgtgact	tgaagccggg	tgatgaagct	aagatcactg	660
gacctgttgg	caaggaataat	cttatgccaa	aagaccocaa	tgccaccatc	atcatgcttg	720
gaacagggaac	tgggaatagt	ccattcagat	cattttgtg	gaaaatgttc	tttgaggagc	780
acgaggacta	caagttccaat	ggtttggcgt	ggcttttctt	gggtgtacc	acaagc	

(2) INFORMATION FOR SEQ ID NO:2594:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 84 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..84

(D) OTHER INFORMATION: / Ceres Seq. ID 1573728

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2594:

Phe	Phe	Phe	Ala	Tyr	Tyr	Phe	Phe	Asp	Phe	Asp	Leu	Pro	Ser	Val	His	
1				5						10				15		
Leu	Leu	Leu	Leu	Leu	Leu	Ile	Asn	His	Gly	Cys	Cys	Tyr	Lys	Cys	Cys	
				20				25					30			
Ser	Leu	Phe	Thr	Phe	Leu	Gln	Val	Ile	Leu	Ser	Pro	His	Gln	Asn	Leu	
				35			40					45				
Leu	Cys	Ile	Pro	Ser	Lys	Asp	Phe	Pro	Gln	Glu	Glu	His	Ser	Val	Leu	
				50			55					60				
Gln	Lys	Ser	Cys	Val	Ser	Glu	Gly	Ser	Gly	Asp	Asn	Arg	Tyr	Tyr	Arg	
				65		70			75					80		
Gly	Thr	Thr	Ser													

(2) INFORMATION FOR SEQ ID NO:2595:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 122 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..122

(D) OTHER INFORMATION: / Ceres Seq. ID 1573729

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2595:

Met	Ala	Ala	Ala	Ile	Ser	Ala	Ala	Val	Ser	Leu	Pro	Ser	Ser	Lys	Ser	
1				5						10				15		
Ser	Ser	Leu	Leu	Thr	Lys	Ile	Ser	Ser	Val	Ser	Pro	Gln	Arg	Ile	Phe	
				20				25				30				
Leu	Lys	Lys	Ser	Thr	Val	Cys	Tyr	Arg	Arg	Val	Val	Ser	Val	Lys	Ala	
				35			40					45				
Gln	Val	Thr	Thr	Asp	Thr	Thr	Glu	Ala	Pro	Pro	Val	Lys	Val	Val	Lys	
				50			55				60					

Glu Ser Lys Lys Gln Glu Glu Gly Ile Val Val Asn Lys Phe Lys Pro
65 70 75 80
Lys Asn Pro Tyr Thr Gly Arg Cys Leu Leu Asn Thr Lys Ile Thr Gly
85 90 95
Asp Asp Ala Pro Gly Glu Thr Trp His Ile Val Phe Thr Thr Glu Gly
100 105 110
Glu Xaa Phe Arg Ile Glu Lys Asp Asn Arg
115 120

(2) INFORMATION FOR SEQ ID NO:2596:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1275 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1275

(D) OTHER INFORMATION: / Ceres Seq. ID 1573730

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2596:

```

aatctttttt tttttgttta ttattttttt gactttgac tcccatcagt tcatctcttt 60
cttctttctt tgatcaacca tgggtgtctg tataagtgtc gcagtctctt taccttcttc 120
caagtcatcc tctctctcca ccaaaatctc ctctgtatcc cctcaaagga ttttctctaa 180
gaagagcaca gtgtgtttta gaagagtgtt gtcagtgaa gctcagggtg caacagatac 240
taccgaggca ccaccaggtta aagtagtcaa ggaagtctaa aaacaggaga aagggattgt 300
tgtcaacaaa ttcaaaccta agaaccctta cactggctgc tgctttttga acaccaagat 360
caccgggtgt gacgtctccg gtgagacttg gcacattgtc ttcaccaccg aaggtgaggt 420
tcctgtatga gaaggacaat cgataggagt gattccagag ggaatagaca agaaccggaa 480
gcgcgcaaa ctcaggcttt actctatcgc gagttagtgc attggtgact ttggagactc 540
caagaccgtt tctctctgtg tcaagagact agttttacaa aatgatggcg gagagattgt 600
taagggggtc tgctccaact tcttgtgtga cttgaagcgg ggtgatgaag ctaagatcac 660
tggacctgtt ggcaaggaaa tgccttatgc aaaagaccoc aatgccacca tcatctgct 720
tggaacagga actggaatag ctccattcag atcatttttg tggaaaatgt tctttgagga 780
gcacgaggac tacaagtcca atggtttggc gtggtctttc ttgggtgtac ccagaagcag 840
ctcactgcta tacaaggagg agtttgagaa gatgaaggag aagaaccagc acaacttcag 900
gctggacttt gcggtgagca gagagcagac gaacgagaag ggagagaaaa tgtacattca 960
gacaagaatg ccagagtatg cagAaagagc tgtgggagtt gctgaagaaa gacaacacct 1020
tgttttacct gtgtgtgtctt aagggtatgg agaagggatc cgtatgacatt atggtctcgc 1080
ttgctgtcaa agatgggcta gattgtgttg attacaaaga gcaatttgaag agggatgaac 1140
agtggaatgt tgaagtctac taaggaaagt tctgaggagg taattatata atgtagataa 1200
aaagcttcag atgcattgtg aaatcttcac atctgcttct tttttcttcc tcaaggattt 1260
tcaatcaaaa catcc

```

(2) INFORMATION FOR SEQ ID NO:2597:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 320 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..320

(D) OTHER INFORMATION: / Ceres Seq. ID 1573731

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2597:

```

Met Ala Ala Ala Ile Ser Ala Ala Val Ser Leu Pro Ser Ser Lys Ser
1 5 10 15
Ser Ser Leu Leu Thr Lys Ile Ser Ser Val Ser Pro Gln Arg Ile Phe
20 25 30
Leu Lys Lys Ser Thr Val Cys Tyr Arg Arg Val Val Ser Val Lys Ala
35 40 45
Gln Val Thr Thr Asp Thr Thr Glu Ala Pro Pro Val Lys Val Val Lys

```


50	55	60
Glu Ser Lys Lys Gln	Glu Glu Gly Ile Val	Val Asn Lys Phe Lys Pro
65	70	75
Lys Asn Pro Tyr Thr	Gly Arg Cys Leu Leu	Asn Thr Lys Ile Thr Gly
85	90	95
Asp Asp Ala Pro Gly	Glu Thr Trp His Ile Val	Phe Thr Thr Glu Gly
100	105	110
Glu Val Pro Tyr Arg	Glu Gly Gln Ser Ile Gly	Val Ile Pro Glu Gly
115	120	125
Ile Asp Lys Asn Gly	Lys Pro His Lys Leu Arg	Leu Tyr Ser Ile Ala
130	135	140
Ser Ser Ala Ile Gly	Asp Phe Gly Asp Ser	Lys Thr Val Ser Leu Cys
145	150	155
Val Lys Arg Leu Val	Tyr Thr Asn Asp Gly	Gly Glu Ile Val Lys Gly
165	170	175
Val Cys Ser Asn Phe	Leu Cys Asp Leu Lys	Pro Gly Asp Glu Ala Lys
180	185	190
Ile Thr Gly Pro Val	Gly Lys Glu Met Leu	Met Pro Lys Asp Pro Asn
195	200	205
Ala Thr Ile Ile Met	Leu Gly Thr Gly Ile	Ala Pro Phe Arg
210	215	220
Ser Phe Leu Trp Lys	Met Phe Phe Glu Glu	His Glu Asp Tyr Lys Phe
225	230	235
Asn Gly Leu Ala Trp	Leu Phe Leu Gly Val	Pro Arg Ser Ser Ser Leu
245	250	255
Leu Tyr Lys Glu Glu	Phe Glu Lys Met Lys	Glu Lys Asn Pro Asp Asn
260	265	270
Phe Arg Leu Asp Phe	Ala Val Ser Arg Glu	Gln Thr Asn Glu Lys Gly
275	280	285
Glu Lys Met Tyr Ile	Gln Thr Arg Met Ala	Glu Tyr Ala Glu Arg Ala
290	295	300
Val Gly Val Ala Glu	Glu Arg Gln His Leu	Cys Glu His Val Trp Ser
305	310	315
		320

(2) INFORMATION FOR SEQ ID NO:2598:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1339 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1339
- (D) OTHER INFORMATION: / Ceres Seq. ID 1573732

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2598:

aattattact	ttaattctct	ttccgcctct	ctattcttct	tcttctttag	gatcaatcac	60
cggttagctt	tcttcccatc	cgctctctcg	tttacgacca	gtatacagag	gctggagctg	120
gggaagaaaa	ggattgtcta	tggaggggaga	cgctcggaata	ggttttggtat	gccagaatac	180
tatggatggg	aaggcgagta	atggaaatgg	tttagagaag	actgtacctt	ctgtgtgcct	240
taaggtctat	gcattgtgtac	ctgaggatga	tgctaagtgt	cactccactg	ttgtttctgg	300
gtggtttctg	gaacctcacc	ctcgctctgg	gaaaaaaggc	ggcaaaagcag	tctatttcaa	360
caaccttatg	tggccaggag	aagcacactc	actgaaagtt	gagaaaagtc	tgttcaaaga	420
caagtcgagt	tttcaggagg	tcttagtggt	cgagtcagcc	acgtacggaa	aggtgcttgt	480
tctagatggg	atcgtaacgc	tgaccgaaaa	agatgaatgt	gcataccagg	agatgatagc	540
ccatctgcct	ttatgtctta	tattctcccc	taaaaatggt	ctgtgttgtt	gtggaggtga	600
tggtgtgtgt	tttcagagaa	ttctcgcaca	tagttcttgt	gaggttatgt	atatctgtga	660
gatatgaca	atggttatag	atgtgtctaa	gaagTtcTtc	cccgagttag	cggttggtgt	720
tgacgatcct	cggtgtcaac	ttcacattag	tgaatgtgct	gagttctctc	gtaaaatccc	780
tgaagggaag	tatgatgcga	tcattgttga	ttcttcagat	cccgtaggtc	ctgctcttgc	840

(2) INFORMATION FOR SEO ID NO:2599:

(A) LENGTH: 359 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: lin

MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..359

(D) OTHER INFORMATION: / Ceres Seq. ID 1573733

```
(x1) SEQUENCE DESCRIPTION: SEQ ID NO:2599:
```

Met	Glu	Gly	Asp	Val	Gly	Ile	Gly	Leu	Val	Cys	Gln	Asn	Thr	Met	Asp
1				5				10						15	
Gly	Lys	Ala	Ser	Asn	Gly	Asn	Gly	Leu	Glu	Lys	Thr	Val	Pro	Ser	Cys
			20					25					30		
Cys	Leu	Lys	Ala	Met	Ala	Cys	Val	Pro	Glu	Asp	Asp	Ala	Lys	Cys	His
		35					40					45			
Ser	Thr	Val	Val	Ser	Gly	Trp	Phe	Ser	Glu	Pro	His	Pro	Arg	Ser	Gly
	50					55					60				
Lys	Lys	Gly	Gly	Lys	Ala	Val	Tyr	Phe	Asn	Asn	Pro	Met	Trp	Pro	Gly
65					70					75					80
Glu	Ala	His	Ser	Leu	Lys	Val	Glu	Lys	Val	Leu	Phe	Lys	Asp	Lys	Ser
				85					90					95	
Asp	Phe	Gln	Glu	Val	Leu	Val	Phe	Glu	Ser	Ala	Thr	Tyr	Gly	Lys	Val
			100					105					110		
Leu	Val	Leu	Asp	Gly	Ile	Val	Gln	Leu	Thr	Glu	Lys	Asp	Glu	Cys	Ala
		115					120					125			
Tyr	Gln	Glu	Met	Ile	Ala	His	Leu	Pro	Leu	Cys	Ser	Ile	Ser	Ser	Pro
	130					135					140				
Lys	Asn	Val	Leu	Val	Val	Gly	Gly	Gly	Asp	Gly	Gly	Val	Lys	Arg	Gly
145					150					155					160
Ile	Ser	Arg	His	Ser	Ser	Val	Glu	Val	Ile	Asp	Ile	Cys	Glu	Ile	Asp
				165					170					175	
Lys	Met	Val	Ile	Asp	Val	Ser	Lys	Lys	Phe	Phe	Pro	Glu	Leu	Ala	Val
			180						185				190		
Gly	Phe	Asp	Asp	Pro	Arg	Val	Gln	Leu	His	Ile	Ser	Asp	Ala	Ala	Glu
		195					200					205			
Phe	Leu	Arg	Lys	Ser	Pro	Glu	Gly	Lys	Tyr	Asp	Ala	Ile	Ile	Val	Asp
	210					215				220					
Ser	Ser	Asp	Pro	Val	Gly	Pro	Ala	Leu	Ala	Leu	Val	Glu	Lys	Pro	Phe
225					230					235					240
Phe	Glu	Thr	Leu	Ala	Arg	Ala	Leu	Lys	Pro	Gly	Gly	Val	Leu	Cys	Asn
				245					250					255	
Met	Ala	Glu	Ser	Met	Trp	Leu	His	Thr	His	Leu	Ile	Glu	Asp	Met	Ile
		260						265					270		
Ser	Ile	Cys	Arg	Gln	Thr	Phe	Lys	Ser	Val	His	Tyr	Ala	Trp	Ser	Ser
		275					280					285			
Val	Pro	Thr	Tyr	Pro	Ser	Gly	Val	Ile	Gly	Phe	Val	Leu	Cys	Ser	Thr
	290					295				300					
Glu	Gly	Pro	Ala	Val	Asp	Phe	Lys	Asn	Pro	Ile	Asn	Pro	Ile	Glu	Lys
305					310					315					320

Leu Asp Gly Ala Met Thr His Lys Arg Glu Leu Lys Phe Tyr Asn Ser
325 330 335
Asp Met His Arg Ala Ala Phe Ala Leu Pro Thr Phe Leu Arg Arg Glu
340 345 350
Val Ala Ser Leu Leu Ala Ser
355

(2) INFORMATION FOR SEQ ID NO:2600:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 345 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..345

(D) OTHER INFORMATION: / Ceres Seq. ID 1573734

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2600:

Met Asp Gly Lys Ala Ser Asn Gly Asn Gly Leu Glu Lys Thr Val Pro
1 5 10 15
Ser Cys Cys Leu Lys Ala Met Ala Cys Val Pro Glu Asp Asp Ala Lys
20 25 30
Cys His Ser Thr Val Val Ser Gly Trp Phe Ser Glu Pro His Pro Arg
35 40 45
Ser Gly Lys Lys Gly Gly Lys Ala Val Tyr Phe Asn Asn Pro Met Trp
50 55 60
Pro Gly Glu Ala His Ser Leu Lys Val Glu Lys Val Leu Phe Lys Asp
65 70 75 80
Lys Ser Asp Phe Gln Glu Val Leu Val Phe Glu Ser Ala Thr Tyr Gly
85 90 95
Lys Val Leu Val Leu Asp Gly Ile Val Gln Leu Thr Glu Lys Asp Glu
100 105 110
Cys Ala Tyr Gln Glu Met Ile Ala His Leu Pro Leu Cys Ser Ile Ser
115 120 125
Ser Pro Lys Asn Val Leu Val Val Gly Gly Gly Asp Gly Gly Val Leu
130 135 140
Arg Glu Ile Ser Arg His Ser Ser Val Glu Val Ile Asp Ile Cys Glu
145 150 155 160
Ile Asp Lys Met Val Ile Asp Val Ser Lys Lys Phe Phe Pro Glu Leu
165 170 175
Ala Val Gly Phe Asp Asp Pro Arg Val Gln Leu His Ile Ser Asp Ala
180 185 190
Ala Glu Phe Leu Arg Lys Ser Pro Glu Gly Lys Tyr Asp Ala Ile Ile
195 200 205
Val Asp Ser Ser Asp Pro Val Gly Pro Ala Leu Ala Leu Val Glu Lys
210 215 220
Pro Phe Phe Glu Thr Leu Ala Arg Ala Leu Lys Pro Gly Gly Val Leu
225 230 235 240
Cys Asn Met Ala Glu Ser Met Trp Leu His Thr His Leu Ile Glu Asp
245 250 255
Met Ile Ser Ile Cys Arg Gln Thr Phe Lys Ser Val His Tyr Ala Trp
260 265 270
Ser Ser Val Pro Thr Tyr Pro Ser Gly Val Ile Gly Phe Val Leu Cys
275 280 285
Ser Thr Glu Gly Pro Ala Val Asp Phe Lys Asn Pro Ile Asn Pro Ile
290 295 300
Glu Lys Leu Asp Gly Ala Met Thr His Lys Arg Glu Leu Lys Phe Tyr
305 310 315 320
Asn Ser Asp Met His Arg Ala Ala Phe Ala Leu Pro Thr Phe Leu Arg
325 330 335
Arg Glu Val Ala Ser Leu Leu Ala Ser

340

345

(2) INFORMATION FOR SEQ ID NO:2601:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 323 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..323

(D) OTHER INFORMATION: / Ceres Seq. ID 1573735

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2601:

Met	Ala	Cys	Val	Pro	Glu	Asp	Asp	Ala	Lys	Cys	His	Ser	Thr	Val	Val	
1			5					10						15		
Ser	Gly	Trp	Phe	Ser	Glu	Pro	His	Pro	Arg	Ser	Gly	Lys	Glu	Gly	Gly	
			20				25					30				
Lys	Ala	Val	Tyr	Phe	Asn	Asn	Pro	Met	Trp	Pro	Gly	Glu	Ala	His	Ser	
			35				40					45				
Leu	Lys	Val	Glu	Lys	Val	Leu	Phe	Lys	Asp	Lys	Ser	Asp	Phe	Gln	Glu	
			50			55				60						
Val	Leu	Val	Phe	Glu	Ser	Ala	Thr	Tyr	Gly	Lys	Val	Leu	Val	Leu	Asp	
65				70				75						80		
Gly	Ile	Val	Gln	Leu	Thr	Glu	Lys	Asp	Glu	Cys	Ala	Tyr	Gln	Glu	Met	
			85					90				95				
Ile	Ala	His	Leu	Pro	Leu	Cys	Ser	Ile	Ser	Ser	Pro	Lys	Asn	Val	Leu	
			100				105					110				
Val	Val	Gly	Gly	Gly	Asp	Gly	Gly	Val	Leu	Arg	Glu	Ile	Ser	Arg	His	
			115			120					125					
Ser	Ser	Val	Glu	Val	Ile	Asp	Ile	Cys	Glu	Ile	Asp	Lys	Met	Val	Ile	
			130			135					140					
Asp	Val	Ser	Lys	Lys	Phe	Phe	Pro	Glu	Leu	Ala	Val	Gly	Phe	Asp	Asp	
145				150						155				160		
Pro	Arg	Val	Gln	Leu	His	Ile	Ser	Asp	Ala	Ala	Glu	Phe	Leu	Arg	Lys	
			165					170						175		
Ser	Pro	Glu	Gly	Lys	Tyr	Asp	Ala	Ile	Ile	Val	Asp	Ser	Ser	Asp	Pro	
			180			185						190				
Val	Gly	Pro	Ala	Leu	Ala	Leu	Val	Glu	Lys	Pro	Phe	Phe	Glu	Thr	Leu	
			195			200					205					
Ala	Arg	Ala	Leu	Lys	Pro	Gly	Gly	Val	Leu	Cys	Asn	Met	Ala	Glu	Ser	
			210			215					220					
Met	Trp	Leu	His	Thr	His	Leu	Ile	Glu	Asp	Met	Ile	Ser	Ile	Cys	Arg	
225				230						235				240		
Gln	Thr	Phe	Lys	Ser	Val	His	Tyr	Ala	Trp	Ser	Ser	Val	Pro	Thr	Tyr	
			245					250						255		
Pro	Ser	Gly	Val	Ile	Gly	Phe	Val	Leu	Cys	Ser	Thr	Glu	Gly	Pro	Ala	
			260				265						270			
Val	Asp	Phe	Lys	Asn	Pro	Ile	Asn	Pro	Ile	Glu	Lys	Leu	Asp	Gly	Ala	
			275			280					285					
Met	Thr	His	Lys	Arg	Glu	Leu	Lys	Phe	Tyr	Asn	Ser	Asp	Met	His	Arg	
			290			295					300					
Ala	Ala	Phe	Ala	Leu	Pro	Thr	Phe	Leu	Arg	Arg	Glu	Val	Ala	Ser	Leu	
			305		310				315					320		
Leu	Ala	Ser														

(2) INFORMATION FOR SEQ ID NO:2602:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1444 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1444

(D) OTHER INFORMATION: / Ceres Seq. ID 1573736

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2602:

```
aaaaatatcaa aacacgagac agatttgatt ccatttttat tactgttact atcatccaaa      60
acottgggtat ttgtagccat gagtcttggt tcagatctca tcaaccttaa cctctcagac      120
tcacatgaca aaatcattgc tgaatacata tgggttggtg gttctggaat ggacatgaga      180
agcaaaagcca ggaactctacc tggaccagtg actgaccctt cgcagctacc aaagtggaa      240
tatgatgggtt caagcacagg caaagctcct ggtgaagaca gtgaagtcat ctatatagtta      300
ataatctttc ttctctgatt ttttaataag ttctctctca ttgttttttt ttctgattct      360
tgtttactaa tccttttggt gtttgtatat cttgttttag cctcgaagcc atattcaaa      420
atcctttccg tagaggaaa aacattcttg tcatgtgcga tgcgtacact ccgcggggtg      480
aaccaatccg gactaaacaa agacacgctg cggctaaggt ctttagcaac cctgatgttg      540
cagctgaagt gccatgggat ggtattgagc aagaatacac ttactccaag aaagatgtga      600
ggtggcctgt ttggttgctt attggcggtt atcccgcccc tcaggggaccg tactattgcg      660
gtattggagc agacaaatct tttggcagag atgtgtttga tctcactac aaggcctggt      720
tatacgctgt aatcaacatt agtggcatca atggagaagt catgccgggt cagtgggagt      780
tcacagtcgg tccagctggt ggtatctcgg ctgctgatga aattttgggtc gctcgtttaca      840
ttttggagag gatacacagag attgctgggt tagtgggtac ttttgaccgc aaaccgattc      900
ccgggtgact gaagcgtctg ggtgctcact gcaactacag taccaagtca atgaggggaag      960
aaggcggtta cgagatcatc aagaaagcaa tcgataaatT gggactgaga cacaaagarc      1020
rcattgctgc ttacsgtgaa ggcaatgagc gtgctctcac aggacaccac gagactgctg      1080
acatacaaac ttctcttttg ggtgttgcca accgtggagc atcgatccga gttaggcagtg      1140
atcaggagaa agaaggagaa ggatactttg aggacaggag ccagactctg aacatggatc      1200
cttaacattg tacttccatg attgcagaga ccaccatcct ctggaatcct tgatgatcat      1260
cagatcaaga aaaaatcttg aatgtcactc aaattttgtg ttcttgcaag attcaaaagt      1320
tgtgtctctc atcaagcaat gtcttaggat aagtcaaaaga ttgctctgc ttattctgct      1380
ttttatttacc ttcacatcct attgaaaaaa ttattgtgta ttattatga ataaacatta      1440
tctt
```

(2) INFORMATION FOR SEQ ID NO:2603:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 266 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..266

(D) OTHER INFORMATION: / Ceres Seq. ID 1573737

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2603:

```
Met Cys Asp Ala Tyr Thr Pro Ala Gly Glu Pro Ile Pro Thr Asn Lys
1      5      10      15
Arg His Ala Ala Ala Lys Val Phe Ser Asn Pro Asp Val Ala Ala Glu
20     25     30
Val Pro Trp Tyr Gly Ile Glu Gln Glu Tyr Thr Leu Leu Gln Lys Asp
35     40     45
Val Arg Trp Pro Val Gly Trp Pro Ile Gly Gly Tyr Pro Gly Pro Gln
50     55     60
Gly Pro Tyr Tyr Cys Gly Ile Gly Ala Asp Lys Ser Phe Gly Arg Asp
65     70     75     80
Val Val Asp Ser His Tyr Lys Ala Cys Leu Tyr Ala Gly Ile Asn Ile
85     90     95
Ser Gly Ile Asn Gly Glu Val Met Pro Gly Gln Trp Glu Phe Gln Val
100    105    110
Gly Pro Ala Val Gly Ile Ser Ala Ala Asp Glu Ile Trp Val Ala Arg
115    120    125
Tyr Ile Leu Glu Arg Ile Thr Glu Ile Ala Gly Val Val Val Ser Phe
130    135    140
```

```

Asp Pro Lys Pro Ile Pro Gly Asp Trp Asn Gly Ala Gly Ala His Cys
145                               150           155           160
Asn Tyr Ser Thr Lys Ser Met Arg Glu Gly Tyr Glu Ile Ile
                               165           170           175
Lys Lys Ala Ile Asp Lys Leu Gly Leu Arg His Lys Xaa Xaa Ile Ala
                               180           185           190
Ala Tyr Xaa Glu Gly Asn Glu Arg Arg Leu Thr Gly His His Glu Thr
                               195           200           205
Ala Asp Ile Asn Thr Phe Leu Trp Gly Val Ala Asn Arg Gly Ala Ser
                               210           215           220
Ile Arg Val Gly Arg Asp Thr Glu Lys Glu Gly Lys Gly Tyr Phe Glu
225                               230           235           240
Asp Arg Arg Pro Ala Ser Asn Met Asp Pro Tyr Ile Val Thr Ser Met
                               245           250           255
Ile Ala Glu Thr Thr Ile Leu Trp Asn Pro
                               260           265

```

(2) INFORMATION FOR SEQ ID NO:2604:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 163 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..163
- (D) OTHER INFORMATION: / Ceres Seq. ID 1573738

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2604:

```

Met Pro Gly Gln Trp Glu Phe Gln Val Gly Pro Ala Val Gly Ile Ser
1                               5           10           15
Ala Ala Asp Glu Ile Trp Val Ala Arg Tyr Ile Leu Glu Arg Ile Thr
                               20           25           30
Glu Ile Ala Gly Val Val Val Ser Phe Asp Pro Lys Pro Ile Pro Gly
                               35           40           45
Asp Trp Asn Gly Ala Gly Ala His Cys Asn Tyr Ser Thr Lys Ser Met
50                               55           60
Arg Glu Glu Gly Gly Tyr Glu Ile Ile Lys Lys Ala Ile Asp Lys Leu
65                               70           75           80
Gly Leu Arg His Lys Xaa Xaa Ile Ala Ala Tyr Xaa Glu Gly Asn Glu
                               85           90           95
Arg Arg Leu Thr Gly His His Glu Thr Ala Asp Ile Asn Thr Phe Leu
                               100          105          110
Trp Gly Val Ala Asn Arg Gly Ala Ser Ile Arg Val Gly Arg Asp Thr
                               115          120          125
Glu Lys Glu Gly Lys Gly Tyr Phe Glu Asp Arg Arg Pro Ala Ser Asn
130          135          140
Met Asp Pro Tyr Ile Val Thr Ser Met Ile Ala Glu Thr Thr Ile Leu
145          150          155          160
Trp Asn Pro

```

(2) INFORMATION FOR SEQ ID NO:2605:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1464 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1464
- (D) OTHER INFORMATION: / Ceres Seq. ID 1573751

aggttctact	gcgaagttt	caacagattc	gccggagaat	cttcggaatc	acggcggaga	60
aatggctcta	taacgcctc	ctacacgatc	caacatcatc	actcgtccct	tctccgcgcg	120
cttcagcgca	ttaattctca	ccgacacaac	tcgcatacaa	atcagagatt	cgcttctctt	180
caacagctca	ttaatgtgat	cacgctgcag	ctccgtcgca	tcaatcagct	ragagctctc	240
cgattttctc	agaanccat	cggtgtgatc	taactatgga	aatcgmscc	gatctctctt	300
acaacggcga	gctaattcca	gggttttgcg	atctctca	cgcccaagaa	cggtagctca	360
tagCvgtgga	agctgcstai	ccgaagaaga	accggtattt	tactgtttat	cgctgataact	420
gtatttttct	aggtcgtggt	ggttcgcttc	atgaagtttt	ctcagagctt	atgggaagac	480
aagctggttg	tctaaagggt	aaagttggat	ctatgcattc	ctataaaga	gaatcgtcgt	540
tttacgggtg	tcatgggatt	gttgtgtgct	aggttccatt	aggtttgtgt	attgcttttg	600
ctcagaagta	taataaggaa	gaggtctgtc	caatttgcct	tgttgttgat	ggtgcgtcga	660
atccaggaca	gttgtttgaa	ctgttgaata	tttctgcctc	tggaggtttg	ctgcgaattt	720
tgtctcgcga	gacaatcac	gttgaaatgt	gaactcgtga	atggagagct	gctaaagatc	780
ctctcttacta	caagcgtggt	tattatgttc	ctgtaactca	ggtagatggt	atggatgcgt	840
ttgtctgcga	acaaactgtc	aaattttctc	agcacatgc	gttggaagaa	gggcccaata	900
ttcttgagat	ggacacatca	aggttaccag	ctactccat	ctctgtactc	ggagacaact	960
accgtaccgg	agatgagata	tctggttgta	ggcaggaacg	ggatccaatt	ggagaataaa	1020
agaagctggt	actatctcat	gacctatgca	ccggaagaag	gcttaaggat	atggagaagg	1080
aaattagaaa	agaagtatag	gacgcgctat	ccaagactga	ggattcccca	atgcagaagc	1140
ctcttgagct	ctttaccaat	gtgtatgtga	agggatttgg	caccgatgca	tttggaacctg	1200
acagaaagta	agtcnaaagt	tcctcttcgt	gcatcatggag	ctcttgttgc	ttaaaactgcc	1260
acgtgtctatg	agaaagtattg	ctgatagaga	aattcatgaa	tatgaataaa	gatctgtattg	1320
tatactctct	ctctcccctc	cccccccctc	tctgattttt	aatctctctg	tctcttttgt	1380
tacaanaact	agggagaaca	tgttatctct	gtgaagcttt	agtagtctcg	tgtttaatat	1440
tcaancaatc	gaattgaact	ctctct				

Ala	Lys	Leu	Ile	20	Xaa	Gly	Phe	Cys	25	His	Leu	Tyr	Asp	Gly	Gln	30	Glu	Ala	15
Val	Ala	Ile	Gly	35	Xaa	Glu	Ala	Xaa	40	Ile	Thr	Lys	Lys	Asp	Ala	Ile	Ile		
Thr	Ala	Tyr	Arg	50	Asp	His	Cys	Ile	55	Phe	Leu	Gly	Arg	Gly	Gly	Ser	Leu		
His	Glu	Val	Phe	65	Ser	Glu	Leu	Met	70	Gly	Arg	Gln	75	Ala	Gly	Cys	Ser	Lys	
Gly	Lys	Gly	Gly	85	Ser	Met	His	Phe	90	Tyr	Lys	Lys	Glu	Ser	Ser	Phe	Tyr		
Gly	Gly	His	Gly	100	Ile	Val	Gly	Ala	105	Gln	Val	Pro	Leu	Gly	Cys	Gly	Ile		
Ala	Phe	Ala	Gln	115	Lys	Tyr	Asn	Lys	120	Glu	Glu	Ala	Val	Thr	Phe	Ala	Leu		
Tyr	Gly	Asp	Gly	130	Ala	Ala	Asn	Gln	135	Gly	Gln	Leu	Phe	Glu	Ala	Leu	Asn		
Ile	Ser	Ala	Leu	145	Trp	Asp	Leu	Pro	150	Ala	Ile	Leu	Val	Cys	Glu	Asn	Asn		
His	Tyr	Gly	Met	165	Gly	Thr	Ala	Glu	170	Arg	Ala	Ala	Lys	Ser	Pro	Ser	Leu		
Tyr	Tyr	Lys	Arg	175	Gly	Asp	Tyr	Val	180	Pro	Gly	Leu	Lys	Val	Asp	Gly	Met		

180	185	190
Asp Ala Phe Ala Val Lys Gln Ala Cys Lys Phe Ala Lys Gln His Ala		
195	200	205
Leu Glu Lys Gly Pro Ile Ile Leu Glu Met Asp Thr Tyr Arg Tyr His		
210	215	220
Gly His Ser Met Ser Asp Pro Gly Ser Thr Tyr Arg Thr Arg Asp Glu		
225	230	235
Ile Ser Gly Val Arg Gln Glu Arg Asp Pro Ile Glu Arg Ile Lys Lys		
	245	250
Leu Val Leu Ser His Asp Leu Ala Thr Glu Lys Glu Leu Lys Asp Met		
	260	265
Glu Lys Glu Ile Arg Lys Glu Val Asp Asp Ala Ile Ala Lys Ala Lys		
	275	280
Asp Cys Pro Met Pro Glu Pro Ser Glu Leu Phe Thr Asn Val Tyr Val		
	290	295
Lys Gly Phe Gly Thr Glu Ser Phe Gly Pro Asp Arg Lys Glu Val Lys		
305	310	315
Ala Ser Leu Pro		320

(2) INFORMATION FOR SEQ ID NO:2607:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 321 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..321

(D) OTHER INFORMATION: / Ceres Seq. ID 1573753

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2607:

Met Arg Arg Met Glu Ile Xaa Xaa Asp Ser Leu Tyr Lys Ala Lys Leu	
1	5
Ile Xaa Gly Phe Cys His Leu Tyr Asp Gly Gln Glu Ala Val Ala Ile	
	10
	15
Gly Xaa Glu Ala Xaa Ile Thr Lys Lys Asp Ala Ile Ile Thr Ala Tyr	
	20
	25
Arg Asp His Cys Ile Phe Leu Gly Arg Gly Gly Ser Leu His Glu Val	
	30
	35
Phe Ser Glu Leu Met Gly Arg Gln Ala Gly Cys Ser Lys Gly Lys Gly	
	40
	45
Gly Ser Met His Phe Tyr Lys Lys Glu Ser Ser Phe Tyr Gly Gly His	
	50
	55
Gly Ile Val Gly Ala Gln Val Pro Leu Gly Cys Gly Ile Ala Phe Ala	
	60
	65
Gln Lys Tyr Asn Lys Glu Glu Ala Val Thr Phe Ala Leu Tyr Gly Asp	
	70
	75
Gly Ala Ala Asn Gln Gly Gln Leu Phe Glu Ala Leu Asn Ile Ser Ala	
	80
	85
Leu Trp Asp Leu Pro Ala Ile Leu Val Cys Glu Asn Asn His Tyr Gly	
	90
	95
Met Gly Thr Ala Glu Trp Arg Ala Ala Lys Ser Pro Ser Tyr Tyr Lys	
	100
	105
Arg Gly Asp Tyr Val Pro Gly Leu Lys Val Asp Gly Met Asp Ala Phe	
	110
	115
Ala Val Lys Gln Ala Cys Lys Phe Ala Lys Gln His Ala Leu Glu Lys	
	120
	125
Gly Pro Ile Ile Leu Glu Met Asp Thr Tyr Arg Tyr His Gly His Ser	
	130
	135
Met Ser Asp Pro Gly Ser Thr Tyr Arg Thr Arg Asp Glu Ile Ser Gly	
	140
	145
	150
	155
	160
	165
	170
	175
	180
	185
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	195
	200
	205
	210
	215
	220
	225
	230
	235
	240

Val Arg Gln Glu Arg Asp Pro Ile Glu Arg Ile Lys Lys Leu Val Leu
245 250 255
Ser His Asp Leu Ala Thr Glu Lys Glu Leu Lys Asp Met Glu Lys Glu
260 265 270
Ile Arg Lys Glu Val Asp Asp Ala Ile Ala Lys Ala Lys Asp Cys Pro
275 280 285
Met Pro Glu Pro Ser Glu Leu Phe Thr Asn Val Tyr Val Lys Gly Phe
290 295 300
Gly Thr Glu Ser Phe Gly Pro Asp Arg Lys Glu Val Lys Ala Ser Leu
305 310 315 320
Pro

(2) INFORMATION FOR SEQ ID NO:2608:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 318 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..318

(D) OTHER INFORMATION: / Ceres Seq. ID 1573754

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2608:

Met Glu Ile Xaa Xaa Asp Ser Leu Tyr Lys Ala Lys Leu Ile Xaa Gly
1 5 10 15
Phe Cys His Leu Tyr Asp Gly Gln Glu Ala Val Ala Ile Gly Xaa Glu
20 25 30
Ala Xaa Ile Thr Lys Lys Asp Ala Ile Ile Thr Ala Tyr Arg Asp His
35 40 45
Cys Ile Phe Leu Gly Arg Gly Gly Ser Leu His Glu Val Phe Ser Glu
50 55 60
Leu Met Gly Arg Gln Ala Gly Cys Ser Lys Gly Lys Gly Ser Met
65 70 75 80
His Phe Tyr Lys Lys Glu Ser Ser Phe Tyr Gly Gly His Gly Ile Val
85 90 95
Gly Ala Gln Val Pro Leu Gly Cys Gly Ile Ala Phe Ala Gln Lys Tyr
100 105 110
Asn Lys Glu Glu Ala Val Thr Phe Ala Leu Tyr Gly Asp Gly Ala Ala
115 120 125
Asn Gln Gly Gln Leu Phe Glu Ala Leu Asn Ile Ser Ala Leu Trp Asp
130 135 140
Leu Pro Ala Ile Leu Val Cys Glu Asn Asn His Tyr Gly Met Gly Thr
145 150 155 160
Ala Glu Trp Arg Ala Ala Lys Ser Pro Ser Tyr Tyr Lys Arg Gly Asp
165 170 175
Tyr Val Pro Gly Leu Lys Val Asp Gly Met Asp Ala Phe Ala Val Lys
180 185 190
Gln Ala Cys Lys Phe Ala Lys Gln His Ala Leu Glu Lys Gly Pro Ile
195 200 205
Ile Leu Glu Met Asp Thr Tyr Arg Tyr His Gly His Ser Met Ser Asp
210 215 220
Pro Gly Ser Thr Tyr Arg Thr Arg Asp Glu Ile Ser Gly Val Arg Gln
225 230 235 240
Glu Arg Asp Pro Ile Glu Arg Ile Lys Lys Leu Val Leu Ser His Asp
245 250 255
Leu Ala Thr Glu Lys Glu Leu Lys Asp Met Glu Lys Glu Ile Arg Lys
260 265 270
Glu Val Asp Asp Ala Ile Ala Lys Ala Lys Asp Cys Pro Met Pro Glu
275 280 285
Pro Ser Glu Leu Phe Thr Asn Val Tyr Val Lys Gly Phe Gly Thr Glu

290 295 300
Ser Phe Gly Pro Asp Arg Lys Glu Val Lys Ala Ser Leu Pro
305 310 315

(2) INFORMATION FOR SEQ ID NO:2609:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1336 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1336
- (D) OTHER INFORMATION: / Ceres Seq. ID 1573759

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2609:

tactttggcg	gtgctgagaa	gaaagatgag	agggttcttg	ttctgtatt	gggttcttta	60
acaagcatct	atgacagggc	aagggaattg	ttctattatt	tgaaggagg	ggtagtgtat	120
tttgccgaag	agcatagcga	Nggcttggtg	acattctcgg	tttgaagaa	gatacgaaca	180
agggcaatc	ccgaaatggg	atgaggatca	tctatttcac	tttggggcg	attcagcggg	240
tgccgaagtt	gtcggtgtat	tgacagaaat	gcttgagat	caggcatctg	aagggtttga	300
agaaacgaat	gagaattggg	ttctgagtg	gacatcggt	tccggggcat	tcaatggaac	360
taccaggcac	tacttagatg	gcattcgccg	agatgatgga	gtgagcatga	aaccaataatg	420
ttgtttgcag	ctgtgtcgta	taggcgtgat	aatgacgat	tggttggaac	tttcatggct	480
aaagacttat	tacaatttcg	ggttcgatca	cttcaacatt	tttggaaga	agacgggtgt	540
gagaggtctc	gttgattgcc	taattggaaa	cacaggctct	tttgcttctg	gcagttggat	600
cttacctgat	ctcacaatcc	aaggctcaac	aagtattaac	tccaatctcc	agacgttccc	660
aaacacttat	tacttcagct	acgcgactaa	acgcacccgc	agagtcatgg	gtatgacaat	720
cccttcagggt	gtttctggaa	tccaccgcgt	gctctctctc	cgctctcttc	abatgagcnc	780
Aatgaaatt	ccgcacaagt	gtctctctcc	cttataaagg	ctacagggat	gaggaactggc	840
aagagaaacg	ccgggcattg	aacacaatat	caatgacaca	tccgaggcta	ctgtgtgacg	900
atccgagccg	gttcataaag	agcgattcgg	aattgcaaac	attacaaccc	gggattctgtg	960
attataagat	agtggaaagc	gatcacataa	gtttcatagt	gaacagagag	agagctgggtg	1020
ttcagtttga	tctgatatac	gacagcatct	tccaacgttg	caggaaacat	gtttttagaa	1080
agattctctca	gactctcccc	aatcaatctc	cttctctctc	tggttcacat	tcatacaccac	1140
gaataaaca	ctttgtacat	tgatcacatg	caaaaaaaaa	attgttttagg	gtgtgtacgt	1200
tgagggctta	agttttttgt	taggctattt	actactaata	cagattattc	attgttcttc	1260
ttgttctctc	ctcgatttgt	tgtaactgaa	aataataatc	ttccattttg	aaaattataa	1320
tattgtttag	ttcgcc					

(2) INFORMATION FOR SEQ ID NO:2610:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 182 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..182
- (D) OTHER INFORMATION: / Ceres Seq. ID 1573760

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2610:

Met	Leu	Ala	Asp	Gln	Ala	Phe	Glu	Gly	Phe	Glu	Glu	Thr	Asn	Glu	Asn
1				5				10				15			
Trp	Val	Leu	Ser	Val	Thr	Ser	Leu	Ser	Gly	Ala	Phe	Asn	Gly	Thr	Thr
				20				25				30			
Arg	Thr	Tyr	Leu	Asp	Gly	Met	Arg	Thr	Asp	Asp	Gly	Val	Ser	Met	Lys
				35				40				45			
Pro	Ile	Cys	Leu	Leu	Gln	Leu	Cys	Arg	Ile	Gly	Val	Ile	Met	Tyr	Asp
				50				55				60			
Trp	Leu	Asp	Ile	Ser	Trp	Leu	Lys	Thr	Tyr	Tyr	Asn	Phe	Gly	Phe	Asp
				65				70				75			80
His	Phe	Asn	Ile	Ser	Trp	Lys	Lys	Thr	Gly	Val	Arg	Gly	Leu	Val	Asp

85 90 95
Cys Leu Met Gly Asn Thr Gly Pro Phe Ala Ser Gly Asp Trp Ile Leu
100 105 110
Pro Asp Leu Thr Ile Gln Gly Ser Thr Ser Ile Asn Ser Asn Leu Gln
115 120 125
Thr Phe Pro Asn Thr Tyr Tyr Phe Ser Tyr Ala Thr Lys Arg Thr Arg
130 135 140
Arg Val Met Gly Met Thr Ile Pro Ser Gly Val Leu Gly Ile His Pro
145 150 155 160
Met Leu Phe Leu Arg Val Phe Xaa Met Ser Xaa Met Glu Ile Pro Thr
165 170 175
Arg Cys Leu Ser Ser Leu
180

(2) INFORMATION FOR SEQ ID NO:2611:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 144 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..144

(D) OTHER INFORMATION: / Ceres Seq. ID 1573761

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2611:

Met Arg Thr Asp Asp Gly Val Ser Met Lys Pro Ile Cys Leu Leu Gln
1 5 10 15
Leu Cys Arg Ile Gly Val Ile Met Tyr Asp Trp Leu Asp Ile Ser Trp
20 25 30
Leu Lys Thr Tyr Tyr Asn Phe Gly Phe Asp His Phe Asn Ile Ser Trp
35 40 45
Lys Lys Thr Gly Val Arg Gly Leu Val Asp Cys Leu Met Gly Asn Thr
50 55 60
Gly Pro Phe Ala Ser Gly Asp Trp Ile Leu Pro Asp Leu Thr Ile Gln
65 70 75 80
Gly Ser Thr Ser Ile Asn Ser Asn Leu Gln Thr Phe Pro Asn Thr Tyr
85 90 95
Tyr Phe Ser Tyr Ala Thr Lys Arg Thr Arg Arg Val Met Gly Met Thr
100 105 110
Ile Pro Ser Gly Val Leu Gly Ile His Pro Met Leu Phe Leu Arg Val
115 120 125
Phe Xaa Met Ser Xaa Met Glu Ile Pro Thr Arg Cys Leu Ser Ser Leu
130 135 140

(2) INFORMATION FOR SEQ ID NO:2612:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 136 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..136

(D) OTHER INFORMATION: / Ceres Seq. ID 1573762

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2612:

Met Lys Pro Ile Cys Leu Leu Gln Leu Cys Arg Ile Gly Val Ile Met
1 5 10 15
Tyr Asp Trp Leu Asp Ile Ser Trp Leu Lys Thr Tyr Tyr Asn Phe Gly
20 25 30

Phe Asp His Phe Asn Ile Ser Trp Lys Lys Thr Gly Val Arg Gly Leu
35 40 45
Val Asp Cys Leu Met Gly Asn Thr Gly Pro Phe Ala Ser Gly Asp Trp
50 55 60
Ile Leu Pro Asp Leu Thr Ile Gln Gly Ser Thr Ser Ile Asn Ser Asn
65 70 75 80
Leu Gln Thr Phe Pro Asn Thr Tyr Tyr Phe Ser Tyr Ala Thr Lys Arg
85 90 95
Thr Arg Arg Val Met Gly Met Thr Ile Pro Ser Gly Val Leu Gly Ile
100 105 110
His Pro Met Leu Phe Leu Arg Val Phe Xaa Met Ser Xaa Met Glu Ile
115 120 125
Pro Thr Arg Cys Leu Ser Ser Leu
130 135

(2) INFORMATION FOR SEQ ID NO:2613:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 590 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..590
- (D) OTHER INFORMATION: / Ceres Seq. ID 1573790

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2613:

atcacttact	taacatacta	agagagttat	tagaacttgc	aaaaaatggc	ttccaaggct	60
ttgattctgt	taggtctctt	ctcagttctt	ctcgtcgtct	ccgaagtgtc	tgccgcaagg	120
caatcgggca	tgggtgaagcc	agagagtgag	gaaactgtgc	aacctgaagg	ttatggcggt	180
ggccacggag	gacatggtgg	tcacggaggg	ggaggaggcc	acggacatgg	aggacacaa	240
ggaggagggg	gccacggact	tgacggatac	ggaggacact	acggaggtgg	tgaggaggga	300
tacggaggtg	gaggaggaca	ccacggaggga	ggaggccacg	ggctaaccga	acctgttcag	360
actaagccgg	gtgtttaaaa	ctatataata	ttcttactac	catgcatgat	tgcatatata	420
tatatacgct	tatgtattat	ctatatgcct	ataaataaac	catgggtgag	ttgtaacgca	480
GtgcNcttca	gaaatgttcg	gaataaattt	ccataatatt	agtataatgt	ctctctgttt	540
gaattataaa	ctcgcgctgtt	tgcataataa	aatctcttgt	agctaggctg		

(2) INFORMATION FOR SEQ ID NO:2614:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 110 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..110
- (D) OTHER INFORMATION: / Ceres Seq. ID 1573791

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2614:

Met	Ala	Ser	Lys	Ala	Leu	Ile	Leu	Leu	Gly	Leu	Phe	Ser	Val	Leu	Leu
1				5					10				15		
Val	Val	Ser	Glu	Val	Ser	Ala	Ala	Arg	Gln	Ser	Gly	Met	Val	Lys	Pro
				20				25					30		
Glu	Ser	Glu	Glu	Thr	Val	Gln	Pro	Glu	Gly	Tyr	Gly	Gly	Gly	His	Gly
				35				40				45			
Gly	His	Gly	Gly	His	Gly	Gly	Gly	Gly	Gly	His	Gly	His	Gly	Gly	His
				50				55				60			
Asn	Gly	Gly	Gly	Gly	His	Gly	Leu	Asp	Gly	Tyr	Gly	Gly	His	Tyr	Gly
				65				70				75		80	
Gly	Gly	Gly	Gly	Gly	Tyr	Gly	Gly	Gly	Gly	Gly	His	His	Gly	Gly	Gly
				85				90				95			
Gly	His	Gly	Leu	Asn	Glu	Pro	Val	Gln	Thr	Lys	Pro	Gly	Val		

100 105 110

(2) INFORMATION FOR SEQ ID NO:2615:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 82 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..82
(D) OTHER INFORMATION: / Ceres Seq. ID 1573792
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2615:
Met Val Lys Pro Glu Ser Glu Glu Thr Val Gln Pro Glu Gly Tyr Gly
1 5 10 15
Gly Gly His Gly Gly His Gly Gly His Gly Gly Gly Gly His Gly
20 25 30
His Gly Gly His Asn Gly Gly Gly His Gly Leu Asp Gly Tyr Gly
35 40 45
Gly His Tyr Gly Gly Gly Gly Gly Tyr Gly Gly Gly Gly His
50 55 60
His Gly Gly Gly Gly His Gly Leu Asn Glu Pro Val Gln Thr Lys Pro
65 70 75 80
Gly Val

(2) INFORMATION FOR SEQ ID NO:2616:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 57 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..57
(D) OTHER INFORMATION: / Ceres Seq. ID 1573793
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2616:
Met Ala Val Ala Thr Glu Asp Met Val Val Thr Glu Gly Glu Ala
1 5 10 15
Thr Asp Met Glu Asp Thr Thr Glu Glu Gly Ala Thr Asp Leu Thr Asp
20 25 30
Thr Glu Asp Thr Thr Glu Val Val Glu Glu Asp Thr Glu Val Glu Glu
35 40 45
Asp Thr Thr Glu Glu Glu Ala Thr Gly
50 55

(2) INFORMATION FOR SEQ ID NO:2617:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 461 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..461
(D) OTHER INFORMATION: / Ceres Seq. ID 1573798
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2617:
atcacttact taacatacta agagagttat tagaacttgc aaaaaaatggc ttccaaggct 60
ttgattctgt taggtctctt ctacgttctt ctgctgctct ccgaagtgtc tgccgcaagg 120
aatcgggcat ggtgaagcca gagagtggag aaactgtgca acctgaagggt tatggcgggt 180
gccacggagg acatggtggt cacggagggg gaggaggcca cggacatgga ggacacaacg 240

gaggtggagg aggcacacac ggaggaggag gccacggcgt aaacgaacct gttcagacta 300
agccgggtgt ttaaaactat ataatatctt cactaccatg catgattgca tatatatata 360
tacgcttatg tattatctat atgctataa ataaaccatg gtgagttgt aacgcagtcg 420
Tcttcagaaa tggctggaat aaatttccat aatattagta t

(2) INFORMATION FOR SEQ ID NO:2618:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 103 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..103
- (D) OTHER INFORMATION: / Ceres Seq. ID 1573799

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2618:

His	Leu	Leu	Asn	Ile	Leu	Arg	Glu	Leu	Glu	Leu	Ala	Lys	Asn	Gly
1			5						10				15	
Phe	Gln	Gly	Phe	Asp	Ser	Val	Arg	Ser	Leu	Ser	Ser	Ser	Arg	Arg
			20					25				30		
Leu	Arg	Ser	Val	Cys	Arg	Lys	Glu	Ser	Gly	Met	Val	Lys	Pro	Glu
			35				40					45		
Glu	Glu	Thr	Val	Gln	Pro	Glu	Gly	Tyr	Gly	Gly	Gly	His	Gly	Gly
			50			55					60			
Gly	Gly	His	Gly	Gly	Gly	Gly	Gly	His	Gly	His	Gly	Gly	His	Asn
			65			70			75				80	
Gly	Gly	Gly	Gly	His	His	Gly	Gly	Gly	Gly	His	Gly	Leu	Asn	Glu
			85					90					95	
Val	Gln	Thr	Lys	Pro	Gly	Val								
			100											

(2) INFORMATION FOR SEQ ID NO:2619:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 61 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..61
- (D) OTHER INFORMATION: / Ceres Seq. ID 1573800

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2619:

Met	Val	Lys	Pro	Glu	Ser	Glu	Glu	Thr	Val	Gln	Pro	Glu	Gly	Tyr	Gly
1			5						10				15		
Gly	Gly	His	Gly	Gly	His	Gly	Gly	His	Gly	Gly	Gly	Gly	Gly	His	Gly
			20				25					30			
His	Gly	Gly	His	Asn	Gly	Gly	Gly	Gly	His	His	Gly	Gly	Gly	Gly	Gly
			35				40					45			
His	Gly	Leu	Asn	Glu	Pro	Val	Gln	Thr	Lys	Pro	Gly	Val			
			50			55					60				

(2) INFORMATION FOR SEQ ID NO:2620:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 596 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..596
- (D) OTHER INFORMATION: / Ceres Seq. ID 1573801

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2620:

```
actcatcact tacttaacat actaagagag ttattagatc ttgaaaaaca tggcttccaa 60
ggctttgatt ctgttgggtc tcttcgcaat tctctgggtg gtctccgaag ttctcgccgc 120
aaggcaKctg ggcattgtga agccagagag gaaactgtgc aacctgaagg ttatcacgga 180
ggacatgggt gtacaggagg gggaggccac tacggaggag gaggccacgg gcatggaggga 240
cacaacggag gagggggcca cggacttgac ggatacggag gaggacatgg aggacactac 300
ggaggaggag gaggacacta cggaggagga ggaggccacg gtggtgtgtg acactatgga 360
ggtggaggac accatggagg agggaggtcac gggctgaacg aacctgttca gacgaagccg 420
ggtgtttaaa agttataact atcaataaaa ttaccatgcg ataattgcac ctctatatac 480
acttatgtct tatatgtatc catcaaaata aacctgggtg agtttgaat gcagttccctt 540
cagaaatgtg tggaataatg ttccacaata ataatagaat atctctgttg attctg
```

(2) INFORMATION FOR SEQ ID NO:2621:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 142 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..142
- (D) OTHER INFORMATION: / Ceres Seq. ID 1573802

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2621:

```
Thr His His Leu Leu Asn Ile Leu Arg Glu Leu Leu Asp Leu Glu Lys
1 5 10 15
His Gly Phe Gln Gly Phe Asp Ser Val Gly Ser Leu Arg Asn Ser Ser
20 25 30
Gly Gly Leu Arg Ser Phe Cys Arg Lys Ala Xaa Gly His Gly Glu Ala
35 40 45
Arg Glu Glu Thr Val Gln Pro Glu Gly Tyr His Gly Gly His Gly Gly
50 55 60
His Gly Gly Gly Gly His Tyr Gly Gly Gly His Gly His Gly Gly
65 70 75 80
His Asn Gly Gly Gly His Gly Leu Asp Gly Tyr Gly Gly Gly His
85 90 95
Gly Gly His Tyr Gly Gly Gly Gly Gly His Tyr Gly Gly Gly Gly
100 105 110
His Gly Gly Gly Gly His Tyr Gly Gly Gly Gly His His Gly Gly Gly
115 120 125
Gly His Gly Leu Asn Glu Pro Val Gln Thr Lys Pro Gly Val
130 135 140
```

(2) INFORMATION FOR SEQ ID NO:2622:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..115
- (D) OTHER INFORMATION: / Ceres Seq. ID 1573803

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2622:

```
Met Ala Ser Lys Ala Leu Ile Leu Leu Gly Leu Phe Ala Ile Leu Leu
1 5 10 15
Val Val Ser Glu Val Ser Ala Ala Arg Xaa Ser Gly Met Val Lys Pro
20 25 30
Glu Arg Lys Leu Cys Asn Leu Lys Val Ile Thr Glu Asp Met Val Val
35 40 45
Thr Gly Gly Glu Ala Thr Thr Glu Glu Ala Thr Gly Met Glu Asp
50 55 60
```

Thr Thr Glu Glu Gly Ala Thr Asp Leu Thr Asp Thr Glu Glu Asp Met
65 70 75 80
Glu Asp Thr Thr Glu Glu Glu Asp Thr Thr Glu Glu Glu Ala
85 90 95
Thr Val Val Val Asp Thr Met Glu Val Glu Asp Thr Met Glu Glu Glu
100 105 110
Val Thr Gly
115

(2) INFORMATION FOR SEQ ID NO:2623:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 87 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..87

(D) OTHER INFORMATION: / Ceres Seq. ID 1573804

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2623:

Met Val Lys Pro Glu Arg Lys Leu Cys Asn Leu Lys Val Ile Thr Glu
1 5 10 15
Asp Met Val Val Thr Glu Gly Glu Ala Thr Thr Glu Glu Glu Ala Thr
20 25 30
Gly Met Glu Asp Thr Thr Glu Glu Gly Ala Thr Asp Leu Thr Asp Thr
35 40 45
Glu Glu Asp Met Glu Asp Thr Thr Glu Glu Glu Glu Asp Thr Thr Glu
50 55 60
Glu Glu Glu Ala Thr Val Val Val Asp Thr Met Glu Val Glu Asp Thr
65 70 75 80
Met Glu Glu Glu Val Thr Gly
85

(2) INFORMATION FOR SEQ ID NO:2624:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 587 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..587

(D) OTHER INFORMATION: / Ceres Seq. ID 1573809

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2624:

actcatcaact tacttaacat actaagagag ttattagatc ttgaaaaaca tggcttccaa 60
ggctttgatt ctgttgggtc tcttcgcaat tcttctgggt gtctccgaag ttctgcccgc 120
aaggCaGtNc Ngggcatggt gaagccagag agtgaggaaa ctgtgcaacc tgaaggttat 180
cacggaggac atggtgggtca cggaggggga gcccactacg gaggaggagg ccacgggcat 240
ggaggacaca acggaggagg gggccacgga cttgacggat acggaggagg acatggagga 300
cactacggag gaggaggagg acactacgga ggaggatcac gtggtggtga aggaggaggt 360
tacggaggaa cgggtggtgg tggaggatgg taattccott aattagggtt aggattacca 420
atgaatgttc tctctctgc ttgttatgct tctacttggt ttgtgtggt ctctattttg 480
ttctggttct gcttagatt tgatgtaaca gttcgtgatt aggtattttg gtatctggaa 540
acgtaatggt aagtcacttg tcattttcta aataacaaat ttcttcg

(2) INFORMATION FOR SEQ ID NO:2625:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 130 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..130

(D) OTHER INFORMATION: / Ceres Seq. ID 1573810

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2625:

Thr His His Leu Leu Asn Ile Leu Arg Glu Leu Leu Asp Leu Glu Lys
1 5 10 15
His Gly Phe Gln Gly Phe Asp Ser Val Gly Ser Leu Arg Asn Ser Ser
20 25 30
Gly Gly Leu Arg Ser Phe Cys Arg Lys Ala Xaa Xaa Gly Met Val Lys
35 40 45
Pro Glu Ser Glu Glu Thr Val Gln Pro Glu Gly Tyr His Gly Gly His
50 55 60
Gly Gly His Gly Gly Gly Gly His Tyr Gly Gly Gly His Gly His
65 70 75 80
Gly Gly His Asn Gly Gly Gly Gly His Gly Leu Asp Gly Tyr Gly Gly
85 90 95
Gly His Gly Gly His Tyr Gly Gly Gly Gly His Tyr Gly Gly Gly
100 105 110
Tyr Gly Gly Gly Glu Gly Gly Tyr Gly Gly Ser Gly Gly Gly Gly
115 120 125
Gly Trp
130

(2) INFORMATION FOR SEQ ID NO:2626:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 85 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..85

(D) OTHER INFORMATION: / Ceres Seq. ID 1573811

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2626:

Met Val Lys Pro Glu Ser Glu Glu Thr Val Gln Pro Glu Gly Tyr His
1 5 10 15
Gly Gly His Gly Gly His Gly Gly Gly Gly His Tyr Gly Gly Gly Gly
20 25 30
His Gly His Gly Gly His Asn Gly Gly Gly Gly His Gly Leu Asp Gly
35 40 45
Tyr Gly Gly Gly His Gly Gly His Tyr Gly Gly Gly Gly His Tyr
50 55 60
Gly Gly Gly Tyr Gly Gly Gly Glu Gly Gly Gly Tyr Gly Gly Ser Gly
65 70 75 80
Gly Gly Gly Gly Trp
85

(2) INFORMATION FOR SEQ ID NO:2627:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 71 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..71

(D) OTHER INFORMATION: / Ceres Seq. ID 1573812

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2627:

Met Val Val Thr Glu Gly Glu Ala Thr Thr Glu Glu Glu Ala Thr Gly
1 5 10 15

Met Glu Asp Thr Thr Glu Glu Gly Ala Thr Asp Leu Thr Asp Thr Glu
20 25 30
Glu Asp Met Glu Asp Thr Thr Glu Glu Glu Asp Thr Thr Glu Glu
35 40 45
Asp Thr Val Val Val Lys Glu Glu Val Thr Glu Glu Ala Val Val Val
50 55 60
Glu Asp Gly Asn Ser Phe Asn
65 70

(2) INFORMATION FOR SEQ ID NO:2628:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 550 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..550
(D) OTHER INFORMATION: / Ceres Seq. ID 1573813

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2628:

atcacttact taacatacta agagagttat tagaacttgc aaaaaatggc ttccaaggct	60
ttgattctgt taggtctctt ctcagttctt ctcgtcgtct ccgaagtgtc tgccgcaagg	120
CaaNtcgggc atggtgaagc cagagagtga ggaactgtg caacctgaag gttatrgcgg	180
tggccacgga ggacatgggt gtcacggarg gggaggaggc caggacatg gaggacacaa	240
cggaggaggg ggccacggac ttgacggata cggaggagggt ggaggacact atggaggarg	300
tggaggacac tggcaggagg gtggaggaca ctacggagga ggtggaggac actacggagg	360
aggtggccac gggctaaacg aacctgttca gactaagcgg ggtgtttaaa actatataat	420
atcttcacta ccatgcatag ttgcatatat atatatacgc ttatgtatta tctatatgcc	480
tataaataaa ccatggtgag ttgtaacgc agtgccttca gaaatgttcg gaataaattt	540
ccataatatt	

(2) INFORMATION FOR SEQ ID NO:2629:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 92 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..92
(D) OTHER INFORMATION: / Ceres Seq. ID 1573814

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2629:

Met Val Lys Pro Glu Ser Glu Glu Thr Val Gln Pro Glu Gly Tyr Xaa	
1 5 10 15	
Gly Gly His Gly Gly His Gly Gly His Gly Xaa Gly Gly Gly His Gly	
20 25 30	
His Gly Gly His Asn Gly Gly Gly Gly His Gly Leu Asp Gly Tyr Gly	
35 40 45	
Gly Gly Gly Gly His Tyr Gly Gly Xaa Gly Gly His Tyr Gly Gly Gly	
50 55 60	
Gly Gly His Tyr Gly Gly Gly Gly His Tyr Gly Gly Gly Gly His	
65 70 75 80	
Gly Leu Asn Glu Pro Val Gln Thr Lys Pro Gly Val	
85 90	

(2) INFORMATION FOR SEQ ID NO:2630:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 60 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..60

(D) OTHER INFORMATION: / Ceres Seq. ID 1573815

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2630:

```
Met Val Val Thr Xaa Gly Glu Glu Ala Thr Asp Met Glu Asp Thr Thr
1          5          10          15
Glu Glu Gly Ala Thr Asp Leu Thr Asp Thr Glu Glu Val Glu Asp Thr
20          25          30
Met Glu Xaa Val Glu Asp Thr Thr Glu Glu Val Glu Asp Thr Thr Glu
35          40          45
Glu Val Glu Asp Thr Thr Glu Glu Val Ala Thr Gly
50          55          60
```

(2) INFORMATION FOR SEQ ID NO:2631:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 49 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..49

(D) OTHER INFORMATION: / Ceres Seq. ID 1573816

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2631:

```
Met Glu Asp Thr Thr Glu Glu Gly Ala Thr Asp Leu Thr Asp Thr Glu
1          5          10          15
Glu Val Glu Asp Thr Thr Met Glu Xaa Val Glu Asp Thr Thr Glu Val
20          25          30
Glu Asp Thr Thr Glu Glu Val Glu Asp Thr Thr Glu Glu Val Ala Thr
35          40          45
Gly
```

(2) INFORMATION FOR SEQ ID NO:2632:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 597 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..597

(D) OTHER INFORMATION: / Ceres Seq. ID 1573817

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2632:

```
atcaacttact taacatacta agagagtatt tagactctga aaaacatggc ttccaagggt 60
ttgattctctg ttggtctctt cgcaattctt ctggttggtc cgaagatttc tgccgcaagg 120
CaTgTcgggc atggtgaagc cagagagtga ggaactgtg caacctgaag gttatcacgg 180
aggacatggt ggtcacggag ggggaggcca ctacggagga ggaggccacg ggcattggag 240
acacaacgga ggagggggccc acggacttaa cggatacgga ggaggacatg gaggacata 300
cggaggagga ggaggacact acggaggarg agggagccac ggtgtgtgtg gacactatgg 360
agggtggagga caccatggag gavgagotca cgggctgaac gaacctgttc agacgaagcc 420
gggtgtttaa aagttataac tatcaataa attocaccat cataattgca tctctatata 480
cacttatgtc ttatatgtat ccatcaaaat aaaccatggt gagtttgtaa tgcagtttct 540
tcagaaatgt gtggaaataa ttttcacaat aataatagaa tatctctgtt gattctg
```

(2) INFORMATION FOR SEQ ID NO:2633:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 102 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..102

(D) OTHER INFORMATION: / Ceres Seq. ID 1573818

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2633:

Met	Ser	Gly	Met	Val	Lys	Pro	Glu	Ser	Glu	Glu	Thr	Val	Gln	Pro	Glu
1			5						10					15	
Gly	Tyr	His	Gly	Gly	His	Gly	Gly	His	Gly	Gly	Gly	Gly	His	Tyr	Gly
			20					25					30		
Gly	Gly	Gly	His	Gly	His	Gly	Gly	His	Asn	Gly	Gly	Gly	Gly	His	Gly
			35					40					45		
Leu	Asn	Gly	Tyr	Gly	Gly	Gly	His	Gly	Gly	His	Tyr	Gly	Gly	Gly	Gly
			50				55				60				
Gly	His	Tyr	Gly	Gly	Xaa	Gly	Gly	His	Gly	Gly	Gly	Gly	His	Tyr	Gly
					70					75				80	
Gly	Gly	Gly	His	His	Gly	Gly	Xaa	Gly	His	Gly	Leu	Asn	Glu	Pro	Val
				85					90					95	
Gln	Thr	Lys	Pro	Gly	Val										
				100											

(2) INFORMATION FOR SEQ ID NO:2634:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 99 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..99

(D) OTHER INFORMATION: / Ceres Seq. ID 1573819

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2634:

Met	Val	Lys	Pro	Glu	Ser	Glu	Glu	Thr	Val	Gln	Pro	Glu	Gly	Tyr	His
1			5						10					15	
Gly	Gly	His	Gly	Gly	His	Gly	Gly	Gly	Gly	His	Tyr	Gly	Gly	Gly	Gly
			20					25					30		
His	Gly	His	Gly	Gly	His	Asn	Gly	Gly	Gly	His	Gly	Leu	Asn	Gly	
			35				40				45				
Tyr	Gly	Gly	Gly	His	Gly	Gly	His	Tyr	Gly	Gly	Gly	Gly	Gly	His	Tyr
			50				55				60				
Gly	Gly	Xaa	Gly	Gly	His	Gly	Gly	Gly	Gly	His	Tyr	Gly	Gly	Gly	Gly
					70				75					80	
His	His	Gly	Gly	Xaa	Gly	His	Gly	Leu	Asn	Glu	Pro	Val	Gln	Thr	Lys
				85					90					95	
Pro	Gly	Val													

(2) INFORMATION FOR SEQ ID NO:2635:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 70 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..70

(D) OTHER INFORMATION: / Ceres Seq. ID 1573820

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2635:

Met	Val	Val	Thr	Glu	Gly	Glu	Ala	Thr	Thr	Glu	Glu	Glu	Ala	Thr	Gly
1			5						10					15	
Met	Glu	Asp	Thr	Thr	Glu	Glu	Gly	Ala	Thr	Asp	Leu	Thr	Asp	Thr	Glu

20 25 30
Glu Asp Met Glu Asp Thr Thr Glu Glu Glu Asp Thr Thr Glu Xaa
35 40 45
Glu Glu Ala Thr Val Val Val Asp Thr Met Glu Val Glu Asp Thr Met
50 55 60
Glu Xaa Glu Val Thr Gly
65 70

(2) INFORMATION FOR SEQ ID NO:2636:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 537 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..537
- (D) OTHER INFORMATION: / Ceres Seq. ID 1573821

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2636:

atcaccttact	taacatacta	agagagttat	tagatcttga	aaaacatggc	ttccaaggct	60
ttgattctgt	tgggtctctt	cgcaattctt	ctgggtgtct	ccgaagtctc	tgccgcaagg	120
CaKtGcgggc	atgggtgaagc	cagagagtga	ggaaactgtg	caacctgaag	gttatcacgg	180
aggacatggt	ggtcacggar	ggggaggcca	ctacggagga	ggaggccaag	ggcatggagg	240
acacaacgga	ggagggggcc	acggacttga	cggatacggg	ggagacatg	gaggacacta	300
cggargagga	ggaggacact	acggargagg	aggaggccac	ggtgtgtgtg	gacactatgg	360
aggtggagga	caccatggag	gaggaggcca	cgggctgaac	gaacctgttc	agacgaaggg	420
tgaggacaa	gaggcaggga	agaaggattt	cattcagata	ctcaagactc	ttgaatctga	480
gcttggagac	aaactctact	ttagtggcga	tgactttggc	tatgtagaca	ttaaggg	

(2) INFORMATION FOR SEQ ID NO:2637:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 135 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..135
- (D) OTHER INFORMATION: / Ceres Seq. ID 1573822

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2637:

Met	Val	Lys	Pro	Glu	Ser	Glu	Glu	Thr	Val	Gln	Pro	Glu	Gly	Tyr	His
1		5						10				15			
Gly	Gly	His	Gly	Gly	His	Gly	Xaa	Gly	Gly	His	Tyr	Gly	Gly	Gly	Gly
		20					25					30			
His	Gly	His	Gly	Gly	His	Asn	Gly	Gly	Gly	His	Gly	Leu	Asp	Gly	
		35				40				45					
Tyr	Gly	Gly	Gly	His	Gly	Gly	His	Tyr	Gly	Xaa	Gly	Gly	Gly	His	Tyr
		50			55			60							
Gly	Xaa	Gly	Gly	His	Gly	Gly	Gly	His	Tyr	Gly	Gly	Gly	Gly		
		65			70			75					80		
His	His	Gly	Gly	Gly	Gly	His	Gly	Leu	Asn	Glu	Pro	Val	Gln	Thr	Lys
		85					90						95		
Gly	Glu	Glu	Gln	Glu	Ala	Gly	Lys	Lys	Asp	Phe	Ile	Gln	Ile	Leu	Lys
		100					105						110		
Thr	Leu	Glu	Ser	Glu	Leu	Gly	Asp	Lys	Pro	Tyr	Phe	Ser	Gly	Asp	Asp
		115					120					125			
Phe	Gly	Tyr	Val	Asp	Ile	Lys									
		130				135									

(2) INFORMATION FOR SEQ ID NO:2638:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 70 amino acids

- (B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..70
(D) OTHER INFORMATION: / Ceres Seq. ID 1573823

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2638:
Met Val Val Thr Xaa Gly Glu Ala Thr Thr Glu Glu Glu Ala Thr Gly
1 5 10 15
Met Glu Asp Thr Thr Glu Glu Gly Ala Thr Asp Leu Thr Asp Thr Glu
20 25 30
Glu Asp Met Glu Asp Thr Thr Xaa Glu Glu Glu Asp Thr Thr Xaa Glu
35 40 45
Glu Glu Ala Thr Val Val Val Asp Thr Met Glu Val Glu Asp Thr Met
50 55 60
Glu Glu Glu Val Thr Gly
65 70

- (2) INFORMATION FOR SEQ ID NO:2639:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1021 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..1021
(D) OTHER INFORMATION: / Ceres Seq. ID 1573832
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2639:

aataaaaaatt tgtttctttc ttctctgttt ttttttgott tgcgtttcaa gagagagaga 60
gagagagata caaagagaga aatttgggtt ttgtttgaac gaagcttctt cggtctctct 120
tctccgtctt acgattgtca acgcgtgtgtt ccattcttcaa tttgtttctt attttagcac 180
aagtttctcg agcttcaaat actgtttcag atcaatcaat cagtcaatca tggcgtagctc 240
tggaaaacaa aacatcaacg ccaaatgtgt attactagga gatgttggag ctggaaaaac 300
aagtcttgtg ctacggtttg tgaagatca gttttgtgaa ttccaggaat caaccattgg 360
tgcagctttt ttctctcaaa cattggctgt gaattgatcg actgtgaagt ttgagatag 420
ggatacagct ggtcaggaac gataccacag ttggctcca atgtactaca ggggtgcagc 480
tgctgtctatt attgtctttg acattactaa tcaagcctca tttagagagg cgaaraaatg 540
ggttcaggaa ctgcaggcac aaggtaaacc taatatggtg atggctcttg ctggaaaacaa 600
agctgattta tttagcgcaa ggaaggtgtc tgcagaggag gcagagatat atgctcaaga 660
gaacagcctt ttctttatg aaacctcagc gaagaccgca acaaatgtca aagacatatt 720
ctacgaataa cggaaaaagg taccacgtat acagccagct gaaaaccgca caggaattgt 780
tctcccaaac gggccagggt ctacggcagt gaggttcatcg tgttgtgctt agattcgtac 840
ctgaagagag atctcatttg gttagtaca tagtagagaa catctggact ttcattgttt 900
tgcttctctt tgcgtttgtg tactttactt tgcttgcaat gacaacaaca acagtgtata 960
tcattgatgat acttattctg cctttgtgaa atcttgaaga tatttgtatt tggagagatt 1020
t

- (2) INFORMATION FOR SEQ ID NO:2640:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 276 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..276
(D) OTHER INFORMATION: / Ceres Seq. ID 1573833
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2640:

```

Ile Lys Ile Cys Phe Phe Leu Leu Cys Phe Phe Leu Leu Ser Ser Ser
1      5      10      15
Arg Glu Arg Glu Arg Glu Ile Gln Arg Glu Lys Phe Gly Cys Leu Leu
20      25      30
Thr Glu Ala Ser Ser Val Ser Leu Leu Arg Leu Thr Ile Val Asn Ala
35      40      45
Trp Phe His Leu Gln Phe Cys Phe Tyr Phe Ser Arg Ser Phe Ser Ser
50      55      60
Phe Lys Tyr Cys Phe Arg Ser Ile Asn Gln Ser Ile Met Ala Ser Ser
65      70      75
Gly Asn Lys Asn Ile Asn Ala Lys Leu Val Leu Leu Gly Asp Val Gly
85      90      95
Ala Gly Lys Ser Ser Leu Val Leu Arg Phe Val Lys Asp Gln Phe Val
100     105     110
Glu Phe Gln Glu Ser Thr Ile Gly Ala Ala Phe Phe Ser Gln Thr Leu
115     120     125
Ala Val Asn Asp Ala Thr Val Lys Phe Glu Ile Trp Asp Thr Ala Gly
130     135     140
Gln Glu Arg Tyr His Ser Ser Leu Ala Pro Met Tyr Tyr Arg Gly Ala Ala
145     150     155
Ala Ala Ile Ile Val Phe Asp Ile Thr Asn Gln Ala Ser Phe Glu Arg
165     170     175
Ala Xaa Lys Trp Val Gln Glu Leu Gln Ala Gln Gly Asn Pro Asn Met
180     185     190
Val Met Ala Leu Ala Gly Asn Lys Ala Asp Leu Leu Asp Ala Arg Lys
195     200     205
Val Ser Ala Glu Glu Ala Glu Ile Tyr Ala Gln Glu Asn Ser Leu Phe
210     215     220
Phe Met Glu Thr Ser Ala Lys Thr Ala Thr Asn Val Lys Asp Ile Phe
225     230     235
Tyr Glu Ile Ala Lys Arg Leu Pro Arg Ile Gln Pro Ala Glu Asn Pro
245     250     255
Thr Gly Met Val Leu Pro Asn Gly Pro Gly Ala Thr Ala Val Ser Ser
260     265     270
Ser Cys Cys Ala
275

```

(2) INFORMATION FOR SEQ ID NO:2641:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 200 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..200
- (D) OTHER INFORMATION: / Ceres Seq. ID 1573834

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2641:

```

Met Ala Ser Ser Gly Asn Lys Asn Ile Asn Ala Lys Leu Val Leu Leu
1      5      10      15
Gly Asp Val Gly Ala Gly Lys Ser Ser Leu Val Leu Arg Phe Val Lys
20      25      30
Asp Gln Phe Val Glu Phe Gln Glu Ser Thr Ile Gly Ala Ala Phe Phe
35      40      45
Ser Gln Thr Leu Ala Val Asn Asp Ala Thr Val Lys Phe Glu Ile Trp
50      55      60
Asp Thr Ala Gly Gln Glu Arg Tyr His Ser Leu Ala Pro Met Tyr Tyr
65      70      75
Arg Gly Ala Ala Ala Ala Ile Ile Val Phe Asp Ile Thr Asn Gln Ala
85      90      95
Ser Phe Glu Arg Ala Xaa Lys Trp Val Gln Glu Leu Gln Ala Gln Gly

```

100	105	110
Asn Pro Asn Met Val Met	Ala Leu Ala Gly Asn Lys Ala Asp Leu Leu	
115	120	125
Asp Ala Arg Lys Val Ser	Ala Glu Glu Ala Glu Ile Tyr Ala Gln Glu	
130	135	140
Asn Ser Leu Phe Phe Met	Glu Thr Ser Ala Lys Thr Ala Thr Asn Val	
145	150	155
Lys Asp Ile Phe Tyr Glu	Ile Ala Lys Arg Leu Pro Arg Ile Gln Pro	
165	170	175
Ala Glu Asn Pro Thr Gly Met Val	Leu Pro Asn Gly Pro Gly Ala Thr	
180	185	190
Ala Val Ser Ser Ser Cys Cys Ala		
195	200	

(2) INFORMATION FOR SEQ ID NO:2642:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 375 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..375
- (D) OTHER INFORMATION: / Ceres Seq. ID 1573857

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2642:

gagcgggact	tactttgtgg	ttgctgatca	cactccattt	ggaatggaga	acgatgttgc	60
tttctgtgag	tatcttattg	aagaagtgtg	ggtcgttgcg	atcccaacga	gcgtctttta	120
tctgaatcca	gaagaaggga	agaatttgg	taggtttgcg	ttctgtaaag	acgaagagac	180
gttcgtgtgt	gcaattgaga	ggaatgaagca	gaagcttaag	agaaaagtct	gaagtgttgaa	240
ttagaaagat	accttatttt	tatctagtgt	tgtaacttct	tcttcggttc	catttcggga	300
gagactttga	tttagcaaa	caaatacata	aagtaaaagt	tacgtGtate	aaatgcaata	360
atagtcttta	gagtc					

(2) INFORMATION FOR SEQ ID NO:2643:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 76 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..76
- (D) OTHER INFORMATION: / Ceres Seq. ID 1573858

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2643:

Ser Gly Thr Tyr Phe Val Val Ala Asp His Thr Pro Phe Gly Met Glu	
1	5
Asn Asp Val Ala Phe Cys Glu Tyr Leu Ile Glu Glu Val Gly Val Val	
20	25
Ala Ile Pro Thr Ser Val Phe Tyr Leu Asn Pro Glu Glu Gly Lys Asn	
35	40
Leu Val Arg Phe Ala Phe Cys Lys Asp Glu Glu Thr Leu Arg Gly Ala	
50	55
Ile Glu Arg Met Lys Glu Lys Leu Lys Arg Lys Val	
65	70
	75

(2) INFORMATION FOR SEQ ID NO:2644:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..40
(D) OTHER INFORMATION: / Ceres Seq. ID 1573859

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2644:

Ala Gly Leu Thr Leu Trp Leu Leu Ile Thr Leu His Leu Glu Trp Arg
1 5 10 15
Thr Met Leu Leu Ser Val Ser Ile Leu Lys Lys Leu Gly Ser Leu
20 25 30
Arg Ser Gln Arg Ala Ser Phe Ile
35 40

(2) INFORMATION FOR SEQ ID NO:2645:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 62 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..62
(D) OTHER INFORMATION: / Ceres Seq. ID 1573860

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2645:

Met Glu Asn Asp Val Ala Phe Cys Glu Tyr Leu Ile Glu Glu Val Gly
1 5 10 15
Val Val Ala Ile Pro Thr Ser Val Phe Tyr Leu Asn Pro Glu Glu Gly
20 25 30
Lys Asn Leu Val Arg Phe Ala Phe Cys Lys Asp Glu Glu Thr Leu Arg
35 40 45
Gly Ala Ile Glu Arg Met Lys Gln Lys Leu Lys Arg Lys Val
50 55 60

(2) INFORMATION FOR SEQ ID NO:2646:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1076 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..1076
(D) OTHER INFORMATION: / Ceres Seq. ID 1573864

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2646:

atttttgatt	gcgtcatctt	cttctttgga	aatgtctttg	atttagcatt	tcagttcgct	60
caaaaacatca	aattctacct	tccttagctt	tcacattaga	ttctggtaat	tattaacaca	120
aaaaaaagat	aagccagaat	acgaacaac	caaaaaaaga	ggattttttt	ttttttttt	180
ttctttccga	tgcttccgac	caataattac	cgaatctccg	gcgaaccacc	gtctactacg	240
cgcgtctctc	caccgcctaa	accgaaaaca	aggattctct	ctctatttct	cggttggtga	300
atcattgttt	caattcttct	ttcttctctc	gttcttatcg	gtatcgccct	tggtcttctc	360
ctccctctcc	ttctctcttc	ttccatcggt	caccaccgac	gtcgtcgctg	taatcgccga	420
caagaatctc	cagatgggtt	atcttcaaga	ttcgtgaaaa	agcttctctc	attcaaatc	480
ttcgaaacct	gcacatacac	acggtacgag	agcgattgtg	tgggtttgtt	tgatggattc	540
agacaaggac	aattggtgtg	gaattcttct	ggttggtggc	acgtgtttca	tcgaagtgt	600
gtggagacct	ggttgctcaa	agcctcgacg	tgctctattK	tcagagata	gggttagatt	660
gtggaggagg	gattccacaag	aaggagaatt	aaggagatgt	tttggtcata	qaagaatgat	720
tttgctagat	ttgtaatatt	gtgtggttat	gtagacgtgg	actcagtcta	atggatgata	780
agaattctca	aaactgaagc	tacgaagagg	tacaatacaa	gcccaaggat	ctttctccca	840
tagagaagta	gcgggttgat	cttatggtaa	tatataagca	ctaaagcagat	gggcggttga	900
tcattataac	cctcactacc	attaccaaaa	agcaatagcc	aagagctttt	tttttcattt	960
ttcttttgaa	agccatggat	cggttttctg	ttctgaatgt	tataatggag	gttcgcggtta	1020
ttctaaatga	atcccgcaaa	ctcttctca	agaacaaaaa	gttgatgttc	tcagcc	

(2) INFORMATION FOR SEQ ID NO:2647:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 153 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..153

(D) OTHER INFORMATION: / Ceres Seq. ID 1573865

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2647:

Met	Pro	Pro	Thr	Asn	Asn	Tyr	Arg	Ile	Ser	Gly	Glu	Pro	Pro	Ser	Thr	
1			5						10					15		
Thr	Pro	Ser	Pro	Pro	Pro	Pro	Lys	Pro	Lys	Thr	Arg	Ile	Leu	Ser	Leu	
			20					25					30			
Phe	Leu	Val	Gly	Val	Ile	Met	Phe	Ser	Ile	Phe	Phe	Leu	Phe	Leu	Val	
		35					40					45				
Leu	Ile	Gly	Ile	Ala	Ser	Val	Leu	Ile	Leu	Pro	Leu	Leu	Leu	Ser	Ser	
		50				55					60					
Leu	His	Arg	His	His	Arg	Arg	Arg	Arg	Arg	Asn	Arg	Arg	Gln	Glu	Ser	
65				70					75				80			
Ser	Asp	Gly	Leu	Ser	Ser	Arg	Phe	Val	Lys	Lys	Leu	Pro	Gln	Phe	Lys	
			85					90					95			
Phe	Ser	Glu	Pro	Ser	Thr	Tyr	Thr	Arg	Tyr	Glu	Ser	Asp	Cys	Val	Val	
			100					105					110			
Cys	Phe	Asp	Gly	Phe	Arg	Gln	Gly	Gln	Trp	Cys	Arg	Asn	Leu	Pro	Gly	
		115				120						125				
Cys	Gly	His	Val	Phe	His	Arg	Lys	Cys	Val	Asp	Thr	Trp	Leu	Leu	Lys	
		130				135						140				
Ala	Ser	Thr	Cys	Pro	Ile	Xaa	Gln	Ser								
145					150											

(2) INFORMATION FOR SEQ ID NO:2648:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 115 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..115

(D) OTHER INFORMATION: / Ceres Seq. ID 1573866

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2648:

Met	Phe	Ser	Ile	Phe	Phe	Leu	Phe	Leu	Val	Leu	Ile	Gly	Ile	Ala	Ser	
1			5						10					15		
Val	Leu	Ile	Leu	Pro	Leu	Leu	Leu	Ser	Ser	Leu	His	Arg	His	His	Arg	
			20					25					30			
Arg	Arg	Arg	Arg	Asn	Arg	Arg	Gln	Glu	Ser	Ser	Asp	Gly	Leu	Ser	Ser	
			35				40					45				
Arg	Phe	Val	Lys	Lys	Leu	Pro	Gln	Phe	Lys	Phe	Ser	Glu	Pro	Ser	Thr	
		50				55				60						
Tyr	Thr	Arg	Tyr	Glu	Ser	Asp	Cys	Val	Val	Cys	Phe	Asp	Gly	Phe	Arg	
65				70					75				80			
Gln	Gly	Gln	Trp	Cys	Arg	Asn	Leu	Pro	Gly	Cys	Gly	His	Val	Phe	His	
			85					90				95				
Arg	Lys	Cys	Val	Asp	Thr	Trp	Leu	Leu	Lys	Ala	Ser	Thr	Cys	Pro	Ile	
			100					105					110			
Xaa	Gln	Ser														
		115														

(2) INFORMATION FOR SEQ ID NO:2649:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 505 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..505
(D) OTHER INFORMATION: / Ceres Seq. ID 1573867

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2649:

atcaatcgga	ttatctgcac	ttgtttcaat	ggcgcatcta	atatctctca	agctggtgct	60
cttgcttgcc	ttacaccoga	aggacttgag	gcaatgcata	aggtgattgg	attctataaa	120
gaaaacacaa	acataatcat	tgacacattc	acatctctcg	ggatgatgt	atatggagga	180
aatgcgcctt	acgtatgggt	tcacttcccg	aaccaaaagt	catgggatgt	gtttgctgag	240
attctggaga	agactcatgt	ggttacaact	ccaggaagt	ggttggacc	agggggtgaa	300
gggttgcttc	gtgtcagtc	ctttggtcac	agagagaaca	tcttagaggc	atgtcgaaga	360
ttcaagcagc	tttacaatat	aagaaccttg	tttgtaatcg	tttcctcatc	tcattccacct	420
ctttaatgac	atgatttgag	ttaaaataat	gtcgtttcca	Tgtgkktstg	gaattttag	480
aagacacttt	tgacaccagt	gttttc				

(2) INFORMATION FOR SEQ ID NO:2650:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 126 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..126
(D) OTHER INFORMATION: / Ceres Seq. ID 1573868

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2650:

Ile	Asn	Arg	Ile	Ile	Cys	Thr	Cys	Phe	Asn	Gly	Ala	Ser	Asn	Ile	Ser
1		5						10						15	
Gln	Ala	Gly	Ala	Leu	Ala	Cys	Leu	Thr	Pro	Glu	Gly	Leu	Glu	Ala	Met
		20						25						30	
His	Lys	Val	Ile	Gly	Phe	Tyr	Lys	Glu	Asn	Thr	Asn	Ile	Ile	Ile	Asp
		35						40						45	
Thr	Phe	Thr	Ser	Leu	Gly	Tyr	Asp	Val	Tyr	Gly	Gly	Asn	Ala	Pro	Tyr
		50						55						60	
Val	Trp	Val	His	Phe	Pro	Asn	Gln	Ser	Ser	Trp	Asp	Val	Phe	Ala	Glu
		65						70						75	
Ile	Leu	Glu	Lys	Thr	His	Val	Val	Thr	Thr	Pro	Gly	Ser	Gly	Phe	Gly
		85						90						95	
Pro	Gly	Gly	Glu	Gly	Phe	Val	Arg	Val	Ser	Ala	Phe	Gly	His	Arg	Glu
		100						105						110	
Asn	Ile	Leu	Glu	Ala	Cys	Arg	Arg	Phe	Lys	Gln	Leu	Tyr	Lys		
		115						120						125	

(2) INFORMATION FOR SEQ ID NO:2651:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 95 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..95
(D) OTHER INFORMATION: / Ceres Seq. ID 1573869

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2651:

Met His Lys Val Ile Gly Phe Tyr Lys Glu Asn Thr Asn Ile Ile Ile

1	5	10	15
Asp Thr Phe Thr Ser Leu Gly Tyr Asp Val Tyr Gly Asn Ala Pro			
	20	25	30
Tyr Val Trp Val His Phe Pro Asn Gln Ser Ser Trp Asp Val Phe Ala			
	35	40	45
Glu Ile Leu Glu Lys Thr His Val Val Thr Thr Pro Gly Ser Gly Phe			
	50	55	60
Gly Pro Gly Gly Glu Gly Phe Val Arg Val Ser Ala Phe Gly His Arg			
	65	70	75
Glu Asn Ile Leu Glu Ala Cys Arg Arg Phe Lys Gln Leu Tyr Lys			
	85	90	95

(2) INFORMATION FOR SEQ ID NO:2652:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1687 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1687
- (D) OTHER INFORMATION: / Ceres Seq. ID 1573899

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2652:

aattctcttgc	tctatttttc	gtcaccctag	ccgttttact	ctcttgcgat	atctctgaga	60
tttggtttgac	agtctctaac	catgggttaa	gagaagtttc	acatcaacat	ttgtggtcatt	120
ggccacgtgc	attcttgaaa	gtcgaccacc	actggacact	tgatctacaa	gttgggtgggt	180
attgacaagc	gtgtcattga	gaggttcgag	aaggaggctg	ctgagatgaa	caagaggttcc	240
ttcaagtacg	catgggtttt	ggacaaactt	aaggctgagc	gtgagcgtgg	tatcaccattc	300
gacattgtcc	tctggaaagt	cgagaccacc	aagtactact	gcactgtcat	tgatgtctct	360
ggccatcgtg	atttcatcaa	gaacatgac	actggtacct	cccaggctga	ttgtgtctgc	420
cttatcatcg	actccaccac	tggtgtgttt	gaggctggta	tctccaagga	tggtcagacc	480
cgtgagcagc	ctctcctctg	tttcacctt	ggtgtcaaac	agatgatctg	ctgttgttaac	540
aagatggatg	ccactaccct	caagtactcc	aaggccaggt	acgatgaat	tatcaaggag	600
gtgtcttctt	acttgaagaa	ggttggttac	aaccocgaca	aaatcccat	tggtcccatc	660
tctggattcg	aggggtgaca	catgattgag	aggtccacca	acctagactg	gtacaaaggga	720
ccaactcttc	ttgaggctct	tgaccagatc	aacgagccca	agaggccact	agacaaagccc	780
cttcgtctcc	cacttcaggga	tgctacaag	attggtggta	ttgaaacggt	gccagtgagg	840
cgtgttgaga	ctgttatgat	caagcctggt	atggttttga	cctttgtctc	cacagggttg	900
accactgagg	tcaagtctgt	tgagatgcac	cacgagcttc	tcttggaggc	acttcagggt	960
gacacagctg	ggttcaatgt	taagaatgtt	gctgtcaagg	atcttaagag	aggggtacgtc	1020
gcactcaact	ccaagatga	ccctgcgaag	ggtgtcgtca	acttcaacct	ccaggtctatc	1080
atcatgaacc	accctgggtc	gattgtgaac	ggttacgccc	cagtcctgtc	ttgccacacc	1140
tctcacattg	cagtcgaagt	ctctgagatc	ttgaccaaga	ttgacaggcg	ctgttcttaag	1200
gagatgtaga	agagagccaa	gttcttgaag	aatggtgatg	ctggtatggt	gaagatgaat	1260
ccaaccaagg	ccatggttgt	ggagaccctt	tctgagtacc	caccacttgg	acgttttcgt	1320
gtgaggggaca	tgaggcgagc	tggttcagtc	ggtgttatca	agagtgttga	caagaaggag	1380
ccaaccggag	ccaaggttac	caaggctgcc	gtcaagaagg	gtgcgaagtg	aacctatctc	1440
aaaactctat	ctgcgcagg	tgaatcaaa	gacagtgtta	gtttttattc	aatagtttgg	1500
tatttgtctg	cgtgtctctg	ttcttgtttc	gtttttctcc	cgtcagagcg	ttgttctcgt	1560
atttgggttc	ttgatcggag	gtggcggatc	tacacacaca	ttcttctcgt	tttttctgtt	1620
ttttttgttt	tctcattttg	aactgtttaa	aatttctggt	atatgaatga	atgtttttccc	1680
tgcggtc						

(2) INFORMATION FOR SEQ ID NO:2653:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 449 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide

(B) LOCATION: 1..449

(D) OTHER INFORMATION: / Ceres Seq. ID 1573900

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2653:

Met	Gly	Lys	Glu	Lys	Phe	His	Ile	Asn	Ile	Val	Val	Ile	Gly	His	Val
1			5					10					15		
Asp	Ser	Gly	Lys	Ser	Thr	Thr	Thr	Gly	His	Leu	Ile	Tyr	Lys	Leu	Gly
			20					25					30		
Gly	Ile	Asp	Lys	Arg	Val	Ile	Glu	Arg	Phe	Glu	Lys	Glu	Ala	Ala	Glu
			35					40					45		
Met	Asn	Lys	Arg	Ser	Phe	Lys	Tyr	Ala	Trp	Val	Leu	Asp	Lys	Leu	Lys
			50				55				60				
Ala	Glu	Arg	Glu	Arg	Gly	Ile	Thr	Ile	Asp	Ile	Ala	Leu	Trp	Lys	Phe
					70				75					80	
Glu	Thr	Thr	Lys	Tyr	Tyr	Cys	Thr	Val	Ile	Asp	Ala	Pro	Gly	His	Arg
				85				90						95	
Asp	Phe	Ile	Lys	Asn	Met	Ile	Thr	Gly	Thr	Ser	Gln	Ala	Asp	Cys	Ala
			100					105					110		
Xaa	Leu	Ile	Ile	Asp	Ser	Thr	Thr	Gly	Gly	Phe	Glu	Ala	Gly	Ile	Ser
			115				120					125			
Lys	Asp	Gly	Gln	Thr	Arg	Glu	His	Ala	Leu	Leu	Ala	Phe	Thr	Leu	Gly
			130				135				140				
Val	Lys	Gln	Met	Ile	Cys	Cys	Cys	Asn	Lys	Met	Asp	Ala	Thr	Thr	Pro
					150				155					160	
Lys	Tyr	Ser	Lys	Ala	Arg	Tyr	Asp	Glu	Ile	Ile	Lys	Glu	Val	Ser	Ser
				165				170						175	
Tyr	Leu	Lys	Lys	Val	Gly	Tyr	Asn	Pro	Asp	Lys	Ile	Pro	Phe	Val	Pro
			180					185					190		
Ile	Ser	Gly	Phe	Glu	Gly	Asp	Asn	Met	Ile	Glu	Arg	Ser	Thr	Asn	Leu
			195				200					205			
Asp	Trp	Tyr	Lys	Gly	Pro	Thr	Leu	Leu	Glu	Ala	Leu	Asp	Gln	Ile	Asn
						215					220				
Glu	Pro	Lys	Arg	Pro	Ser	Asp	Lys	Pro	Leu	Arg	Leu	Pro	Leu	Gln	Asp
					230				235					240	
Val	Tyr	Lys	Ile	Gly	Gly	Ile	Gly	Thr	Val	Pro	Val	Gly	Arg	Val	Glu
				245				250						255	
Thr	Gly	Met	Ile	Lys	Pro	Gly	Met	Val	Val	Thr	Phe	Ala	Pro	Thr	Gly
			260				265					270			
Leu	Thr	Thr	Glu	Val	Lys	Ser	Val	Glu	Met	His	His	Glu	Ser	Leu	Leu
			275				280					285			
Glu	Ala	Leu	Pro	Gly	Asp	Asn	Val	Gly	Phe	Asn	Val	Lys	Asn	Val	Ala
			290			295					300				
Val	Lys	Asp	Leu	Lys	Arg	Gly	Tyr	Val	Ala	Ser	Asn	Ser	Lys	Asp	Asp
					310				315					320	
Pro	Ala	Lys	Gly	Ala	Ala	Asn	Phe	Thr	Ser	Gln	Val	Ile	Ile	Met	Asn
				325				330						335	
His	Pro	Gly	Gln	Ile	Gly	Asn	Gly	Tyr	Ala	Pro	Val	Leu	Asp	Cys	His
				340				345					350		
Thr	Ser	His	Ile	Ala	Val	Lys	Phe	Ser	Glu	Ile	Leu	Thr	Lys	Ile	Asp
			355				360					365			
Arg	Arg	Ser	Gly	Lys	Glu	Ile	Glu	Lys	Glu	Pro	Lys	Phe	Leu	Lys	Asn
			370			375					380				
Gly	Asp	Ala	Gly	Met	Val	Lys	Met	Thr	Pro	Thr	Lys	Pro	Met	Val	Val
					390				395					400	
Glu	Thr	Phe	Ser	Glu	Tyr	Pro	Pro	Leu	Gly	Arg	Phe	Ala	Val	Arg	Asp
				405				410						415	
Met	Arg	Gln	Thr	Val	Ala	Val	Gly	Val	Ile	Lys	Ser	Val	Asp	Lys	Lys
			420				425					430			
Asp	Pro	Thr	Gly	Ala	Lys	Val	Thr	Lys	Ala	Ala	Val	Lys	Lys	Gly	Ala
			435				440					445			

Lys

(2) INFORMATION FOR SEQ ID NO:2654:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 401 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..401

(D) OTHER INFORMATION: / Ceres Seq. ID 1573901

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2654:

```

Met Asn Lys Arg Ser Phe Lys Tyr Ala Trp Val Leu Asp Lys Leu Lys
1      5      10      15
Ala Glu Arg Glu Arg Gly Ile Thr Ile Asp Ile Ala Leu Trp Lys Phe
20      25      30
Glu Thr Thr Lys Tyr Tyr Cys Thr Val Ile Asp Ala Pro Gly His Arg
35      40      45
Asp Phe Ile Lys Asn Met Ile Thr Gly Thr Ser Gln Ala Asp Cys Ala
50      55      60
Xaa Leu Ile Ile Asp Ser Thr Thr Gly Gly Phe Glu Ala Gly Ile Ser
65      70      75      80
Lys Asp Gly Gln Thr Arg Glu His Ala Leu Ala Phe Thr Leu Gly
85      90      95
Val Lys Gln Met Ile Cys Cys Cys Asn Lys Met Asp Ala Thr Thr Pro
100      105      110
Lys Tyr Ser Lys Ala Arg Tyr Asp Glu Ile Ile Lys Glu Val Ser Ser
115      120      125
Tyr Leu Lys Lys Val Gly Tyr Asn Pro Asp Lys Ile Pro Phe Val Pro
130      135      140
Ile Ser Gly Phe Glu Gly Asp Asn Met Ile Glu Arg Ser Thr Asn Leu
145      150      155      160
Asp Trp Tyr Lys Gly Pro Thr Leu Leu Glu Ala Leu Asp Gln Ile Asn
165      170      175
Glu Pro Lys Arg Pro Ser Asp Lys Pro Leu Arg Leu Pro Leu Gln Asp
180      185      190
Val Tyr Lys Ile Gly Gly Ile Gly Thr Val Pro Val Gly Arg Val Glu
195      200      205
Thr Gly Met Ile Lys Pro Gly Met Val Val Thr Phe Ala Pro Thr Gly
210      215      220
Leu Thr Thr Glu Val Lys Ser Val Glu Met His His Glu Ser Leu Leu
225      230      235      240
Glu Ala Leu Pro Gly Asp Asn Val Gly Phe Asn Val Lys Asn Val Ala
245      250      255
Val Lys Asp Leu Lys Arg Gly Tyr Val Ala Ser Asn Ser Lys Asp Asp
260      265      270
Pro Ala Lys Gly Ala Ala Asn Phe Thr Ser Gln Val Ile Ile Met Asn
275      280      285
His Pro Gly Gln Ile Gly Asn Gly Tyr Ala Pro Val Leu Asp Cys His
290      295      300
Thr Ser His Ile Ala Val Lys Phe Ser Glu Ile Leu Thr Lys Ile Asp
305      310      315      320
Arg Arg Ser Gly Lys Glu Ile Glu Lys Glu Pro Lys Phe Leu Lys Asn
325      330      335
Gly Asp Ala Gly Met Val Lys Met Thr Pro Thr Lys Pro Met Val Val
340      345      350
Glu Thr Phe Ser Glu Tyr Pro Pro Leu Gly Arg Phe Ala Val Arg Asp
355      360      365
Met Arg Gln Thr Val Ala Val Gly Val Ile Lys Ser Val Asp Lys Lys
370      375      380
Asp Pro Thr Gly Ala Lys Val Thr Lys Ala Ala Val Lys Lys Gly Ala

```

385 390 395 400
Lys

(2) INFORMATION FOR SEQ ID NO:2655:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 348 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..348

(D) OTHER INFORMATION: / Ceres Seq. ID 1573902

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2655:

Met Ile Thr Gly Thr Ser Gln Ala Asp Cys Ala Xaa Leu Ile Asp
1 5 10 15
Ser Thr Thr Gly Gly Phe Glu Ala Gly Ile Ser Lys Asp Gly Gln Thr
20 25 30
Arg Glu His Ala Leu Leu Ala Phe Thr Leu Gly Val Lys Gln Met Ile
35 40 45
Cys Cys Cys Asn Lys Met Asp Ala Thr Thr Pro Lys Tyr Ser Lys Ala
50 55 60
Arg Tyr Asp Glu Ile Ile Lys Glu Val Ser Ser Tyr Leu Lys Lys Val
65 70 75 80
Gly Tyr Asn Pro Asp Lys Ile Pro Phe Val Pro Ile Ser Gly Phe Glu
85 90 95
Gly Asp Asn Met Ile Glu Arg Ser Thr Asn Leu Asp Trp Tyr Lys Gly
100 105 110
Pro Thr Leu Leu Glu Ala Leu Asp Gln Ile Asn Glu Pro Lys Arg Pro
115 120 125
Ser Asp Lys Pro Leu Arg Leu Pro Leu Gln Asp Val Tyr Lys Ile Gly
130 135 140
Gly Ile Gly Thr Val Pro Val Gly Arg Val Glu Thr Gly Met Ile Lys
145 150 155 160
Pro Gly Met Val Val Thr Phe Ala Pro Thr Gly Leu Thr Thr Glu Val
165 170 175
Lys Ser Val Glu Met His His Glu Ser Leu Leu Glu Ala Leu Pro Gly
180 185 190
Asp Asn Val Gly Phe Asn Val Lys Asn Val Ala Val Lys Asp Leu Lys
195 200 205
Arg Gly Tyr Val Ala Ser Asn Ser Lys Asp Asp Pro Ala Lys Gly Ala
210 215 220
Ala Asn Phe Thr Ser Gln Val Ile Ile Met Asn His Pro Gly Gln Ile
225 230 235 240
Gly Asn Gly Tyr Ala Pro Val Leu Asp Cys His Thr Ser His Ile Ala
245 250 255
Val Lys Phe Ser Glu Ile Leu Thr Lys Ile Asp Arg Arg Ser Gly Lys
260 265 270
Glu Ile Glu Lys Glu Pro Lys Phe Leu Lys Asn Gly Asp Ala Gly Met
275 280 285
Val Lys Met Thr Thr Pro Thr Lys Pro Met Val Val Glu Thr Phe Ser Glu
290 295 300
Tyr Pro Pro Leu Gly Arg Phe Ala Val Arg Asp Met Arg Gln Thr Val
305 310 315 320
Ala Val Gly Val Ile Lys Ser Val Asp Lys Lys Asp Pro Thr Gly Ala
325 330 335
Lys Val Thr Lys Ala Ala Val Lys Lys Gly Ala Lys
340 345

(2) INFORMATION FOR SEQ ID NO:2656:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 660 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..660
(D) OTHER INFORMATION: / Ceres Seq. ID 1573909
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2656:
agggtttctg tttgcgcgt caggtttcgt gaaaagaatc tatcttgagc aatgtctcca 60
gctaaagtgt atgtcaccac gaaagccgac cctaaggcta aggccttgaa agctgcgaaa 120
gcagtgaaat ctggccaaat ctgtaaaagc cctgcgaaga agatcaggac aaaggttact 180
ttccacaggc cMaaGacat tgaccgttcc tagaaagcct aagtacccaa agatcagtcg 240
tactccaagg aacaaaattgg atcattacca gatcctcaag taccctetca ctactgaatc 300
tgccatgaaa aagattgaag acaacaacac cttagtcttc attggtgaca tccgtgctga 360
caagaaaaag atcaaatgat ctgtcaagaa gatgtatgac attcagacca agaaagtcaa 420
cacctcatt aggcccgatg gaacaaagaa ggcgtatgtg aggttgactc ctgattatga 480
tgctttggat gtggctaaca aaatcgggat catctaactc gatcattgtc gctctgtgat 540
tttacttttt ctggtttttc tcttccatag tctcagtttt gctagagaag ttaagatatt 600
actatcacca tctctttgtt atgcttttat ctttggtattc aaaaagatta tatgtttggc 660

(2) INFORMATION FOR SEQ ID NO:2657:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 53 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..53
(D) OTHER INFORMATION: / Ceres Seq. ID 1573910
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2657:
Met Ser Pro Ala Lys Val Asp Val Thr Lys Lys Ala Asp Pro Lys Ala
1 5 10 15
Lys Ala Leu Lys Ala Ala Lys Ala Val Lys Ser Gly Gln Ile Val Lys
20 25 30
Lys Pro Ala Lys Lys Ile Arg Thr Lys Val Thr Phe His Arg Xaa Lys
35 40 45
Asp Ile Asp Arg Ser
50

(2) INFORMATION FOR SEQ ID NO:2658:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 70 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..70
(D) OTHER INFORMATION: / Ceres Seq. ID 1573911
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2658:
Met Lys Lys Ile Glu Asp Asn Asn Thr Leu Val Phe Ile Val Asp Ile
1 5 10 15
Arg Ala Asp Lys Lys Lys Ile Lys Asp Ala Val Lys Lys Met Tyr Asp
20 25 30
Ile Gln Thr Lys Lys Val Asn Thr Leu Ile Arg Pro Asp Gly Thr Lys
35 40 45
Lys Ala Tyr Val Arg Leu Thr Pro Asp Tyr Asp Ala Leu Asp Val Ala

50 55 60
Asn Lys Ile Gly Ile Ile
65 70
(2) INFORMATION FOR SEQ ID NO:2659:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 41 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..41
(D) OTHER INFORMATION: / Ceres Seq. ID 1573912
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2659:
Met Tyr Asp Ile Gln Thr Lys Lys Val Asn Thr Leu Ile Arg Pro Asp
1 5 10 15
Gly Thr Lys Lys Ala Tyr Val Arg Leu Thr Pro Asp Tyr Asp Ala Leu
20 25 30
Asp Val Ala Asn Lys Ile Gly Ile Ile
35 40

(2) INFORMATION FOR SEQ ID NO:2660:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 559 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..559
(D) OTHER INFORMATION: / Ceres Seq. ID 1573920
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2660:
aattcaactga ttattgtttt aaggcaaat aagatcatct tcaaaatctt ctcatgctc 60
ttccaatttt ctagaataaa catgtcttgc tgtggtggaa gctgtggttg tggatctgcc 120
tgcaagtgcg gcaatgggtg cggagggtgc aaaaggtacc ctgacttgga gaacaccgcc 180
accgagactc ttgtctctcg ttgtgctcgc gcgatgaact ctcatgaca ggcttccggT 240
cgSagacttt cgttgccgag aatgatgcct gcaaatgcgg atctgactgc aagtgcaccc 300
cttgtaactg caaatgaaga acttcataaa ccctaagtct gtaataaccc taatgttatg 360
ttagggtttg ttaatatgaa taattggctg atttttccgg tagttttgcc ggcgacgttg 420
gtctttctct tcttcttctt cttctgtgtg tgtttttatg gtttggtcac taagatatct 480
ctgcaaatgt ttaattttgt gactttatta atcctaagac tattatgggt ttgtattaaa 540
gtttgcttct tcttgcctc

(2) INFORMATION FOR SEQ ID NO:2661:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 111 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..111
(D) OTHER INFORMATION: / Ceres Seq. ID 1573921
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2661:
Asn Ser Leu Ile Ile Val Leu Arg Gln Ile Lys Ile Ile Phe Lys Ile
1 5 10 15
Phe Ser Asp Leu Phe Gln Phe Ser Arg Lys Asn Met Ser Cys Cys Gly
20 25 30
Gly Ser Cys Gly Cys Gly Ser Ala Cys Lys Cys Gly Asn Gly Cys Gly
35 40 45

Gly Cys Lys Arg Tyr Pro Asp Leu Glu Asn Thr Ala Thr Glu Thr Leu
50 55 60
Val Leu Gly Val Ala Pro Ala Met Asn Ser Gln Tyr Glu Ala Ser Gly
65 70 75 80
Xaa Arg Leu Ser Leu Pro Arg Met Met Pro Ala Asn Ala Asp Leu Thr
85 90 95
Ala Ser Ala Thr Leu Val Pro Ala Asn Glu Glu Leu His Lys Pro
100 105 110

(2) INFORMATION FOR SEQ ID NO:2662:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 84 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..84
- (D) OTHER INFORMATION: / Ceres Seq. ID 1573922

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2662:

Met Ser Cys Cys Gly Gly Ser Cys Gly Cys Gly Ser Ala Cys Lys Cys
1 5 10 15
Gly Asn Gly Cys Gly Gly Cys Lys Arg Tyr Pro Asp Leu Glu Asn Thr
20 25 30
Ala Thr Glu Thr Leu Val Leu Gly Val Ala Pro Ala Met Asn Ser Gln
35 40 45
Tyr Glu Ala Ser Gly Xaa Arg Leu Ser Leu Pro Arg Met Met Pro Ala
50 55 60
Asn Ala Asp Leu Thr Ala Ser Ala Thr Leu Val Pro Ala Asn Glu Glu
65 70 75 80
Leu His Lys Pro

(2) INFORMATION FOR SEQ ID NO:2663:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 67 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..67
- (D) OTHER INFORMATION: / Ceres Seq. ID 1573923

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2663:

Met Leu Gly Leu Leu Ile Cys Asn Asn Trp Leu Ile Phe Pro Val Val
1 5 10 15
Leu Pro Ala Thr Leu Val Phe Leu Phe Phe Phe Phe Cys Val Cys
20 25 30
Phe Tyr Gly Leu Val Ile Lys Ile Ser Leu Gln Ser Phe Ile Phe Val
35 40 45
Thr Leu Leu Ile Leu Arg Leu Leu Trp Val Cys Ile Lys Val Cys Phe
50 55 60
Phe Leu Ala
65

(2) INFORMATION FOR SEQ ID NO:2664:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1211 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..1211
(D) OTHER INFORMATION: / Ceres Seq. ID 1573941

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2664:

aaaagcaaca	tgaagacaaa	ttaagctggt	tcttcttctt	gttcttgggtc	tctgtggaaa	60
atatgtttgt	tgtctgttct	ctttctcacc	gagacgatca	ccgcgcgtgaa	gctgccgcca	120
aaattgtatta	tccgcgtgtg	aatcgctttc	ggagactcca	ctgtcgacac	aggaatgaac	180
aacaatgtca	aaaccggtgt	taagtgtgat	tttcttctct	atgggtatcaa	tttccaaagc	240
ggagttgcc	cggggagatt	ctgcgatgga	cgagtcctcg	ccgattttgct	agccgaagaa	300
ctgggaataa	aatcaattgt	accagcatca	ctagatccga	atctaaaatc	gaaagatctt	360
ttaaccggtg	tatgttttgc	ctccggaggt	tctggtatg	atcctataac	accgaaactt	420
gtggcgagta	tatcattaga	agatcaattg	agttatttgc	aggagtagat	agagaaagtg	480
aagaatatag	ttggggaagc	aagaaaaagc	ttcatagtag	ccaacagctt	attcttattg	540
gtcgcaggca	gcgacgacat	agccaataca	tactatactc	tacgtgcaag	acctgaatac	600
gacgtcgatt	catacactac	tcttatgtct	gactctgcct	cagaatttgt	gactaaacta	660
tactgatatg	gagtgagaag	agtagctgtg	tttgggtcac	caccaattgg	gtgtgtacca	720
tccagagaaa	cgttaggagg	aggtatcttg	agagattgtg	ctgataatta	caacgaagca	780
gcaaaacttt	ttaattcaaa	gcctctccca	aaattggatt	cgttgcgtta	aacctaccgc	840
ggcatcaaac	cgatctacat	taatatctat	gatcctcttt	tgcacatcat	ccagaatcct	900
gcaaatatgt	ggtttgaagt	gtctaataaa	ggatgctgtg	gaacaggagc	catagaagtt	960
gctgtgttgt	gcaataaaaa	cacatctctt	gtatgtcccg	acgtgtctac	ctatgtgttt	1020
tgggacagnt	tatcatctca	cagagaaaaa	ttacaaaagta	ttagtctcac	tgttgattaa	1080
caaatattgt	aaatcagttg	tctgaattaa	aaactatttt	cacggcataa	tgattgatta	1140
tattttatct	catcttgttt	gtattatttg	ataattgtat	tcgatttaaa	taaaaattaat	1200
atttcttgtt	t					

(2) INFORMATION FOR SEQ ID NO:2665:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 359 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..359
(D) OTHER INFORMATION: / Ceres Seq. ID 1573942

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2665:

Lys	Ser	Asn	Met	Lys	Asp	Asn	Ser	Ser	Trp	Ser	Cys	Ser	Cys	Ser	Trp
1				5					10					15	
Ser	Ser	Trp		Lys	Ile	Cys	Leu	Leu	Ser	Val	Leu	Thr	Glu	Thr	
				20					25				30		
Ile	Thr	Ala	Val	Lys	Leu	Pro	Pro	Lys	Leu	Ile	Ile	Pro	Ala	Val	Ile
				35					40				45		
Ala	Phe	Gly	Asp	Ser	Ile	Val	Asp	Thr	Gly	Met	Asn	Asn	Val	Lys	
				50					55				60		
Thr	Val	Val	Lys	Cys	Asp	Phe	Leu	Pro	Tyr	Gly	Ile	Asn	Phe	Gln	Ser
				65					70				75		80
Gly	Val	Ala	Thr	Gly	Arg	Phe	Cys	Asp	Gly	Arg	Val	Pro	Ala	Asp	Leu
				85					90				95		
Leu	Ala	Glu	Glu	Leu	Gly	Ile	Lys	Ser	Ile	Val	Pro	Ala	Tyr	Leu	Asp
				100					105				110		
Pro	Asn	Leu	Lys	Ser	Lys	Asp	Leu	Leu	Thr	Gly	Val	Ser	Phe	Ala	Ser
				115					120				125		
Gly	Gly	Ser	Gly	Tyr	Asp	Pro	Ile	Thr	Pro	Lys	Leu	Val	Ala	Val	Ile
				130					135				140		
Ser	Leu	Glu	Asp	Gln	Leu	Ser	Tyr	Phe	Glu	Glu	Tyr	Ile	Glu	Lys	Val
				145					150				155		160
Lys	Asn	Ile	Val	Gly	Glu	Ala	Arg	Lys	Asp	Phe	Ile	Val	Ala	Asn	Ser
				165					170				175		
Leu	Phe	Leu	Leu	Val	Ala	Gly	Ser	Asp	Asp	Ile	Ala	Asn	Thr	Tyr	Tyr

180 185 190
Thr Leu Arg Ala Arg Pro Glu Tyr Asp Val Asp Ser Tyr Thr Thr Leu
195 200 205
Met Ser Asp Ser Ala Ser Glu Phe Val Thr Lys Leu Tyr Gly Tyr Gly
210 215 220
Val Arg Arg Val Ala Val Phe Gly Ala Pro Pro Ile Gly Cys Val Pro
225 230 235
Ser Gln Arg Thr Leu Gly Gly Ile Leu Arg Asp Cys Ala Asp Asn
245 250 255
Tyr Asn Glu Ala Ala Lys Leu Phe Asn Ser Lys Leu Ser Pro Lys Leu
260 265 270
Asp Ser Leu Arg Lys Thr Leu Pro Gly Ile Lys Pro Ile Tyr Ile Asn
275 280 285
Ile Tyr Asp Pro Leu Phe Asp Ile Ile Gln Asn Pro Ala Asn Tyr Gly
290 295 300
Phe Glu Val Ser Asn Lys Gly Cys Cys Gly Thr Gly Ala Ile Glu Val
305 310 315
Ala Val Leu Cys Asn Lys Ile Thr Ser Ser Val Cys Pro Asp Val Ser
325 330 335
Thr His Val Phe Trp Asp Xaa Leu Ser Ser Tyr Arg Glu Asn Leu Gln
340 345 350
Ser Ile Ser Leu Thr Val Asp
355

(2) INFORMATION FOR SEQ ID NO:2666:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 356 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..356
- (D) OTHER INFORMATION: / Ceres Seq. ID 1573943

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2666:

Met Lys Asp Asn Ser Ser Trp Ser Cys Ser Cys Ser Trp Ser Ser Trp
1 5 10 15
Lys Ile Cys Leu Leu Ser Val Leu Phe Leu Thr Glu Thr Ile Thr Ala
20 25 30
Val Lys Leu Pro Pro Lys Leu Ile Ile Pro Ala Val Ile Ala Phe Gly
35 40 45
Asp Ser Ile Val Asp Thr Gly Met Asn Asn Asn Val Lys Thr Val Val
50 55 60
Lys Cys Asp Phe Leu Pro Tyr Gly Ile Asn Phe Gln Ser Gly Val Ala
65 70 75 80
Thr Gly Arg Phe Cys Asp Gly Arg Val Pro Ala Asp Leu Leu Ala Glu
85 90 95
Glu Leu Gly Ile Lys Ser Ile Val Pro Ala Tyr Leu Asp Pro Asn Leu
100 105 110
Lys Ser Lys Asp Leu Leu Thr Gly Val Ser Phe Ala Ser Gly Gly Ser
115 120 125
Gly Tyr Asp Pro Ile Thr Pro Lys Leu Val Ala Val Ile Ser Leu Glu
130 135 140
Asp Gln Leu Ser Tyr Phe Glu Glu Tyr Ile Glu Lys Val Lys Asn Ile
145 150 155 160
Val Gly Glu Ala Arg Lys Asp Phe Ile Val Ala Asn Ser Leu Phe Leu
165 170 175
Leu Val Ala Gly Ser Asp Asp Ile Ala Asn Thr Tyr Tyr Thr Leu Arg
180 185 190
Ala Arg Pro Glu Tyr Asp Val Asp Ser Tyr Thr Thr Leu Met Ser Asp
195 200 205

Ser Ala Ser Glu Phe Val Thr Lys Leu Tyr Gly Tyr Gly Val Arg Arg
210 215 220
Val Ala Val Phe Gly Ala Pro Pro Ile Gly Cys Val Pro Ser Gln Arg
225 230 235 240
Thr Leu Gly Gly Gly Ile Leu Arg Asp Cys Ala Asp Asn Tyr Asn Glu
245 250 255
Ala Ala Lys Leu Phe Asn Ser Lys Leu Ser Pro Lys Leu Asp Ser Leu
260 265 270
Arg Lys Thr Leu Pro Gly Ile Lys Pro Ile Tyr Ile Asn Ile Tyr Asp
275 280 285
Pro Leu Phe Asp Ile Ile Gln Asn Pro Ala Asn Tyr Gly Phe Glu Val
290 295 300
Ser Asn Lys Gly Cys Cys Gly Thr Gly Ala Ile Glu Val Ala Val Leu
305 310 315 320
Cys Asn Lys Ile Thr Ser Ser Val Cys Pro Asp Val Ser Thr His Val
325 330 335
Phe Trp Asp Xaa Leu Ser Ser Tyr Arg Glu Asn Leu Gln Ser Ile Ser
340 345 350
Leu Thr Val Asp
355

(2) INFORMATION FOR SEQ ID NO:2667:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 301 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..301

(D) OTHER INFORMATION: / Ceres Seq. ID 1573944

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2667:

Met Asn Asn Asn Val Lys Thr Val Val Lys Cys Asp Phe Leu Pro Tyr
1 5 10 15
Gly Ile Asn Phe Gln Ser Gly Val Ala Thr Gly Arg Phe Cys Asp Gly
20 25 30
Arg Val Pro Ala Asp Leu Leu Ala Glu Glu Leu Gly Ile Lys Ser Ile
35 40 45
Val Pro Ala Tyr Leu Asp Pro Asn Leu Lys Ser Lys Asp Leu Leu Thr
50 55 60
Gly Val Ser Phe Ala Ser Gly Gly Ser Gly Tyr Asp Pro Ile Thr Pro
65 70 75 80
Lys Leu Val Ala Val Ile Ser Leu Glu Asp Gln Leu Ser Tyr Phe Glu
85 90 95
Glu Tyr Ile Glu Lys Val Lys Asn Ile Val Gly Glu Ala Arg Lys Asp
100 105 110
Phe Ile Val Ala Asn Ser Leu Phe Leu Leu Val Ala Gly Ser Asp Asp
115 120 125
Ile Ala Asn Thr Tyr Tyr Thr Leu Arg Ala Arg Pro Glu Tyr Asp Val
130 135 140
Asp Ser Tyr Thr Thr Leu Met Ser Asp Ser Ala Ser Glu Phe Val Thr
145 150 155 160
Lys Leu Tyr Gly Tyr Gly Val Arg Arg Val Ala Val Phe Gly Ala Pro
165 170 175
Pro Ile Gly Cys Val Pro Ser Gln Arg Thr Leu Gly Gly Gly Ile Leu
180 185 190
Arg Asp Cys Ala Asp Asn Tyr Asn Glu Ala Ala Lys Leu Phe Asn Ser
195 200 205
Lys Leu Ser Pro Lys Leu Asp Ser Leu Arg Lys Thr Leu Pro Gly Ile
210 215 220
Lys Pro Ile Tyr Ile Asn Ile Tyr Asp Pro Leu Phe Asp Ile Ile Gln

(2) INFORMATION FOR SEQ ID NO:2668:

(A) LENGTH: 1257 base pairs

MOLECULE TYPE: DNA (g

(D) OTHER INFORMATION: / Ceres Seq. ID 1573949

gtaatctcaa	tcaacaacaa	ttcccccttc	tcgatcatca	aatctctcaac	agaaaaaaaa	60
aattccccaa	agctctctca	aaatccccaa	acagatctct	cgatctcttc	cgatctgtct	120
ttctctctaa	tcctggtttg	tttgatttaa	ttgattgaa	gatgtcgacg	gctttgtaata	180
tgcactctta	tgaatttgtg	aaagaagtaa	agagatgaaa	ctgtcgacgt	cgaaagtctg	240
gaggtctaaag	agtttcccg	aagagctggc	gtggacgtgg	tggacctaat	agctggcaat	300
gagctggaa	aggaagtggga	ctgtctcgta	gaggtctctt	tgctgttaat	tctgcggcat	360
catcatcctt	ctccataaac	aaagcttccc	cagcgaagag	gagcttgcca	ttgcagaaat	420
agaagtgttt	gtatgaagaa	acctctagag	ctgttggggt	ctcaggaagt	gaagtgcgaa	480
ccacagttta	tattaccaac	cttgtacag	gagtgcacaa	tgaagatata	agggcaactc	540
atgtctgagt	ttggagagctg	raaagatgat	caattcacta	tgcacaaaat	gggcgtccaa	600
gtggagtctg	tcgaatttgt	tatatgagaa	gaagtgaac	aattcaagct	tgcagaaat	660
acalacaagt	tacttttggg	tgggaagcct	atgaaactgt	agattctggg	tggaaagtat	720
gaatctgtct	ctgtcgcaga	tcgttgtta	gtgactgtgt	tgaatggaa	gtaggaagag	780
agttctctca	tggcacaagg	agttgaaggt	gggagagtag	gaaggaggaag	aggttcaggt	840
ctctctggaa	cagccctctc	agctcaacaa	aaccaacaa	gtgttcgag	tggtcgagag	900
ggggtccgtg	ctcagaggcag	aggtcttgt	ggagcgagag	ggaataaaa	tgtgtggcca	960
gttggaagaa	agccggcgga	gaagtctgtg	cgcgactctg	acaaagatct	cggaagctat	1020
catgtctga	ctatgaacat	ctcttaaa	gaagactctg	atcttctgt	gtacttttgt	1080
gtctttttat	ctgtagtctc	gactaaatat	gtgccaaagt	ttgttttgt	ttaataactg	1140
ttaggaatgc	tctactctgc	ttcttgtttc	ctcttttttt	tgttcaacat	ttcaacagta	1200
cttttgttta	tttaagattaa	aaagagattta	gctgttaatg	agaaagctgt	tcttgttc	

(2) INFORMATION FOR SEQ ID NO:2669:

(ii) MOLECULE TYPE: peptide

(D) OTHER INFORMATION: / Ceres Seq. ID 1573950

Met	Ser	Asp	Ala	Leu	Asn	Met	Thr	Leu	Asp	Glu	Ile	Val	Lys	Lys	Ser
1				5				10					15		
Lys	Ser	Glu	Arg	Ser	Ala	Ala	Ala	Arg	Ser	Gly	Gly	Lys	Gly	Val	Ser
			20					25					30		
Arg	Lys	Ser	Gly	Arg	Gly	Arg	Gly	Gly	Pro	Asn	Gly	Val	Val	Gly	Ala
			35				40					45			
Gly	Arg	Gly	Gly	Gly	Pro	Val	Arg	Arg	Gly	Pro	Leu	Ala	Val	Asn	Thr

(ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1..118
(D) OTHER INFORMATION: / Ceres Seq. ID 1573952
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2671:
Met Lys Leu Glu Ile Leu Gly Gly Ser Thr Glu Ser Ala Pro Val Ala
1 5 10 15
Ala Arg Val Asn Val Thr Gly Leu Asn Gly Arg Met Lys Arg Ser Val
20 25 30
Phe Ile Gly Gln Gly Val Arg Gly Gly Arg Val Gly Arg Gly Arg Gly
35 40 45
Ser Gly Pro Ser Gly Arg Arg Leu Pro Val Gln Gln Asn Gln Gln Gly
50 55 60
Gly Arg Gly Gly Arg Gly Gly Val Arg Gly Arg Gly Arg Gly Ala Gly
65 70 75 80
Gly Gly Arg Gly Asn Lys Ser Gly Gly Arg Gly Gly Lys Lys Pro Val
85 90 95
Glu Lys Ser Ala Ala Asp Leu Asp Lys Asp Leu Glu Ser Tyr His Ala
100 105 110
Glu Ala Met Asn Ile Ser
115

(2) INFORMATION FOR SEQ ID NO:2672:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 600 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..600
(D) OTHER INFORMATION: / Ceres Seq. ID 1573953
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2672:

ggatcatata ttgtctgtat gagcattgtt tcagcacaa gccaagcaaa gcaggggatg 60
agcagttgaa cttgttccgt ttcctcctc ttgtagctcc catcaagtgc acggttttcc 120
cgcttgttca gaaccaacaa ttcgaggaag cagccaaagt tatttccaa gaactcgct 180
ctgtcgggat ctcccataag attgacatca ctggtacatc gatagggaag agatatgca 240
gaaccgatga gcttggagtg ccatttgcaa taacagtggg ctcggataca tcagtgacaa 300
tcagagaaaag agacagcaaa gatcaagtc gagtcacatt gaaggaggca gcttccgttg 360
tgagctcagt ctacaggggg aaaatgacgt ggcaagacgt ctggggcaacc ttccctcacc 420
attcttctgc tgctgcagac gagtagctag ctccctgttt ttttccGaa ttaaaaacca 480
aagtgttaaa ttaattgttg ctgaattctac tcatttttaa tgttttgttt cttagtgtca 540
cgtaaaaagt tcgataccag attgttagac gaagyggtca taaagtataa actctctgtc 600

(2) INFORMATION FOR SEQ ID NO:2673:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 147 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..147
(D) OTHER INFORMATION: / Ceres Seq. ID 1573954
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2673:

Ile Ile Tyr Cys Leu Tyr Glu His Cys Phe Ser Thr Arg Pro Ser Lys
1 5 10 15
Ala Gly Asp Glu Gln Leu Asn Leu Phe Arg Phe Pro Pro Leu Val Ala
20 25 30
Pro Ile Lys Cys Thr Val Phe Pro Leu Val Gln Asn Gln Gln Phe Glu
35 40 45

Glu Ala Ala Lys Val Ile Ser Lys Glu Leu Ala Ser Val Gly Ile Ser
50 55 60
His Lys Ile Asp Ile Thr Gly Thr Ser Ile Gly Lys Arg Tyr Ala Arg
65 70 75 80
Thr Asp Glu Leu Gly Val Pro Phe Ala Ile Thr Val Asp Ser Asp Thr
85 90 95
Ser Val Thr Ile Arg Glu Arg Asp Ser Lys Asp Gln Val Arg Val Thr
100 105 110
Leu Lys Glu Ala Ala Ser Val Val Ser Ser Val Ser Glu Gly Lys Met
115 120 125
Thr Trp Gln Asp Val Trp Ala Thr Phe Pro His His Ser Ser Ala Ala
130 135 140
Ala Asp Glu
145

(2) INFORMATION FOR SEQ ID NO:2674:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1146 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1146
- (D) OTHER INFORMATION: / Ceres Seq. ID 1573955

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2674:

aattgcaaat	caaatggatc	gtcttaagct	tattttctcc	gttttcgttt	tgtctttctt	60
tatcgctctc	gtttcgtcgt	ctgatgtcaa	cgacggcgat	gatctcgtga	tcgcgcaggt	120
ggttgggtga	gccgagccct	aggttttgac	ctcagaggat	cactttttctc	tcttcaagcg	180
gaagttcggg	aaggtctcac	cttccaacga	ggagcatgac	tatagattct	cggtttgagt	240
tcctgaagaa	gcacttgggg	gttagaagtg	gctttaagct	tctttaaagt	gccaaacaag	300
ctccgattct	ccctaccgaa	aattctccctg	aggattttga	ttggagagat	catggcgccg	360
ttaactcccg	caaaaatcac	ggatcttgcg	gctcttgcgt	gagtttccgc	gccactggag	420
ctttggaagg	tgttaacttc	ctcgtctaccg	gcagactcgt	cagcctcagc	gaacaacagc	480
tcgtcgactg	tgatcacgag	tgtgatcccg	aggagcagaa	tttcttcgca	ctctgttggt	540
aatgggtggc	taatgaacag	cgcttttgaa	tacaccctca	aaaccggagg	gctcatgaaa	600
gaagaagact	atcctttacac	cggaaaggac	ggcaagacct	gcaagctaga	caagtccaag	660
atcgttgcc	ctgtctccaa	cttcagtggt	atctccattg	atgaagaaca	gattgtgcga	720
aacctgtgca	agaacgggac	tcttgctgtga	gccatcaacg	ctggctatat	gcagacttac	780
attggaggag	tctcatgccc	ttacatattg	accaggaggc	tcaaccaacg	tgtcttattg	840
gttggtctatg	gagcggcagg	tacgctccg	gctagggtca	aggagaagcc	ttactggatc	900
atcaagaact	cgtggggaga	gaacttgggt	gaaaatgggt	tctacaaaat	ctgcaaaagg	960
cgtaacattt	gttggtgtga	cagtatggtc	tccactgttg	cagccaccgt	ctcaaccacc	1020
gccattataa	catctcgtca	ataagtttta	attacttttg	tgatttgat	gagcgcgtc	1080
tctttgcgct	gctgactctc	tctatttate	tctgcttctt	gcttgtaaat	aaaatgcggt	1140
ctattg						

(2) INFORMATION FOR SEQ ID NO:2675:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 246 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..246
- (D) OTHER INFORMATION: / Ceres Seq. ID 1573956

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2675:

Met Pro Thr Arg Leu Arg Phe Ser Leu Pro Lys Ile Ser Leu Arg Ile
1 5 10 15
Leu Ile Gly Glu Ile Met Ala Pro Leu Leu Pro Ser Lys Ile Arg Asp

20	25	30
Leu Ala Ala Leu Ala Gly Val Ser Ala Pro Leu Glu Leu Trp Lys Val		
35	40	45
Leu Thr Ser Ser Leu Pro Ala Asp Ser Ser Ala Ser Ala Asn Asn Ser		
50	55	60
Ser Ser Thr Val Ile Thr Ser Val Ile Pro Arg Arg Gln Ile Ser Cys		
65	70	75
Asp Ser Gly Cys Asn Gly Gly Leu Met Asn Ser Ala Phe Glu Tyr Thr		
85	90	95
Leu Lys Thr Gly Gly Leu Met Lys Glu Glu Asp Tyr Pro Tyr Thr Gly		
100	105	110
Lys Asp Gly Lys Thr Cys Lys Leu Asp Lys Ser Lys Ile Val Ala Ser		
115	120	125
Val Ser Asn Phe Ser Val Ile Ser Ile Asp Glu Glu Gln Ile Ala Ala		
130	135	140
Asn Leu Val Lys Asn Gly Pro Leu Ala Val Ala Ile Asn Ala Gly Tyr		
145	150	155
Met Gln Thr Tyr Ile Gly Gly Val Ser Cys Pro Tyr Ile Cys Thr Arg		
165	170	175
Arg Leu Asn His Gly Val Leu Leu Val Gly Tyr Gly Ala Ala Gly Tyr		
180	185	190
Ala Pro Ala Arg Phe Lys Glu Lys Pro Tyr Trp Ile Ile Lys Asn Ser		
195	200	205
Trp Gly Glu Thr Trp Gly Glu Asn Gly Phe Tyr Lys Ile Cys Lys Gly		
210	215	220
Arg Asn Ile Cys Gly Val Asp Ser Met Val Ser Thr Val Ala Ala Thr		
225	230	235
Val Ser Thr Thr Ala His		240
245		

(2) INFORMATION FOR SEQ ID NO:2676:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 225 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..225

(D) OTHER INFORMATION: / Ceres Seq. ID 1573957

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2676:

Met Ala Pro Leu Leu Pro Ser Lys Ile Arg Asp Leu Ala Ala Leu Ala		
1	5	10
Gly Val Ser Ala Pro Leu Glu Leu Trp Lys Val Leu Thr Ser Ser Leu		
20	25	30
Pro Ala Asp Ser Ser Ala Ser Ala Asn Asn Ser Ser Ser Thr Val Ile		
35	40	45
Thr Ser Val Ile Pro Arg Arg Gln Ile Ser Cys Asp Ser Gly Cys Asn		
50	55	60
Gly Gly Leu Met Asn Ser Ala Phe Glu Tyr Thr Leu Lys Thr Gly Gly		
65	70	75
Leu Met Lys Glu Glu Asp Tyr Pro Tyr Thr Gly Lys Asp Gly Lys Thr		
85	90	95
Cys Lys Leu Asp Lys Ser Lys Ile Val Ala Ser Val Ser Asn Phe Ser		
100	105	110
Val Ile Ser Ile Asp Glu Glu Gln Ile Ala Ala Asn Leu Val Lys Asn		
115	120	125
Gly Pro Leu Ala Val Ala Ile Asn Ala Gly Tyr Met Gln Thr Tyr Ile		
130	135	140
Gly Gly Val Ser Cys Pro Tyr Ile Cys Thr Arg Leu Asn His Gly		
145	150	155
		160

Val Leu Leu Val Gly Tyr Gly Ala Ala Gly Tyr Ala Pro Ala Arg Phe
165 170 175
Lys Glu Lys Pro Tyr Trp Ile Ile Lys Asn Ser Trp Gly Glu Thr Trp
180 185 190
Gly Glu Asn Gly Phe Tyr Lys Ile Cys Lys Gly Arg Asn Ile Cys Gly
195 200 205
Val Asp Ser Met Val Ser Thr Val Ala Ala Thr Val Ser Thr Thr Ala
210 215 220

His
225

(2) INFORMATION FOR SEQ ID NO:2677:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 158 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..158
- (D) OTHER INFORMATION: / Ceres Seq. ID 1573958

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2677:

Met	Asn	Ser	Ala	Phe	Glu	Tyr	Thr	Leu	Lys	Thr	Gly	Gly	Leu	Met	Lys
1				5					10					15	
Glu	Glu	Asp	Tyr	Pro	Tyr	Thr	Gly	Lys	Asp	Gly	Lys	Thr	Cys	Lys	Leu
				20				25					30		
Asp	Lys	Ser	Lys	Ile	Val	Ala	Ser	Val	Ser	Asn	Phe	Ser	Val	Ile	Ser
				35				40					45		
Ile	Asp	Glu	Glu	Gln	Ile	Ala	Ala	Asn	Leu	Val	Lys	Asn	Gly	Pro	Leu
				50				55				60			
Ala	Val	Ala	Ile	Asn	Ala	Gly	Tyr	Met	Gln	Thr	Tyr	Ile	Gly	Gly	Val
65				70				75						80	
Ser	Cys	Pro	Tyr	Ile	Cys	Thr	Arg	Arg	Leu	Asn	His	Gly	Val	Leu	Leu
				85				90						95	
Val	Gly	Tyr	Gly	Ala	Ala	Gly	Tyr	Ala	Pro	Ala	Arg	Phe	Lys	Glu	Lys
				100				105					110		
Pro	Tyr	Trp	Ile	Ile	Lys	Asn	Ser	Trp	Gly	Glu	Thr	Trp	Gly	Glu	Asn
				115				120					125		
Gly	Phe	Tyr	Lys	Ile	Cys	Lys	Gly	Arg	Asn	Ile	Cys	Gly	Val	Asp	Ser
				130				135					140		
Met	Val	Ser	Thr	Val	Ala	Ala	Thr	Val	Ser	Thr	Thr	Ala	His		
145				150				155							

(2) INFORMATION FOR SEQ ID NO:2678:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 883 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..883
- (D) OTHER INFORMATION: / Ceres Seq. ID 1573960

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2678:

aaaaaaaaat	catcgtgAaa	cggtcgaagg	ccattttcct	tggacgacca	tcggcggttaa	60
ggagagagct	tagatctcgt	gcgctcgtgc	gacgttggtt	tccggcgttg	tcaaaatggg	120
gttgctcatt	ggaaagtgtg	tcacgcaggct	cttgcgaag	aaagagatgc	gtattctgat	180
ggttggtctc	gatcgtcgtg	gtaagacgac	tatctctcac	aagctcaaac	ttggagagat	240
cgtcaccact	attccaacca	tggggttcaa	cgttgagact	gttgaataca	agaacatcag	300
cttcaccgtg	tgggatgttg	gggggtcaaga	caagatccgt	ccattgtgga	gacattactt	360
ccagaacaca	cagggactta	tctttgttgt	ggacagcaat	gatcgtgacc	gtgtgtgtga	420

```

agccagggag  gagcttcaca  ggatgctgaa  tgaggtatgaa  ttgagggatg  cagttctgct  480
tgtatttgct  aacaagcaag  atcttcccaa  cgcatgaac   gctgctgaga  taactgacaa  540
gcttggggctt  cattctcttc  gtcaacgaca  ctggtacatt  cagagcacat  gtgccacctc  600
tgaggaagga  ctctatgagg  gacttgactg  gctctccaac  aacatcgcaa  gcaaggcata  660
gatggaatgt  tagccaagatt  cctcttctgc  ttgtttgggt  tacaaatcaa  agacagaggt  720
ctgtttctct  agtactaaaa  gatttattat  tatattcttc  ttctgcactt  atctcaaacg  780
cagatcattt  tacactttgt  acttccccct  caataacttg  ttacttctct  cgtttgcttc  840
cgaatttgag  tatatcattt  ttacatctgc  ttttcatcaa  agc

```

(2) INFORMATION FOR SEQ ID NO:2679:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 181 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..181
- (D) OTHER INFORMATION: / Ceres Seq. ID 1573961

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2679:

```

Met Gly Leu Ser Phe Gly Lys Leu Phe Ser Arg Leu Phe Ala Lys Lys
1      5      10      15
Glu Met Arg Ile Leu Met Val Gly Leu Asp Ala Ala Gly Lys Thr Thr
20      25      30
Ile Leu Tyr Lys Leu Lys Leu Gly Glu Ile Val Thr Thr Ile Pro Thr
35      40      45
Ile Gly Phe Asn Val Glu Thr Val Glu Tyr Lys Asn Ile Ser Phe Thr
50      55      60
Val Trp Asp Val Gly Gly Gln Asp Lys Ile Arg Pro Leu Trp Arg His
65      70      75      80
Tyr Phe Gln Asn Thr Gln Gly Leu Ile Phe Val Val Asp Ser Asn Asp
85      90      95
Arg Asp Arg Val Val Glu Ala Arg Asp Glu Leu His Arg Met Leu Asn
100     105     110
Glu Asp Glu Leu Arg Asp Ala Val Leu Leu Val Phe Ala Asn Lys Gln
115     120     125
Asp Leu Pro Asn Ala Met Asn Ala Ala Glu Ile Thr Asp Lys Leu Gly
130     135     140
Leu His Ser Leu Arg Gln Arg His Trp Tyr Ile Gln Ser Thr Cys Ala
145     150     155     160
Thr Ser Gly Glu Gly Leu Tyr Glu Gly Leu Asp Trp Leu Ser Asn Asn
165     170     175
Ile Ala Ser Lys Ala
180

```

(2) INFORMATION FOR SEQ ID NO:2680:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 164 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..164
- (D) OTHER INFORMATION: / Ceres Seq. ID 1573962

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2680:

```

Met Arg Ile Leu Met Val Gly Leu Asp Ala Ala Gly Lys Thr Thr Ile
1      5      10      15
Leu Tyr Lys Leu Lys Leu Gly Glu Ile Val Thr Thr Ile Pro Thr Ile
20      25      30
Gly Phe Asn Val Glu Thr Val Glu Tyr Lys Asn Ile Ser Phe Thr Val

```

(2) INFORMATION FOR SEQ ID NO:2681:

(A) LENGTH: 160 amino acids

(C) STRANDEDNESS:

(D) TOPOLOGY: lin

MOLECULE TYPE: peptid

(1X) FLETCORE.
(A) NAM

(B) LOCATION: 1..160

(D) OTHER INFORMATION:

SEQUENCE DESCRIPTION: SEQ ID NO:2681:

Val Gly Leu Asp Ala Ala Gly Lys Thr Thr Il

(2) INFORMATION FOR SEQ ID NO:2682:

(A) LENGTH: 771 base pairs

(B) TYPE: nucleic acid

```
(C) STRANDEDNESS: single
```

(D) TOPOLOGY: linear

MOLECULE TYPE: DNA (g

```
(ix) FEATURE:
```

(IX) FLATONE.
(A) NAM

(A) NAME/REF: —
(B) LOCATION: 1

(B) LOCATION: 1..771

(D) OTHER INFORMATION: / Ceres Seq. ID 1573964

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2682:

acaaatccaaat	caaaacacac	agagagaaga	aaaactcaga	agaaaaagcca	aagagtga	60
caaaaaatggc	gtgcagcact	ctctcaatcg	caacaacaat	cogttcctca	tcttattccta	120
ctctcgtcttc	ctcaaatcac	ttcccttccc	gaacccamcac	catcgaaatc	ccctctcgct	180
tcgggtggttg	ttcatcatcc	acattgaccc	accgtgcaac	ccatctccgt	ccaatcgccg	240
ccgtcgaaagc	tcggagagaaa	atcgagaaga	toggatccga	aatctcacc	ctaaccctcg	300
aagaagctcg	tatctctgct	gactatctcc	aagacaaat	cggtgtctcc	ccactctctt	360
tagCccccgc	agcagcGgcg	gttgctgctc	cagccgacgg	tggcgcgccg	gctgtagtgg	420
aagagcaaac	agagttcgat	gtggttatca	atgaagttcc	cagcagttcc	cgtattgcaag	480
tgattaaagc	tgttagggct	ttaaactagct	tggcggtgaa	ggaagctaag	gagctaatacg	540
aaggattacc	aaagaagttt	aaagaaggtta	tcactaaaga	tgaagctgaa	gaagctaaga	600
agactcttga	agaagctggg	gctaagaatct	ccattgctta	aggtttttat	taaaaaaaaaa	660
aaagaagttg	ttatcttttc	tggaaattga	ttggtctttt	gtgtgtgtta	gtatagtttg	720
cgtctggaat	tgttgagaaa	ttgttgtaat	ttgaatcaca	tttggtttcc	c	

(2) INFORMATION FOR SEQ ID NO:2683:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 212 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..212

(D) OTHER INFORMATION: / Ceres Seq. ID 1573965

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2683:

Asn	Pro	Ile	Lys	Thr	His	Arg	Glu	Lys	Lys	Asn	Ser	Glu	Glu	Lys	Pro
1			5							10				15	
Lys	Ser	Glu	Thr	Lys	Met	Ala	Ser	Thr	Thr	Leu	Ser	Ile	Ala	Thr	Thr
			20						25				30		
Ile	Arg	Ser	Ser	Ser	Tyr	Pro	Thr	Leu	Ala	Ser	Ile	Asn	His	Phe	Pro
			35				40					45			
Ser	Arg	Thr	Xaa	Thr	Ile	Glu	Phe	Pro	Ser	Arg	Phe	Gly	Gly	Ser	
			50			55				60					
Ser	Ser	Thr	Leu	Thr	His	Arg	Ala	Thr	His	Leu	Arg	Pro	Ile	Ala	Ala
			65		70				75				80		
Val	Glu	Ala	Pro	Glu	Lys	Ile	Glu	Lys	Ile	Gly	Ser	Glu	Ile	Ser	Ser
			85					90					95		
Leu	Thr	Leu	Glu	Glu	Ala	Arg	Ile	Leu	Val	Asp	Tyr	Leu	Gln	Asp	Lys
			100					105					110		
Phe	Gly	Val	Ser	Pro	Leu	Ser	Leu	Ala	Pro	Ala	Ala	Ala	Ala	Val	Ala
			115				120					125			
Ala	Pro	Ala	Asp	Gly	Gly	Ala	Ala	Ala	Val	Val	Glu	Glu	Gln	Thr	Glu
			130				135				140				
Phe	Asp	Val	Val	Ile	Asn	Glu	Val	Pro	Ser	Ser	Ser	Arg	Ile	Ala	Val
			145		150				155					160	
Ile	Lys	Ala	Val	Arg	Ala	Leu	Thr	Ser	Leu	Ala	Leu	Lys	Glu	Ala	Lys
			165					170					175		
Glu	Leu	Ile	Glu	Gly	Leu	Pro	Lys	Lys	Phe	Lys	Glu	Gly	Ile	Thr	Lys
			180					185					190		
Asp	Glu	Ala	Glu	Glu	Ala	Lys	Lys	Thr	Leu	Glu	Glu	Ala	Gly	Ala	Lys
			195				200					205			
Val	Ser	Ile	Ala												
			210												

(2) INFORMATION FOR SEQ ID NO:2684:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 191 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..191

(D) OTHER INFORMATION: / Ceres Seq. ID 1573966

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2684:

Met	Ala	Ser	Thr	Thr	Leu	Ser	Ile	Ala	Thr	Thr	Ile	Arg	Ser	Ser	Ser		
1				5					10					15			
Tyr	Pro	Thr	Leu	Ala	Ser	Ile	Asn	His	Phe	Pro	Ser	Arg	Thr	Xaa	Thr		
				20				25					30				
Ile	Glu	Phe	Pro	Ser	Arg	Phe	Gly	Gly	Gly	Ser	Ser	Ser	Thr	Leu	Thr		
				35			40					45					
His	Arg	Ala	Thr	His	Leu	Arg	Pro	Ile	Ala	Ala	Val	Glu	Ala	Pro	Glu		
	50					55					60						
Lys	Ile	Glu	Lys	Ile	Gly	Ser	Glu	Ile	Ser	Ser	Leu	Thr	Leu	Glu	Glu		
	65				70				75					80			
Ala	Arg	Ile	Leu	Val	Asp	Tyr	Leu	Gln	Asp	Lys	Phe	Gly	Val	Ser	Pro		
				85					90				95				
Leu	Ser	Leu	Ala	Pro	Ala	Ala	Ala	Val	Ala	Ala	Pro	Ala	Asp	Gly			
			100				105					110					
Gly	Ala	Ala	Ala	Val	Val	Glu	Glu	Gln	Thr	Glu	Phe	Asp	Val	Val	Ile		
			115				120					125					
Asn	Glu	Val	Pro	Ser	Ser	Ser	Arg	Ile	Ala	Val	Ile	Lys	Ala	Val	Arg		
	130					135					140						
Ala	Leu	Thr	Ser	Leu	Ala	Leu	Lys	Glu	Ala	Lys	Glu	Leu	Ile	Glu	Gly		
	145				150				155					160			
Leu	Pro	Lys	Lys	Phe	Lys	Glu	Gly	Ile	Thr	Lys	Asp	Glu	Ala	Glu	Glu		
			165				170							175			
Ala	Lys	Lys	Thr	Leu	Glu	Glu	Ala	Gly	Ala	Lys	Val	Ser	Ile	Ala			
			180				185						190				

(2) INFORMATION FOR SEQ ID NO:2685:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 547 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..547

(D) OTHER INFORMATION: / Ceres Seq. ID 1573980

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2685:

ttttccagaa	atctctcaact	atcgccatcg	attttagcag	acattgaaga	agatggggagt	60
attcacattc	gtatgcaaga	atggaggcgg	cgcgtggagc	gcGaaGCaac	acgaaggaga	120
acttgaatct	tcagcttctt	ctacctacga	gctccagcgt	aagCtcgttc	aggatatctct	180
ctccgctgat	tcctccgggtg	gcgttcagtc	ttcgttttct	cttgctctccc	ctacctccgc	240
cgtattccag	gtaattgttg	gtggtgggtg	tggtggagga	ttctctgctg	gaggagctgc	300
ctcaagtggg	ggtggtgcgg	gtgaagctgc	agctgccctc	aaggaagatg	agaagaagaa	360
agaagaatca	gaagaggaa	aggagacttc	ggattcgatc	tctttgtgta	agattgaaat	420
agtattttgg	aggtgtgtgt	ttgagctttc	catttttgtg	tggggtgttt	cttcctattgt	480
caagtgtgat	atgtacacat	gctttcaata	atatttcgtg	agtaatgaca	agtttctctt	540
tcgatcc						

(2) INFORMATION FOR SEQ ID NO:2686:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 152 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..152

(D) OTHER INFORMATION: / Ceres Seq. ID 1573981

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2686:

Met Gly Val Phe Thr Phe Val Cys Lys Asn Gly Gly Gly Ala Trp Ser
1 5 10 15
Ala Lys Gln His Glu Gly Glu Leu Glu Ser Ser Ala Ser Ser Thr Tyr
20 25 30
Glu Leu Gln Arg Lys Leu Val Gln Val Ser Leu Ser Ala Asp Ser Ser
35 40 45
Gly Gly Val Gln Ser Ser Phe Ser Leu Val Ser Pro Thr Ser Ala Val
50 55 60
Phe Gln Val Ile Val Gly Gly Gly Gly Gly Gly Phe Ser Ala Gly
65 70 75 80
Gly Ala Ala Ser Ser Gly Gly Gly Ala Gly Ala Ala Ala Ala Pro
85 90 95
Lys Glu Asp Glu Lys Lys Lys Glu Glu Ser Glu Glu Glu Thr
100 105 110
Ser Asp Ser Ile Ser Leu Val Lys Ile Glu Ile Val Phe Trp Arg Cys
115 120 125
Trp Phe Glu Leu Ser Ile Phe Val Trp Gly Val Ser Ser Ile Val Lys
130 135 140
Cys Asp Met Leu His Cys Phe Gln
145 150

(2) INFORMATION FOR SEQ ID NO:2687:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 727 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..727

(D) OTHER INFORMATION: / Ceres Seq. ID 1573982

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2687:

aacataagtc tctctctttac attttgaaac cctaatttct caaaaaaaaaa gtctgaagtt 60
gagtagccgt gctttgtcgg cggccttggc tggggccacca atgatgaaga tcttcaaagg 120
acgtttctcc agttcggcga cgttatcgat tctaagatca ttaacgaccg cgagagtggg 180
agatcaaggg gattcggatt cgtcaccttc aaggacgaga aagccatgag gtagtgcgatt 240
gaagagatga acggttaaga gctcgatgga cgtgtcatca ccgtgaacga ggctcagtcg 300
agagtgatcg cgggtggcgg aggaggccgt gttggaagcg gtggtgggta ccgcagcgga 360
ggcgtgggtg gatactcagg aggcggtggc ggcggatact caggaggagg cggtgggtggt 420
tacgagagac gtacgggagg ttacggatct gttggaggcg gtggtggccg aggatcacgtt 480
gggtgtggac gccgtgaggg aggtggctac ggaggcggtg atggtMggaa gttacggcgg 540
cgggtgtggc sgctggtaat caaagataga gttgttttgc tgctgctgct ctgttttttg 600
tttagatttg gatttgtgtc accactttct gtttggttat cgttcgtttg gtttactttt 660
ttgatgaaac agtttcgttt aagtcttctt ttgtctggatc gaaatgttaa ttgcgcgtgtt 720
gtttacc

(2) INFORMATION FOR SEQ ID NO:2688:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 226 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..226

(D) OTHER INFORMATION: / Ceres Seq. ID 1573983

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2688:

Met Ser Glu Val Glu Tyr Arg Cys Phe Val Gly Gly Leu Ala Trp Ala


```

1           5           10           15
Thr Asn Asp Glu Asp Leu Gln Arg Thr Phe Ser Gln Phe Gly Asp Val
20
Ile Asp Ser Lys Ile Ile Asn Asp Arg Glu Ser Gly Arg Ser Arg Gly
35
Phe Gly Phe Val Thr Phe Lys Asp Glu Lys Ala Met Arg Asp Ala Ile
50
Glu Glu Met Asn Gly Lys Glu Leu Asp Gly Arg Val Ile Thr Val Asn
65
Glu Ala Gln Ser Arg Gly Ser Gly Gly Gly Gly Gly Gly Arg Gly Gly
85
Ser Gly Gly Gly Tyr Arg Ser Gly Gly Gly Gly Gly Tyr Ser Gly Gly
100
Gly Gly Gly Tyr Ser Gly Gly Gly Gly Gly Tyr Glu Arg Arg
115
Ser Gly Gly Tyr Gly Ser Gly Gly Gly Gly Gly Arg Gly Tyr Gly
130
Gly Gly Gly Arg Arg Glu Gly Gly Gly Tyr Gly Gly Asp Gly Xaa
145
Lys Leu Arg Arg Arg Trp Trp Xaa Leu Val Ile Lys Asp Arg Val Val
165
Cys Val Leu Leu Leu Cys Phe Trp Phe Arg Phe Gly Phe Val Ser Pro
180
Leu Leu Val Trp Leu Ser Phe Val Trp Phe Thr Phe Leu Met Lys Gln
195
Phe Arg Leu Ser Leu Leu Cys Leu Asp Arg Asn Val Asn Ser Arg Val
210
Val Tyr
225

```

(2) INFORMATION FOR SEQ ID NO:2689:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 167 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..167
- (D) OTHER INFORMATION: / Ceres Seq. ID 1573984

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2689:

```

Met Arg Asp Ala Ile Glu Glu Met Asn Gly Lys Glu Leu Asp Gly Arg
1           5           10           15
Val Ile Thr Val Asn Glu Ala Gln Ser Arg Gly Ser Gly Gly Gly Gly
20
Gly Gly Arg Gly Gly Ser Gly Gly Gly Tyr Arg Ser Gly Gly Gly Gly
35
Gly Tyr Ser Gly Gly Gly Gly Gly Gly Tyr Ser Gly Gly Gly Gly Gly
50
Gly Tyr Glu Arg Arg Ser Gly Gly Tyr Gly Ser Gly Gly Gly Gly Gly
65
Gly Arg Gly Tyr Gly Gly Gly Gly Arg Arg Glu Gly Gly Gly Tyr Gly
85
Gly Gly Asp Gly Xaa Lys Leu Arg Arg Trp Trp Xaa Leu Val Ile
100
Lys Asp Arg Val Val Cys Val Leu Leu Cys Phe Trp Phe Arg Phe
115
Gly Phe Val Ser Pro Leu Leu Val Trp Leu Ser Phe Val Trp Phe Thr
130
Phe Leu Met Lys Gln Phe Arg Leu Ser Leu Leu Cys Leu Asp Arg Asn
145
150
155
160

```

Val Asn Ser Arg Val Val Tyr
165

(2) INFORMATION FOR SEQ ID NO:2690:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 160 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..160
- (D) OTHER INFORMATION: / Ceres Seq. ID 1573985

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2690:

Met	Asn	Gly	Lys	Glu	Leu	Asp	Gly	Arg	Val	Ile	Thr	Val	Asn	Glu	Ala
1			5						10					15	
Gln	Ser	Arg	Gly	Ser	Gly	Gly	Gly	Gly	Gly	Arg	Gly	Gly	Ser	Gly	
			20					25				30			
Gly	Gly	Tyr	Arg	Ser	Gly	Gly	Gly	Gly	Tyr	Ser	Gly	Gly	Gly	Gly	
		35					40				45				
Gly	Gly	Tyr	Ser	Gly	Gly	Gly	Gly	Gly	Tyr	Glu	Arg	Arg	Ser	Gly	
		50				55				60					
Gly	Tyr	Gly	Ser	Gly	Gly	Gly	Gly	Gly	Arg	Gly	Tyr	Gly	Gly	Gly	
		65			70				75					80	
Gly	Arg	Arg	Glu	Gly	Gly	Gly	Tyr	Gly	Gly	Asp	Gly	Xaa	Lys	Leu	
			85					90					95		
Arg	Arg	Arg	Trp	Trp	Xaa	Leu	Val	Ile	Lys	Asp	Arg	Val	Val	Cys	Val
			100					105					110		
Leu	Leu	Leu	Cys	Phe	Trp	Phe	Arg	Phe	Gly	Phe	Val	Ser	Pro	Leu	Leu
			115				120					125			
Val	Trp	Leu	Ser	Phe	Val	Trp	Phe	Thr	Phe	Leu	Met	Lys	Gln	Phe	Arg
		130				135					140				
Leu	Ser	Leu	Leu	Cys	Leu	Asp	Arg	Asn	Val	Asn	Ser	Arg	Val	Val	Tyr
			145		150				155						160

(2) INFORMATION FOR SEQ ID NO:2691:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 954 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..954
- (D) OTHER INFORMATION: / Ceres Seq. ID 1573986

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2691:

aacaaaaaga	ttaaacaaga	agagaagaat	atggcgagag	ggaagatcca	gatcaagagg	60
atagagaacc	agacaaacag	acaagtgcag	tattcaaaga	gaagaaatgg	tttattcaag	120
aaagcacatg	agctcacggt	tttgtgtgat	gctagggttt	cgattatcat	gttctctagc	180
tccaacaagc	ttcatgagta	tatcagccct	aacaccacaa	cgaaggagat	cgtagatctg	240
taccaaaacta	tttctgatgt	cgatgttttg	gccactcaat	atgagcgaat	gcaagaaacc	300
aagaggaaac	tggttgagagc	aaatagaagt	ctccggaact	agatcaagca	gaggctaggt	360
gagtggtttg	acaagcttga	cattcaggag	ctcgctgcgt	ttgaggatga	aatggaaacc	420
actttcaaac	tcgttcgcga	gcgcaagttc	aaatctcttg	ggaatcagat	cgagaccacc	480
aagaaaaaga	acaaaagtca	acaagacata	caaaaagaatc	tcatacatga	gctaactaag	540
agctgaagat	ccctcactat	gactagtaga	caatggagga	gattacgact	caagttcttg	600
ataccaaatc	gaagggtcac	gtGcttacgc	tcttctgttc	caccagaacc	atcaccacta	660
ttaccocaaac	catggccttc	atgcaccctc	tgccctctgac	atcattacct	tcattctctc	720
tgaaataatta	aaggctaaaa	ggtttgcttg	tgccatcatt	gtctatctaa	tttattagta	780

actacttataa acataaggca tgggtgttgcg aaaaccttaa actgtcatgt tctttagtta 840
tgtatttttaa agcctaaga aatatggatt gtgtgatcag tagtgcttag gctttattgtg 900
tgtggaatgt ttccaagact ttatcatgt atcgtattat tatattgacc accc

(2) INFORMATION FOR SEQ ID NO:2692:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 181 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..181
- (D) OTHER INFORMATION: / Ceres Seq. ID 1573987

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2692:

Asn Lys Lys Ile Lys Gln Arg Glu Lys Asn Met Ala Arg Gly Lys Ile
1 5 10 15
Gln Ile Lys Arg Ile Glu Asn Gln Thr Asn Arg Gln Val Thr Tyr Ser
20 25 30
Lys Arg Arg Asn Gly Leu Phe Lys Lys Ala His Glu Leu Thr Val Leu
35 40 45
Cys Asp Ala Arg Val Ser Ile Ile Met Phe Ser Ser Ser Asn Lys Leu
50 55 60
His Glu Tyr Ile Ser Pro Asn Thr Thr Thr Lys Glu Ile Val Asp Leu
65 70 75 80
Tyr Gln Thr Ile Ser Asp Val Asp Val Trp Ala Thr Gln Tyr Glu Arg
85 90 95
Met Gln Glu Thr Lys Arg Lys Leu Leu Glu Thr Asn Arg Asn Leu Arg
100 105 110
Thr Gln Ile Lys Gln Arg Leu Gly Glu Cys Leu Asp Lys Leu Asp Ile
115 120 125
Gln Glu Leu Arg Arg Leu Glu Asp Glu Met Glu Asn Thr Phe Lys Leu
130 135 140
Val Arg Glu Arg Lys Phe Lys Ser Leu Gly Asn Gln Ile Glu Thr Thr
145 150 155 160
Lys Lys Lys Asn Lys Ser Gln Gln Asp Ile Gln Lys Asn Leu Ile His
165 170 175
Glu Leu Thr Lys Ser
180

(2) INFORMATION FOR SEQ ID NO:2693:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 171 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..171
- (D) OTHER INFORMATION: / Ceres Seq. ID 1573988

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2693:

Met Ala Arg Gly Lys Lys Ile Gln Ile Lys Arg Ile Glu Asn Gln Thr Asn
1 5 10 15
Arg Gln Val Thr Tyr Ser Lys Arg Arg Asn Gly Leu Phe Lys Lys Ala
20 25 30
His Glu Leu Thr Val Leu Cys Asp Ala Arg Val Ser Ile Ile Met Phe
35 40 45
Ser Ser Ser Asn Lys Leu His Glu Tyr Ile Ser Pro Asn Thr Thr Thr
50 55 60
Lys Glu Ile Val Asp Leu Tyr Gln Thr Ile Ser Asp Val Asp Val Tyr
65 70 75 80

Ala Thr Gln Tyr Glu Arg Met Gln Glu Thr Lys Arg Lys Leu Leu Glu
85 90 95
Thr Asn Arg Asn Leu Arg Thr Gln Ile Lys Gln Arg Leu Gly Glu Cys
100 105 110
Leu Asp Lys Leu Asp Ile Gln Glu Leu Arg Arg Leu Glu Asp Glu Met
115 120 125
Glu Asn Thr Phe Lys Leu Val Arg Glu Arg Lys Phe Lys Ser Leu Gly
130 135 140
Asn Gln Ile Glu Thr Thr Lys Lys Lys Asn Lys Ser Gln Gln Asp Ile
145 150 155 160
Gln Lys Asn Leu Ile His Glu Leu Thr Lys Ser
165 170

(2) INFORMATION FOR SEQ ID NO:2694:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..125

(D) OTHER INFORMATION: / Ceres Seq. ID 1573989

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2694:

Met Phe Ser Ser Ser Asn Lys Leu His Glu Tyr Ile Ser Pro Asn Thr
1 5 10 15
Thr Thr Lys Glu Ile Val Asp Leu Tyr Gln Thr Ile Ser Asp Val Asp
20 25 30
Val Trp Ala Thr Gln Tyr Glu Arg Met Gln Glu Thr Lys Arg Lys Leu
35 40 45
Leu Glu Thr Asn Arg Asn Leu Arg Thr Gln Ile Lys Gln Arg Leu Gly
50 55 60
Glu Cys Leu Asp Lys Leu Asp Ile Gln Glu Leu Arg Arg Leu Glu Asp
65 70 75 80
Glu Met Glu Asn Thr Phe Lys Leu Val Arg Glu Arg Lys Phe Lys Ser
85 90 95
Leu Gly Asn Gln Ile Glu Thr Thr Lys Lys Lys Asn Lys Ser Gln Gln
100 105 110
Asp Ile Gln Lys Asn Leu Ile His Glu Leu Thr Lys Ser
115 120 125

(2) INFORMATION FOR SEQ ID NO:2695:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 767 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..767
- (D) OTHER INFORMATION: / Ceres Seq. ID 1573990

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2695:

ataccaataa gcaatttgct cattagagaa cacagaaaaa aaaaaaacaa tggcaactca 60
agccgcggg atcttcaact ccgcataaac aaccgcgcga acctcggcg tcaagaaact 120
ccactttttc tcaacaaccc accgtcccaa atccctctcc ttcacaaaaa ccgcaatccg 180
cgccgagaaa acagatttct ccgcgcgcgc tgctgcagcc ccgcaccaaa aagaagctcc 240
cgtgggattc acgccaccgc agctagaccc aaacacacgc tctccgatct tcgctggaag 300
cacccggtggt tcttctacgta aagcgcaagt ggaagagttc tacgttatca tcgtggaact 360
accgaagaaa cagatctttg agatgcccag aggaggagca gcgatcatga gagaaggtcc 420
gaatctctcg aagctagcga ggaaaagaga gtgtttagct ttggggacaa ggcttagatc 480
caagtacaag atcacttacc agttttacag agtggttctc aacggtgagg ttcaatatct 540

tcctcctctaaa gatgtgtgttt atccagagaa ggcgaatcca ggaagagaag gtgttggtct 600
caacatgaga tctattggga aaaatgttag tcccatgaa gtaagtta ctggcaacaa 660
aagttagat ttgtaagatc tgtaactaa aaaaaAccaa aaactatgtg catgtgtgta 720
tgattatgac tatgtttcat gtTaattttt aatggatttt gKttttg

(2) INFORMATION FOR SEQ ID NO:2696:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 106 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..106

(D) OTHER INFORMATION: / Ceres Seq. ID 1573991

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2696:

Ile Pro Ile Ser Asn Leu Leu Ile Arg Glu Gln Arg Lys Lys Lys Asn
1 5 10 15
Asn Gly Asn Ser Ser Arg Arg Asp Leu Gln Leu Arg His Asn Asn Arg
20 25 30
Arg Asn Leu Arg Arg Gln Glu Thr Pro Leu Phe Leu Asn Asn Pro Pro
35 40 45
Ser Gln Ile Pro Leu Leu His Gln Asn Arg Asn Pro Arg Arg Glu Asn
50 55 60
Arg Phe Leu Arg Arg Cys Cys Ser Pro Arg His Glu Arg Ser Ser
65 70 75 80
Arg Gly Ile His Ala Thr Ala Ala Arg Pro Lys His Thr Val Ser Asp
85 90 95
Leu Arg Trp Lys His Arg Trp Ser Ser Thr
100 105

(2) INFORMATION FOR SEQ ID NO:2697:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 208 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..208

(D) OTHER INFORMATION: / Ceres Seq. ID 1573992

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2697:

Met Ala Thr Gln Ala Ala Gly Ile Phe Asn Ser Ala Ile Thr Thr Ala
1 5 10 15
Ala Thr Ser Gly Val Lys Lys Leu His Phe Phe Ser Thr Thr His Arg
20 25 30
Pro Lys Ser Leu Ser Phe Thr Lys Thr Ala Ile Arg Ala Glu Lys Thr
35 40 45
Asp Ser Ser Ala Ala Ala Ala Ala Pro Ala Thr Lys Glu Ala Pro
50 55 60
Val Gly Phe Thr Pro Pro Gln Leu Asp Pro Asn Thr Pro Ser Pro Ile
65 70 75 80
Phe Ala Gly Ser Thr Gly Gly Leu Leu Arg Lys Ala Gln Val Glu Glu
85 90 95
Phe Tyr Val Ile Thr Trp Asn Ser Pro Lys Glu Gln Ile Phe Glu Met
100 105 110
Pro Thr Gly Gly Ala Ala Ile Met Arg Glu Gly Pro Asn Leu Leu Lys
115 120 125
Leu Ala Arg Lys Glu Gln Cys Leu Ala Leu Gly Thr Arg Leu Arg Ser
130 135 140
Lys Tyr Lys Ile Thr Tyr Gln Phe Tyr Arg Val Phe Pro Asn Gly Glu

145											150											155											160														
Val	Gln	Tyr	Leu	His	Pro	Lys	Asp	Gly	Val	Tyr	Pro	Glu	Lys	Ala	Asn	Val	Gln	Tyr	Leu	His	Pro	Lys	Asp	Gly	Val	Tyr	Pro	Glu	Lys	Ala	Asn																
															165																170																175
Pro	Gly	Arg	Glu	Gly	Val	Gly	Leu	Asn	Met	Arg	Ser	Ile	Gly	Lys	Asn	Pro	Gly	Arg	Glu	Gly	Val	Gly	Leu	Asn	Met	Arg	Ser	Ile	Gly	Lys	Asn																
															180																185																190
Val	Ser	Pro	Ile	Glu	Val	Lys	Phe	Thr	Gly	Lys	Gln	Ser	Tyr	Asp	Leu	Val	Ser	Pro	Ile	Glu	Val	Lys	Phe	Thr	Gly	Lys	Gln	Ser	Tyr	Asp	Leu																
															195																200																205

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 800 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..800

(D) OTHER INFORMATION: / Ceres Seq. ID 1573995

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2698:

(A1) SUBSEQUENT						
taatttagga	gaagagcaac	cgttgaaacg	tacggcgagt	ggtggtggtg	gtgtctcgac	60
tggtcttgat	atgagtcgcc	gaagtccatc	gggactctgac	gtcagcgacg	aatctagttg	120
gtgtgcacac	gtgttttaaac	caacgcttga	atctcaggtg	acagcgctac	actctggtga	180
agatctctcca	acttatcttta	gtttgtctct	tctcttgaac	gcgagacagc	ttcaggtaca	240
cgcagcgctgc	caacttaacc	agaatcacgt	tatggacggt	gagttacatg	cgaGctgtt	300
tcoggttaga	aaggaagacg	aagctggaag	agaagaagaa	gcgacgaag	ggatctaggt	360
tgcatctgtg	ggtgagttca	tgcgtgtggt	tcaggagatg	ataaggacag	aggtgaggag	420
ttacatggcg	gatttacacg	gaggaaacgt	cggtgtgagt	agttctggcg	gcggtaggtg	480
cgggtcgtgt	atgcacacaa	gtgttaaacg	cgcgtcgtgt	gggttttagc	agtttatagt	540
gaaccagcat	ggaattggga	agtaggaagta	gagtgataag	aaacagtttt	ccctctgttt	600
ctcggggaaaa	taaaagttttc	aggtcttttc	gtgtatagac	cagtagatga	gacgcagcaa	660
ggagagcaaac	aaactcaaaa	atgttttttc	atcatcatca	tatgatcttc	tttctgtatt	720
caattaaaag	caaaagcaaga	tcatttatta	acaatttaca	caaaacttga	gaagaaaagt	780
caaaaaactc	tctcaaacctc					

(2) INFORMATION FOR SEQ ID NO:2699:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 189 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

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(ix) FEATURE:
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{A} NAME/KEY: peptide
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(B) LOCATION: 1..189

(D) OTHER INFORMATION: / Ceres Seq. ID 1573996

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2699:

Asn	Leu	Gly	Glu	Glu	Gln	Pro	Leu	Lys	Arg	Thr	Ala	Ser	Gly	Gly	Gly
1			5						10				15		
Gly	Val	Ser	Thr	Gly	Leu	Tyr	Met	Ser	Pro	Gly	Ser	Pro	Ser	Gly	Ser
		20						25					30		
Asp	Val	Ser	Glu	Gln	Ser	Ser	Gly	Gly	Ala	His	Val	Phe	Lys	Pro	Thr
		35					40					45			
Val	Arg	Ser	Glu	Val	Thr	Ala	Ser	Ser	Ser	Gly	Glu	Asp	Pro	Pro	Thr
	50					55					60				
Tyr	Leu	Ser	Leu	Ser	Leu	Pro	Trp	Thr	Asp	Glu	Thr	Val	Arg	Val	Asn
65					70				75						80
Glu	Pro	Val	Gln	Leu	Asn	Gln	Asn	Thr	Val	Met	Asp	Gly	Gly	Tyr	Thr
			85					90					95		
Ala	Glu	Leu	Phe	Pro	Val	Arg	Lys	Glu	Glu	Gln	Val	Glu	Val	Glu	Glu
		100						105					110		

Glu Glu Ala Lys Gly Ile Ser Gly Gly Phe Gly Gly Glu Phe Met Thr
115 120 125
Val Val Gln Glu Met Ile Arg Thr Glu Val Arg Ser Tyr Met Ala Asp
130 135 140
Leu Gln Arg Gly Asn Val Gly Gly Ser Ser Ser Gly Gly Gly Gly
145 150 155 160
Gly Ser Cys Met Pro Gln Ser Val Asn Ser Arg Arg Val Gly Phe Arg
165 170 175
Glu Phe Ile Val Asn Gln Ile Gly Ile Gly Lys Met Glu
180 185

(2) INFORMATION FOR SEQ ID NO:2700:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 166 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..166

(D) OTHER INFORMATION: / Ceres Seq. ID 1573997

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2700:

Met Ser Pro Gly Ser Pro Ser Gly Ser Asp Val Ser Glu Gln Ser Ser
1 5 10 15
Gly Gly Ala His Val Phe Lys Pro Thr Val Arg Ser Glu Val Thr Ala
20 25 30
Ser Ser Ser Gly Glu Asp Pro Pro Thr Tyr Leu Ser Leu Ser Leu Pro
35 40 45
Trp Thr Asp Glu Thr Val Arg Val Asn Glu Pro Val Gln Leu Asn Gln
50 55 60
Asn Thr Val Met Asp Gly Gly Tyr Thr Ala Glu Leu Phe Pro Val Arg
65 70 75 80
Lys Glu Glu Gln Val Glu Val Glu Glu Glu Ala Lys Gly Ile Ser
85 90 95
Gly Gly Phe Gly Gly Glu Phe Met Thr Val Val Gln Glu Met Ile Arg
100 105 110
Thr Glu Val Arg Ser Tyr Met Ala Asp Leu Gln Arg Gly Asn Val Gly
115 120 125
Gly Ser Ser Ser Gly Gly Gly Gly Gly Ser Cys Met Pro Gln Ser
130 135 140
Val Asn Ser Arg Arg Val Gly Phe Arg Glu Phe Ile Val Asn Gln Ile
145 150 155 160
Gly Ile Gly Lys Met Glu
165

(2) INFORMATION FOR SEQ ID NO:2701:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 99 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..99

(D) OTHER INFORMATION: / Ceres Seq. ID 1573998

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2701:

Met Asp Gly Gly Tyr Thr Ala Glu Leu Phe Pro Val Arg Lys Glu Glu
1 5 10 15
Gln Val Glu Val Glu Glu Glu Glu Ala Lys Gly Ile Ser Gly Gly Phe
20 25 30
Gly Gly Glu Phe Met Thr Val Val Gln Glu Met Ile Arg Thr Glu Val

35	40	45
Arg Ser Tyr Met Ala Asp Leu Gln Arg Gly Asn Val Gly Gly Ser Ser		
50	55	60
Ser Gly Gly Gly Gly Gly Gly Ser Cys Met Pro Gln Ser Val Asn Ser		
65	70	75
Arg Arg Val Gly Phe Arg Glu Phe Ile Val Asn Gln Ile Gly Ile Gly		
85	90	95
Lys Met Glu		

(2) INFORMATION FOR SEQ ID NO:2702:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1114 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1114
- (D) OTHER INFORMATION: / Ceres Seq. ID 1573999

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2702:

aaaaaaaaa	aaaaaactca	gagcagagga	gatcgagaga	gacaaagaga	gacaaagaga	60
gagagagaga	gagagagaga	gagagagaga	gagagatctt	caacaagcaa	tgcttatatc	120
catggcggtta	ttctctccgc	cgatctcttc	ctcacttcaa	aaccttaatc	tcattcccaa	180
gatctcaacc	tctcttctct	ccaccaaaacg	tttctctcta	atctccgctc	ctagagcttc	240
ctccgacaat	ggtaacgaatt	cccccgctgt	gaaaattccg	aagcctcgct	ctgtagctgt	300
agaggaagtt	ccggttaaat	ctccggcgga	aagctctctc	gcttctgaaa	acggcgccgt	360
tggaaggtgaa	gcgactgatt	cgagtactga	gacggtaaat	aaatatcaaa	atgcgaagt	420
ggttaatgga	acttgaggat	tgaaacagtt	cgagaaagat	ggcaaaaactg	attgggattc	480
tgttatcggt	tctgaggcaa	agagagagaaa	atggcttgaa	gataaccggg	aaacaacgag	540
taacgacgag	cttgtgtgtc	tcgatacttc	gattattcca	tggtgggcat	ggatgaagag	600
ataccatcta	cctgaagctg	aactttctca	tggtcgtgct	gcgatgatag	ggtttctcat	660
ggcttacttt	gttgatagtc	ttaccggagt	aggacttggt	gatcaaatgg	ggaattttct	720
ctgcaaaaaca	ctcttggtttg	tggtcgtagc	tggagtcttc	ttcatccgta	agaatgaaga	780
tttagacaaa	cttaaggatc	tggtcgatga	gactacgtta	tatgacaaac	aatggcaagc	840
tgcatggaaa	gagccagatt	catcaGacag	tttcttcaaa	gaagtgaaca	agttctttaca	900
atcttttcatt	ttcttttttt	tggtatgcaa	taactctgtg	atcagtgaaa	gtttatctct	960
actgaactac	tgatcttcag	attttgtaat	ctttctgctt	taaaaaatctc	tatgaagtag	1020
tctcaaaagat	aatgtatcga	aggtctttga	cttgtaaaagc	agacctattt	cgttttgacg	1080
cttgataatt	taatcaataa	gagatttttt	tttt			

(2) INFORMATION FOR SEQ ID NO:2703:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 312 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..312
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574000

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2703:

Lys Lys Lys Lys Lys Lys	Leu Arg Ala Glu Glu Ile Glu Arg	Asp Lys Glu
1	5	10
Arg Gln Arg Glu Arg Glu Arg	Glu Arg Glu Arg Glu Arg	Glu Arg Asp
20	25	30
Leu Gln Gln Ala Met Ser Ile	Ser Met Ala Leu Phe Ser	Pro Pro Ile
35	40	45
Ser Ser Ser Leu Gln Asn Pro	Asn Leu Ile Pro Lys Ile	Ser Thr Ser
50	55	60
Leu Leu Ser Thr Lys Arg Phe	Ser Leu Ile Ser Val	Pro Arg Ala Ser

(2) INFORMATION FOR SEQ ID NO:2704:

(A) LENGTH: 276 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..276

(D) OTHER INFORMATION: / Ceres Seq. ID 1574001

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2704:

Met	Ser	Pro	Ile	Ser	Met	Ala	Leu	Phe	Ser	Pro	Pro	Ile	Ser	Ser	Ser	Leu
1				5					10						15	
Gln	Asn	Pro	Asn	Leu	Ile	Pro	Lys	Ile	Ser	Thr	Ser	Leu	Leu	Ser	Thr	
			20					25					30			
Lys	Arg	Phe	Ser	Leu	Ile	Ser	Val	Pro	Arg	Ala	Ser	Ser	Asp	Asn	Gly	
		35					40					45				
Thr	Thr	Ser	Pro	Val	Val	Lys	Ile	Pro	Lys	Pro	Ala	Ser	Val	Ala	Val	
	50					55					60					
Glu	Glu	Val	Pro	Val	Lys	Ser	Pro	Ala	Glu	Ser	Ser	Ser	Ala	Ser	Glu	
65					70					75					80	
Asn	Gly	Ala	Val	Gly	Gly	Glu	Ala	Thr	Asp	Ser	Ser	Thr	Glu	Thr	Val	
				85					90					95		
Ile	Lys	Tyr	Gln	Asn	Ala	Lys	Trp	Val	Asn	Gly	Thr	Trp	Asp	Leu	Lys	
			100					105					110			
Gln	Phe	Glu	Lys	Asp	Gly	Lys	Thr	Asp	Trp	Asp	Ser	Val	Ile	Val	Ser	
		115					120					125				
Glu	Ala	Lys	Arg	Arg	Lys	Trp	Leu	Glu	Asp	Asn	Pro	Glu	Thr	Thr	Ser	
	130					135					140					

Asn Asp Glu Leu Val Val Phe Asp Thr Ser Ile Ile Pro Trp Trp Ala
145 150 155 160
Trp Met Lys Arg Tyr His Leu Pro Glu Ala Glu Leu Leu Asn Gly Arg
165 170 175
Ala Ala Met Ile Gly Phe Phe Met Ala Tyr Phe Val Asp Ser Leu Thr
180 185 190
Gly Val Gly Leu Val Asp Gln Met Gly Asn Phe Phe Cys Lys Thr Leu
195 200 205
Leu Phe Val Ala Val Ala Gly Val Leu Phe Ile Arg Lys Asn Glu Asp
210 215 220
Leu Asp Lys Leu Lys Asp Leu Phe Asp Glu Thr Thr Leu Tyr Asp Lys
225 230 235 240
Gln Trp Gln Ala Ala Trp Lys Glu Pro Asp Ser Ser Asp Ser Phe Phe
245 250 255
Lys Glu Val Asn Lys Phe Leu Gln Ser Phe Ile Phe Leu Phe Leu Leu
260 265 270
Cys Asn Asn Leu
275

(2) INFORMATION FOR SEQ ID NO:2705:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 272 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..272

(D) OTHER INFORMATION: / Ceres Seq. ID 1574002

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2705:

Met Ala Leu Phe Ser Pro Pro Ile Ser Ser Ser Leu Gln Asn Pro Asn
1 5 10 15
Leu Ile Pro Lys Ile Ser Thr Ser Leu Leu Ser Thr Lys Arg Phe Ser
20 25 30
Leu Ile Ser Val Pro Arg Ala Ser Asp Asn Gly Thr Thr Ser Pro
35 40 45
Val Val Lys Ile Pro Lys Pro Ala Ser Val Ala Val Glu Glu Val Pro
50 55 60
Val Lys Ser Pro Ala Glu Ser Ser Ser Ala Ser Glu Asn Gly Ala Val
65 70 75 80
Gly Gly Glu Ala Thr Asp Ser Ser Thr Glu Thr Val Ile Lys Tyr Gln
85 90 95
Asn Ala Lys Trp Val Asn Gly Thr Trp Asp Leu Lys Gln Phe Glu Lys
100 105 110
Asp Gly Lys Thr Asp Trp Asp Ser Val Ile Val Ser Glu Ala Lys Arg
115 120 125
Arg Lys Trp Leu Glu Asp Asn Pro Glu Thr Thr Ser Asn Asp Glu Leu
130 135 140
Val Val Phe Asp Thr Ser Ile Ile Pro Trp Trp Ala Trp Met Lys Arg
145 150 155 160
Tyr His Leu Pro Glu Ala Glu Leu Leu Asn Gly Arg Ala Ala Met Ile
165 170 175
Gly Phe Phe Met Ala Tyr Phe Val Asp Ser Leu Thr Gly Val Gly Leu
180 185 190
Val Asp Gln Met Gly Asn Phe Phe Cys Lys Thr Leu Leu Phe Val Ala
195 200 205
Val Ala Gly Val Leu Phe Ile Arg Lys Asn Glu Asp Leu Asp Lys Leu
210 215 220
Lys Asp Leu Phe Asp Glu Thr Thr Leu Tyr Asp Lys Gln Trp Gln Ala
225 230 235 240
Ala Trp Lys Glu Pro Asp Ser Ser Asp Ser Phe Phe Lys Glu Val Asn

	245		250		255										
Lys	Phe	Leu	Gln	Ser	Phe	Ile	Phe	Leu	Phe	Leu	Leu	Cys	Asn	Asn	Leu
	260							265						270	

(2) INFORMATION FOR SEQ ID NO:2706:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 551 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..551
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574006

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2706:

ataa	caaaaa	agaatt	tgaa	ccaaca	aaagc	aaaaca	tgaa	aggc	acattc	acta	acttgc	60
ttgt	gtcctc	cctc	attgca	cttg	tttgtg	ccaatg	tcgg	tgct	aggaaa	gttatc	tcctcg	120
aagata	ccca	attca	aggat	gaaaaa	atctt	tcctc	ggagg	cagt	ggcagc	ggtgat	ggct	180
tagggc	ttgg	cctt	ggtgga	ggag	ctggtc	ttgg	tgggc	ttgg	gattggg	gctggg	atcg	240
gcgc	gggagc	cgga	ctaggg	ttag	gtggag	gcgt	tgggg	aggag	cccggt	ggcg	gactcg	300
ttgg	ccttcc	ttga	acgtat	tgaca	agtg	gcgt	gtgaga	gctg	attctc	agct	tattac	360
taatta	aatta	agtt	actttc	attc	ctctta	taaa	atctag	aggg	tttgaa	tttc	ggattt	420
cttc	agcttt	aatt	taaac	tcaat	atttg	aaccaa	aaaaa	ggct	ttagct	actaga	gagta	480
atgc	tcgtaa	tcgt	tattag	tgta	Acgcgc	gttc	tgatat	tctt	atgtgc	aAgt	gtggaa	540
cg	ttctctt	t										

(2) INFORMATION FOR SEQ ID NO:2707:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 103 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..103
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574007

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2707:

Lys	Gln	Lys	Glu	Phe	Glu	Pro	Thr	Lys	Gln	Asn	Met	Lys	Gly	Thr	Phe
1			5						10				15		
Thr	Asn	Leu	Leu	Val	Leu	Leu	Leu	Ile	Ala	Leu	Val	Cys	Ala	Asn	Val
			20					25					30		
Gly	Ala	Arg	Lys	Val	Ile	Ser	Glu	Asp	Thr	Gln	Phe	Lys	Asp	Glu	Lys
		35					40					45			
Ser	Phe	Leu	Gly	Gly	Ser	Gly	Ser	Gly	Asp	Gly	Leu	Gly	Leu	Gly	Leu
	50						55				60				
Gly	Gly	Gly	Ala	Gly	Leu	Gly	Gly	Leu	Gly	Ile	Gly	Ala	Gly	Ile	Gly
	65						70			75				80	
Ala	Gly	Ala	Gly	Leu	Gly	Leu	Gly	Gly	Gly	Gly	Gly	Gly	Ala	Gly	
			85				90						95		
Gly	Gly	Leu	Val	Gly	Leu	Pro									
			100												

(2) INFORMATION FOR SEQ ID NO:2708:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 92 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2708:

(2) INFORMATION FOR SEQ ID NO:2709:

(D) OTHER INFORMATION: / Ceres Seq. ID 1574009

(2) INFORMATION FOR SEO ID NO:2710:

(xi) SEQUENCE DESCRIPTION															
Lys	Asn	Lys	Gln	Lys	Asn	Gln	Cys	Ser	Ala	Leu	Thr	Arg	Ser	Thr	Thr
1				5					10					15	
Met	Ala	Val	Ser	Phe	Asn	Thr	Thr	Leu	His	Gln	Pro	Ser	Leu	Ser	Pro
			20					25					30		

```

Ser Cys Ser Ile Lys Leu Tyr Ser Gly Leu Lys Pro Gln Ser Ala Ser
      35              40              45
Phe Leu Ala Ser Gly Tyr Gln Asn Leu Asn Lys Glu Phe Tyr Gly Arg
      50              55              60
Val His Lys Ser Leu Gln Ser Gly Thr Gly Lys Ala Ser Arg Ser Arg
      65              70              75              80
Val Lys Met Met Pro Ile Gly Thr Pro Arg Val Pro Tyr Arg Asn Arg
      85              90              95
Glu Glu Gly Thr Trp Gln Xaa Val Asp Ile Trp Asn Ala Leu Tyr Arg
      100             105
Glu Arg Val Ile Phe Ile Gly Gln Asn Ile Asp Glu Glu Phe Ser Asn
      115             120             125
Gln Ile Leu Ala Thr Met Leu Tyr Leu Asp Thr Leu Asp Asp Ser Arg
      130             135             140
Arg Ile Tyr Met Tyr Leu Asn Gly Pro Gly Gly Asp Leu Thr Pro Ser
      145             150             155             160
Leu Ala Ile Tyr Asp Thr Met Lys Ser Leu Lys Ser Pro Val Gly Thr
      165             170             175
His Cys Val Gly Leu Ala Tyr Asn Leu Ala Gly Phe Leu Leu Ala Ala
      180             185             190
Gly Glu Lys Gly His Arg Phe Ala Met Pro Leu Ser Arg Ile Ala Leu
      195             200             205
Gln Ser Pro Ala Gly Ala Ala Arg Gly Gln Ala Asp Asp Ile Gln Asn
      210             215             220
Glu Ala Lys Glu Leu Ser Arg Ile Arg Asp Tyr Leu Phe Asn Glu Leu
      225             230             235             240
Ala Lys Asn Thr Gly Gln Pro Ala Glu Arg Val Phe Lys Asp Leu Ser
      245             250             255
Arg Val Lys Arg Phe Asn Ala Glu Glu Ala Ile Glu Tyr Gly Leu Ile
      260             265             270
Asp Lys Ile Val Arg Pro Pro Arg Ile Lys Glu Asp Ala Pro Arg Gln
      275             280             285
Asp Glu Ser Ala Gly Leu Gly
      290             295

```

(2) INFORMATION FOR SEQ ID NO:2711:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 279 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..279
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574011

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2711:

```

Met Ala Val Ser Phe Asn Thr Thr Leu His Gln Pro Ser Leu Ser Pro
1      5              10              15
Ser Cys Ser Ile Lys Leu Tyr Ser Gly Leu Lys Pro Gln Ser Ala Ser
      20              25              30
Phe Leu Ala Ser Gly Tyr Gln Asn Leu Asn Lys Glu Phe Tyr Gly Arg
      35              40              45
Val His Lys Ser Leu Gln Ser Gly Thr Gly Lys Ala Ser Arg Ser Arg
      50              55              60
Val Lys Met Met Pro Ile Gly Thr Pro Arg Val Pro Tyr Arg Asn Arg
      65              70              75              80
Glu Glu Gly Thr Trp Gln Xaa Val Asp Ile Trp Asn Ala Leu Tyr Arg
      85              90              95
Glu Arg Val Ile Phe Ile Gly Gln Asn Ile Asp Glu Glu Phe Ser Asn
      100             105             110
Gln Ile Leu Ala Thr Met Leu Tyr Leu Asp Thr Leu Asp Asp Ser Arg

```

(2) INFORMATION FOR SEO ID NO:2712:

(A) LENGTH: 213 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(A) NAME/KEY: peptide

(B) LOCATION: 1..213

(D) OTHER INFORMATION: / Ceres Seq. ID 1574012

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2712:

[illegible]

(2) INFORMATION FOR SEQ ID NO:2713:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 597 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..597
(D) OTHER INFORMATION: / Ceres Seq. ID 1574013

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2713:

tctcKSGatt	aaagaggttg	atctagcgat	tgttcgcat	cttggtacgc	tocagcgatt	60
accgagtatt	gttgggtatg	ctaacgccat	ggaattagct	ttaactgctc	ggagattctc	120
tgagagtgaa	gcaaaggatc	ttggtttgtt	ttctaaagtt	ttcggtatct	aatcggaagt	180
tgacaacggc	gtcagtacaa	tcgctgaagg	aataggaggc	aagtcctcct	tagctgtgac	240
agggacaaag	gcagtgttat	taagaagcag	agaggtgagt	gtagaacaag	gacttgacta	300
tgtagcaact	tggaactcgg	ctatgcttat	atcagatgat	ctcaacgaag	ctgtttctgc	360
tcagatgatg	aaaaacaaaac	ctcggtttgc	taaaactgtga	tacagctctc	gtgttgcttc	420
tttgtcttcc	aaagctcttc	tggtactaaa	agtaataaga	tattacttca	aataagttta	480
gttattgata	gttcctcta	tacggattag	ggctatagat	aaaatggctc	tctacacatg	540
agaatatgat	taatactctg	cacaatgcac	attggtaaat	gctatacctc	aatgttt	

(2) INFORMATION FOR SEQ ID NO:2714:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 132 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..132
(D) OTHER INFORMATION: / Ceres Seq. ID 1574014

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2714:

Leu	Xaa	Ile	Lys	Glu	Val	Asp	Leu	Ala	Ile	Val	Ala	Asp	Leu	Gly	Thr
1															
Leu	Gln	Arg	Leu	Pro	Ser	Ile	Val	Gly	Tyr	Ala	Asn	Ala	Met	Glu	Leu
Ala	Leu	Thr	Ala	Arg	Arg	Phe	Ser	Gly	Gly	Glu	Ala	Lys	Asp	Leu	Gly
Leu	Val	Ser	Lys	Val	Phe	Gly	Ser	Lys	Ser	Glu	Leu	Asp	Asn	Gly	Val
Ser	Thr	Ile	Ala	Glu	Gly	Ile	Gly	Gly	Lys	Ser	Pro	Leu	Ala	Val	Thr
Gly	Thr	Lys	Ala	Val	Leu	Leu	Arg	Ser	Arg	Glu	Val	Ser	Val	Glu	Gln
Gly	Leu	Asp	Tyr	Val	Ala	Thr	Trp	Asn	Ser	Ala	Met	Leu	Ile	Ser	Asp
Asp	Leu	Asn	Glu	Ala	Val	Ser	Ala	Gln	Met	Met	Lys	Thr	Lys	Pro	Arg
Phe	Ala	Lys	Leu												

(2) INFORMATION FOR SEQ ID NO:2715:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 103 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide

(B) LOCATION: 1..103

(D) OTHER INFORMATION: / Ceres Seq. ID 1574015

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2715:

Met Glu Leu Ala Leu Thr Ala Arg Arg Phe Ser Gly Gly Glu Ala Lys
1 5 10 15
Asp Leu Gly Leu Val Ser Lys Val Phe Gly Ser Lys Ser Glu Leu Asp
20 25 30
Asn Gly Val Ser Thr Ile Ala Glu Gly Ile Gly Lys Ser Pro Leu
35 40 45
Ala Val Thr Gly Thr Lys Ala Val Leu Leu Arg Ser Arg Glu Val Ser
50 55 60
Val Glu Gln Gly Leu Asp Tyr Val Ala Thr Trp Asn Ser Ala Met Leu
65 70 75 80
Ile Ser Asp Asp Leu Asn Glu Ala Val Ser Ala Gln Met Met Lys Thr
85 90 95
Lys Pro Arg Phe Ala Lys Leu
100

(2) INFORMATION FOR SEQ ID NO:2716:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2259 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..2259

(D) OTHER INFORMATION: / Ceres Seq. ID 1574021

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2716:

gcctcgctct	cgccgctgctg	ccacaacaa	tctccgactt	cgtttctctc	atctatcatc	60
gtcgtgtctca	acccttattta	tctcttaatt	tatcattaaa	acaaaaaaac	caaaaaaaac	120
ctctagctct	tcgtttcttc	aatcccagca	aaaaaaatgg	ctcaggttca	agctctctct	180
tcacattctc	ctctctctcc	tgctgttggt	aacgacgggg	ctgcgacggc	ttctgttacc	240
cctggaatgc	gcgtcgggcg	cggtggagac	ggagtcaact	acggtgctct	ttgttctctc	300
tatgtcggag	atctggattt	caatgtcacc	gattctcagc	tttatgacta	tttcaccagag	360
gtgtgtcagg	ttgtatctgt	tcgtgtttgt	cgtgatgctg	ctaccaatac	ttctcttggt	420
tatggttatg	tcaactacag	caacaccgac	gatgcggaga	agggcaatga	gaagtgtgaac	480
tcagtttctc	tcaattggaa	gatgattcgg	attacttact	cttctcgtga	ctcttctgcc	540
cgtagaagtg	gggttgggaa	tttgtttgta	aagaatttgg	ataagtcagt	tgacaacaaa	600
acccctgcac	aggcgttttc	cggtgttggg	actattgtgt	cctgtaaggt	tgctactgat	660
cacatgggtc	agctctagag	atattgggtt	gtgcagtttg	acactaagga	ttcagctaaag	720
aagtctattg	agaaagctga	cgggaaagtg	ttgaatgaca	aacagatttt	tggtggacct	780
tttcttcgtc	aggaggaagc	agagtctgct	gctgataaga	tgaagttttc	taattgtttat	840
gtgaagaatc	tttcggagtc	gactactgac	gatgagttga	agactacttt	tggttcagtat	900
ggtagtatct	cgagcgctgt	agttatgagg	gatggagatg	ggaaatccag	gtgttttggg	960
ttgttcaact	ttgagaatcc	tgaagatgca	gctcgtgctg	ttgaagctct	caatggaagc	1020
aaagtgtgat	ataaggagtg	gtatgtgggt	aaagctcagS	aagaaatctc	agagggaaact	1080
tgagtgtgagc	cggagatatg	aacaaggctc	aagtgatggt	ggaaaacaat	ttgatggggt	1140
gaatttttat	gttaagaatcc	ttgatgatac	cgctcacgag	gagaagttgc	gcgagttggt	1200
tgccgaattt	tgtaacaatca	ctctcttgca	ggttatcgcg	gacctagctg	gtactagcaa	1260
aggatcagga	tttgtttgct	tctctgctgc	cagtgaagct	tcaagtagtc	tgaatgaaat	1320
gaatgtgtaa	atggtttggtg	gcaaaacggt	gtatgttgct	cttgacacgc	ggaaaagaaga	1380
aaggagggct	aagctgcagc	cacagttttc	tcaaatgaga	cctgcattta	tcccgggtgt	1440
gggtctctga	atgccaatat	tcaacaggtg	tgctccaggt	cttgacaacac	agctttttta	1500
cggtcaagga	cctccaccac	tcattcctca	ccagcctgga	tttgatatac	agcctcagct	1560
ggttctcggg	atgaggccgg	cctttttttg	tggaaccgatg	atgcagccag	gtcagcaagg	1620
tcacaccacg	gtggcagacg	gttcagtgat	ggacccatgc	gccatcagca	tcagcagcca	1680
atgctctaca	tgcagccaca	gatgatgcca	agaggacgag	ggatccggta	cccttctggt	1740
gttagaatac	tgctctagcg	tccaatgcca	ggaggaatgg	ttccagttgt	tatgacacat	1800
aatgtaatgc	cgatatatgc	gcctatgtcc	gctgtgcatt	tggtactctc	ccctgtcaat	1860
gctacacctg	ctcaacagag	aacacttctt	ggtagagatc	tattaccatt	agtggaacag	1920

atagagagtg agcagcgtgc gaaagtgc ggtatgcttc tggaaatgga tcagaccgag 1980
gttttgcac tcgtcgagtc accagagcct ctaaatgcc aagtttcaga ggcattagat 2040
gtgttgagaa acgtgaaatca gccatottca caggggaagt aaggcaacaa aagtgggaagt 2100
ccaagtgtac ttttggcttc actttccatc aatgatcaat tatgagaagc ttttgttcga 2160
gttttttttt ttttactttg actctctctc tctctatctc tctctctgat tgacaaattt 2220
ttgcgggaat ctatttgctg ttttagactt ttttgcctc

(2) INFORMATION FOR SEQ ID NO:2717:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 304 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..304
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574022

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2717:

Met	Ala	Gln	Val	Gln	Ala	Pro	Ser	Ser	His	Ser	Pro	Pro	Pro	Ala
1		5						10					15	
Val	Val	Asn	Asp	Gly	Ala	Ala	Thr	Ala	Ser	Ala	Thr	Pro	Gly	Ile
		20						25					30	Gly
Val	Gly	Gly	Gly	Gly	Asp	Gly	Val	Thr	His	Gly	Ala	Leu	Cys	Ser
		35					40					45		Leu
Tyr	Val	Gly	Asp	Leu	Asp	Phe	Asn	Val	Thr	Asp	Ser	Gln	Leu	Tyr
		50				55				60				Asp
Tyr	Phe	Thr	Glu	Val	Cys	Gln	Val	Val	Ser	Val	Arg	Val	Cys	Arg
65			70							75				80
Ala	Ala	Thr	Asn	Thr	Ser	Leu	Gly	Tyr	Gly	Tyr	Val	Asn	Tyr	Ser
			85					90					95	Asn
Thr	Asp	Asp	Ala	Glu	Lys	Ala	Met	Gln	Lys	Leu	Asn	Tyr	Ser	Tyr
			100					105				110		Leu
Asn	Gly	Lys	Met	Ile	Arg	Ile	Thr	Tyr	Ser	Ser	Arg	Asp	Ser	Ser
			115				120					125		Ala
Arg	Arg	Ser	Gly	Val	Gly	Asn	Leu	Phe	Val	Lys	Asn	Leu	Asp	Lys
			130			135				140				Ser
Val	Asp	Asn	Lys	Thr	Leu	His	Glu	Ala	Phe	Ser	Gly	Cys	Gly	Thr
145				150						155				160
Val	Ser	Cys	Lys	Val	Ala	Thr	Asp	His	Met	Gly	Gln	Ser	Arg	Gly
			165					170						175
Gly	Phe	Val	Gln	Phe	Asp	Thr	Lys	Asp	Ser	Ala	Lys	Asn	Ala	Ile
			180					185				190		Glu
Lys	Leu	Asn	Gly	Lys	Val	Leu	Asn	Asp	Lys	Gln	Ile	Phe	Val	Gly
			195				200					205		Pro
Phe	Leu	Arg	Lys	Glu	Glu	Arg	Glu	Ser	Ala	Ala	Asp	Lys	Met	Lys
			210				215				220			Phe
Thr	Asn	Val	Tyr	Val	Lys	Asn	Leu	Ser	Glu	Ala	Thr	Thr	Asp	Asp
225				230						235				Glu
Leu	Lys	Thr	Thr	Phe	Gly	Gln	Tyr	Gly	Ser	Ile	Ser	Ser	Ala	Val
			245					250						255
Met	Arg	Asp	Gly	Asp	Gly	Lys	Ser	Arg	Cys	Phe	Gly	Phe	Val	Asn
			260					265				270		Phe
Glu	Asn	Pro	Glu	Asp	Ala	Ala	Arg	Ala	Val	Glu	Ala	Leu	Asn	Gly
			275				280					285		Lys
Lys	Phe	Asp	Asp	Lys	Glu	Trp	Tyr	Val	Gly	Lys	Ala	Gln	Xaa	Glu
			290			295					300			Ile

(2) INFORMATION FOR SEQ ID NO:2718:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 257 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..257
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1574023

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2718:

```
Met Glu Met Gly Asn Pro Gly Val Leu Asp Leu Ser Thr Leu Arg Ile
1      5      10      15
Leu Lys Met Gln Leu Val Leu Leu Lys Leu Ser Met Glu Arg Ser Leu
20      25      30
Met Ile Arg Ser Gly Met Trp Val Lys Leu Xaa Lys Lys Ser Glu Arg
35      40      45
Glu Leu Glu Leu Ser Arg Arg Tyr Glu Gln Gly Ser Ser Asp Gly Gly
50      55      60
Asn Lys Phe Asp Gly Leu Asn Leu Tyr Val Lys Asn Leu Asp Asp Thr
65      70      75      80
Val Thr Asp Glu Lys Leu Arg Glu Leu Phe Ala Glu Phe Gly Thr Ile
85      90      95
Thr Ser Cys Lys Val Met Arg Asp Pro Ser Gly Thr Ser Lys Gly Ser
100      105      110
Gly Phe Val Ala Phe Ser Ala Ala Ser Glu Ala Ser Arg Val Leu Asn
115      120      125
Glu Met Asn Gly Lys Met Val Gly Gly Lys Pro Leu Tyr Val Ala Leu
130      135      140
Ala Gln Arg Lys Glu Glu Arg Arg Ala Lys Leu Gln Ala Gln Phe Ser
145      150      155      160
Gln Met Arg Pro Ala Phe Ile Pro Gly Val Gly Pro Arg Met Pro Ile
165      170      175
Phe Thr Gly Gly Ala Pro Gly Leu Gly Gln Gln Ile Phe Tyr Gly Gln
180      185      190
Gly Pro Pro Pro Ile Ile Pro His Gln Pro Gly Phe Gly Tyr Gln Pro
195      200      205
Gln Leu Val Pro Gly Met Arg Pro Ala Phe Phe Gly Gly Pro Met Met
210      215      220
Gln Pro Gly Gln Gln Gly Pro His Gln Val Ala Asp Gly Gln Val Met
225      230      235      240
Asp Pro Cys Ala Ile Ser Ile Ser Ser Gln Cys Leu Thr Cys Ser His
245      250      255
Arg
```

(2) INFORMATION FOR SEQ ID NO:2719:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 255 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..255
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1574024

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2719:

```
Met Gly Asn Pro Gly Val Leu Asp Leu Ser Thr Leu Arg Ile Leu Lys
1      5      10      15
Met Gln Leu Val Leu Leu Lys Leu Ser Met Glu Arg Ser Leu Met Ile
20      25      30
Arg Ser Gly Met Trp Val Lys Leu Xaa Lys Lys Ser Glu Arg Glu Leu
35      40      45
```

Glu	Leu	Ser	Arg	Arg	Tyr	Glu	Gln	Gly	Ser	Ser	Asp	Gly	Gly	Asn	Lys		
50						55					60						
Phe	Asp	Gly	Leu	Asn	Leu	Tyr	Val	Lys	Asn	Leu	Asp	Asp	Thr	Val	Thr		
65					70					75					80		
Asp	Glu	Lys	Leu	Arg	Glu	Leu	Phe	Ala	Glu	Phe	Gly	Thr	Ile	Thr	Ser		
			85						90					95			
Cys	Lys	Val	Met	Arg	Asp	Pro	Ser	Gly	Thr	Ser	Lys	Gly	Ser	Gly	Phe		
			100						105					110			
Val	Ala	Phe	Ser	Ala	Ala	Ser	Glu	Ala	Ser	Arg	Val	Leu	Asn	Glu	Met		
			115						120					125			
Asn	Gly	Lys	Met	Val	Gly	Gly	Lys	Pro	Leu	Tyr	Val	Ala	Leu	Ala	Gln		
			130				135					140					
Arg	Lys	Glu	Glu	Arg	Arg	Ala	Lys	Leu	Gln	Ala	Gln	Phe	Ser	Gln	Met		
145					150					155					160		
Arg	Pro	Ala	Phe	Ile	Pro	Gly	Val	Gly	Pro	Arg	Met	Pro	Ile	Phe	Thr		
				165					170					175			
Gly	Gly	Ala	Pro	Gly	Leu	Gly	Gln	Gln	Ile	Phe	Tyr	Gly	Gln	Gly	Pro		
			180						185					190			
Pro	Pro	Ile	Ile	Pro	His	Gln	Pro	Gly	Phe	Gly	Tyr	Gln	Pro	Gln	Leu		
			195				200						205				
Val	Pro	Gly	Met	Arg	Pro	Ala	Phe	Phe	Gly	Gly	Pro	Met	Met	Gln	Pro		
			210				215					220					
Gly	Gln	Gln	Gly	Pro	His	Gln	Val	Ala	Asp	Gly	Gln	Val	Met	Asp	Pro		
225					230						235				240		
Cys	Ala	Ile	Ser	Ile	Ser	Ser	Gln	Cys	Leu	Thr	Cys	Ser	His	Arg			
			245						250					255			

(2) INFORMATION FOR SEQ ID NO:2720:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 927 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..927
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574025

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2720:

atctttcatt	cttctaagcc	ctagctcaaa	gctttctctc	tcaaatccgc	catgactaaa	60
cagcacgcga	actggtctcc	ttacgataac	aatggaggaa	catgtgtggc	catcgctgga	120
tcggattact	gtgttatcgc	gcgcgatact	cggatgtcta	ctggttacag	tattcttagt	180
cgcgattact	ccaaaatcca	taaaactagcg	gacagacctg	ttttgtcttc	ctctggtctc	240
caggctgattg	tgaaagcttt	cgagaaggtt	ctcaaatcca	gacacttgat	ctatcaacat	300
cagcataaca	agcagatgag	ctgtctctgca	atggcccagc	ttctctccaa	cacgctttat	360
ttcaagcggg	ttttccctta	ctatgccttt	aatgttctag	gagggcttga	cgaggaagga	420
aaagggtgtg	tctttactta	cgacgctgtt	ggctcatacg	agagagttgg	atacgggtgc	480
caaggttctg	gtttccacat	catcatgcct	ttccttgaca	atcagctcaa	gtctccaagt	540
cctctttttg	tacctaaaca	ggattcaaac	acgCcccttt	cogaagctga	agcagttgac	600
ttggttAaaa	ctgttttcgc	atctgcacca	Tgagagggat	atctacactg	gagacaagct	660
tgagattatg	atacttaagg	cgcagcgtat	caagaccgaa	ctcatggacc	tgaggaaaga	720
ctaagctcct	ttagtgcatt	tagccaacct	tatcggtttg	ttatttcact	tcaacatcga	780
gcttctcgag	ttgtagaact	cgtatgaact	gtactgggtg	ttgatatttt	acagttaaaa	840
tcatgactcg	tggttgaagt	ttctccaaaa	ctgtttccct	atgtatgaga	atcactcgaa	900
tcttgtcttt	aatcaatgt	ttctccc				

(2) INFORMATION FOR SEQ ID NO:2721:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 193 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..193

(D) OTHER INFORMATION: / Ceres Seq. ID 1574026

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2721:

```
Met Thr Lys Gln His Ala Asn Trp Ser Pro Tyr Asp Asn Asn Gly Gly
1      5      10      15
Thr Cys Val Ala Ile Ala Gly Ser Asp Tyr Cys Val Ile Ala Ala Asp
      20      25      30
Thr Arg Met Ser Thr Gly Tyr Ser Ile Leu Ser Arg Asp Tyr Ser Lys
      35      40      45
Ile His Lys Leu Ala Asp Arg Pro Val Leu Ser Ser Ser Gly Phe Gln
      50      55      60
Ala Asp Val Lys Ala Leu Gln Lys Val Leu Lys Ser Arg His Leu Ile
65      70      75      80
Tyr Gln His Gln His Asn Lys Gln Met Ser Cys Pro Ala Met Ala Gln
      85      90      95
Leu Leu Ser Asn Thr Leu Tyr Phe Lys Arg Phe Phe Pro Tyr Tyr Ala
      100      105      110
Phe Asn Val Leu Gly Gly Leu Asp Glu Glu Gly Lys Gly Cys Val Phe
      115      120      125
Thr Tyr Asp Ala Val Gly Ser Tyr Glu Arg Val Gly Tyr Gly Ala Gln
      130      135      140
Gly Ser Gly Ser Thr Leu Ile Met Pro Phe Leu Asp Asn Gln Leu Lys
145      150      155      160
Ser Pro Ser Pro Leu Leu Leu Pro Lys Gln Asp Ser Asn Thr Pro Leu
      165      170      175
Ser Glu Ala Glu Ala Val Asp Leu Val Lys Thr Val Phe Ala Ser Ala
      180      185      190
Thr
```

(2) INFORMATION FOR SEQ ID NO:2722:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 159 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..159

(D) OTHER INFORMATION: / Ceres Seq. ID 1574027

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2722:

```
Met Ser Thr Gly Tyr Ser Ile Leu Ser Arg Asp Tyr Ser Lys Ile His
1      5      10      15
Lys Leu Ala Asp Arg Pro Val Leu Ser Ser Ser Gly Phe Gln Ala Asp
      20      25      30
Val Lys Ala Leu Gln Lys Val Leu Lys Ser Arg His Leu Ile Tyr Gln
      35      40      45
His Gln His Asn Lys Gln Met Ser Cys Pro Ala Met Ala Gln Leu Leu
      50      55      60
Ser Asn Thr Leu Tyr Phe Lys Arg Phe Phe Pro Tyr Tyr Ala Phe Asn
65      70      75      80
Val Leu Gly Gly Leu Asp Glu Glu Gly Lys Gly Cys Val Phe Thr Tyr
      85      90      95
Asp Ala Val Gly Ser Tyr Glu Arg Val Gly Tyr Gly Ala Gln Gly Ser
      100      105      110
Gly Ser Thr Leu Ile Met Pro Phe Leu Asp Asn Gln Leu Lys Ser Pro
      115      120      125
Ser Pro Leu Leu Leu Pro Lys Gln Asp Ser Asn Thr Pro Leu Ser Glu
      130      135      140
```

Ala Glu Ala Val Asp Leu Val Lys Thr Val Phe Ala Ser Ala Thr
145 150 155

(2) INFORMATION FOR SEQ ID NO:2723:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..105
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574028

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2723:

Met Ser Cys Pro Ala Met Ala Gln Leu Leu Ser Asn Thr Leu Tyr Phe
1 5 10 15
Lys Arg Phe Phe Pro Tyr Tyr Ala Phe Asn Val Leu Gly Gly Leu Asp
20 25 30
Glu Glu Gly Lys Gly Cys Val Phe Thr Tyr Asp Ala Val Gly Ser Tyr
35 40 45
Glu Arg Val Gly Tyr Gly Ala Gln Gly Ser Gly Ser Thr Leu Ile Met
50 55 60
Pro Phe Leu Asp Asn Gln Leu Lys Ser Pro Ser Pro Leu Leu Leu Pro
65 70 75 80
Lys Gln Asp Ser Asn Thr Pro Leu Ser Glu Ala Glu Ala Val Asp Leu
85 90 95
Val Lys Thr Val Phe Ala Ser Ala Thr
100 105

(2) INFORMATION FOR SEQ ID NO:2724:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1117 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1117
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574029

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2724:

tttgatgact gttcacgac ccaatgtcact atccatcgaa atccctggaag ttgagttcgg 60
tgaagctcgcg gatattggcg aagaagcaat ctattataga catttcaaac cggtgatctt 120
gtggagcctt caaaactgga ttggtattgg gcttgagagg aagatgagaa cagctttggc 180
cactgtcaat cgtatgtttg cgaagatcat atcttcaaga agaaaaggagg agataagtcg 240
cgccaaaaac gagccatatt ccaaggacgc gttgacgtat tatatgaatg tggacacgag 300
caaatataag ctcttgaaac ctaataaaga taagtttata agagatgtta tttttagtct 360
agtgttagca ggaaggagaca ccacaagctc agttctcact tggttctttt ggcttctttc 420
taagcatcct caagttatgg ccaagctcag acatgagatc aacacaaagt ttgataatga 480
agatctagag aagctcgtgt atctgcatcg tgcattgtcc gaatcaatga gactctaccc 540
gccactctcc ttcaaccaca agtctCctgc gaaGccagat gtaacttccaa gcgggcacaa 600
agttgatgca aattcaaaga tcgtgatatg tatctatgca ttggggaggga tgagatctgt 660
atggggagaa gacgcattgg atttcaaacc agagagatgg atttcagaca atggaggtct 720
aagacatgaa ccttcaatca agttcatggc tttaaattct ggctcgagaa cttgcttggt 780
taaaaaacta gctctcttgc agatgaagat ggtagctctg gagatcatac gaaactatga 840
ctttaaggtc attgaaggtc acaaggctga accaattcct tctatctctc tccgtatgaa 900
acatgggtctt taacttcacg tcacaaagaa gatatgatta ttatgcttcg ttggttctta 960
cggaacactt taacttttcc ttattttaa atgtgttact ctatgtttgt cccacgttat 1020
aactactgtt attacgtact aagtacggtt ttgtgccac gtcatgtcta taaataaatt 1080
aatatcgtca aataaagtatt agacatcct cgtccat

(2) INFORMATION FOR SEQ ID NO:2725:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 311 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..311
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1574030

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2725:

Leu Met Thr Gly Tyr Asp Pro Met Ser Leu Ser Ile Glu Ile Leu Glu
1 5 10 15
Val Glu Phe Gly Glu Ala Ala Asp Ile Gly Glu Glu Ala Ile Tyr Tyr
20 25 30
Arg His Phe Lys Pro Val Ile Leu Trp Arg Leu Gln Asn Trp Ile Gly
35 40 45
Ile Gly Leu Glu Arg Lys Met Arg Thr Ala Leu Ala Thr Val Asn Arg
50 55 60
Met Phe Ala Lys Ile Ile Ser Ser Arg Arg Lys Glu Glu Ile Ser Arg
65 70 75 80
Ala Lys Thr Glu Pro Tyr Ser Lys Asp Ala Leu Thr Tyr Tyr Met Asn
85 90 95
Val Asp Thr Ser Ser Lys Tyr Lys Leu Leu Lys Pro Asn Lys Asp Lys Phe
100 105 110
Ile Arg Asp Val Ile Phe Ser Leu Val Leu Ala Gly Arg Asp Thr Thr
115 120 125
Ser Ser Val Leu Thr Trp Phe Phe Trp Leu Leu Ser Lys His Pro Gln
130 135 140
Val Met Ala Lys Leu Arg His Glu Ile Asn Thr Lys Phe Asp Asn Glu
145 150 155 160
Asp Leu Glu Lys Leu Val Tyr Leu His Ala Ala Leu Ser Glu Ser Met
165 170 175
Arg Leu Tyr Pro Pro Leu Pro Phe Asn His Lys Ser Pro Ala Lys Pro
180 185 190
Asp Val Leu Pro Ser Gly His Lys Val Asp Ala Asn Ser Lys Ile Val
195 200 205
Ile Cys Ile Tyr Ala Leu Gly Arg Met Arg Ser Val Trp Gly Glu Asp
210 215 220
Ala Leu Asp Phe Lys Pro Glu Arg Trp Ile Ser Asp Asn Gly Gly Leu
225 230 235 240
Arg His Glu Pro Ser Tyr Lys Phe Met Ala Phe Asn Ser Gly Pro Arg
245 250 255
Thr Cys Leu Gly Lys Asn Leu Ala Leu Leu Gln Met Lys Met Val Ala
260 265 270
Leu Glu Ile Ile Arg Asn Tyr Asp Phe Lys Val Ile Glu Gly His Lys
275 280 285
Val Glu Pro Ile Pro Ser Ile Leu Leu Arg Met Lys His Gly Leu Lys
290 295 300
Val Thr Val Thr Lys Lys Ile
305 310

(2) INFORMATION FOR SEQ ID NO:2726:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 310 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..310
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1574031

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2726:

Met Thr Gly Tyr Asp Pro Met Ser Leu Ser Ile Glu Ile Leu Glu Val
1 5 10 15
Glu Phe Gly Glu Ala Ala Asp Ile Gly Glu Glu Ala Ile Tyr Tyr Arg
20 25 30
His Phe Lys Pro Val Ile Leu Trp Arg Leu Gln Asn Trp Ile Gly Ile
35 40 45
Gly Leu Glu Arg Lys Met Arg Thr Ala Leu Ala Thr Val Asn Arg Met
50 55 60
Phe Ala Lys Ile Ile Ser Ser Arg Arg Lys Glu Glu Ile Ser Arg Ala
65 70 75 80
Lys Thr Glu Pro Tyr Ser Lys Asp Ala Leu Thr Tyr Tyr Met Asn Val
85 90 95
Asp Thr Ser Lys Tyr Lys Leu Leu Lys Pro Asn Lys Asp Lys Phe Ile
100 105 110
Arg Asp Val Ile Phe Ser Leu Val Leu Ala Gly Arg Asp Thr Thr Ser
115 120 125
Ser Val Leu Thr Trp Phe Phe Trp Leu Leu Ser Lys His Pro Gln Val
130 135 140
Met Ala Lys Leu Arg His Glu Ile Asn Thr Lys Phe Asp Asn Glu Asp
145 150 155 160
Leu Glu Lys Leu Val Tyr Leu His Ala Ala Leu Ser Glu Ser Met Arg
165 170 175
Leu Tyr Pro Pro Leu Pro Phe Asn His Lys Ser Pro Ala Lys Pro Asp
180 185 190
Val Leu Pro Ser Gly His Lys Val Asp Ala Asn Ser Lys Ile Val Ile
195 200 205
Cys Ile Tyr Ala Leu Gly Arg Met Arg Ser Val Trp Gly Glu Asp Ala
210 215 220
Leu Asp Phe Lys Pro Glu Arg Trp Ile Ser Asp Asn Gly Gly Leu Arg
225 230 235 240
His Glu Pro Ser Tyr Lys Phe Met Ala Phe Asn Ser Gly Pro Arg Thr
245 250 255
Cys Leu Gly Lys Asn Leu Ala Leu Gln Met Lys Met Val Ala Leu
260 265 270
Glu Ile Ile Arg Asn Tyr Asp Phe Lys Val Ile Glu Gly His Lys Val
275 280 285
Glu Pro Ile Pro Ser Ile Leu Leu Arg Met Lys His Gly Leu Lys Val
290 295 300
Thr Val Thr Lys Lys Ile
305 310

(2) INFORMATION FOR SEQ ID NO:2727:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 304 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..304
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574032

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2727:

Met Ser Leu Ser Ile Glu Ile Leu Glu Val Glu Phe Gly Glu Ala Ala
1 5 10 15
Asp Ile Gly Glu Glu Ala Ile Tyr Tyr Arg His Phe Lys Pro Val Ile
20 25 30
Leu Trp Arg Leu Gln Asn Trp Ile Gly Ile Gly Leu Glu Arg Lys Met
35 40 45
Arg Thr Ala Leu Ala Thr Val Asn Arg Met Phe Ala Lys Ile Ile Ser
50 55 60

Ser	Arg	Arg	Lys	Glu	Glu	Ile	Ser	Arg	Ala	Lys	Thr	Glu	Pro	Tyr	Ser	
65				70						75				80		
Lys	Asp	Ala	Leu	Thr	Tyr	Tyr	Met	Asn	Val	Asp	Thr	Ser	Lys	Tyr	Lys	
			85						90					95		
Leu	Leu	Lys	Pro	Asn	Lys	Asp	Lys	Phe	Ile	Arg	Asp	Val	Ile	Phe	Ser	
			100					105					110			
Leu	Val	Leu	Ala	Gly	Arg	Asp	Thr	Thr	Ser	Ser	Val	Leu	Thr	Trp	Phe	
		115					120					125				
Phe	Trp	Leu	Leu	Ser	Lys	His	Pro	Gln	Val	Met	Ala	Lys	Leu	Arg	His	
	130					135					140					
Glu	Ile	Asn	Thr	Lys	Phe	Asp	Asn	Glu	Asp	Leu	Glu	Lys	Leu	Val	Tyr	
145				150						155				160		
Leu	His	Ala	Ala	Leu	Ser	Glu	Ser	Met	Arg	Leu	Tyr	Pro	Pro	Leu	Pro	
			165						170					175		
Phe	Asn	His	Lys	Ser	Pro	Ala	Lys	Pro	Asp	Val	Leu	Pro	Ser	Gly	His	
			180					185					190			
Lys	Val	Asp	Ala	Asn	Ser	Lys	Ile	Val	Ile	Cys	Ile	Tyr	Ala	Leu	Gly	
		195					200					205				
Arg	Met	Arg	Ser	Val	Trp	Gly	Glu	Asp	Ala	Leu	Asp	Phe	Lys	Pro	Glu	
	210					215					220					
Arg	Trp	Ile	Ser	Asp	Asn	Gly	Gly	Leu	Arg	His	Glu	Pro	Ser	Tyr	Lys	
225				230						235				240		
Phe	Met	Ala	Phe	Asn	Ser	Gly	Pro	Arg	Thr	Cys	Leu	Gly	Lys	Asn	Leu	
			245					250						255		
Ala	Leu	Leu	Gln	Met	Lys	Met	Val	Ala	Leu	Glu	Ile	Ile	Arg	Asn	Tyr	
		260					265						270			
Asp	Phe	Lys	Val	Ile	Glu	Gly	His	Lys	Val	Glu	Pro	Ile	Pro	Ser	Ile	
	275					280						285				
Leu	Leu	Arg	Met	Lys	His	Gly	Leu	Lys	Val	Thr	Val	Thr	Lys	Lys	Ile	
	290					295					300					

(2) INFORMATION FOR SEQ ID NO:2728:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 923 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..923
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574038

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2728:

agtgcgcgaga	aagataaaca	aaatggcggc	aatcagaacg	atgacgaaca	tgattctacg	60
cgagttcatc	catcatccac	ttctcttcca	ctcttcatcg	aaatcgtgtc	aatctctttt	120
taccatgtct	ccgtctcact	cccctaattt	ctccaaattca	ccctaattcc	cgggtctgat	180
ccgtccgatg	tgcggcatcg	acctccgggtg	gaagcgggtgg	tgatcggaaa	gtctcttcac	240
ggtttgtcgca	ggtgcaacag	atgcttcatg	aagccgaaga	gagagctagt	tcgcgtggca	300
atgagcctac	tcctcaaatc	actctagaca	atgttacact	taactttgct	agaagtgggtg	360
gtcctgcgagg	ccagaatgtg	aacaaattga	ataccaaaagt	agatatgcgc	ttcaatgtta	420
agaacgcgta	ttgctgagtg	gacaggatca	gagagaaaat	cttactgacg	gagaagaatc	480
ggatcaacaa	ggatggtgaa	cttgtgatat	cttcaaccaa	aaccagaacg	cagaaggcca	540
acatcgcgca	tgcacttgaa	aaactacagg	cgatcattga	tgccgctctt	tatgttccac	600
ctccaccatc	agaagaacag	aagaagaaaa	tagtaaaagt	ggctgcgaaa	gctgacataa	660
aacgacttaa	aagcaaaaaa	gttctgtcag	acaagaaaat	tgccgagaaga	agcccgcgta	720
gtttacagtga	ttaaaactta	aaccatacaa	tggagtcacg	gtgtattcta	aagcttttaa	780
cttaaaatga	tgtgtatttt	cttggaaatt	aatgtaaacac	aaacaacaaa	tcatccaata	840
aaaattgcag	tatatggagt	tttatgtaca	aaccactctt	atacaaaata	tgaacaaaaa	900
aagtatcaaa	cataaacattc	ctc				

(2) INFORMATION FOR SEQ ID NO:2729:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 157 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..157
(D) OTHER INFORMATION: / Ceres Seq. ID 1574039
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2729:
Met Leu His Glu Ala Glu Glu Arg Ala Ser Ser Ala Gly Asn Glu Pro
1 5 10 15
Thr Pro Gln Ile Thr Leu Asp Asn Val Thr Leu Asn Phe Ala Arg Ser
20 25 30
Gly Gly Pro Gly Gly Gln Asn Val Asn Lys Leu Asn Thr Lys Val Asp
35 40 45
Met Arg Phe Asn Val Lys Asn Ala Tyr Trp Leu Ser Asp Arg Ile Arg
50 55 60
Glu Lys Ile Leu Leu Thr Glu Lys Asn Arg Ile Asn Lys Asp Gly Glu
65 70 75 80
Leu Val Ile Ser Ser Thr Lys Thr Arg Thr Gln Lys Gly Asn Ile Asp
85 90 95
Asp Ala Leu Glu Lys Leu Gln Ala Ile Ile Asp Ala Ala Ser Tyr Val
100 105 110
Pro Pro Pro Pro Ser Glu Glu Gln Lys Lys Lys Ile Val Lys Leu Ala
115 120 125
Ala Lys Ala Asp Asn Lys Arg Leu Lys Ser Lys Lys Val Leu Ser Asp
130 135 140
Lys Lys Ser Ala Arg Arg Ser Arg Gly Ser Tyr Asp Asp
145 150 155
(2) INFORMATION FOR SEQ ID NO:2730:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 109 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..109
(D) OTHER INFORMATION: / Ceres Seq. ID 1574040
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2730:
Met Arg Phe Asn Val Lys Asn Ala Tyr Trp Leu Ser Asp Arg Ile Arg
1 5 10 15
Glu Lys Ile Leu Leu Thr Glu Lys Asn Arg Ile Asn Lys Asp Gly Glu
20 25 30
Leu Val Ile Ser Ser Thr Lys Thr Arg Thr Gln Lys Gly Asn Ile Asp
35 40 45
Asp Ala Leu Glu Lys Leu Gln Ala Ile Ile Asp Ala Ala Ser Tyr Val
50 55 60
Pro Pro Pro Pro Ser Glu Glu Gln Lys Lys Lys Ile Val Lys Leu Ala
65 70 75 80
Ala Lys Ala Asp Asn Lys Arg Leu Lys Ser Lys Lys Val Leu Ser Asp
85 90 95
Lys Lys Ser Ala Arg Arg Ser Arg Gly Ser Tyr Asp Asp
100 105
(2) INFORMATION FOR SEQ ID NO:2731:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 506 base pairs
(B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..506
(D) OTHER INFORMATION: / Ceres Seq. ID 1574041
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2731:
ggactatctta ttacttggtc cacaataat gtacttagta cgcgcccaaca agtatatctg 60
cgtaaaactag gtggtgcgaa gccaaatatg gatgaaaacg caagcaaaat aataagtgcg 120
ggacgagcaaa agagatctat tgctcagcct gacgatgctg gcgaacatt tagacaatta 180
aaagagcaag agaagcgag Caagaagaac aaggcggttg cgaagatac agttgaattg 240
gtagaagaat ctcagtctga atcagaagaa gggtctgatg atgagggaag agaggctcgt 300
gaaggagcgt tagCttcgag cacaacaagc aagccgcttc ctgaggttgg ccaacgaaga 360
agcaaaaagat cgaagcgga acgcactgta tagaaccaaa gcaaacgaaa ttgcaagtaa 420
ggaagagaaa agagagagat ttgaatcttg ttccttagtt tgatcttttg atatattatt 480
gcatacacca tgtccggtaa ttatcc

(2) INFORMATION FOR SEQ ID NO:2732:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 130 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..130
(D) OTHER INFORMATION: / Ceres Seq. ID 1574042
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2732:
Gly Leu Ser Ile Tyr Trp Leu Thr Asn Asn Val Leu Ser Thr Ala Gln
1 5 10 15
Gln Val Tyr Leu Arg Lys Leu Gly Gly Ala Lys Pro Asn Met Asp Glu
20 25 30
Asn Ala Ser Lys Ile Ile Ser Ala Gly Arg Ala Lys Arg Ser Ile Ala
35 40 45
Gln Pro Asp Asp Ala Gly Glu Thr Phe Arg Gln Leu Lys Glu Gln Glu
50 55 60
Lys Arg Ser Lys Lys Asn Lys Ala Val Ala Lys Asp Thr Val Glu Leu
65 70 75 80
Val Glu Glu Ser Gln Ser Glu Ser Glu Glu Gly Ser Asp Asp Glu Glu
85 90 95
Glu Glu Ala Arg Glu Gly Ala Leu Ala Ser Ser Thr Thr Ser Lys Pro
100 105 110
Leu Pro Glu Val Gly Gln Arg Arg Ser Lys Arg Ser Lys Arg Lys Arg
115 120 125
Thr Val
130

(2) INFORMATION FOR SEQ ID NO:2733:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 101 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..101
(D) OTHER INFORMATION: / Ceres Seq. ID 1574043
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2733:
Met Asp Glu Asn Ala Ser Lys Ile Ile Ser Ala Gly Arg Ala Lys Arg
1 5 10 15

Ser Ile Ala Gln Pro Asp Asp Ala Gly Glu Thr Phe Arg Gln Leu Lys
20 25 30
Glu Gln Glu Lys Arg Ser Lys Lys Asn Lys Ala Val Ala Lys Asp Thr
35 40 45
Val Glu Leu Val Glu Glu Ser Gln Ser Glu Ser Glu Glu Gly Ser Asp
50 55 60
Asp Glu Glu Glu Glu Ala Arg Glu Gly Ala Leu Ala Ser Ser Thr Thr
65 70 75 80
Ser Lys Pro Leu Pro Glu Val Gly Gln Arg Arg Ser Lys Arg Ser Lys
85 90 95
Arg Lys Arg Thr Val
100

(2) INFORMATION FOR SEQ ID NO:2734:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1496 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1496
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574044

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2734:

acggaccgac gcttgctctg tgctcatcgt tctcttcttc accttattcca tgggtggttta 60
gttcatgatt ttggagtttt taagaacttt ttctactaga actcgaaatc ttccaagtttc 120
tggtttttat tcgataaagta ctagtataat gcgagatatac aaagtcacaaat ctgattcttaa 180
ggagttttcta acatcatctg atgaagaaga agaatacagtt tccattagag ttgcgtcttc 240
ttcttctctg agtagtggtta aatcgacgcc tgagattgag aaaaagtatg ttcacagagt 300
ttacgatacgc attgctcttc attttagctc tactaggttt gctaagtggc ctaaaagttgc 360
tgcttctctc gaatcgttac cgtctggatc ggtgattctc gatgccggtt gcggtaacgg 420
gaagtatttg ggggtgaatc ctagtgtgtt ctctaatggt tgtgataaa gtcatctctt 480
gattaaaaatc tgtctggata aagggaaga ggttttgggt gcagatgctg ttaactctKbc 540
ttatagagag gagtttggcg atcgacgatc ttcatagagc gttttgcatc atttgagtagc 600
agagaataga aggaagaaga ctattgaaga gcttgttcgt ttgtttaagc ctggtggatt 660
tgtttctcatt actgtctcggg ctgtgtaaca ggagatatac tcgttgccta cgaataggac 720
acctttgtct gctaagtatg ttgaggaatg ggttgggtcca ggtagtcgga tgaatagtc 780
tcgtgtgagg aacaatccgt tcttttagtct tgagagtatc ccagagactg aggtgagtagc 840
aaaggagcaa aaggttgaga acagtcagtt catcggctct gagagcattc cagagagcga 900
ggagagtagc acagagcaga aaggtgagag tattattcca gaaaccaaaag ctagtatagt 960
agagcaaaag atgagaatac tgttgaggag tcattggagg ctctgaagaa gagtcaacaa 1020
gagtactttg tgccatggca ttaccatac caccgtgctg aagtgagtagg tgcattctgcg 1080
tctgcacttg caagtggtct tgcaaaagaa gatgatagaa aaggagctgt ttgttacaac 1140
agatactacc atgtcttttag cgaaggcgaa cttgaaaggt tggcatctgg agtaggcaat 1200
gcaatgatag ttgatagatt ttctgacaag tcgaattggt gtattgtctt tcagaaagaa 1260
gctttaaacc aagattgaac ttgtgtttca aacttatcaa atctttgtgac tattggaact 1320
ccattgcatc tgtaatcggg aattattatt gcatttttca tggttgtagt ttgagattct 1380
gtggcagctc attttccctg caatttgggt tctttaaagg gttttgtatt atgtgttaaca 1440
caaatcaaaag aaagaatctt ctctacatga taacaaaaat gtcagaaata tgattt

(2) INFORMATION FOR SEQ ID NO:2735:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 313 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..313
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574045

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2735:

Met Ile Leu Asp Val Leu Arg Thr Phe Ser Thr Arg Thr Arg Asn Leu
1 5 10 15
Pro Ser Ser Gly Phe Tyr Ser Ile Ser Thr Ser Ile Met Arg Asp Ile
20 25 30
Lys Val Lys Ser Asp Ser Lys Glu Phe Leu Thr Ser Ser Asp Glu Glu
35 40 45
Glu Glu Ser Val Ser Ile Arg Val Ser Ser Ser Ser Leu Ser Ser
50 55 60
Val Lys Ser Thr Pro Glu Ile Glu Lys Lys Tyr Val His Arg Val Tyr
65 70 75 80
Asp Ala Ile Ala Pro His Phe Ser Ser Thr Arg Phe Ala Lys Trp Pro
85 90 95
Lys Val Ala Ala Phe Leu Glu Ser Leu Pro Ser Gly Ser Val Ile Leu
100 105 110
Asp Ala Gly Cys Gly Asn Gly Lys Tyr Leu Gly Leu Asn Pro Ser Cys
115 120 125
Phe Phe Ile Gly Cys Asp Ile Ser His Pro Leu Ile Lys Ile Cys Ser
130 135 140
Asp Lys Gly Gln Glu Val Leu Val Ala Asp Ala Val Asn Xaa Xaa Tyr
145 150 155 160
Arg Glu Glu Phe Gly Asp Ala Ala Ile Ser Ile Ala Val Leu His His
165 170 175
Leu Ser Thr Glu Asn Arg Arg Lys Lys Ala Ile Glu Glu Leu Val Arg
180 185 190
Val Val Lys Pro Gly Gly Phe Val Leu Ile Thr Val Trp Ala Ala Glu
195 200 205
Gln Glu Asp Thr Ser Leu Leu Thr Lys Trp Thr Pro Leu Ser Ala Lys
210 215 220
Tyr Val Glu Glu Trp Val Gly Pro Gly Ser Pro Met Asn Ser Pro Arg
225 230 235 240
Val Arg Asn Asn Pro Phe Phe Ser Leu Glu Ser Ile Pro Glu Thr Glu
245 250 255
Val Ser Thr Lys Glu Gln Lys Val Glu Asn Ser Gln Phe Ile Gly Leu
260 265 270
Glu Ser Ile Pro Glu Ser Glu Glu Ser Xaa Arg Glu Gln Lys Gly Glu
275 280 285
Ser Ile Ile Pro Glu Thr Lys Ala Ser Ile Val Glu Gln Arg Met Arg
290 295 300
Asn Leu Leu Arg Ser His Trp Arg Leu
305 310

(2) INFORMATION FOR SEQ ID NO:2736:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 285 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..285

(D) OTHER INFORMATION: / Ceres Seq. ID 1574046

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2736:

Met Arg Asp Ile Lys Val Lys Ser Asp Ser Lys Glu Phe Leu Thr Ser
1 5 10 15
Ser Asp Glu Glu Glu Glu Ser Val Ser Ile Arg Val Ser Ser Ser Ser
20 25 30
Ser Leu Ser Ser Val Lys Ser Thr Pro Glu Ile Glu Lys Lys Tyr Val
35 40 45
His Arg Val Tyr Asp Ala Ile Ala Pro His Phe Ser Ser Thr Arg Phe
50 55 60
Ala Lys Trp Pro Lys Val Ala Ala Phe Leu Glu Ser Leu Pro Ser Gly

65	70	75	80
Ser Val Ile Leu	Asp Ala Gly Cys	Gly Asn Gly Lys Tyr Leu	Gly Leu
	85	90	95
Asn Pro Ser Cys Phe Phe Ile Gly Cys Asp Ile Ser His Pro Leu Ile			
	100	105	110
Lys Ile Cys Ser Asp Lys Gly Gln Glu Val Leu Val Ala Asp Ala Val			
	115	120	125
Asn Xaa Xaa Tyr Arg Glu Glu Phe Gly Asp Ala Ala Ile Ser Ile Ala			
	130	135	140
Val Leu His His Leu Ser Thr Glu Asn Arg Arg Lys Lys Ala Ile Glu			
	145	150	155
Glu Leu Val Arg Val Val Lys Pro Gly Gly Phe Val Leu Ile Thr Val			
	165	170	175
Trp Ala Ala Glu Gln Glu Asp Thr Ser Leu Leu Thr Lys Trp Thr Pro			
	180	185	190
Leu Ser Ala Lys Tyr Val Glu Glu Trp Val Gly Pro Gly Ser Pro Met			
	195	200	205
Asn Ser Pro Arg Val Arg Asn Asn Pro Phe Phe Ser Leu Glu Ser Ile			
	210	215	220
Pro Glu Thr Glu Val Ser Thr Lys Glu Gln Lys Val Glu Asn Ser Gln			
	225	230	235
Phe Ile Gly Leu Glu Ser Ile Pro Glu Ser Glu Glu Ser Xaa Arg Glu			
	245	250	255
Gln Lys Gly Glu Ser Ile Ile Pro Glu Thr Lys Ala Ser Ile Val Glu			
	260	265	270
Gln Arg Met Arg Asn Leu Leu Arg Ser His Trp Arg Leu			
	275	280	285

(2) INFORMATION FOR SEQ ID NO:2737:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1342 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1342

(D) OTHER INFORMATION: / Ceres Seq. ID 1574047

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2737:

attgtgttgc	cttcttcttt	ctttctgact	caaaacctta	aatcaattct	cgcgattaag	60
caaaacctta	gattattct	actcttcgaa	gtcgatttca	atggaaaggt	ctcgtcagc	120
catcgogagg	aagacatggg	agctagagaa	caacattctc	ccagtggaac	caaccgattc	180
agcctccgac	agtatattcc	actacgacga	cgcttcacaa	gcocaaatcc	agcaggagaa	240
gccatggccc	tccgatccta	actacttcaa	gcgcgttcac	atctcagccc	ttgctctctt	300
caagatgggt	gttcacgctc	gctccgggtg	cacaatcgag	atcatgggtc	ttatgcaggg	360
taaaaccgag	gggtatacaa	tcactgttat	ggatgctttt	gctttgcgtg	ttgaagggtac	420
tgagactagg	gttaatgctc	agtctgatgc	ctatgagtat	atgggtgaat	acctctcagc	480
cagcaagctg	gctgggaggt	tgagagaacgt	tgttggatgg	tatcactctc	acctggggtta	540
tggatgttgg	ctctcgggta	ttgatgttct	gacacagatg	cttaaccaac	agtatcagga	600
gccattctta	gctgtttgtta	ttgatccaac	aaggactgtt	tcggctggta	aggttgagat	660
tgggggcattc	agaacatatc	cagagggaca	taagatctcg	gatgatcatg	tttctgagta	720
tcagactatc	ctctttaaca	agattgagga	ctttggtgta	cattgcaaac	agtaactactc	780
attggacatc	acttatttca	agtcattctc	cgatagtcac	cttctggatc	tCcttcggaa	840
caagtaactg	gtgaacatc	tttcttcttc	cccaactgtt	ggcaatggag	actatgtttg	900
cgggcacaata	ctgagacttg	ctgagaagct	cgagcaagcg	gagagtcacg	tcgctaactc	960
ccggtatgga	ggaattgcgc	cagccgggtca	ccaaaggagg	aaaggaggat	agcctcaact	1020
cgcgaagata	actcgggata	gtgcacaagt	aactgtcgag	caggtccatg	gactaatgtc	1080
acaggttatc	aaagacatct	tggtcaaatc	cgctcgtcag	tccaagaagt	ctgctgcagca	1140
ctcatcagat	ccagagccca	tgattacatc	gtgaagttgg	tctattcttt	tggtttttttg	1200
ctgcggaaat	tgcattatcg	tttgacccag	tttatgaggc	aatgcccatt	gttccctata	1260
tctctagtgt	agtatctgct	tcagacaaag	atctttgggt	tattaatga	cattaacata	1320

aatcgatcat tatgtttttg tg

(2) INFORMATION FOR SEQ ID NO:2738:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 357 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..357

(D) OTHER INFORMATION: / Ceres Seq. ID 1574048

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2738:

Met	Glu	Gly	Ser	Ser	Ser	Ala	Ile	Ala	Arg	Lys	Thr	Trp	Glu	Leu	Glu
1			5						10					15	
Asn	Asn	Ile	Leu	Pro	Val	Glu	Pro	Thr	Asp	Ser	Ala	Ser	Asp	Ser	Ile
			20					25					30		
Phe	His	Tyr	Asp	Asp	Ala	Ser	Gln	Ala	Lys	Ile	Gln	Gln	Glu	Lys	Pro
		35					40					45			
Trp	Ala	Ser	Asp	Pro	Asn	Tyr	Phe	Lys	Arg	Val	His	Ile	Ser	Ala	Leu
	50					55				60					
Ala	Leu	Leu	Lys	Met	Val	Val	His	Ala	Arg	Ser	Gly	Gly	Thr	Ile	Glu
65				70					75					80	
Ile	Met	Gly	Leu	Met	Gln	Gly	Lys	Thr	Glu	Gly	Asp	Thr	Ile	Ile	Val
			85						90					95	
Met	Asp	Ala	Phe	Ala	Leu	Pro	Val	Glu	Gly	Thr	Glu	Thr	Arg	Val	Asn
			100					105					110		
Ala	Gln	Ser	Asp	Ala	Tyr	Glu	Tyr	Met	Val	Glu	Tyr	Ser	Gln	Thr	Ser
		115					120					125			
Lys	Leu	Ala	Gly	Arg	Leu	Glu	Asn	Val	Val	Gly	Trp	Tyr	His	Ser	His
	130					135					140				
Pro	Gly	Tyr	Gly	Cys	Trp	Leu	Ser	Gly	Ile	Asp	Val	Ser	Thr	Gln	Met
145				150					155					160	
Leu	Asn	Gln	Gln	Tyr	Gln	Glu	Pro	Phe	Leu	Ala	Val	Val	Ile	Asp	Pro
		165						170						175	
Thr	Arg	Thr	Val	Ser	Ala	Gly	Lys	Val	Glu	Ile	Gly	Ala	Phe	Arg	Thr
		180					185						190		
Tyr	Pro	Glu	Gly	His	Lys	Ile	Ser	Asp	Asp	His	Val	Ser	Glu	Tyr	Gln
	195					200						205			
Thr	Ile	Pro	Leu	Asn	Lys	Ile	Glu	Asp	Phe	Gly	Val	His	Cys	Lys	Gln
	210					215					220				
Tyr	Tyr	Ser	Leu	Asp	Ile	Thr	Tyr	Phe	Lys	Ser	Ser	Leu	Asp	Ser	His
225			230						235					240	
Leu	Leu	Asp	Leu	Leu	Arg	Asn	Lys	Tyr	Trp	Val	Asn	Thr	Leu	Ser	Ser
		245							250					255	
Ser	Pro	Leu	Leu	Gly	Asn	Gly	Asp	Tyr	Val	Ala	Gly	Gln	Ile	Ser	Asp
		260						265					270		
Leu	Ala	Glu	Lys	Leu	Glu	Gln	Ala	Glu	Ser	Gln	Leu	Ala	Asn	Ser	Arg
		275					280					285			
Tyr	Gly	Gly	Ile	Ala	Pro	Ala	Gly	His	Gln	Arg	Arg	Lys	Glu	Asp	Glu
	290					295					300				
Pro	Gln	Leu	Ala	Lys	Ile	Thr	Arg	Asp	Ser	Ala	Lys	Ile	Thr	Val	Glu
305				310					315					320	
Gln	Val	His	Gly	Leu	Met	Ser	Gln	Val	Ile	Lys	Asp	Ile	Leu	Phe	Asn
		325						330						335	
Ser	Ala	Arg	Gln	Ser	Lys	Lys	Ser	Ala	Asp	Asp	Ser	Ser	Asp	Pro	Glu
		340					345						350		
Pro	Met	Ile	Thr	Ser											
		355													

(2) INFORMATION FOR SEQ ID NO:2739:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 289 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..289
(D) OTHER INFORMATION: / Ceres Seq. ID 1574049
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2739:

Met Val Val His Ala Arg Ser Gly Gly Thr Ile Glu Ile Met Gly Leu
1 5 10 15
Met Gln Gly Lys Thr Glu Gly Asp Thr Ile Ile Val Met Asp Ala Phe
20 25 30
Ala Leu Pro Val Glu Gly Thr Glu Thr Arg Val Asn Ala Gln Ser Asp
35 40 45
Ala Tyr Glu Tyr Met Val Glu Tyr Ser Gln Thr Ser Lys Leu Ala Gly
50 55 60
Arg Leu Glu Asn Val Val Gly Trp Tyr His Ser His Pro Gly Tyr Gly
65 70 75 80
Cys Trp Leu Ser Gly Ile Asp Val Ser Thr Gln Met Leu Asn Gln Gln
85 90 95
Tyr Gln Glu Pro Phe Leu Ala Val Val Ile Asp Pro Thr Arg Thr Val
100 105 110
Ser Ala Gly Lys Val Glu Ile Gly Ala Phe Arg Thr Tyr Pro Glu Gly
115 120 125
His Lys Ile Ser Asp Asp His Val Ser Glu Tyr Gln Thr Ile Pro Leu
130 135 140
Asn Lys Ile Glu Asp Phe Gly Val His Cys Lys Gln Tyr Tyr Ser Leu
145 150 155 160
Asp Ile Thr Tyr Phe Lys Ser Ser Leu Asp Ser His Leu Leu Asp Leu
165 170 175
Leu Arg Asn Lys Tyr Trp Val Asn Thr Leu Ser Ser Ser Pro Leu Leu
180 185 190
Gly Asn Gly Asp Tyr Val Ala Gly Gln Ile Ser Asp Leu Ala Glu Lys
195 200 205
Leu Glu Gln Ala Glu Ser Gln Leu Ala Asn Ser Arg Tyr Gly Gly Ile
210 215 220
Ala Pro Ala Gly His Gln Arg Arg Lys Glu Asp Glu Pro Gln Leu Ala
225 230 235 240
Lys Ile Thr Arg Asp Ser Ala Lys Ile Thr Val Glu Gln Val His Gly
245 250 255
Leu Met Ser Gln Val Ile Lys Asp Ile Leu Phe Asn Ser Ala Arg Gln
260 265 270
Ser Lys Lys Ser Ala Asp Asp Ser Ser Asp Pro Glu Pro Met Ile Thr
275 280 285
Ser

(2) INFORMATION FOR SEQ ID NO:2740:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 276 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..276
(D) OTHER INFORMATION: / Ceres Seq. ID 1574050

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2740:

Met Gly Leu Met Gln Gly Lys Thr Glu Gly Asp Thr Ile Ile Val Met

1	5	10	15
Asp Ala Phe Ala Leu Pro Val Glu Gly Thr Glu Thr Arg Val Asn Ala			
20	25	30	
Gln Ser Asp Ala Tyr Glu Tyr Met Val Glu Tyr Ser Gln Thr Ser Lys			
35	40	45	
Leu Ala Gly Arg Leu Glu Asn Val Val Gly Trp Tyr His Ser His Pro			
50	55	60	
Gly Tyr Gly Cys Trp Leu Ser Gly Ile Asp Val Ser Thr Gln Met Leu			
65	70	75	80
Asn Gln Gln Tyr Gln Glu Pro Phe Leu Ala Val Ile Asp Pro Thr			
85	90	95	
Arg Thr Val Ser Ala Gly Lys Val Glu Ile Gly Ala Phe Arg Thr Tyr			
100	105	110	
Pro Glu Gly His Lys Ile Ser Asp Asp His Val Ser Glu Tyr Gln Thr			
115	120	125	
Ile Pro Leu Asn Lys Ile Glu Asp Phe Gly Val His Cys Lys Gln Tyr			
130	135	140	
Tyr Ser Leu Asp Ile Thr Tyr Phe Lys Ser Ser Leu Asp Ser His Leu			
145	150	155	160
Leu Asp Leu Leu Arg Asn Lys Tyr Trp Val Asn Thr Leu Ser Ser Ser			
165	170	175	
Pro Leu Leu Gly Asn Gly Asp Tyr Val Ala Gly Gln Ile Ser Asp Leu			
180	185	190	
Ala Glu Lys Leu Glu Gln Ala Glu Ser Gln Leu Ala Asn Ser Arg Tyr			
195	200	205	
Gly Gly Ile Ala Pro Ala Gly His Gln Arg Arg Lys Glu Asp Glu Pro			
210	215	220	
Gln Leu Ala Lys Ile Thr Arg Asp Ser Ala Lys Ile Thr Val Glu Gln			
225	230	235	240
Val His Gly Leu Met Ser Gln Val Ile Lys Asp Ile Leu Phe Asn Ser			
245	250	255	
Ala Arg Gln Ser Lys Lys Ser Ala Asp Asp Ser Ser Pro Glu Pro			
260	265	270	
Met Ile Thr Ser			
275			

(2) INFORMATION FOR SEQ ID NO:2741:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1950 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1950

(D) OTHER INFORMATION: / Ceres Seq. ID 1574059

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2741:

aacagagtcg	cacacactaa	aatggcggttc	cgcgtttttgc	tctcttcttc	actcaccgca	60
ctctctcatct	tctccgcgct	tctctcttct	ttcgccgctt	cttctctccga	cgacgttgac	120
gagagagatc	tcagcttctc	cgaagatctc	aaagaagacg	acgttcccg	cgctgactca	180
ctctcttctc	caactggtat	tgacgaattc	gaaggaggag	aagaagaaga	tcccgatatg	240
tacaacgacg	atgacgatga	agaagagagat	ttttccgac	taggtaatcc	ggattccgat	300
cogttaccga	cgccggagat	tgatgagaaa	gacgttggtg	ttatcaagga	cggtaaactc	360
actgatgtga	ttgagaataa	tcaatacgtt	ttggttgagt	tttatgtccc	gtggtgtggt	420
cattgtcagt	ctcttgcctc	tgagtatgct	gcgtctgcc	cgagcttaa	ggaagatggt	480
gtgtgttttg	ctaagattga	tgccgaggag	gagaatgagt	tagctcaagg	gtatcgttgt	540
cagggtcttc	cgacgcttct	ttttctcggt	gatgtgtgac	acaagcctta	cactggagga	600
aggactaaa	aaacaattgt	gacatgggtg	aagaagaaga	ttggtcctgg	tgtgtataat	660
ctaactacat	tagatgatgc	tgagaaaagt	ttgacttctg	ggaacaaaat	tgtttttgga	720
tacttgaact	ccttggtggg	tggtgagcac	gatcagctta	atgctgtctc	caaagctgaa	780
gacgatgtga	acttttatca	aacagtgaat	cctgatgttg	caaagatggt	tcaccttgat	840

ccggagtgcta	aaaggcctgc	tcttgctcta	gttaagaagg	aagaggagaa	aattagccat	900
tttgatggag	aatttggttaa	gtctgtctcta	gttagttttg	tgctctgccaa	caagcttgtct	960
ttggctctctg	ttttccacag	agagactgct	ccggaatttt	ttgagagtgt	taatcaagaaa	1020
cagtttgtgt	tggtttgaac	caaaaatgaa	tctgaaaagg	ttcttacgga	atttcaagaa	1080
gcagcgaaat	cattcaaaag	aaagctcatc	ttgtatctg	tggtatctgga	taatgaggat	1140
taagggaagc	cagtcgctga	atactttggt	gtgtctggaa	atggctccaa	acttattggc	1200
tacacaggga	atgaagacca	taaaaaatat	tttttcgatg	gcgagatcca	gtcagataaa	1260
attaagatat	ttgggggagc	tttctggaac	gacaagttaa	agccttttca	taagtacagc	1320
ccattctctg	aaaagaacga	tgaagatgtg	aaaatagtgg	ttggagataa	ctttgatgaa	1380
attgtctctg	acgatttcaa	agatgtgctt	ctcgaggtct	acgcaccatg	gtgtggccat	1440
tgccaagccc	ttgagccaat	gtataacaaa	cttgccaagc	atttacgaag	tattgattct	1500
ctcgctcata	ccaagatgga	tggacaaccc	aatgaacatc	ccaaggcmaa	ggctgagggg	1560
ttccctacca	ttctctctct	ccCtgcgggc	aaacagactt	cagagccgat	tactgtagat	1620
acagaccgca	ctgTggttgc	attttacaag	ttcttaagga	aaacgcgaac	gatccatttc	1680
aaactggaga	aaactgcctc	aaccgaatca	cctaaaactg	cagagtccac	accaaaaagta	1740
gaaactacgc	agaccaaaga	atcacccgat	agcacgacaa	agagtacgca	aagtgactcg	1800
aaggacgaat	tggtatcaga	aaagggatata	atatatatta	catgtctcct	taagtgtgta	1860
tatgtatgat	cagaattgtc	acatcatgag	tttgacttag	ataaagatgg	gaattaaagt	1920
aattttagtt	ttgagaaga	caatttcttc				

(2) INFORMATION FOR SEQ ID NO:2742:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 604 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..604
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574060

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2742:

Asn	Arg	Val	Ala	His	Thr	Lys	Met	Ala	Phe	Arg	Val	Leu	Leu	Leu	Phe
1				5					10					15	
Ser	Leu	Thr	Ala	Leu	Leu	Ile	Phe	Ser	Ala	Val	Ser	Pro	Ser	Phe	Ala
				20				25				30			
Ala	Ser	Ser	Ser	Asp	Asp	Val	Asp	Glu	Asp	Leu	Ser	Phe	Leu	Glu	
				35			40			45					
Asp	Leu	Lys	Glu	Asp	Asp	Val	Pro	Gly	Ala	Asp	Ser	Leu	Ser	Ser	Ser
				50			55			60					
Thr	Gly	Phe	Asp	Glu	Phe	Glu	Gly	Gly	Glu	Glu	Asp	Pro	Asp	Met	
65				70				75							
Tyr	Asn	Asp	Asp	Asp	Asp	Glu	Glu	Gly	Asp	Phe	Ser	Asp	Leu	Gly	Asn
				85				90					95		
Pro	Asp	Ser	Asp	Pro	Leu	Pro	Thr	Pro	Glu	Ile	Asp	Glu	Lys	Asp	Val
				100				105				110			
Val	Val	Ile	Lys	Glu	Arg	Asn	Phe	Thr	Asp	Val	Ile	Glu	Asn	Asn	Gln
				115			120				125				
Tyr	Val	Leu	Val	Glu	Phe	Tyr	Ala	Pro	Trp	Cys	Gly	His	Cys	Gln	Ser
				130			135			140					
Leu	Ala	Pro	Glu	Tyr	Ala	Ala	Ala	Ala	Thr	Glu	Leu	Lys	Glu	Asp	Gly
145				150				155					160		
Val	Val	Leu	Ala	Lys	Ile	Asp	Ala	Thr	Glu	Glu	Asn	Glu	Leu	Ala	Gln
				165				170					175		
Glu	Tyr	Arg	Val	Gln	Gly	Phe	Pro	Thr	Leu	Leu	Phe	Phe	Val	Asp	Gly
				180				185				190			
Glu	His	Lys	Pro	Tyr	Thr	Gly	Gly	Arg	Thr	Lys	Glu	Thr	Ile	Val	Thr
				195			200				205				
Trp	Val	Lys	Lys	Lys	Ile	Gly	Pro	Gly	Val	Tyr	Asn	Leu	Thr	Thr	Leu
				210			215			220					
Asp	Asp	Ala	Glu	Lys	Val	Leu	Thr	Ser	Gly	Asn	Lys	Val	Val	Leu	Gly
225				230				235							

Tyr Leu Asn Ser Leu Val Gly Val Glu His Asp Gln Leu Asn Ala Ala
245 250 255
Ser Lys Ala Glu Asp Asp Val Asn Phe Tyr Gln Thr Val Asn Pro Asp
260 265 270
Val Ala Lys Met Phe His Leu Asp Pro Glu Ser Lys Arg Pro Ala Leu
275 280 285
Val Leu Val Lys Lys Glu Glu Glu Lys Ile Ser His Phe Asp Gly Glu
290 295 300
Phe Val Lys Ser Ala Leu Val Ser Phe Val Ser Ala Asn Lys Leu Ala
305 310 315
Leu Val Ser Val Phe Thr Arg Glu Thr Ala Pro Glu Ile Phe Glu Ser
325 330 335
Ala Ile Lys Lys Gln Leu Leu Leu Phe Val Thr Lys Asn Glu Ser Glu
340 345 350
Lys Val Leu Thr Glu Phe Gln Glu Ala Ala Lys Ser Phe Lys Gly Lys
355 360 365
Leu Ile Phe Val Ser Val Asp Leu Asp Asn Glu Asp Tyr Gly Lys Pro
370 375 380
Val Ala Glu Tyr Phe Gly Val Ser Gly Asn Gly Pro Lys Leu Ile Gly
385 390 395
Tyr Thr Gly Asn Glu Asp His Lys Lys Tyr Phe Phe Asp Gly Glu Ile
405 410 415
Gln Ser Asp Lys Ile Lys Ile Phe Gly Glu Asp Phe Leu Asn Asp Lys
420 425 430
Leu Lys Pro Phe Tyr Lys Ser Asp Pro Ile Pro Glu Lys Asn Asp Glu
435 440 445
Asp Val Lys Ile Val Val Gly Asp Asn Phe Asp Glu Ile Val Leu Asp
450 455 460
Asp Ser Lys Asp Val Leu Leu Glu Val Tyr Ala Pro Trp Cys Gly His
465 470 475
Cys Gln Ala Leu Glu Pro Met Tyr Asn Lys Leu Ala Lys His Leu Arg
485 490 495
Ser Ile Asp Ser Leu Val Ile Thr Lys Met Asp Gly Thr Thr Asn Glu
500 505 510
His Pro Lys Ala Lys Ala Glu Gly Phe Pro Thr Ile Leu Phe Phe Pro
515 520 525
Ala Gly Asn Lys Thr Ser Glu Pro Ile Thr Val Asp Thr Asp Arg Thr
530 535 540
Val Val Ala Phe Tyr Lys Phe Leu Arg Lys His Ala Thr Ile Pro Phe
545 550 555
Lys Leu Glu Lys Pro Ala Ser Thr Glu Ser Pro Lys Thr Ala Glu Ser
565 570 575
Thr Pro Lys Val Glu Thr Thr Glu Thr Lys Glu Ser Pro Asp Ser Thr
580 585 590
Thr Lys Ser Ser Gln Ser Asp Ser Lys Asp Glu Leu
595 600

(2) INFORMATION FOR SEQ ID NO:2743:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 597 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..597
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574061

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2743:

Met Ala Phe Arg Val Leu Leu Leu Phe Ser Leu Thr Ala Leu Leu Ile
1 5 10 15
Phe Ser Ala Val Ser Pro Ser Phe Ala Ala Ser Ser Ser Asp Asp Val

20					25					30						
Asp	Asp	Glu	Glu	Asp	Leu	Ser	Phe	Leu	Glu	Asp	Leu	Lys	Glu	Asp	Asp	Val
Pro	Gly	Ala	Asp	Ser	Leu	Ser	Ser	Ser	Thr	Gly	Phe	Asp	Glu	Phe	Glu	
Gly	Gly	Glu	Glu	Glu	Asp	Pro	Asp	Met	Tyr	Asn	Asp	Asp	Asp	Asp	Asp	Glu
65					70					75						80
Glu	Gly	Asp	Phe	Ser	Asp	Leu	Gly	Asn	Pro	Asp	Ser	Asp	Pro	Leu	Pro	
Thr	Pro	Glu	Ile	Asp	Glu	Lys	Asp	Val	Val	Val	Ile	Lys	Glu	Arg	Asn	
Phe	Thr	Asp	Val	Ile	Glu	Asn	Asn	Gln	Tyr	Val	Leu	Val	Glu	Phe	Tyr	
Ala	Pro	Trp	Cys	Gly	His	Cys	Gln	Ser	Leu	Ala	Pro	Glu	Tyr	Ala	Ala	
Ala	Ala	Thr	Glu	Leu	Lys	Glu	Asp	Gly	Val	Val	Leu	Ala	Lys	Ile	Asp	
145					150					155					160	
Ala	Thr	Glu	Glu	Asn	Glu	Leu	Ala	Gln	Glu	Tyr	Arg	Val	Gln	Gly	Phe	
					165					170					175	
Pro	Thr	Leu	Leu	Phe	Phe	Val	Asp	Gly	Glu	His	Lys	Pro	Tyr	Thr	Gly	
Gly	Arg	Thr	Lys	Glu	Thr	Ile	Val	Thr	Trp	Val	Lys	Lys	Lys	Ile	Gly	
Pro	Gly	Val	Tyr	Asn	Leu	Thr	Thr	Leu	Asp	Asp	Ala	Glu	Lys	Val	Leu	
Thr	Ser	Gly	Asn	Lys	Val	Val	Leu	Gly	Tyr	Leu	Asn	Ser	Leu	Val	Gly	
225					230					235					240	
Val	Glu	His	Asp	Gln	Leu	Asn	Ala	Ala	Ser	Lys	Ala	Glu	Asp	Asp	Val	
					245					250					255	
Asn	Phe	Tyr	Gln	Thr	Val	Asn	Pro	Asp	Val	Ala	Lys	Met	Phe	His	Leu	
Asp	Pro	Glu	Ser	Lys	Arg	Pro	Ala	Leu	Val	Leu	Val	Lys	Lys	Glu	Glu	
Glu	Lys	Ile	Ser	His	Phe	Asp	Gly	Glu	Phe	Val	Lys	Ser	Ala	Leu	Val	
Ser	Phe	Val	Ser	Ala	Asn	Lys	Leu	Ala	Leu	Val	Ser	Val	Phe	Thr	Arg	
305					310					315					320	
Glu	Thr	Ala	Pro	Glu	Ile	Phe	Glu	Ser	Ala	Ile	Lys	Lys	Gln	Leu	Leu	
					325					330					335	
Leu	Phe	Val	Thr	Lys	Asn	Glu	Ser	Glu	Lys	Val	Leu	Thr	Glu	Phe	Gln	
Glu	Ala	Ala	Lys	Ser	Phe	Lys	Gly	Lys	Leu	Ile	Phe	Val	Ser	Val	Asp	
Leu	Asp	Asn	Glu	Asp	Tyr	Gly	Lys	Pro	Val	Ala	Glu	Tyr	Phe	Gly	Val	
Ser	Gly	Asn	Gly	Pro	Lys	Leu	Ile	Gly	Tyr	Thr	Gly	Asn	Glu	Asp	His	
385					390					395					400	

Gly Phe Pro Thr Ile Leu Phe Phe Pro Ala Gly Asn Lys Thr Ser Glu
515 520 525
Pro Ile Thr Val Asp Thr Asp Arg Thr Val Val Ala Phe Tyr Lys Phe
530 535 540
Leu Arg Lys His Ala Thr Ile Pro Phe Lys Leu Glu Lys Pro Ala Ser
545 550 555 560
Thr Glu Ser Pro Lys Thr Ala Glu Ser Thr Pro Lys Val Glu Thr Thr
565 570 575
Glu Thr Lys Glu Ser Pro Asp Ser Thr Thr Lys Ser Ser Gln Ser Asp
580 585 590
Ser Lys Asp Glu Leu
595

(2) INFORMATION FOR SEQ ID NO:2744:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 525 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..525

(D) OTHER INFORMATION: / Ceres Seq. ID 1574062

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2744:

Met Tyr Asn Asp Asp Asp Asp Glu Glu Gly Asp Phe Ser Asp Leu Gly
1 5 10 15
Asn Pro Asp Ser Asp Pro Leu Pro Thr Pro Glu Ile Asp Glu Lys Asp
20 25 30
Val Val Val Ile Lys Glu Arg Asn Phe Thr Asp Val Ile Glu Asn Asn
35 40 45
Gln Tyr Val Leu Val Glu Phe Tyr Ala Pro Trp Cys Gly His Cys Gln
50 55 60
Ser Leu Ala Pro Glu Tyr Ala Ala Ala Ala Thr Glu Leu Lys Glu Asp
65 70 75 80
Gly Val Val Leu Ala Lys Ile Asp Ala Thr Glu Glu Asn Glu Leu Ala
85 90 95
Gln Glu Tyr Arg Val Gln Gly Phe Pro Thr Leu Leu Phe Phe Val Asp
100 105 110
Gly Glu His Lys Pro Tyr Thr Gly Gly Arg Thr Lys Glu Thr Ile Val
115 120 125
Thr Trp Val Lys Lys Lys Ile Gly Pro Gly Val Tyr Asn Leu Thr Thr
130 135 140
Leu Asp Asp Ala Glu Lys Val Leu Thr Ser Gly Asn Lys Val Val Leu
145 150 155 160
Gly Tyr Leu Asn Ser Leu Val Gly Val Glu His Asp Gln Leu Asn Ala
165 170 175
Ala Ser Lys Ala Glu Asp Asp Val Asn Phe Tyr Gln Thr Val Asn Pro
180 185 190
Asp Val Ala Lys Met Phe His Leu Asp Pro Glu Ser Lys Arg Pro Ala
195 200 205
Leu Val Leu Val Lys Lys Glu Glu Lys Ile Ser His Phe Asp Gly
210 215 220
Glu Phe Val Lys Ser Ala Leu Val Ser Phe Val Ser Ala Asn Lys Leu
225 230 235 240
Ala Leu Val Ser Val Phe Thr Arg Glu Thr Ala Pro Glu Ile Phe Glu
245 250 255
Ser Ala Ile Lys Lys Gln Leu Leu Leu Phe Val Thr Lys Asn Glu Ser
260 265 270
Glu Lys Val Leu Thr Glu Phe Gln Glu Ala Ala Lys Ser Phe Lys Gly
275 280 285
Lys Leu Ile Phe Val Ser Val Asp Leu Asp Asn Glu Asp Tyr Gly Lys

290	295	300
Pro Val Ala Glu Tyr Phe Gly Val Ser Gly Asn Gly Pro Lys Leu Ile		
305	310	315
Gly Tyr Thr Gly Asn Glu Asp His Lys Lys Tyr Phe Phe Asp Gly Glu		
	325	330
Ile Gln Ser Asp Lys Ile Lys Ile Phe Gly Glu Asp Phe Leu Asn Asp		
	340	345
Lys Leu Lys Pro Phe Tyr Lys Ser Asp Pro Ile Pro Glu Lys Asn Asp		
	355	360
Glu Asp Val Lys Ile Val Val Gly Asp Asn Phe Asp Glu Ile Val Leu		
	370	375
Asp Asp Ser Lys Asp Val Leu Leu Glu Val Tyr Ala Pro Trp Cys Gly		
385	390	395
His Cys Gln Ala Leu Glu Pro Met Tyr Asn Lys Leu Ala Lys His Leu		
	405	410
Arg Ser Ile Asp Ser Leu Val Ile Thr Lys Met Asp Gly Thr Thr Asn		
	420	425
Glu His Pro Lys Ala Lys Ala Glu Gly Phe Pro Thr Ile Leu Phe Phe		
	435	440
Pro Ala Gly Asn Lys Thr Ser Glu Pro Ile Thr Val Asp Thr Asp Arg		
	450	455
Thr Val Val Ala Phe Tyr Lys Phe Leu Arg Lys His Ala Thr Ile Pro		
465	470	475
Phe Lys Leu Glu Lys Pro Ala Ser Thr Glu Ser Pro Lys Thr Ala Glu		
	485	490
Ser Thr Pro Lys Val Glu Thr Thr Glu Thr Lys Glu Ser Pro Asp Ser		
	500	505
Thr Thr Lys Ser Ser Gln Ser Asp Ser Lys Asp Glu Leu		
	515	520
		525

(2) INFORMATION FOR SEQ ID NO:2745:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 978 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..978
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574066

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2745:

atcagtcact	tattcagact	gttggaaatta	caaagatggg	tgtgtatggt	gaagccagta	60
ctggctttgg	gcaatctcct	gagagtattc	atactcacta	tgggattatg	tcgaacaaga	120
atgaattgtt	ttccaccatt	ctgcacaaag	agagaagacc	agaagcaacg	caagcttaca	180
tcacaagaaa	caaataccac	cttcacgaag	cattcaatgt	aagtttcac	ttggagaaac	240
ttgcttacc	gatctctaga	gggcatttga	gcttggtaaa	cacaaatggt	gatgacaacc	300
cttcagtcac	cttcaattac	tttaaacacc	cggtggatct	ccaacgctgt	gttggaagcca	360
ttcgctctgt	ttccaaagtg	gtgacgtcta	agcggttctt	aaactacacg	cagKtgGaca	420
agcaaaacgt	acacaagatg	cttagcttaa	gcgtcaagcg	aaacatcaat	ctaaagggcaa	480
agcaactgaa	cgataccaaa	tcaatggctc	agttctgcaa	agacactgtt	gtcaaatctt	540
ggcactacac	tgtgtgagtg	cttgtgggta	aagtgtgtgag	ccctaaccgc	aaagtctctg	600
gtgtcgacag	gcttagagtg	attgatggtt	caacgcttga	cgagctccca	ggaaccaaac	660
cgcaagctac	tatgatgatg	atgggaagat	acatggggag	caagattctt	cgggagagac	720
ttggaataac	agctggtgtt	tagtttgcag	attgagcttt	tatggtagac	aaattcgtag	780
cagataattc	tgatgtggaa	ttgtgttgga	gaatatctct	ctctgtctcc	ttctctgtta	840
tttgatattc	gattcattga	agtataggat	catattgtct	aatgaactgt	gttaacctct	900
attgggcaat	cggtctgtgt	gcttattagc	ttgtgtgaaa	agttaatcac	gttttctgtt	960
tcaatactct	tacaatcg					

(2) INFORMATION FOR SEQ ID NO:2746:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 246 amino acids

(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..246
 (D) OTHER INFORMATION: / Ceres Seq. ID 1574067
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2746:
Gln Ser Leu Ile Gln Thr Val Gly Ile Thr Lys Met Gly Val Tyr Val
1 5 10 15
Glu Ala Ser Thr Gly Phe Gly Gln Ser Pro Glu Ser Ile His Thr His
 20 25 30
Tyr Gly Ile Met Ser Asn Lys Asn Glu Leu Phe Ser Thr Ile Pro Ala
 35 40 45
Lys Gln Arg Arg Pro Glu Ala Thr Gln Ala Tyr Ile Thr Arg Asn Lys
 50 55 60
Tyr Gln Leu His Glu Ala Phe Asn Gly Ser Phe Ile Leu Glu Lys Leu
65 70 75 80
Ala Tyr Pro Ile Ser Arg Gly His Leu Ser Leu Val Asn Thr Asn Val
 85 90 95
Asp Asp Asn Pro Ser Val Thr Phe Asn Tyr Phe Lys His Pro Val Asp
 100 105 110
Leu Gln Arg Cys Val Glu Ala Ile Arg Leu Val Ser Lys Val Val Thr
 115 120 125
Ser Lys Arg Phe Leu Asn Tyr Thr Gln Xaa Asp Lys Gln Asn Val His
 130 135 140
Lys Met Leu Ser Leu Ser Val Lys Ala Asn Ile Asn Leu Arg Pro Lys
145 150 155 160
Gln Leu Asn Asp Thr Lys Ser Met Ala Gln Phe Cys Lys Asp Thr Val
 165 170 175
Val Thr Ile Trp His Tyr His Gly Gly Cys Leu Val Gly Lys Val Val
 180 185 190
Ser Pro Asn Arg Lys Val Leu Gly Val Asp Arg Leu Arg Val Ile Asp
 195 200 205
Gly Ser Thr Phe Asp Glu Ser Pro Gly Thr Asn Pro Gln Ala Thr Met
210 215 220
Met Met Met Gly Arg Tyr Met Gly Val Lys Ile Leu Arg Glu Arg Leu
225 230 235 240
Gly Asn Lys Ala Gly Val
 245
(2) INFORMATION FOR SEQ ID NO:2747:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 235 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..235
 (D) OTHER INFORMATION: / Ceres Seq. ID 1574068
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2747:
Met Gly Val Tyr Val Glu Ala Ser Thr Gly Phe Gly Gln Ser Pro Glu
1 5 10 15
Ser Ile His Thr His Tyr Gly Ile Met Ser Asn Lys Asn Glu Leu Phe
 20 25 30
Ser Thr Ile Pro Ala Lys Gln Arg Arg Pro Glu Ala Thr Gln Ala Tyr
 35 40 45
Ile Thr Arg Asn Lys Tyr Gln Leu His Glu Ala Phe Asn Gly Ser Phe
50 55 60

[illegible]

210

(2) INFORMATION FOR SEQ ID NO:2749:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 827 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..827
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574074

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2749:

tgattccgaa	ttgtttgttt	cgtgttggtg	gttcgcgat	ttgtgtgtcg	aacaagggga	60
aagatcgtag	acgggtctaag	tataagcttg	ttcataccgt	taggactcat	aaaggagctt	120
ttgagaagcg	tttcaactgt	gtttaccaag	agcaagatga	taatgggaag	accgggggtt	180
cgtgtgtcgaa	agatcttatg	gctatagctg	gtgaagctct	taaggcgaat	atcactactt	240
taggtctctt	ggttcttctt	ataagtgcgc	agattctgtt	tttcatgact	ttggttacga	300
agaaactgtt	taactcgaa	ctgaagccgt	atattccgga	tttcaagctt	gcgtttgac	360
attctctgat	ccatgctggt	ggtagagctg	tgattgatga	gottgagaag	aatctgcagc	420
tttcgcagac	ctatgtcgag	gcatcgagaa	tgacactgca	tagatttggg	aacacttctt	480
cgagctcgat	ttggtatgaa	ctggcttaca	tagaggctaa	aggtaggatg	aagaaaggaa	540
accgggtttg	cgagattgct	tttggaaagt	ggtttaagt	taacagtgc	gtttggatgg	600
ctctaaacaa	tgtaaacgct	tcggttagta	gtccgtggga	acactgcac	gaccgatatc	660
cgtgttaagt	cgactcttga	tttaatgaaa	aaccttgg	ttggttagtc	ctagtcttac	720
tagactctgc	ctgttttatt	tttcttctt	tctgtttaag	ctctgtgact	cttaagtgtg	780
cgcttcttga	ttattactct	cggttttat	gctatggcat	ctttatc		

(2) INFORMATION FOR SEQ ID NO:2750:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 225 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..225
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574075

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2750:

Ile	Pro	Asn	Cys	Leu	Phe	Arg	Val	Gly	Gly	Ser	Ala	Ile	Leu	Leu	Ser	
1			5						10					15		
Asn	Lys	Gly	Lys	Asp	Arg	Arg	Arg	Ser	Lys	Tyr	Lys	Leu	Val	His	Thr	
			20					25					30			
Val	Arg	Thr	His	Lys	Gly	Ala	Val	Glu	Lys	Ala	Phe	Asn	Cys	Val	Tyr	
			35				40					45				
Gln	Glu	Gln	Asp	Asp	Asn	Gly	Lys	Thr	Gly	Val	Ser	Leu	Ser	Lys	Asp	
			50				55				60					
Leu	Met	Ala	Ile	Ala	Gly	Glu	Ala	Leu	Lys	Ala	Asn	Ile	Thr	Thr	Leu	
			65			70				75			80			
Gly	Pro	Leu	Val	Leu	Pro	Ile	Ser	Glu	Gln	Ile	Leu	Phe	Phe	Met	Thr	
			85				90					95				
Leu	Val	Thr	Lys	Lys	Leu	Phe	Asn	Ser	Lys	Leu	Lys	Pro	Tyr	Ile	Pro	
			100				105					110				
Asp	Phe	Lys	Leu	Ala	Phe	Asp	His	Phe	Cys	Ile	His	Ala	Gly	Gly	Arg	
			115				120					125				
Ala	Val	Ile	Asp	Glu	Leu	Glu	Lys	Asn	Leu	Gln	Leu	Ser	Gln	Thr	His	
			130			135					140					
Val	Glu	Ala	Ser	Arg	Met	Thr	Leu	His	Arg	Phe	Gly	Asn	Thr	Ser	Ser	
			145			150				155						
Ser	Ser	Ile	Trp	Tyr	Glu	Leu	Ala	Tyr	Ile	Glu	Ala	Lys	Gly	Arg	Met	
			165				170						175			

Lys Lys Gly Asn Arg Val Trp Gln Ile Ala Phe Gly Ser Gly Phe Lys
180 185 190
Cys Asn Ser Ala Val Trp Met Ala Leu Asn Asn Val Lys Pro Ser Val
195 200 205
Ser Ser Pro Trp Glu His Cys Ile Asp Arg Tyr Pro Val Lys Leu Asp
210 215 220

Phe
225

(2) INFORMATION FOR SEQ ID NO:2751:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 160 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
 - (B) LOCATION: 1..160
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1574076
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2751:

Met	Ala	Ile	Ala	Gly	Glu	Ala	Leu	Lys	Ala	Asn	Ile	Thr	Thr	Leu	Gly
1				5				10						15	
Pro	Leu	Val	Leu	Pro	Ile	Ser	Glu	Gln	Ile	Leu	Phe	Phe	Met	Thr	Leu
			20				25						30		
Val	Thr	Lys	Lys	Leu	Phe	Asn	Ser	Lys	Leu	Lys	Pro	Tyr	Ile	Pro	Asp
			35				40						45		
Phe	Lys	Leu	Ala	Phe	Asp	His	Phe	Cys	Ile	His	Ala	Gly	Gly	Arg	Ala
			50				55					60			
Val	Ile	Asp	Glu	Leu	Glu	Lys	Asn	Leu	Gln	Leu	Ser	Gln	Thr	His	Val
			65				70				75			80	
Glu	Ala	Ser	Arg	Met	Thr	Leu	His	Arg	Phe	Gly	Asn	Thr	Ser	Ser	Ser
				85					90					95	
Ser	Ile	Trp	Tyr	Glu	Leu	Ala	Tyr	Ile	Glu	Ala	Lys	Gly	Arg	Met	Lys
			100					105					110		
Lys	Gly	Asn	Arg	Val	Trp	Gln	Ile	Ala	Phe	Gly	Ser	Gly	Phe	Lys	Cys
			115				120						125		
Asn	Ser	Ala	Val	Trp	Met	Ala	Leu	Asn	Asn	Val	Lys	Pro	Ser	Val	Ser
			130				135					140			
Ser	Pro	Trp	Glu	His	Cys	Ile	Asp	Arg	Tyr	Pro	Val	Lys	Leu	Asp	Phe
			145			150				155				160	

(2) INFORMATION FOR SEQ ID NO:2752:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 131 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..131
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574077

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2752:

Met	Thr	Leu	Val	Thr	Lys	Lys	Leu	Phe	Asn	Ser	Lys	Leu	Lys	Pro	Tyr
1				5				10					15		
Ile	Pro	Asp	Phe	Lys	Leu	Ala	Phe	Asp	His	Phe	Cys	Ile	His	Ala	Gly
			20					25					30		
Gly	Arg	Ala	Val	Ile	Asp	Glu	Leu	Glu	Lys	Asn	Leu	Gln	Leu	Ser	Gln
			35				40					45			
Thr	His	Val	Glu	Ala	Ser	Arg	Met	Thr	Leu	His	Arg	Phe	Gly	Asn	Thr

(2) INFORMATION FOR SEO ID NO:2753:

(A) LENGTH: 1167 base pairs

- (B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(A) NAME/KEY: -

- (D) OTHER INFORMATION: / Ceres Seq. ID 1574086

```
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2753:
```

aaatccttat	gtcaggagat	ccattctctct	agtgaattgc	cctttctact	tcaagattgg	60
acctctgcgt	catgggtgac	gggtcgtctgt	tcttcacatc	ctgtctacac	ttctcccaac	120
agctctctct	tcaaacatgt	accaaaggcc	tgacatgatt	accocctggg	ttgacgctca	180
gggccacaacca	ctcgaccocg	gtgaagtatta	ggagacacct	gagattttct	ttgaggtatt	240
tttttagagtg	cttggaagat	gtgtgcagat	ggagagcctc	acaatttggc	acaaccctgc	300
tgacacacatg	attggcaacg	tatatgttca	gtttaaaggaa	gagatgcagc	ctcgacgtgc	360
tttgcgaagct	ctgcaagagta	gtgtctcatc	aggacgtccc	ataattgtcg	attctctctc	420
tgtagcgagat	ttccgcgaag	ccacgctgtg	cgagtatgaa	gaaaaacaac	gcaaccgtgc	480
tggtgattct	ataattctatc	atgtgaagct	gtgtctcagg	gaactaagtc	gaaaattcgc	540
tcggagatat	cgcgcatcat	accgcagagc	aagtagaagc	aggagcagaa	caggagtgat	600
tagcccgatg	aacaagagag	ataatgaccg	acgtgatctc	tctcacagag	aattcagcta	660
tcgggacagca	gatcgcgagt	tttaccgtta	tggaaagtga	aaaagagaca	gtgagaggct	720
ggagagggcaa	gagggggagc	gattacaagg	tagagagaca	gaagacccca	aacggaggag	780
gagccccgggt	ggcggggagg	ggttaaagtg	ggagaggagg	gcaagagtta	agcataggaa	840
caagaaacagg	gagggaaagg	aagagggaag	agcataaaaa	cagttcttta	ctcaaatcac	900
aatttgtctct	atttgtgttc	tcgcctctgt	tctctcggtt	tattctgaaa	tcggtaaatt	960
ctggtgatgat	atttttcatt	tggtctgtct	aatttggaac	ttgaaatgag	tggaaacaac	1020
tctctttagat	tataaaatgt	tgtgggttgt	ttctcttgat	ttttttatag	gaaaaccacg	1080
tctgtccctct	tgttattgat	tttcaacaat	gttctttaga	accttgtact	atctctctgt	1140
ctgttaaacat	taaaagagtt	ctagtttt				

(2) INFORMATION FOR SEQ ID NO:2754:

(A) LENGTH: 291 amino acids

- ```
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
```

## (ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..291  
(D) OTHER INFORMATION: / Ceres Seq. ID 1574087

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2754:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asn | Pro | Tyr | Val | Arg | Arg | Ser | His | Ser | Leu | Val | Asn | Cys | Pro | Phe | Tyr |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Phe | Lys | Ile | Gly | Ala | Cys | Arg | His | Gly | Asp | Arg | Cys | Ser | Arg | Leu | His |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Asn | Arg | Pro | Thr | Ile | Ser | Pro | Thr | Leu | Leu | Leu | Ser | Asn | Met | Tyr | Gln |
|     | 35  |     |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Tyr | Gln | Arg | Pro | Asp | Met | Ile | Thr | Pro | Gly | Val | Asp | Ala | Gln | Gly |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Gln | Pro | Leu | Asp | Pro | Arg | Lys | Ile | Gln | Glu | His | Phe | Glu | Asp | Phe | Phe |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Glu | Asp | Leu | Phe | Glu | Glu | Leu | Gly | Lys | Phe | Gly | Glu | Ile | Glu | Ser | Leu |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Asn | Ile | Cys | Asp | Asn | Leu | Ala | Asp | His | Met | Ile | Gly | Asn | Val | Tyr | Val |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Gln | Phe | Lys | Glu | Glu | Asp | Gln | Ala | Ala | Ala | Ala | Leu | Gln | Ala | Leu | Gln |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Gly | Arg | Phe | Tyr | Ser | Gly | Arg | Pro | Ile | Ile | Ala | Asp | Phe | Ser | Pro | Val |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Thr | Asp | Phe | Arg | Glu | Ala | Thr | Cys | Arg | Gln | Tyr | Glu | Glu | Asn | Asn | Cys |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Asn | Arg | Gly | Gly | Tyr | Cys | Asn | Phe | Met | His | Val | Lys | Leu | Val | Ser | Arg |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Glu | Leu | Arg | Arg | Lys | Leu | Phe | Gly | Arg | Tyr | Arg | Arg | Ser | Tyr | Arg | Arg |

(2) INFORMATION FOR SEO ID NO:2756:

(A) LENGTH: 240 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:

(ii) MOLECULE TYPE: peptide

(A) NAME/KEY: peptide

(D) OTHER INFORMATION

ar Pro Gly Val Asp Ala Gln Gly Gln Pro Leu Asp

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Lys | Ile | Gln | Glu | His | Phe | Glu | Asp | Phe | Phe | Glu | Asp | Leu | Gly | Glu | Glu |
|     |     | 20  |     |     |     |     |     |     |     |     |     | 30  |     |     |     |
| Leu | Gly | Lys | Phe | Gly | Glu | Ile | Glu | Ser | Leu | Asn | Ile | Cys | Asp | Asn | Leu |
|     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |
| Ala | Asp | His | Met | Ile | Gly | Asn | Val | Tyr | Val | Gln | Phe | Lys | Glu | Glu | Asp |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Gln | Ala | Ala | Ala | Ala | Leu | Gln | Ala | Leu | Gln | Gly | Arg | Phe | Tyr | Ser | Gly |
|     | 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Arg | Pro | Ile | Ile | Ala | Asp | Phe | Ser | Pro | Val | Thr | Asp | Phe | Arg | Glu | Ala |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Thr | Cys | Arg | Gln | Tyr | Glu | Glu | Asn | Asn | Cys | Asn | Arg | Gly | Gly | Tyr | Cys |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Asn | Phe | Met | His | Val | Lys | Leu | Val | Ser | Arg | Glu | Leu | Arg | Arg | Lys | Leu |
|     |     | 115 |     |     |     | 120 |     |     |     |     |     | 125 |     |     |     |
| Phe | Gly | Arg | Tyr | Arg | Arg | Ser | Tyr | Arg | Arg | Gly | Ser | Arg | Ser | Arg | Ser |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Arg | Ser | Arg | Ser | Ile | Ser | Pro | Arg | Asn | Lys | Arg | Asp | Asn | Asp | Arg | Arg |
|     | 145 |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Asp | Pro | Ser | His | Arg | Glu | Phe | Ser | His | Arg | Asp | Arg | Asp | Arg | Glu | Phe |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Tyr | Arg | His | Gly | Ser | Gly | Lys | Arg | Ser | Ser | Asp | Arg | Ser | Glu | Arg | Gln |
|     |     | 180 |     |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Glu | Arg | Asp | Gly | Ser | Arg | Gly | Arg | Arg | Gln | Ala | Ser | Pro | Lys | Arg | Gly |
|     |     | 195 |     |     |     | 200 |     |     |     |     |     | 205 |     |     |     |
| Gly | Ser | Pro | Gly | Gly | Gly | Arg | Glu | Gly | Ser | Glu | Glu | Arg | Arg | Ala | Arg |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Ile | Glu | Gln | Glu | Asn | Arg | Glu | Arg | Glu | Gly | Lys | Glu | Glu | Gly | Gly | Ala |
|     | 225 |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |

(i) SEQUENCE CHARACTERISTICS:

```
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
```

(A) NAME/KEY: -  
(B) LOCATION: 1..662  
(D) OTHER INFORMATION: / Ceres Seq. ID 1574093

(2) INFORMATION FOR SEQ ID NO:2758:

```
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
```

[illegible]

(2) INFORMATION FOR SEQ ID NO:2759:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 195 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..195  
(D) OTHER INFORMATION: / Ceres Seq. ID 1574095  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2759:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Leu | Pro | Gly | Val | Glu | Cys | Ala | Arg | Arg | Arg | Phe | His | Gly | Gly |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ala | Pro | Pro | Ile | Glu | Ser | Ser | Asn | Thr | Ala | Ser | Val | Ala | Ala | Ala |
|     |     |     | 20  |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Gly | His | Val | Trp | Thr | Arg | Arg | Pro | Ser | Phe | Ser | Leu | Tyr | Thr | Thr |
|     |     | 35  |     |     |     |     | 40  |     |     |     | 45  |     |     | Asn |
| His | Glu | Ser | His | Gln | Ala | His | Val | Ser | Phe | Ser | Glu | Arg | Ser | Val |
|     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     | Arg |
| Asn | Lys | Ser | Tyr | Gly | Glu | Asp | Asn | Asp | Glu | Lys | Leu | Asp | Gly | Ala |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Lys | Glu | Ala | Lys | Gln | Arg | Leu | Asn | Lys | Arg | Leu | Arg | Ile | Pro | Pro |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     | 95  | Arg |
| Thr | Ser | Ser | Gly | Lys | Met | Val | Lys | Thr | Lys | Gly | Ile | Asn | Trp | Ser |
|     |     |     | 100 |     |     |     | 105 |     |     |     |     | 110 |     | Lys |
| Glu | Arg | Val | Asn | Leu | Ser | Gly | Thr | Tyr | Arg | Pro | Arg | Trp | Val | Gly |
|     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     | Leu |
| Lys | Lys | Ser | Arg | Gly | Arg | Leu | Met | Glu | Trp | Phe | Lys | Arg | Arg | Val |
|     |     | 130 |     |     |     | 135 |     |     |     | 140 |     |     |     | Arg |
| Glu | Gln | Gln | Asp | Cys | Ala | Ile | Cys | Leu | Asp | Arg | Phe | Lys | Lys | Gly |
| 145 |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Thr | Leu | Val | His | Leu | Pro | Cys | Ala | His | Lys | Phe | His | Ser | Ile | Cys |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     | 175 | Leu |
| Leu | Pro | Trp | Leu | Asp | Thr | Asn | Val | Tyr | Cys | Pro | Tyr | Cys | Arg | Thr |
|     |     |     | 180 |     |     |     | 185 |     |     |     |     |     | 190 | Asp |
| Ile | Trp | Asn |     |     |     |     |     |     |     |     |     |     |     |     |
|     |     | 195 |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2760:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1396 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
(A) NAME/KEY: -  
(B) LOCATION: 1..1396  
(D) OTHER INFORMATION: / Ceres Seq. ID 1574100  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2760:

|             |             |             |             |             |            |     |
|-------------|-------------|-------------|-------------|-------------|------------|-----|
| aaagatgaaa  | agtaataacc  | ttcctctctt  | gccctttttg  | ctggctctggg | tgaacatatg | 60  |
| aaaaattttt  | cttgctcaag  | ttaatgataa  | aaggttgttg  | taggtattgt  | tgctctggct | 120 |
| ctgggtgtag  | gtctatgaaa  | tcaacccata  | tcgtgaatgg  | actgcaacat  | ggatatcttc | 180 |
| tccacgtggg  | attgggagca  | tttgatcatg  | tccaatccgt  | caaggactga  | agatgacagc | 240 |
| aaacagctac  | ctactgagtg  | ggaaattgaa  | aaaggtgaag  | gaattgaatc  | tatagttcca | 300 |
| cattttctcag | gcccttgagag | agtcagtaGg  | tggtctctgcc | accagcttct  | ggcacactgc | 360 |
| tgtatcgaaa  | agctccacagt | cgacctctat  | caactcatca  | tctcccgaag  | ccaaacgatg | 420 |
| caagcttgca  | tcagaaagt   | cccttgagag  | tctttgcagc  | aacatagact  | ttgtccaggt | 480 |
| gaaggctccc  | acagctctcg  | aggtatccgt  | tgctcagctc  | gaatcagatc  | tttgtttaaa | 540 |
| actaggaag   | cggacatact  | ctggaagaata | ctggggtaga  | aacaataatg  | aaatttcagc | 600 |
| ggtttctatg  | aagttgttaa  | ctccatctgt  | tgtcgtggg   | aaatccaaat  | tgtgtggtca | 660 |
| gagcatgcc   | gtcccgcgt   | gccaaattga  | tggctgtgaa  | ctggatctct  | catctgctaa | 720 |

```

gggttatcat cgtaagcaca aagtctgcga aaagcattca aagtgcctaa aagttagcgt 780
gagtgccctg gaacgtcggt tctgcacaac gtgtagcagg ttccatgctg tctctgaatt 840
tgatgagaag aaacgaagct ccgcaaaacg tctttctcat cataatgcga ggcgtcgtaa 900
gccacaagga gtattttcaa tgaatccgca gagggtgtat gatcgaagac agcatacaaa 960
tatgttgttg aatgggggtg cctttaacgc gagatctgaa gaaatgtatg aatggggtaa 1020
taacacttat gatacaagac ctagacaaac ggaaaaaaac tttactctga gcttcacagag 1080
aggtaatggc tctgaggacc agctggttgc tagtagcagc cgtatgttCc tctacatctc 1140
aaacctcagg tgggttccca gcaggaaggt ccaagtttca acttcattggc gaagatgtgg 1200
gagaatactc aggagtcttc catgaatctc aagatatcca ccgtgctctc tctcttctgt 1260
caacctcttc ggatccctcg gcccaaccac atgtgcagcc attttctcta ctctgttcat 1320
atgatgttgg accaaaatag atgagtaagt aatgtgtaat ttgtaaacct gttactcagt 1380
aggtggatac tttccc

```

(2) INFORMATION FOR SEQ ID NO:2761:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 121 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..121
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574101

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2761:

```

Met Asp Cys Asn Met Val Ser Ser Ser Gln Trp Asp Trp Glu His Leu
1 5 10 15
Ile Met Ser Asn Pro Ser Arg Thr Glu Asp Asp Ser Lys Gln Leu Pro
 20 25 30
Thr Glu Trp Glu Ile Glu Lys Gly Glu Gly Ile Glu Ser Ile Val Pro
 35 40 45
His Phe Ser Gly Leu Glu Arg Val Ser Arg Trp Leu Cys His Gln Leu
 50 55 60
Leu Ala His Cys Cys Ile Glu Lys Leu Thr Val Asp Leu Tyr Gln Leu
 65 70 75
Ile Ile Ser Arg Ser Gln Thr Met Gln Ala Cys Ile Arg Lys Phe Pro
 85 90 95
Trp Arg Phe Leu Gln Gln His Arg Leu Cys Pro Gly Glu Gly Ser His
 100 105 110
Ser Ser Arg Gly Ile Arg Cys Leu Ser
 115 120

```

(2) INFORMATION FOR SEQ ID NO:2762:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 205 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..205
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574102

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2762:

```

Met Lys Leu Leu Thr Pro Ser Val Val Ala Gly Lys Ser Lys Lys Cys
1 5 10 15
Gly Gln Ser Met Pro Val Pro Arg Cys Gln Ile Asp Gly Cys Glu Leu
 20 25 30
Asp Leu Ser Ser Ala Lys Gly Tyr His Arg Lys His Lys Val Cys Glu
 35 40 45
Lys His Ser Lys Cys Pro Lys Val Ser Val Ser Gly Leu Glu Arg Arg
 50 55 60
Phe Cys Gln Gln Cys Ser Arg Phe His Ala Val Ser Glu Phe Asp Glu

```

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Lys | Lys | Arg | Ser | Cys | Arg | Lys | Arg | Leu | Ser | His | His | Asn | Ala | Arg | Arg |
|     |     |     |     | 85  |     |     |     |     |     | 90  |     |     |     | 95  |     |
| Arg | Lys | Pro | Gln | Gly | Val | Phe | Ser | Met | Asn | Pro | Glu | Arg | Val | Tyr | Asp |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Arg | Arg | Gln | His | Thr | Asn | Met | Leu | Trp | Asn | Gly | Val | Ser | Leu | Asn | Ala |
|     |     | 115 |     |     |     |     | 120 |     |     |     | 125 |     |     |     |     |
| Arg | Ser | Glu | Glu | Met | Tyr | Glu | Trp | Gly | Asn | Asn | Thr | Tyr | Asp | Thr | Lys |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Pro | Arg | Gln | Thr | Glu | Lys | Ser | Phe | Thr | Leu | Ser | Phe | Gln | Arg | Gly | Asn |
|     | 145 |     |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |     |
| Gly | Ser | Glu | Asp | Gln | Leu | Val | Ala | Ser | Ser | Ser | Arg | Met | Phe | Leu | Tyr |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |     |
| Ile | Ser | Asn | Leu | Arg | Trp | Val | Pro | Ser | Arg | Lys | Val | Gln | Val | Ser | Thr |
|     |     | 180 |     |     |     |     | 185 |     |     |     |     |     | 190 |     |     |
| Ser | Trp | Arg | Arg | Cys | Gly | Arg | Ile | Leu | Arg | Ser | Pro | Pro |     |     |     |
|     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2763:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 186 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..186
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574103

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2763:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Pro | Val | Pro | Arg | Cys | Gln | Ile | Asp | Gly | Cys | Glu | Leu | Asp | Leu | Ser |
| 1   |     |     |     |     | 5   |     |     | 10  |     |     |     |     | 15  |     |     |
| Ser | Ala | Lys | Gly | Tyr | His | Arg | Lys | His | Lys | Val | Cys | Glu | Lys | His | Ser |
|     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |     |
| Lys | Cys | Pro | Lys | Val | Ser | Val | Ser | Gly | Leu | Glu | Arg | Arg | Phe | Cys | Gln |
|     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| Gln | Cys | Ser | Arg | Phe | His | Ala | Val | Ser | Glu | Phe | Asp | Glu | Lys | Lys | Arg |
|     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |
| Ser | Cys | Arg | Lys | Arg | Leu | Ser | His | His | Asn | Ala | Arg | Arg | Arg | Lys | Pro |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Gln | Gly | Val | Phe | Ser | Met | Asn | Pro | Glu | Arg | Val | Tyr | Asp | Arg | Arg | Gln |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| His | Thr | Asn | Met | Leu | Trp | Asn | Gly | Val | Ser | Leu | Asn | Ala | Arg | Ser | Glu |
|     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |     |
| Glu | Met | Tyr | Glu | Trp | Gly | Asn | Asn | Thr | Tyr | Asp | Thr | Lys | Pro | Arg | Gln |
|     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |     |
| Thr | Glu | Lys | Ser | Phe | Thr | Leu | Ser | Phe | Gln | Arg | Gly | Asn | Gly | Ser | Glu |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Asp | Gln | Leu | Val | Ala | Ser | Ser | Ser | Arg | Met | Phe | Leu | Tyr | Ile | Ser | Asn |
|     | 145 |     |     |     | 150 |     |     |     | 155 |     |     |     |     | 160 |     |
| Leu | Arg | Trp | Val | Pro | Ser | Arg | Lys | Val | Gln | Val | Ser | Thr | Ser | Trp | Arg |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |     |
| Arg | Cys | Gly | Arg | Ile | Leu | Arg | Ser | Pro | Pro |     |     |     |     |     |     |
|     | 180 |     |     |     |     | 185 |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2764:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1454 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:



- (A) NAME/KEY: -  
(B) LOCATION: 1..1454  
(D) OTHER INFORMATION: / Ceres Seq. ID 1574104

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2764:

|            |             |             |             |            |             |      |
|------------|-------------|-------------|-------------|------------|-------------|------|
| ctgggtgaaa | catagaaaag  | tttctcttgc  | tcaagttaat  | gataaaaagg | tgagagcaat  | 60   |
| aaaagctgat | aagccttgtc  | tggctcctgg  | aattttgaat  | tttcttttct | tatcttactt  | 120  |
| atagatttgg | tagttgaggg  | tgtcgtcgat  | aagttgttgt  | aggatttgtt | gctctggctc  | 180  |
| tggttgtagg | tctatgaaat  | caaccocat   | cgtgaatgga  | ctgcaacatg | gtatcttcgt  | 240  |
| cccagtgagg | tggggagcat  | ttagatcatg  | ccaatcgtc   | aaggactgaa | gatgacagca  | 300  |
| aacagctacc | tactgagtgg  | gaaattgaaa  | aagggtgaagg | aattgaatct | atagttccac  | 360  |
| attctcaggg | ccttgagaga  | gtcagtagtg  | gctctgCcac  | cagctctctg | cacactgctg  | 420  |
| tatcgaaaag | ctcacagctg  | acctctatca  | actcatcatc  | tcccgaagcc | aaacagatga  | 480  |
| agcttgcacg | agaaagtctc  | cctggagatt  | cttcgagcaa  | catagacttt | gtccaggtga  | 540  |
| aggtctccac | agctctcgag  | gtatccgttg  | cctcagctga  | atcagatctt | tgtttaaaac  | 600  |
| taggaaagcg | gacatactct  | gaagaatact  | ggggtagaaa  | caataatgaa | atttcagcgg  | 660  |
| tttctatgaa | gttggttaact | ccatctgttg  | tcgtcgggaa  | atccaaattg | tgtggtcaga  | 720  |
| gcatgccagt | cccgctttgc  | caaatgatg   | gctgtgaact  | ggatctctca | tctgctaagg  | 780  |
| gttatcatcg | taagcacaaa  | gtctgcgaaa  | agcattcaaa  | gtgcccgaaa | gttagcgtga  | 840  |
| gtggctcgga | acgtcgggtc  | tgccaaacagt | gtagcaggtt  | ccatgctgtc | tctgaatttg  | 900  |
| atgagaagaa | acgaagctgc  | cgaaaacgtc  | tttctcatca  | taatgcgagg | cgctgtaagc  | 960  |
| cacaaggagt | attttcaatg  | aatcccgaga  | gggtgtatga  | tcgaagacag | catacaaata  | 1020 |
| tggtgtggaa | tgggggtgtc  | cttaacgcga  | gatctgAaag  | aaatgtatga | atggggtaat  | 1080 |
| aacacttatg | atacaaaagc  | tagacaaacg  | gaaaaaagct  | ttactctgag | cttccagagga | 1140 |
| ggtaatggct | ctgaggacca  | gctggttgct  | agtagcagcc  | gtatgtttct | tacatctcaa  | 1200 |
| acctcaggtg | gggtccacgc  | aggaaagtcc  | aagtttcaac  | ttcatggcga | agatgtggga  | 1260 |
| gaatctctga | gagtcctcca  | tgaatctcaa  | gatatccacc  | gtgctctctc | tcttctgtca  | 1320 |
| acctctctgg | atccctctgc  | ccaaccacat  | gtgcagccat  | tttctctact | ctgttcaat   | 1380 |
| gatgtgtgac | caaaaatgat  | gagtaagtga  | tgtgtaattt  | gtaaacctgt | tactcagttg  | 1440 |
| gtggatactt | ttcc        |             |             |            |             |      |

(2) INFORMATION FOR SEQ ID NO:2765:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 284 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..284  
(D) OTHER INFORMATION: / Ceres Seq. ID 1574105

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2765:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Asp | Cys | Asn | Met | Val | Ser | Ser | Ser | Gln | Trp | Asp | Trp | Glu | His | Leu |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     | 15  |     |     |
| Ile | Met | Ser | Asn | Pro | Ser | Arg | Thr | Glu | Asp | Asp | Ser | Lys | Gln | Leu | Pro |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Thr | Glu | Trp | Glu | Ile | Glu | Lys | Gly | Glu | Gly | Ile | Glu | Ser | Ile | Val | Pro |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| His | Phe | Ser | Gly | Leu | Glu | Arg | Val | Ser | Ser | Gly | Ser | Ala | Thr | Ser | Phe |
|     |     |     | 50  |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Trp | His | Thr | Ala | Val | Ser | Lys | Ser | Ser | Gln | Ser | Thr | Ser | Ile | Asn | Ser |
|     |     |     | 65  |     |     | 70  |     |     | 75  |     |     |     | 80  |     |     |
| Ser | Ser | Pro | Glu | Ala | Lys | Arg | Cys | Lys | Leu | Ala | Ser | Glu | Ser | Ser | Pro |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Gly | Asp | Ser | Cys | Ser | Asn | Ile | Asp | Phe | Val | Gln | Val | Lys | Ala | Pro | Thr |
|     |     |     | 100 |     |     |     | 105 |     |     |     |     | 110 |     |     |     |
| Ala | Leu | Glu | Val | Ser | Val | Ala | Ser | Ala | Glu | Ser | Asp | Leu | Cys | Leu | Lys |
|     |     |     | 115 |     |     | 120 |     |     |     |     | 125 |     |     |     |     |
| Leu | Gly | Lys | Arg | Thr | Tyr | Ser | Glu | Glu | Tyr | Trp | Gly | Arg | Asn | Asn | Asn |
|     |     |     | 130 |     |     | 135 |     |     |     | 140 |     |     |     |     |     |
| Glu | Ile | Ser | Ala | Val | Ser | Met | Lys | Leu | Leu | Thr | Pro | Ser | Val | Val | Ala |
|     |     |     | 145 |     |     | 150 |     |     |     | 155 |     |     |     |     | 160 |

Gly Lys Ser Lys Leu Cys Gly Gln Ser Met Pro Val Pro Arg Cys Gln  
165 170 175  
Ile Asp Gly Cys Glu Leu Asp Leu Ser Ser Ala Lys Gly Tyr His Arg  
180 185 190  
Lys His Lys Val Cys Glu Lys His Ser Lys Cys Pro Lys Val Ser Val  
195 200 205  
Ser Gly Leu Glu Arg Arg Phe Cys Gln Gln Cys Ser Arg Phe His Ala  
210 215 220  
Val Ser Glu Phe Asp Glu Lys Lys Arg Ser Cys Arg Lys Arg Leu Ser  
225 230 235  
His His Asn Ala Arg Arg Arg Lys Pro Gln Gly Val Phe Ser Met Asn  
245 250 255  
Pro Glu Arg Val Tyr Asp Arg Arg Gln His Thr Asn Met Leu Trp Asn  
260 265 270  
Gly Val Ser Leu Asn Ala Arg Ser Glu Arg Asn Val  
275 280

(2) INFORMATION FOR SEQ ID NO:2766:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 280 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..280

(D) OTHER INFORMATION: / Ceres Seq. ID 1574106

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2766:

Met Val Ser Ser Ser Gln Trp Asp Trp Glu His Leu Ile Met Ser Asn  
1 5 10 15  
Pro Ser Arg Thr Glu Asp Asp Ser Lys Gln Leu Pro Thr Glu Trp Glu  
20 25 30  
Ile Glu Lys Gly Glu Gly Ile Glu Ser Ile Val Pro His Phe Ser Gly  
35 40 45  
Leu Glu Arg Val Ser Ser Gly Ser Ala Thr Ser Phe Trp His Thr Ala  
50 55 60  
Val Ser Lys Ser Ser Gln Ser Thr Ser Ile Asn Ser Ser Ser Pro Glu  
65 70 75 80  
Ala Lys Arg Cys Lys Leu Ala Ser Glu Ser Ser Pro Gly Asp Ser Cys  
85 90 95  
Ser Asn Ile Asp Phe Val Gln Val Lys Ala Pro Thr Ala Leu Glu Val  
100 105 110  
Ser Val Ala Ser Ala Glu Ser Asp Leu Cys Leu Lys Leu Gly Lys Arg  
115 120 125  
Thr Tyr Ser Glu Glu Tyr Trp Gly Arg Asn Asn Asn Glu Ile Ser Ala  
130 135 140  
Val Ser Met Lys Leu Leu Thr Pro Ser Val Val Ala Gly Lys Ser Lys  
145 150 155 160  
Leu Cys Gly Gln Ser Met Pro Val Pro Arg Cys Gln Ile Asp Gly Cys  
165 170 175  
Glu Leu Asp Leu Ser Ser Ala Lys Gly Tyr His Arg Lys His Lys Val  
180 185 190  
Cys Glu Lys His Ser Lys Cys Pro Lys Val Ser Val Ser Gly Leu Glu  
195 200 205  
Arg Arg Phe Cys Gln Gln Cys Ser Arg Phe His Ala Val Ser Glu Phe  
210 215 220  
Asp Glu Lys Lys Arg Ser Cys Arg Lys Arg Leu Ser His His Asn Ala  
225 230 235 240  
Arg Arg Arg Lys Pro Gln Gly Val Phe Ser Met Asn Pro Glu Arg Val  
245 250 255  
Tyr Asp Arg Arg Gln His Thr Asn Met Leu Trp Asn Gly Val Ser Leu

260 265 270  
Asn Ala Arg Ser Glu Arg Asn Val  
275 280  
(2) INFORMATION FOR SEQ ID NO:2767:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 267 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..267  
(D) OTHER INFORMATION: / Ceres Seq. ID 1574107  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2767:  
Met Ser Asn Pro Ser Arg Thr Glu Asp Asp Ser Lys Gln Leu Pro Thr  
1 5 10 15  
Glu Trp Glu Ile Glu Lys Gly Glu Gly Ile Glu Ser Ile Val Pro His  
20 25 30  
Phe Ser Gly Leu Glu Arg Val Ser Ser Gly Ser Ala Thr Ser Phe Trp  
35 40 45  
His Thr Ala Val Ser Lys Ser Ser Gln Ser Thr Ser Ile Asn Ser Ser  
50 55 60  
Ser Pro Glu Ala Lys Arg Cys Lys Leu Ala Ser Glu Ser Ser Pro Gly  
65 70 75 80  
Asp Ser Cys Ser Asn Ile Asp Phe Val Gln Val Lys Ala Pro Thr Ala  
85 90 95  
Leu Glu Val Ser Val Ala Ser Ala Glu Ser Asp Leu Cys Leu Lys Leu  
100 105 110  
Gly Lys Arg Thr Tyr Ser Glu Glu Tyr Trp Gly Arg Asn Asn Asn Glu  
115 120 125  
Ile Ser Ala Val Ser Met Lys Leu Leu Thr Pro Ser Val Val Ala Gly  
130 135 140  
Lys Ser Lys Leu Cys Gly Gln Ser Met Pro Val Pro Arg Cys Gln Ile  
145 150 155 160  
Asp Gly Cys Glu Leu Asp Leu Ser Ser Ala Lys Gly Tyr His Arg Lys  
165 170 175  
His Lys Val Cys Glu Lys His Ser Lys Cys Pro Lys Val Ser Val Ser  
180 185 190  
Gly Leu Glu Arg Arg Phe Cys Gln Gln Cys Ser Arg Phe His Ala Val  
195 200 205  
Ser Glu Phe Asp Glu Lys Lys Arg Ser Cys Arg Lys Arg Leu Ser His  
210 215 220  
His Asn Ala Arg Arg Arg Lys Pro Gln Gly Val Phe Ser Met Asn Pro  
225 230 235 240  
Glu Arg Val Tyr Asp Arg Arg Gln His Thr Asn Met Leu Trp Asn Gly  
245 250 255  
Val Ser Leu Asn Ala Arg Ser Glu Arg Asn Val  
260 265

(2) INFORMATION FOR SEQ ID NO:2768:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1658 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
(A) NAME/KEY: -  
(B) LOCATION: 1..1658  
(D) OTHER INFORMATION: / Ceres Seq. ID 1574122  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2768:

```

aatttctcaa taacgctctc agagagacca ttgtatgaag ctctcgcgtt ctggaatttg 60
aaaaggaact tgttatggag ataactcacc tgaacgttgt gccccagtcg tctgtgggta 120
cttggagtag taaattagaa acgaaaagat tgggtccaaa tcggtcaaat ttgttatctt 180
caggggtcaa aaaatccaga cttgtgattc gaagtggaaa ttccgatggt tatgtttgtg 240
gtgagaatga tgacttgggt cgtatagcca gaagaggaga atcaacgtca aagggttttg 300
ttcctgggtt gctcgtatga tcaaatgggt aaattgctgc tcgaatcagt cattctcaact 360
gcgagtggaa gcccaagctt agagtacatt atgagaaagc cggttgtgac aatctcgatg 420
ctcctgcggt gttgtttctt cctggccttg gcgttggttc atttcaactt gagaagcagc 480
ttaccgatatt gggaagggat tatcgagtat gggtatttga ttttcttgga cagggtttat 540
ctctccctatt tgaagatcct actaccatga ctgaagaaac cagttcctcg gaagataagg 600
aacacattttg gggatttggg gacaaaactg aaccgtgggc tgatcaactt gtattctctc 660
tggatctctg gagggatcaa gttcagttat ttgtagaaga ggttatcggg gagcctgtgt 720
acattgctgg gaactcactt ggagggtatg tagctctcta ctttgacgca acccatcctc 780
acctgggttaa ggggtgttacc ttgcctaatg caacaccttt ctgggggttc ttccctaact 840
cagtaagatc cccaaagcta ccacgtctct ttccatggcc cggagcattc cctctgccgg 900
aaaagatgaa aaaaatcaca gaattgggtg ggcaaaagat aagtgatctc gaagacatag 960
ctgagatcact taacacaggtc tacacagacc attctaccaa tgttgataaa gtattctcac 1020
gtattgtgga ggtcacacag catccggctg ctgcagcatc gtttgcttca attatgcttg 1080
ctcctgtgtg agagctatct ttctccgaag ctttatctag gtgtaaggaa aacaatgttc 1140
agatatgtct catgtatgga agagaagatc catgggtgag accgttatgg ggaaagaaga 1200
taaagaagga aatccccaac gctccatact acgagatcag cccagcgggt cactgccacc 1260
acgatgaagt cctcgaggtg gtgaactatc tgatgcggcg gtggatcaag cactcggaat 1320
ctgggtggtt tgaaNgcgct cccgcttttg gaggacactg aagaagattg ggaggagtcc 1380
aggaattgga gagaaattga gttcccgaga gatggttgga aaaaagcagt gaactctgtg 1440
ttatatgggt caaactatac gtactggaga ggagttagag aatctttcag atccagtttt 1500
ataagggtgt ttggagggaa gtctgcatag aagaagcatg gaacagtcgt ctagtgtaaa 1560
ttaattgtaa tctatgttgc atccgatgct agcatataaa tgttgtctgt agaatacagt 1620

```

(2) INFORMATION FOR SEQ ID NO:2769:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 428 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..428

(D) OTHER INFORMATION: / Ceres Seq. ID 1574123

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2769:

```

Met Glu Ile Ile Ser Leu Asn Val Val Pro Gln Cys Ser Val Val Thr
1 5 10 15
Trp Ser Ser Phe Ser Leu Ala Thr Lys Arg Leu Val Pro Asn Arg Ser Ser
20 25 30
Leu Leu Phe Ser Gly Val Lys Lys Ser Arg Leu Val Ile Arg Ser Gly
35 40 45
Asn Ser Asp Gly Tyr Val Val Gly Glu Asn Asp Asp Leu Gly Arg Ile
50 55 60
Ala Arg Arg Gly Glu Ser Thr Ser Lys Val Leu Ile Pro Gly Leu Pro
65 70 75 80
Asp Glu Ser Asn Gly Glu Ile Ala Ala Arg Ile Ser His Ser His Cys
85 90 95
Glu Trp Lys Pro Lys Leu Arg Val His Tyr Glu Lys Ala Gly Cys Asp
100 105 110
Asn Leu Asp Ala Pro Ala Val Leu Phe Leu Pro Gly Phe Gly Val Gly
115 120 125
Ser Phe His Tyr Glu Lys Gln Leu Thr Asp Leu Gly Arg Asp Tyr Arg
130 135 140
Val Trp Ala Ile Asp Phe Leu Gly Gln Gly Leu Ser Leu Pro Thr Glu
145 150 155 160
Asp Pro Thr Thr Met Thr Glu Glu Thr Ser Ser Ser Glu Asp Lys Glu

```

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Thr | Glu | Glu | Thr | Ser | Ser | Ser | Glu | Asp | Lys | Glu | Pro | Phe | Trp | Gly |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Phe | Gly | Asp | Lys | Thr | Glu | Pro | Trp | Ala | Asp | Gln | Leu | Val | Phe | Ser | Leu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Asp | Leu | Trp | Arg | Asp | Gln | Val | Gln | Tyr | Phe | Val | Glu | Glu | Val | Ile | Gly |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Glu | Pro | Val | Tyr | Ile | Ala | Gly | Asn | Ser | Leu | Gly | Gly | Tyr | Val | Ala | Leu |
|     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Tyr | Phe | Ala | Ala | Thr | His | Pro | His | Leu | Val | Lys | Gly | Val | Thr | Leu | Leu |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Asn | Ala | Thr | Pro | Phe | Trp | Gly | Phe | Phe | Pro | Asn | Pro | Val | Arg | Ser | Pro |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Lys | Leu | Ala | Arg | Leu | Phe | Pro | Trp | Pro | Gly | Ala | Phe | Pro | Leu | Pro | Glu |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Arg | Val | Lys | Lys | Ile | Thr | Glu | Leu | Val | Trp | Gln | Lys | Ile | Ser | Asp | Pro |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |

Glu Ser Ile Ala Glu Ile Leu Lys Gln Val Tyr Thr Asp His Ser Thr  
130 135 140  
Asn Val Asp Lys Val Phe Ser Arg Ile Val Glu Val Thr Gln His Pro  
145 150 155 160  
Ala Ala Ala Ala Ser Phe Ala Ser Ile Met Leu Ala Pro Gly Gly Glu  
165 170 175  
Leu Ser Phe Ser Glu Ala Leu Ser Arg Cys Lys Glu Asn Asn Val Gln  
180 185 190  
Ile Cys Leu Met Tyr Gly Arg Glu Asp Pro Trp Val Arg Pro Leu Trp  
195 200 205  
Gly Lys Lys Ile Lys Lys Glu Ile Pro Asn Ala Pro Tyr Tyr Glu Ile  
210 215 220  
Ser Pro Ala Gly His Cys Pro His Asp Glu Val Pro Glu Val Val Asn  
225 230 235 240  
Tyr Leu Met Arg Gly Trp Ile Lys His Leu Glu Ser Gly Gly Phe Glu  
245 250 255  
Xaa Ala Pro Ala Phe Gly Gly His  
260

(2) INFORMATION FOR SEQ ID NO:2771:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1267 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1267
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574133

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2771:

|             |             |            |             |             |             |      |
|-------------|-------------|------------|-------------|-------------|-------------|------|
| accctacaca  | caatctctcaa | aacagagtaa | cccaaaaaac  | agagcaatct  | ctaaaaaatc  | 60   |
| tcaagaaaac  | tcactaaaat  | gggttcaacg | gcggagacac  | aattaactcc  | gggtcgaagt  | 120  |
| accgacgacg  | aagctgcccct | cttcgccatg | caactagcca  | gtgcttcogt  | tcttYccgat  | 180  |
| ggctttaaaa  | tcgcgcttag  | agcttgacct | tcttgagatt  | atggccaaga  | atggtttctc  | 240  |
| catgtctcct  | acagagatcg  | cttctaaact | tcggacccaa  | aacctggaag  | ctccggtcat  | 300  |
| gctcgaccgt  | atctcccgct  | ttcttaacgt | ttactccgtc  | ttaaacctgc  | ccaaccgtaa  | 360  |
| actttccggt  | gatggcggtg  | aacggattta | cgggcttggg  | ccggttttga  | agtatttgac  | 420  |
| caagaacgaa  | gatgggtggt  | ccattgctgc | tctttgtctt  | atgaaccaag  | acaaggttct  | 480  |
| catggaaaag  | tggtaccatt  | tgaaggatgc | aattcttgat  | gggtgggattc | cattcaacaa  | 540  |
| ggcttatgga  | atgagcgcgt  | tcgagtacca | cgggactgac  | cctagattca  | acaaggttct  | 600  |
| taacaatgga  | atgtctaac   | attccacaat | caccatgaag  | aagattcttg  | agacctataa  | 660  |
| gggttttgaa  | ggattgaact  | ctttggttga | tgttggtggt  | ggcattgggtg | ctacactcaa  | 720  |
| aatgatgttc  | tccaagtacc  | ctaatcttaa | agggatcaac  | tttgatctcc  | cacatgtcat  | 780  |
| tgaagatgct  | cttctctcat  | ctggatttga | gcattgttga  | ggagatatgt  | ttgtaagtgt  | 840  |
| ccctaaaaggt | gatggccatg  | tcatgaagtg | gatattgcat  | gactggagtg  | acgaacattg  | 900  |
| cgtgaaattc  | ttgaaaaact  | gctacgagtc | acttccagag  | gatggaaaaa  | tgatattagc  | 960  |
| agagtgtata  | cttcacagaga | caccagactc | aagcctctca  | acccaaacaa  | tagtccatgt  | 1020 |
| cagattgcatt | atgttggctc  | acaatcccgg | aggcaacgaga | acgaaccgaga | aagaggtttga | 1080 |
| ggcattagcc  | aaagcatcag  | gcttcaaggg | catcaaaagt  | Gtctgcgacg  | cttttggtgt  | 1140 |
| taaccttatt  | gagttactca  | aaagactcta | aaaacaaaca  | agtttccctat | gaagatgatt  | 1200 |
| tatatgtaaa  | cattatctca  | tatctccttc | cacggttcca  | aaactatgct  | gtttaataat  | 1260 |
| gggttttt    |             |            |             |             |             |      |

(2) INFORMATION FOR SEQ ID NO:2772:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 330 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide

(B) LOCATION: 1..330

(D) OTHER INFORMATION: / Ceres Seq. ID 1574134

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2772:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Leu | Lys | Ser | Ala | Leu | Glu | Leu | Asp | Leu | Leu | Glu | Ile | Met | Ala |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Lys | Asn | Gly | Ser | Pro | Met | Ser | Pro | Thr | Glu | Ile | Ala | Ser | Lys | Leu | Pro |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Thr | Lys | Asn | Pro | Glu | Ala | Pro | Val | Met | Leu | Asp | Arg | Ile | Leu | Arg | Leu |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Leu | Thr | Ser | Tyr | Ser | Val | Leu | Thr | Cys | Ser | Asn | Arg | Lys | Leu | Ser | Gly |
|     |     |     | 50  |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Asp | Gly | Val | Glu | Arg | Ile | Tyr | Gly | Leu | Gly | Pro | Val | Cys | Lys | Tyr | Leu |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Thr | Lys | Asn | Glu | Asp | Gly | Val | Ser | Ile | Ala | Leu | Cys | Leu | Met | Asn |     |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Gln | Asp | Lys | Val | Leu | Met | Glu | Ser | Trp | Tyr | His | Leu | Lys | Asp | Ala | Ile |
|     |     |     | 100 |     |     |     | 105 |     |     |     |     |     | 110 |     |     |
| Leu | Asp | Gly | Gly | Ile | Pro | Phe | Asn | Lys | Ala | Tyr | Gly | Met | Ser | Ala | Phe |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Glu | Tyr | His | Gly | Thr | Asp | Pro | Arg | Phe | Asn | Lys | Val | Phe | Asn | Asn | Gly |
|     |     |     | 130 |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Met | Ser | Asn | His | Ser | Thr | Ile | Thr | Met | Lys | Lys | Ile | Leu | Glu | Thr | Tyr |
| 145 |     |     |     | 150 |     |     |     |     |     | 155 |     |     |     | 160 |     |
| Lys | Gly | Phe | Glu | Gly | Leu | Thr | Ser | Leu | Val | Asp | Val | Gly | Gly | Gly | Ile |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Gly | Ala | Thr | Leu | Lys | Met | Ile | Val | Ser | Lys | Tyr | Pro | Asn | Leu | Lys | Gly |
|     |     |     | 180 |     |     |     | 185 |     |     |     |     |     | 190 |     |     |
| Ile | Asn | Phe | Asp | Leu | Pro | His | Val | Ile | Glu | Asp | Ala | Pro | Ser | His | Pro |
|     |     |     | 195 |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Gly | Ile | Glu | His | Val | Gly | Gly | Asp | Met | Phe | Val | Ser | Val | Pro | Lys | Gly |
|     |     |     | 210 |     |     | 215 |     |     |     | 220 |     |     |     |     |     |
| Asp | Ala | Ile | Phe | Met | Lys | Trp | Ile | Cys | His | Asp | Trp | Ser | Asp | Glu | His |
| 225 |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |     |
| Cys | Val | Lys | Phe | Leu | Lys | Asn | Cys | Tyr | Glu | Ser | Leu | Pro | Glu | Asp | Gly |
|     |     |     | 245 |     |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Lys | Val | Ile | Leu | Ala | Glu | Cys | Ile | Leu | Pro | Glu | Thr | Pro | Asp | Ser | Ser |
|     |     |     | 260 |     |     |     | 265 |     |     |     |     |     | 270 |     |     |
| Leu | Ser | Thr | Lys | Gln | Val | Val | His | Val | Asp | Cys | Ile | Met | Leu | Ala | His |
|     |     |     | 275 |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Asn | Pro | Gly | Gly | Lys | Glu | Arg | Thr | Glu | Lys | Glu | Phe | Glu | Ala | Leu | Ala |
|     |     |     | 290 |     |     | 295 |     |     |     | 300 |     |     |     |     |     |
| Lys | Ala | Ser | Gly | Phe | Lys | Gly | Ile | Lys | Val | Val | Cys | Asp | Ala | Phe | Gly |
| 305 |     |     |     | 310 |     |     |     |     |     | 315 |     |     |     |     | 320 |
| Val | Asn | Leu | Ile | Glu | Leu | Leu | Lys | Lys | Leu |     |     |     |     |     |     |
|     |     |     | 325 |     |     |     |     |     | 330 |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2773:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 316 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..316

(D) OTHER INFORMATION: / Ceres Seq. ID 1574135

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2773:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Lys | Asn | Gly | Ser | Pro | Met | Ser | Pro | Thr | Glu | Ile | Ala | Ser | Lys |
| 1   |     |     | 5   |     |     |     |     |     |     | 10  |     |     |     | 15  |     |
| Leu | Pro | Thr | Lys | Asn | Pro | Glu | Ala | Pro | Val | Met | Leu | Asp | Arg | Ile | Leu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |

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Arg Leu Leu Thr Ser Tyr Ser Val Leu Thr Cys Ser Asn Arg Lys Leu
 35 40 45
Ser Gly Asp Gly Val Glu Arg Ile Tyr Gly Leu Gly Pro Val Cys Lys
 50 55 60
Tyr Leu Thr Lys Asn Glu Asp Gly Val Ser Ile Ala Ala Leu Cys Leu
 65 70 75 80
Met Asn Gln Asp Lys Val Leu Met Glu Ser Trp Tyr His Leu Lys Asp
 85 90 95
Ala Ile Leu Asp Gly Gly Ile Pro Phe Asn Lys Ala Tyr Gly Met Ser
 100 105 110
Ala Phe Glu Tyr His Gly Thr Asp Pro Arg Phe Asn Lys Val Phe Asn
 115 120 125
Asn Gly Met Ser Asn His Ser Thr Ile Thr Met Lys Lys Ile Leu Glu
 130 135 140
Thr Tyr Lys Gly Phe Glu Gly Leu Thr Ser Leu Val Asp Val Gly Gly
 145 150 155 160
Gly Ile Gly Ala Thr Leu Lys Met Ile Val Ser Lys Tyr Pro Asn Leu
 165 170 175
Lys Gly Ile Asn Phe Asp Leu Pro His Val Ile Glu Asp Ala Pro Ser
 180 185 190
His Pro Gly Ile Glu His Val Gly Gly Asp Met Phe Val Ser Val Pro
 195 200 205
Lys Gly Asp Ala Ile Phe Met Lys Trp Ile Cys His Asp Trp Ser Asp
 210 215 220
Glu His Cys Val Lys Phe Leu Lys Asn Cys Tyr Glu Ser Leu Pro Glu
 225 230 235 240
Asp Gly Lys Val Ile Leu Ala Glu Cys Ile Leu Pro Glu Thr Pro Asp
 245 250 255
Ser Ser Leu Ser Thr Lys Gln Val Val His Val Asp Cys Ile Met Leu
 260 265 270
Ala His Asn Pro Gly Gly Lys Glu Arg Thr Glu Lys Glu Phe Glu Ala
 275 280 285
Leu Ala Lys Ala Ser Gly Phe Lys Gly Ile Lys Val Val Cys Asp Ala
 290 295 300
Phe Gly Val Asn Leu Ile Glu Leu Leu Lys Lys Leu
 305 310 315

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(2) INFORMATION FOR SEQ ID NO:2774:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 309 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..309
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574136

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2774:

```

Met Ser Pro Thr Glu Ile Ala Ser Lys Leu Pro Thr Lys Asn Pro Glu
1 5 10 15
Ala Pro Val Met Leu Asp Arg Ile Leu Arg Leu Leu Thr Ser Tyr Ser
 20 25 30
Val Leu Thr Cys Ser Asn Arg Lys Leu Ser Gly Asp Gly Val Glu Arg
 35 40 45
Ile Tyr Gly Leu Gly Pro Val Cys Lys Tyr Leu Thr Lys Asn Glu Asp
 50 55 60
Gly Val Ser Ile Ala Ala Leu Cys Leu Met Asn Gln Asp Lys Val Leu
 65 70 75 80
Met Glu Ser Trp Tyr His Leu Lys Asp Ala Ile Leu Asp Gly Gly Ile
 85 90 95
Pro Phe Asn Lys Ala Tyr Gly Met Ser Ala Phe Glu Tyr His Gly Thr

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|                             |                         |                     |
|-----------------------------|-------------------------|---------------------|
| 100                         | 105                     | 110                 |
| Asp Pro Arg Phe Asn Lys Val | Phe Asn Asn Gly Met Ser | Asn His Ser         |
| 115                         | 120                     | 125                 |
| Thr Ile Thr Met Lys Lys Ile | Leu Glu Thr Tyr Lys Gly | Phe Glu Gly         |
| 130                         | 135                     | 140                 |
| Leu Thr Ser Leu Val Asp Val | Gly Gly Gly Ile Gly Ala | Thr Leu Lys         |
| 145                         | 150                     | 155                 |
| Met Ile Val Ser Lys Tyr     | Pro Asn Leu Lys Gly     | Ile Asn Phe Asp Leu |
| 165                         | 170                     | 175                 |
| Pro His Val Ile Glu Asp Ala | Pro Ser His Pro Gly Ile | Glu His Val         |
| 180                         | 185                     | 190                 |
| Gly Gly Asp Met Phe Val Ser | Val Pro Lys Gly Asp Ala | Ile Phe Met         |
| 195                         | 200                     | 205                 |
| Lys Trp Ile Cys His Asp Trp | Ser Asp Glu His Cys Val | Lys Phe Leu         |
| 210                         | 215                     | 220                 |
| Lys Asn Cys Tyr Glu Ser Leu | Pro Glu Asp Gly Lys Val | Ile Leu Ala         |
| 225                         | 230                     | 235                 |
| Glu Cys Ile Leu Pro Glu Thr | Pro Asp Ser Ser Leu Ser | Thr Lys Gln         |
| 245                         | 250                     | 255                 |
| Val Val His Val Asp Cys Ile | Met Leu Ala His Asn Pro | Gly Gly Lys         |
| 260                         | 265                     | 270                 |
| Glu Arg Thr Glu Lys Glu Phe | Glu Ala Leu Ala Lys Ala | Ser Gly Phe         |
| 275                         | 280                     | 285                 |
| Lys Gly Ile Lys Val Val Cys | Asp Ala Phe Gly Val Asn | Leu Ile Glu         |
| 290                         | 295                     | 300                 |
| Leu Leu Lys Lys Leu         |                         |                     |

(2) INFORMATION FOR SEQ ID NO:2775:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 686 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..686
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574141

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2775:

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| aaaaaccac  | cattcaaac  | aaacacaaaa | acaaaaaaaa | aaacatttcc | ccaaaaaaaa | 60  |
| aaaaacagag | gatgaacaa  | aaccagagca | agtttttgag | aataatctca | acgcctctaa | 120 |
| gagcttttag | caaggccat  | gattttctac | tgagaagcat | cacoggttgc | gcaGctcgga | 180 |
| ctcaatattc | ctctccgcg  | tcogtctcgc | ctctttttcc | aagaagccgg | agctctctct | 240 |
| cgcgcgcctt | ctctctctcc | gcacatctcc | ggagaaccac | cgatttcggg | atagatgaag | 300 |
| attacagcga | gctagtgaga | gctgcgtcgg | tgaggagttt | agggcacaag | aatgatagat | 360 |
| acatgttgat | acaagagaag | ctgcaacagc | agaagcaaca | gaagcaagga | gggttgcta  | 420 |
| agagctcgag | tgctgggagt | gcgaggatag | aggaagagga | agaaacagag | gaaggatctg | 480 |
| tgaatccgaa | Ggtgaagaag | actaagaaag | tctctgatct | tttgatctct | cgtagcaaat | 540 |
| cttacgccgt | tactactagt | accocattct | tgtaacttct | cttcttattt | tttctctctc | 600 |
| ttaattttag | tattttgtgg | attgattatc | attttctagc | tcgatttttc | gtgcactgtg | 660 |
| aaatactatt | ttcttagctt | gatttt     |            |            |            |     |

(2) INFORMATION FOR SEQ ID NO:2776:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 190 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..190

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Lys | Pro | Thr | Ile | Gln | Thr | Lys | His | Lys | Asn | Lys | Lys | Lys | Asn | Ile | Ser |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Pro | Lys | Lys | Lys | Lys | Gln | Arg | Met | Lys | Gln | Asn | Gln | Ser | Lys | Phe | Leu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Arg | Ile | Ile | Ser | Thr | Pro | Leu | Arg | Ala | Leu | Gly | Lys | Ala | Arg | Asp | Phe |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Tyr | Val | Arg | Ser | Ile | Thr | Gly | Cys | Ala | Ala | Arg | Thr | Gln | Tyr | Ser | Ser |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ser | Ala | Ser | Val | Ser | Ala | Pro | Phe | Pro | Arg | Ser | Arg | Ser | Ser | Ser | Ser |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Ala | Ala | Phe | Ser | Ser | Ser | Ala | Ser | Ser | Arg | Arg | Thr | Thr | Asp | Phe | Gly |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Ile | Asp | Glu | Asp | Tyr | Ser | Glu | Leu | Val | Arg | Ala | Ala | Ser | Val | Arg | Ser |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Leu | Gly | His | Lys | Asn | Glu | Ile | Asp | Met | Leu | Ile | Gln | Glu | Lys | Leu | Gln |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Gln | Gln | Lys | Gln | Gln | Lys | Gln | Gly | Gly | Leu | Pro | Lys | Ser | Ser | Ser | Ala |
|     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Gly | Met | Ala | Arg | Ile | Glu | Glu | Glu | Glu | Glu | Thr | Glu | Glu | Gly | Ser | Val |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |     |
| Asn | Pro | Lys | Val | Lys | Lys | Thr | Lys | Lys | Val | Ser | Asp | Leu | Leu | Tyr | Pro |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Arg | Ser | Lys | Ser | Tyr | Ala | Val | Thr | Thr | Ser | Thr | Pro | Ile | Leu |     |     |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |

(2) INFORMATION FOR SEQ ID NO:2778:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 892 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..892  
(D) OTHER INFORMATION: / Ceres Seq. ID 1574148

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2778:

|             |             |            |            |            |             |     |
|-------------|-------------|------------|------------|------------|-------------|-----|
| aatcaaaaaa  | ctatccactc  | tcagccggaa | aatttttctc | tgattcatta | cgacagagag  | 60  |
| aaccatgccg  | gcgaacacaga | ggaccgccga | gGtcaacaga | aacctgatc  | tgatcagggg  | 120 |
| gtgttgtaaa  | tactcgagat  | ccagatgta  | ccataagaga | ggtttggtgg | ctatcaaggc  | 180 |
| caaaaatgga  | ggcgttttcc  | cacgtcacga | cgctaaatct | aaggttgatg | ctccgggtgga | 240 |
| gaagccaccg  | aagtctctatc | cagctgaaga | tgttaaagaa | ccctccccc  | acaggcgccac | 300 |
| ggcaaaacca  | accaagctca  | gagctagcat | tactccaggt | acagtgttga | ttatccctgc  | 360 |
| tggtgagttc  | aagggaaga   | gagttgtctt | ccttaagcag | cttgctctcg | gtttgcttct  | 420 |
| tgtgactgga  | ccattcaaga  | tcaatggtgt | tcctttgaga | cgtgttaacc | aggcctatgt  | 480 |
| gattggcact  | tccacaaagg  | ttgacatttc | tggagtcacc | ctcgataaat | tcgatgataa  | 540 |
| gtactttggc  | aaggttgctg  | agaagaaaaa | gaagaagaca | gaaggagagt | tccttgaggc  | 600 |
| tgagaaagag  | gagaagaagg  | agatccacca | ggtgaagaaa | gatgaccaga | aagctgtgga  | 660 |
| tgcagctttg  | atcaaaagca  | ttgaagcagt | tcagagtttg | aagacttacc | ttggcgcaag  | 720 |
| gtttctcattg | aaacaaggaa  | tgaagcccca | tgagcttggt | ttctagattt | cattactttt  | 780 |
| ttcttgaggt  | ctctagagta  | tctgtctctc | gaagtgtttt | accttctaaa | tggtgtgttt  | 840 |
| gttctgtgtc  | actgaacaca  | tacaattttt | ggcttatata | ttctctgttc | tt          |     |

(2) INFORMATION FOR SEQ ID NO:2779:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 233 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..233  
(D) OTHER INFORMATION: / Ceres Seq. ID 1574149

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2779:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Pro | Ala | Lys | Gln | Arg | Thr | Pro | Lys | Val | Asn | Arg | Asn | Pro | Asp | Leu |
| 1   |     |     |     | 5   |     |     |     |     |     | 10  |     |     |     | 15  |     |
| Ile | Arg | Gly | Val | Gly | Lys | Tyr | Ser | Arg | Ser | Gln | Met | Tyr | His | Lys | Arg |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Gly | Leu | Trp | Ala | Ile | Lys | Ala | Lys | Asn | Gly | Gly | Val | Phe | Pro | Arg | His |
|     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |
| Asp | Ala | Lys | Ser | Lys | Val | Asp | Ala | Pro | Val | Glu | Lys | Pro | Pro | Lys | Phe |
|     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Tyr | Pro | Ala | Glu | Asp | Val | Lys | Lys | Pro | Leu | Pro | Asn | Arg | Arg | Thr | Ala |
|     |     | 65  |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Lys | Pro | Thr | Lys | Leu | Arg | Ala | Ser | Ile | Thr | Pro | Gly | Thr | Val | Leu | Ile |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Ile | Leu | Ala | Gly | Arg | Phe | Lys | Gly | Lys | Arg | Val | Val | Phe | Leu | Lys | Gln |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Leu | Ala | Ser | Gly | Leu | Leu | Leu | Val | Thr | Gly | Pro | Phe | Lys | Ile | Asn | Gly |
|     |     | 115 |     |     |     | 120 |     |     |     |     |     | 125 |     |     |     |
| Val | Pro | Leu | Arg | Arg | Val | Asn | Gln | Ala | Tyr | Val | Ile | Gly | Thr | Ser | Thr |
|     |     | 130 |     |     |     | 135 |     |     |     |     |     | 140 |     |     |     |
| Lys | Val | Asp | Ile | Ser | Gly | Val | Thr | Leu | Asp | Lys | Phe | Asp | Asp | Lys | Tyr |
|     |     | 145 |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |     |
| Phe | Gly | Lys | Val | Ala | Glu | Lys | Lys | Lys | Lys | Lys | Thr | Glu | Gly | Glu | Phe |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | 175 |     |
| Phe | Glu | Ala | Glu | Lys | Glu | Glu | Lys | Lys | Glu | Ile | Pro | Gln | Val | Lys | Lys |

180 185 190  
Asp Asp Gln Lys Ala Val Asp Ala Ala Leu Ile Lys Ala Ile Glu Ala  
195 200 205  
Val Pro Glu Leu Lys Thr Tyr Leu Gly Ala Arg Phe Ser Leu Lys Gln  
210 215 220  
Gly Met Lys Pro His Glu Leu Val Phe  
225 230

(2) INFORMATION FOR SEQ ID NO:2780:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 206 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..206
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574150

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2780:

Met Tyr His Lys Arg Gly Leu Trp Ala Ile Lys Ala Lys Asn Gly Gly  
1 5 10 15  
Val Phe Pro Arg His Asp Ala Lys Ser Lys Val Asp Ala Pro Val Glu  
20 25 30  
Lys Pro Pro Lys Phe Tyr Pro Ala Glu Asp Val Lys Lys Pro Leu Pro  
35 40 45  
Asn Arg Arg Thr Ala Lys Pro Thr Lys Leu Arg Ala Ser Ile Thr Pro  
50 55 60  
Gly Thr Val Leu Ile Ile Leu Ala Gly Arg Phe Lys Gly Lys Arg Val  
65 70 75 80  
Val Phe Leu Lys Gln Leu Ala Ser Gly Leu Leu Val Thr Gly Pro  
85 90 95  
Phe Lys Ile Asn Gly Val Pro Leu Arg Arg Val Asn Gln Ala Tyr Val  
100 105 110  
Ile Gly Thr Ser Thr Lys Val Asp Ile Ser Gly Val Thr Leu Asp Lys  
115 120 125  
Phe Asp Asp Lys Tyr Phe Gly Lys Val Ala Glu Lys Lys Lys Lys  
130 135 140  
Thr Glu Gly Glu Phe Phe Glu Ala Glu Lys Glu Glu Lys Lys Glu Ile  
145 150 155 160  
Pro Gln Val Lys Lys Asp Asp Gln Lys Ala Val Asp Ala Ala Leu Ile  
165 170 175  
Lys Ala Ile Glu Ala Val Pro Glu Leu Lys Thr Tyr Leu Gly Ala Arg  
180 185 190  
Phe Ser Leu Lys Gln Gly Met Lys Pro His Glu Leu Val Phe  
195 200 205

(2) INFORMATION FOR SEQ ID NO:2781:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1013 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1013
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574151

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2781:

cacaacttac tcttgctcgca tgcttaacgcc gttgacgcat tcagaaaatg caaacagtggt 60  
gctgaggagta aaatagggaat tgcacacagt ccagcttggt tcgaaccaca agaccttgag 120  
catgtggag gttccattga acgtgtgctt gatttcatcc taggatggca ttgggtcca 180  
acaacttatg gagattatcc acaatcgatg aaggatcgtg tcggtcatag attgccaaaa 240

(2) INFORMATION FOR SEQ ID NO:2782:

(A) LENGTH: 278 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

MOLECULE TYPE: peptide

```
(ix) FEATURE:
```

(1X) FEATURE:  
(1A) NAM

(A) NAME/KEY: peptide  
(B) LOCATION: 1-278

(B) LOCATION: 1..278  
(D) OTHER INFORMATION:

(D) OTHER INFORMATION: / Ceres Seq. ID 1574152

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2782:

[illegible]

(2) INFORMATION FOR SEQ ID NO:2783:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 209 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..209

(D) OTHER INFORMATION: / Ceres Seq. ID 1574153

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2783:

```
Met Lys Asp Arg Val Gly His Arg Leu Pro Lys Phe Thr Glu Ala Glu
1 5 10 15
Lys Lys Leu Leu Lys Gly Ser Thr Asp Tyr Val Gly Met Asn Tyr Tyr
20 25 30
Thr Ser Val Phe Ala Lys Glu Ile Ser Pro Asp Pro Lys Asn Pro Ser
35 40 45
Trp Thr Thr Asp Ser Leu Val Asp Trp Asp Ser Lys Ser Val Asp Gly
50 55 60
Tyr Lys Ile Gly Ser Lys Pro Phe Asn Gly Lys Leu Asp Val Tyr Ser
65 70 75 80
Lys Gly Leu Arg Tyr Leu Leu Lys Tyr Ile Lys Asp Asn Tyr Gly Asp
85 90 95
Pro Glu Val Ile Ile Ala Glu Asn Gly Tyr Gly Glu Asp Leu Gly Glu
100 105 110
Lys His Asn Asp Val Asn Phe Gly Thr Gln Asp His Asn Arg Lys Tyr
115 120 125
Tyr Ile Gln Arg His Leu Leu Ser Met His Asp Ala Ile Cys Lys Asp
130 135 140
Lys Val Asn Val Thr Gly Tyr Phe Val Trp Ser Leu Met Asp Asn Phe
145 150 155 160
Glu Trp Gln Asp Gly Tyr Lys Ala Arg Phe Gly Leu Tyr Tyr Ile Asp
165 170 175
Phe Gln Asn Asn Leu Thr Arg His Gln Lys Val Ser Gly Lys Trp Tyr
180 185 190
Ser Glu Phe Leu Lys Pro Gln Phe Pro Thr Ser Lys Leu Arg Glu Glu
195 200 205
Leu
```

(2) INFORMATION FOR SEQ ID NO:2784:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 181 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..181

(D) OTHER INFORMATION: / Ceres Seq. ID 1574154

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2784:

```
Met Asn Tyr Tyr Thr Ser Val Phe Ala Lys Glu Ile Ser Pro Asp Pro
1 5 10 15
Lys Asn Pro Ser Trp Thr Thr Asp Ser Leu Val Asp Trp Asp Ser Lys
20 25 30
Ser Val Asp Gly Tyr Lys Ile Gly Ser Lys Pro Phe Asn Gly Lys Leu
35 40 45
Asp Val Tyr Ser Lys Gly Leu Arg Tyr Leu Leu Lys Tyr Ile Lys Asp
50 55 60
Asn Tyr Gly Asp Pro Glu Val Ile Ile Ala Glu Asn Gly Tyr Gly Glu
```

Met Ala Thr Glu Ser Tyr Glu Ala Ala Ile Lys Gly Leu Asn Asp Leu  
1 5 10 15  
Leu Ser Thr Lys Ala Asp Leu Gly Asn Val Ala Ala Ala Lys Ile Lys

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Val | Pro | Pro | Glu | Asp | Gln | Lys | Arg | His | Ser | Gly | Val | Gly | Ala | Ala |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Val | Glu | Tyr | Ala | Val | Val | His | Leu | Lys | Val | Glu | Asn | Ile | Leu | Val | Ile |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     | 30  |     |     |     |
| Gly | His | Ser | Cys | Gly | Gly | Ile | Lys | Gly | Leu | Met | Ser | Ile | Glu | Asp |     |
|     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| Asp | Ala | Ala | Pro | Thr | Gln | Ser | Asp | Phe | Ile | Glu | Asn | Trp | Val | Lys | Ile |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Gly | Ala | Ser | Ala | Arg | Asn | Lys | Ile | Lys | Glu | Glu | His | Lys | Asp | Leu | Ser |
| 65  |     |     |     | 70  |     |     |     |     |     | 75  |     |     |     | 80  |     |
| Tyr | Asp | Asp | Gln | Cys | Asn | Lys | Cys | Glu | Lys | Glu | Ala | Val | Asn | Val | Ser |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Leu | Gly | Asn | Leu | Leu | Ser | Tyr | Pro | Phe | Val | Arg | Ala | Glu | Val | Val | Lys |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     | 110 |     |     |     |
| Asn | Thr | Leu | Ala | Ile | Arg | Gly | Gly | His | Thr | Asn | Phe | Val | Lys | Gly | Thr |
|     |     | 115 |     |     |     | 120 |     |     |     |     |     | 125 |     |     |     |
| Phe | Asp | Leu | Trp | Glu | Leu | Asp | Phe | Lys | Thr | Thr | Pro | Ala | Phe | Ala | Phe |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |



Ser  
145

(2) INFORMATION FOR SEQ ID NO:2788:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 683 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..683

(D) OTHER INFORMATION: / Ceres Seq. ID 1574162

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2788:

|             |             |            |            |             |             |            |     |
|-------------|-------------|------------|------------|-------------|-------------|------------|-----|
| aacaacttaa  | acagatat    | ttt        | cataaggaaa | atgaagggtg  | agtttttcac  | attgatggca | 60  |
| ataatgtctc  | tctcttagc   | cttctcgta  | gtccatggag | gaggagagtc  | tggaacacct  |            | 120 |
| tctaatacag  | cogctacccc  | gactagccca | accgaaGgat | ccagtgggtc  | aagtgggtca  |            | 180 |
| gctcatggac  | ctaattgggg  | atatagtktg | ggatgggggt | cagccccggg  | aggtgtttat  |            | 240 |
| ggctatgggt  | ctgggtcggg  | tctgtcacca | gatggaggag | gaaaaggggc  | tggattcggg  |            | 300 |
| tttggttcgg  | ggctcaggtc  | aggaactgga | tttgggtctg | gctcggggag  | aggaggagcc  |            | 360 |
| acagacgggtg | gttctggcca  | tggaaagtgg | accggacacg | ctgggttaagg | cgggtggctca |            | 420 |
| ggaagtggaa  | atggtagaag  | atctcctgtg | cgtagagaga | ggagccaaca  | ccgctaaaag  |            | 480 |
| aagttttctt  | gttattatta  | ctaccttaac | acaatcacac | atcgtaaga   | tgataaagct  |            | 540 |
| aaaagaagga  | aaaagaaaaa  | tactatagta | gcattctta  | taattaatgc  | ataaataagg  |            | 600 |
| accaaaaggaa | taagtagtgtg | ggctttaatt | accgctgtac | tttgtaatat  | aactaaacct  |            | 660 |
| ataatatatt  | gtgtctctgc  | gcc        |            |             |             |            |     |

(2) INFORMATION FOR SEQ ID NO:2789:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 135 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..135

(D) OTHER INFORMATION: / Ceres Seq. ID 1574163

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2789:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asn | Asn | Leu | Asn | Arg | Tyr | Phe | Ile | Arg | Lys | Met | Lys | Gly | Glu | Phe | Phe |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     | 15  |     |     |
| Thr | Leu | Met | Ala | Ile | Met | Ser | Leu | Leu | Leu | Ala | Phe | Ser | Leu | Val | His |
|     |     |     | 20  |     |     |     | 25  |     |     |     |     | 30  |     |     |     |
| Gly | Gly | Gly | Glu | Ser | Gly | Thr | Pro | Ser | Asn | Ala | Ala | Ala | Thr | Pro | Thr |
|     |     | 35  |     |     |     |     | 40  |     |     |     | 45  |     |     |     |     |
| Ser | Pro | Thr | Glu | Gly | Ser | Ser | Gly | Ser | Gly | Ser | Ala | His | Gly | Pro |     |
|     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Asn | Trp | Gly | Tyr | Ser | Xaa | Gly | Trp | Gly | Ser | Ala | Pro | Gly | Gly | Gly | Tyr |
|     |     | 65  |     |     | 70  |     |     |     | 75  |     |     |     | 80  |     |     |
| Gly | Tyr | Gly | Ser | Gly | Ser | Gly | Ser | Pro | Asp | Gly | Gly | Gly | Lys | Gly |     |
|     |     |     | 85  |     |     |     | 90  |     |     |     |     |     | 95  |     |     |
| Ala | Gly | Phe | Gly | Phe | Gly | Ser | Gly | Ser | Gly | Ser | Gly | Thr | Gly | Phe | Gly |
|     |     |     | 100 |     |     |     | 105 |     |     |     |     |     | 110 |     |     |
| Ser | Gly | Ser | Gly | Gly | Gly | Gly | Ala | Thr | Asp | Gly | Gly | Ser | Gly | His | Gly |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     |     | 125 |     |     |
| Ser | Gly | Thr | Gly | His | Ala | Gly |     |     |     |     |     |     |     |     |     |
|     |     | 130 |     |     | 135 |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2790:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 157 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:

(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..157  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1574164  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2790:  
Met Glu Glu Glu Ser Leu Glu His Leu Leu Met Gln Pro Leu Pro Arg  
1                  5                  10                  15  
Leu Ala Gln Pro Lys Asp Pro Val Val Gln Val Val Gln Leu Met Asp  
                  20                  25                  30  
Leu Ile Gly Asp Ile Val Xaa Asp Gly Val Gln Pro Arg Glu Val Val  
                  35                  40                  45  
Met Ala Met Val Leu Val Arg Val Arg His Gln Met Glu Glu Glu Lys  
50                  55                  60  
Gly Leu Asp Ser Gly Leu Val Arg Gly Gln Val Gln Glu Leu Asp Leu  
65                  70                  75                  80  
Gly Leu Ala Arg Glu Glu Glu Pro Gln Thr Val Val Leu Ala Met  
                  85                  90                  95  
Glu Val Gly Pro Asp Thr Leu Val Lys Ala Val Ala Gln Glu Val Glu  
100                  105                  110  
Met Val Lys Asp Leu Leu Val Val Glu Arg Gly Ala Asn Thr Ala Lys  
115                  120                  125  
Arg Ser Phe Leu Val Ile Ile Thr Thr Leu Thr Gln Ser His Met Arg  
130                  135                  140  
Lys Met Ile Arg Leu Lys Glu Gly Lys Arg Lys Ile Leu  
145                  150                  155

(2) INFORMATION FOR SEQ ID NO:2791:  
    (i) SEQUENCE CHARACTERISTICS:  
        (A) LENGTH: 147 amino acids  
        (B) TYPE: amino acid  
        (C) STRANDEDNESS:  
        (D) TOPOLOGY: linear  
    (ii) MOLECULE TYPE: peptide  
    (ix) FEATURE:  
        (A) NAME/KEY: peptide  
        (B) LOCATION: 1..147  
        (D) OTHER INFORMATION: / Ceres Seq. ID 1574165  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2791:  
Met Gln Pro Leu Pro Arg Leu Ala Gln Pro Lys Asp Pro Val Val Gln  
1                  5                  10                  15  
Val Val Gln Leu Met Asp Leu Ile Gly Asp Ile Val Xaa Asp Gly Val  
                  20                  25                  30  
Gln Pro Arg Glu Val Val Met Ala Met Val Leu Val Arg Val Arg His  
35                  40                  45  
Gln Met Glu Glu Glu Lys Gly Leu Asp Ser Gly Leu Val Arg Gly Gln  
50                  55                  60  
Val Gln Glu Leu Asp Leu Gly Leu Ala Arg Glu Glu Glu Glu Pro Gln  
65                  70                  75                  80  
Thr Val Val Leu Ala Met Glu Val Gly Pro Asp Thr Leu Val Lys Ala  
                  85                  90                  95  
Val Ala Gln Glu Val Glu Met Val Lys Asp Leu Leu Val Val Glu Arg  
100                  105                  110  
Gly Ala Asn Thr Ala Lys Arg Ser Phe Leu Val Ile Ile Thr Thr Leu  
115                  120                  125  
Thr Gln Ser His Met Arg Lys Met Ile Arg Leu Lys Glu Gly Lys Arg  
130                  135                  140  
Lys Ile Leu  
145

(2) INFORMATION FOR SEQ ID NO:2792:  
    (i) SEQUENCE CHARACTERISTICS:

(xi) SEQUENCE DESCRIPTION: Day 15 Revisited

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Pro | Phe | Gly | Leu | Lys | Asn | Ala | Gly | Ala | Thr | Tyr | Gln | Arg | Phe | Val |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Asn | Lys | Ile | Phe | Ala | Leu | Gln | Ile | Gly | Lys | Thr | Met | Glu | Val | Tyr | Ile |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |  |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|--|--|
| 20  |     |     |     |     |     |     |     |     |     | 25  |     |     |     |     | 30  |  |  |  |  |
| Asp | Asp | Met | Leu | Val | Lys | Ser | Met | Thr | Glu | Lys | Asp | His | Ile | Ser | His |  |  |  |  |
| 35  | 35  | 35  |     |     |     |     | 40  |     |     |     | 45  |     |     |     |     |  |  |  |  |
| Leu | Arg | Glu | Cys | Phe | Lys | Gln | Leu | Asn | Leu | Tyr | Asn | Val | Lys | Leu | Asn |  |  |  |  |
| 50  | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |  |  |  |  |
| Pro | Ala | Lys | Cys | Arg | Phe | Gly | Val | Arg | Ser | Gly | Ile | Glu | Ala | Asn | Pro |  |  |  |  |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     |     | 80  |  |  |  |  |
| Lys | Gln | Ile | Glu | Ala | Leu | Phe | Gly | Met | Ala | Ser | Pro | Gln | Asn | Lys | Arg |  |  |  |  |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |  |  |  |  |
| Glu | Val | Gln | Cys | Leu | Thr | Gly | Arg | Val | Ala | Ala | Leu | Asn | Arg | Phe | Ile |  |  |  |  |
|     |     |     |     | 100 |     |     |     | 105 |     |     |     |     |     | 110 |     |  |  |  |  |
| Ser | Arg | Ser | Thr | Glu | Lys | Cys | Leu | Ala | Phe | Tyr | Val | Val | Leu | Arg | Gly |  |  |  |  |
|     |     |     |     | 115 |     |     | 120 |     |     |     |     | 125 |     |     |     |  |  |  |  |
| Asn | Lys | Lys | Phe | Glu | Trp | Thr | Thr | Arg | Cys | Glu | Glu | Ala | Phe | Gln | Glu |  |  |  |  |
|     |     |     |     | 130 |     | 135 |     |     |     |     | 140 |     |     |     |     |  |  |  |  |
| Leu | Lys | Lys | Tyr | Leu | Ala | Thr | Pro | Pro | Ile | Leu | Lys | Pro | Val | Ile |     |  |  |  |  |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |     |  |  |  |  |
| Gly | Glu | Pro | Gln | Tyr | Leu | Tyr | Val | Ala | Val | Ser | Asp | Thr | Thr | Val | Ser |  |  |  |  |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |  |  |  |  |
| Gly | Glu | Leu | Val | Arg | Glu | Asp | Arg | Gly | Glu | Gln | Lys | Leu | Ile | Phe | Tyr |  |  |  |  |
|     |     |     |     | 180 |     |     |     | 185 |     |     |     |     | 190 |     |     |  |  |  |  |
| Val | Ser | Gln | Thr | Phe | Thr | Ser | Ala | Glu | Ser | Arg | Tyr | Pro | Gln | Met | Glu |  |  |  |  |
|     |     |     |     | 195 |     |     | 200 |     |     |     |     | 205 |     |     |     |  |  |  |  |
| Lys | Ser | Ala | Leu | Ala | Val | Val | Met | Ser | Ala | Gln | Lys | Leu | Arg | Pro | Tyr |  |  |  |  |
|     |     |     |     | 210 |     | 215 |     |     |     |     | 220 |     |     |     |     |  |  |  |  |
| Phe | Gln | Ser | His | Ser | Ile | Ile | Val | Met | Gly | Ser | Met | Pro | Leu | Cys | Val |  |  |  |  |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     | 240 |     |  |  |  |  |
| Ile | Leu | His | Ser | Pro | Ser | Gln | Ser | Gly | Arg | Leu | Ala | Lys | Trp | Thr | Ile |  |  |  |  |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |  |  |  |  |
| Glu | Leu | Ser | Glu | Tyr | Asp | Ile | Glu | Tyr | Gln | Asn | Lys | Thr | Cys | Ala | Lys |  |  |  |  |
|     |     |     |     | 260 |     |     |     | 265 |     |     |     |     |     | 270 |     |  |  |  |  |
| Ser | Arg | Leu | Val | Ile | Glu | Ala | Arg | Leu | Gly | Cys | Arg | His | Pro | Ser | His |  |  |  |  |
|     |     |     |     | 275 |     |     | 280 |     |     |     |     | 285 |     |     |     |  |  |  |  |
| Leu | Thr | Asn | Arg | Arg | Gly | Pro | Arg | Val | Val | Ile | Lys | Ile | Lys | Leu | Arg |  |  |  |  |
|     |     |     |     | 290 |     | 295 |     |     |     |     | 300 |     |     |     |     |  |  |  |  |
| Gly | Tyr | Gln | Gln | Cys | Gly | Arg | Leu | Ile | Ala | Asn | Gln | Phe | Asn | Gly | Glu |  |  |  |  |
| 305 |     |     |     |     | 310 |     |     |     | 315 |     |     |     |     | 320 |     |  |  |  |  |
| Tyr | Thr | Thr | Gln | Asp | Lys | Lys | Met | Glu | Ala | Tyr | Leu | Ile | His | Val | Gln |  |  |  |  |
|     |     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |     |  |  |  |  |
| Asn | Leu | Ala | Lys | Asn | Phe | Asp | Glu | Phe | Glu | Leu | Thr | Arg | Ile | Pro | Arg |  |  |  |  |
|     |     |     |     | 340 |     |     |     | 345 |     |     |     |     |     | 350 |     |  |  |  |  |
| Gly | Glu | Asn | Thr | Ser | Ala | Asp | Ala | Leu | Ala | Ala | Leu | Ala | Ser | Thr | Ser |  |  |  |  |
|     |     |     |     | 355 |     | 360 |     |     |     |     | 365 |     |     |     |     |  |  |  |  |
| Asp | Thr | Ile | Leu | Lys | Arg | Val | Ile | Pro | Val | Glu | Phe | Ile | Glu | Lys | Pro |  |  |  |  |
|     |     |     |     | 370 |     | 375 |     |     |     |     | 380 |     |     |     |     |  |  |  |  |
| Ser |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |  |  |

Gln Cys Glu Lys Cys Gln Arg His Ala Gln Thr Ile His Gln Pro Ala  
515 520 525  
Glu Leu Leu Ser Ser Ile Ala Ser Pro Tyr Pro Phe Met Arg Trp Ser  
530 535 540  
Met Asp Ile Ile Gly Pro Met His Pro Ser Lys Glu Lys Lys Ile Val  
545 550 555 560  
Leu Val Leu Thr Asp Tyr Phe Ser Lys Trp Ile Glu Ala Glu Phe Tyr  
565 570 575  
Ala Ser Ile Lys Asp Ala Gln Val Glu Asn Phe Val Leu Lys His Ile  
580 585 590  
Leu Cys Arg His Gly Ile Pro Tyr Glu Ile Val Thr Asp Asn Gly Ser  
595 600 605  
Gln Phe Ile Ser Thr Arg Phe Gln Gly Phe Cys Asp Lys Trp Gly Ile  
610 615 620  
Arg Leu Ser Lys Ser Thr Pro Gln Tyr Pro Gln Gly Asn Gly Gln Ala  
625 630 635 640  
Glu Ala Ala Asn Glu Leu Glu Gly Val Leu Trp Leu His Arg Thr Thr  
645 650 655  
Pro Arg Arg Ala Thr Arg Glu Thr Pro Phe Ala Ser Val Tyr Gly Thr  
660 665 670  
Glu Cys Val Ile Pro Ala Glu Met Ile Val Pro Ser Leu Arg Arg Ser  
675 680 685  
Leu Ser Pro Glu Asp Asp Pro Asp Asn Thr Gln Arg Pro Leu Asp Glu  
690 695 700  
Leu Asp Leu Ile Asp Glu  
705 710

(2) INFORMATION FOR SEQ ID NO:2794:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 683 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..683

(D) OTHER INFORMATION: / Ceres Seq. ID 1574197

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2794:

Met Glu Val Tyr Ile Asp Asp Met Leu Val Lys Ser Met Thr Glu Lys  
1 5 10 15  
Asp His Ile Ser His Leu Arg Glu Cys Phe Lys Gln Leu Asn Leu Tyr  
20 25 30  
Asn Val Lys Leu Asn Pro Ala Lys Cys Arg Phe Gly Val Arg Ser Gly  
35 40 45  
Ile Glu Ala Asn Pro Lys Gln Ile Glu Ala Leu Phe Gly Met Ala Ser  
50 55 60  
Pro Gln Asn Lys Arg Glu Val Gln Cys Leu Thr Gly Arg Val Ala Ala  
65 70 75 80  
Leu Asn Arg Phe Ile Ser Arg Ser Thr Glu Lys Cys Leu Ala Phe Tyr  
85 90 95  
Val Val Leu Arg Gly Asn Lys Lys Phe Glu Trp Thr Thr Arg Cys Glu  
100 105 110  
Glu Ala Phe Gln Glu Leu Lys Lys Tyr Leu Ala Thr Pro Pro Ile Leu  
115 120 125  
Ala Lys Pro Val Ile Gly Glu Pro Gln Tyr Leu Tyr Val Ala Val Ser  
130 135 140  
Asp Thr Thr Val Ser Gly Glu Leu Val Arg Glu Asp Arg Gly Glu Gln  
145 150 155 160  
Lys Leu Ile Phe Tyr Val Ser Gln Thr Phe Thr Ser Ala Glu Ser Arg  
165 170 175  
Tyr Pro Gln Met Glu Lys Leu Ala Leu Val Val Met Ser Ala Gln

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Lys | Leu | Arg | Pro | Tyr | Phe | Gln | Ser | His | Ser | Ile | Ile | Val | Met | Gly | Ser |
| Met | Pro | Leu | Cys | Val | Ile | Leu | His | Ser | Pro | Ser | Gln | Ser | Gly | Arg | Leu |
| Ala | Lys | Trp | Thr | Ile | Glu | Leu | Ser | Glu | Tyr | Asp | Ile | Glu | Tyr | Gln | Asn |
| Lys | Thr | Cys | Ala | Lys | Ser | Arg | Leu | Val | Ile | Glu | Ala | Arg | Leu | Gly | Cys |
| Arg | His | Pro | Ser | His | Leu | Thr | Asn | Arg | Arg | Gly | Pro | Arg | Val | Val | Ile |
| Lys | Ile | Lys | Leu | Arg | Gly | Tyr | Gln | Gln | Cys | Gly | Arg | Leu | Ile | Ala | Asn |
| Gln | Phe | Asn | Gly | Glu | Tyr | Thr | Thr | Gln | Asp | Lys | Lys | Met | Glu | Ala | Tyr |
| Leu | Ile | His | Val | Gln | Asn | Leu | Ala | Lys | Asn | Phe | Asp | Glu | Phe | Glu | Leu |
| Thr | Arg | Ile | Pro | Arg | Gly | Glu | Asn | Thr | Ser | Ala | Asp | Ala | Leu | Ala | Ala |
| Leu | Ala | Ser | Thr | Ser | Asp | Thr | Ile | Leu | Lys | Arg | Val | Ile | Pro | Val | Glu |
| Phe | Ile | Glu | Lys | Pro | Ser | Ile | Glu | Leu | Gly | Lys | Glu | Glu | His | Val | Leu |
| Pro | Ile | Gln | Ile | Ser | Ala | Asp | Gln | Asp | Asp | Pro | Asp | Asp | Cys | Asn | Ser |
| Glu | Trp | Met | Glu | Pro | Ile | Ile | Ser | Tyr | Ile | Ser | Glu | Gly | Lys | Leu | Pro |
| Ser | Asp | Lys | Trp | Lys | Ala | Arg | Lys | Leu | Lys | Ala | Gln | Ala | Ala | Arg | Phe |
| Val | Leu | Val | Asp | Ala | Lys | Leu | Tyr | Lys | Trp | Arg | Leu | Ser | Gly | Pro | Leu |
| Met | Thr | Cys | Val | Glu | Ala | Glu | Ala | Ile | Cys | Lys | Ile | Met | Lys | Glu | Ile |
| His | Gly | Gly | Ser | Cys | Gly | Asn | His | Ser | Gly | Gly | Arg | Ala | Leu | Ala | Ile |
| Lys | Ile | Lys | Arg | Gln | Gly | Phe | Phe | Trp | Pro | Thr | Met | Ile | Lys | Asp | Xaa |
| Glu | Asn | Phe | Ser | Lys | Gln | Cys | Glu | Lys | Cys | Gln | Arg | His | Ala | Gln | Thr |
| Ile | His | Gln | Pro | Ala | Glu | Leu | Leu | Ser | Ser | Ile | Ala | Ser | Pro | Tyr | Pro |
| Phe | Met | Arg | Trp | Ser | Met | Asp | Ile | Ile | Gly | Pro | Met | His | Pro | Ser | Lys |
| Glu | Lys | Lys | Ile | Val | Leu | Val | Leu | Thr | Asp | Tyr | Phe | Ser | Lys | Trp | Ile |
| Glu | Ala | Glu | Phe | Tyr | Ala | Ser | Ile | Lys | Asp | Ala | Gln | Val | Glu | Asn | Phe |
| Val | Leu | Lys | His | Ile | Lys | Cys | Arg | His | Gly | Ile | Pro | Tyr | Glu | Ile | Val |
| Thr | Asp | Asn | Gly | Ser | Gln | Phe | Ile | Ser | Thr | Arg | Phe | Gln | Gly | Phe | Cys |
| Asp | Lys | Trp | Gly | Ile | Arg | Leu | Ser | Lys | Ser | Thr | Pro | Gln | Tyr | Pro | Gln |
| Gly | Asn | Gly | Gln | Ala | Glu | Ala | Ala | Asn | Glu | Leu | Glu | Gly | Val | Leu | Trp |
| Leu | His | Arg | Thr | Thr | Pro | Arg | Arg | Ala | Thr | Arg | Glu | Thr | Pro | Phe | Ala |
| Ser | Val | Tyr | Gly | Thr | Glu | Cys | Val | Ile | Pro | Ala | Glu | Met | Ile | Val | Pro |
| Ser | Leu | Arg | Arg | Ser | Leu | Ser | Pro | Glu | Asp | Asp | Pro | Asp | Asn | Thr | Gln |

Arg Pro Leu Asp Glu Leu Asp Leu Ile Asp Glu  
675 680

(2) INFORMATION FOR SEQ ID NO:2795:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 106 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..106
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574203

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2795:

accgtcgtcg ttgaggcccc accgaagaca ccaccagttc caaatttcga ttctactccc 60  
ttcgactaca ttttgagaga atctggttac aagaacgttt tagtgc

(2) INFORMATION FOR SEQ ID NO:2796:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..35
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574204

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2796:

Thr Val Val Val Glu Ala Pro Pro Lys Thr Pro Pro Val Pro Asn Phe  
1 5 10 15  
Asp Phe Thr Pro Phe Asp Tyr Ile Leu Glu Lys Ser Ala Tyr Lys Asn  
20 25 30  
Val Leu Val  
35

(2) INFORMATION FOR SEQ ID NO:2797:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..33
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574205

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2797:

Pro Ser Ser Leu Arg Pro His Arg Arg His His Gln Phe Gln Ile Ser  
1 5 10 15  
Ile Ser Leu Pro Ser Thr Thr Phe Trp Arg Asn Leu Leu Thr Arg Thr  
20 25 30  
Phe

(2) INFORMATION FOR SEQ ID NO:2798:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 162 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -

(B) LOCATION: 1.162  
(D) OTHER INFORMATION: / Ceres Seq. ID 1574218  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2798:  
acggatacat caaaggcgat agaacaaagc acatcctacc aaaattcttc tacacacacg 60  
atctacaaaa gagcgcgat gtacgagttc tacagatccg ttcgaaatgga atattctggc 120  
tgactttatt acaaaggcgc tacctactgc tactttcaag aa  
(2) INFORMATION FOR SEQ ID NO:2799:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 40 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1.40  
(D) OTHER INFORMATION: / Ceres Seq. ID 1574219  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2799:  
Thr Asp Thr Ser Lys Ala Ile Glu Gln Ser Thr Ser Tyr Gln Asn Ser  
1 5 10 15  
Ser Thr His Thr Ile Tyr Lys Arg Ala Ala Met Tyr Glu Phe Tyr Arg  
20 25 30  
Ser Val Arg Met Glu Tyr Ser Gly  
35 40  
(2) INFORMATION FOR SEQ ID NO:2800:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 53 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1.53  
(D) OTHER INFORMATION: / Ceres Seq. ID 1574220  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2800:  
Gly Tyr Ile Lys Gly Asp Arg Thr Lys His Ile Leu Pro Lys Phe Phe  
1 5 10 15  
Tyr Thr His Asp Leu Gln Lys Ser Gly Asp Val Arg Val Leu Gln Ile  
20 25 30  
Arg Ser Asn Gly Ile Phe Trp Leu Thr Tyr Ser Gln Arg Arg Tyr Leu  
35 40 45  
Leu Leu Leu Ser Arg  
50  
(2) INFORMATION FOR SEQ ID NO:2801:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 581 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
(A) NAME/KEY: -  
(B) LOCATION: 1.581  
(D) OTHER INFORMATION: / Ceres Seq. ID 1574260  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2801:  
ataatggcat aattccatat ttctccagct gttccgcccga gcgaacgacc cacaaccaga 60  
agccaccocat tggcgtagcg gaggcgatcg gagcatcccg tcccaagagg agaaactccg 120  
gccggcgacg cgggggaaaa tggggaagac gccggtgcgg atgaagcgcg tgggtgacgc 180  
gctgtcgccc ttccagcaga aggtgatgcc ggggctgtgg aaggacatca ccaccaagat 240  
ccaccacaag gtcaccgaga actggatctc cgccaagctc ctccctcacc ccgtcgctcg 300



cacctaccaa tacgcatgtt ggtacaaaga gcaggagaag ctttcccaca gatactaaat 360  
gggatgtcct ccaagtttgc gcggcttgct gcagttgaat tttccatgat gggttgtata 420  
atctgtcaat gtcatctttt tgctcagttt tagttcaacc cattttcaacc ttcccatatg 480  
catatacggg atctgtgcct ggcacacata ttttgaggct agctaaatat gaaccttttg 540  
tctcttaagt tgttaaataa agcaaaAtba tctgacagt t

(2) INFORMATION FOR SEQ ID NO:2802:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..53

(D) OTHER INFORMATION: / Ceres Seq. ID 1574261

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2802:

Asn Gly Ile Ile Pro Tyr Phe Ser Ser Cys Ser Ala Glu Arg Thr Thr  
1 5 10 15  
His Asn Gln Lys Pro Pro Ile Gly Val Arg Glu Ala Ile Gly Ala Ser  
20 25 30  
Arg Pro Lys Arg Arg Asn Ser Gly Arg Arg Arg Gly Gly Lys Trp Gly  
35 40 45  
Arg Arg Arg Cys Gly  
50

(2) INFORMATION FOR SEQ ID NO:2803:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 72 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..72

(D) OTHER INFORMATION: / Ceres Seq. ID 1574262

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2803:

Met Gly Lys Thr Pro Val Arg Met Lys Ala Val Val Tyr Ala Leu Ser  
1 5 10 15  
Pro Phe Gln Gln Lys Val Met Pro Gly Leu Trp Lys Asp Ile Thr Thr  
20 25 30  
Lys Ile His His Lys Val Thr Glu Asn Trp Ile Ser Ala Thr Leu Leu  
35 40 45  
Leu Thr Pro Val Val Gly Thr Tyr Gln Tyr Ala Met Trp Tyr Lys Glu  
50 55 60  
Gln Glu Lys Leu Ser His Arg Tyr  
65 70

(2) INFORMATION FOR SEQ ID NO:2804:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 65 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..65

(D) OTHER INFORMATION: / Ceres Seq. ID 1574263

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2804:

Met Lys Ala Val Val Tyr Ala Leu Ser Pro Phe Gln Gln Lys Val Met  
1 5 10 15

Pro Gly Leu Trp Lys Asp Ile Thr Thr Lys Ile His His Lys Val Thr  
20 25 30  
Glu Asn Trp Ile Ser Ala Thr Leu Leu Leu Thr Pro Val Val Gly Thr  
35 40 45  
Tyr Gln Tyr Ala Met Trp Tyr Lys Glu Gln Glu Lys Leu Ser His Arg  
50 55 60

Tyr  
65

(2) INFORMATION FOR SEQ ID NO:2805:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 809 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..809
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574264

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2805:

|             |            |            |             |             |             |     |
|-------------|------------|------------|-------------|-------------|-------------|-----|
| caggatagtt  | tgggtaccct | cgtcgtcgtc | tcactcaccc  | cgccttcacg  | cctccctcac  | 60  |
| caataaaggt  | cccgcccttt | tccgacattc | acagggggga  | caggaataca  | gcggccatgg  | 120 |
| cctcgattcc  | ggcgacgacc | ttcgccgtca | tcttatccgt  | cctcttctgt  | gcgcggcgctg | 180 |
| gcaccgcgct  | cgacaacgac | ctccccgact | acgtcatcca  | gggcccgcgtc | tattgcgaca  | 240 |
| cctgcgcgct  | cgggttcgtg | accaatgtca | ccgagtcacat | cgccggcgccg | aaggtgagggc | 300 |
| tggagtgcac  | gcactctggc | accggcgaag | tcgagcgcctc | catcgacggg  | gtgaccgacg  | 360 |
| ggaacggcgc  | gtacacgwtc | gagctcaagg | acagccacga  | ggaggacatc  | tgcgaggtgg  | 420 |
| ctcttggtga  | gagcccgccg | aaggactGgc | gaccaggtgc  | agggcgacag  | ggaccgcgcc  | 480 |
| ggcgtctctg  | tcaccaggaa | cgtcggcatc | agcgacaacc  | tgcgccccgc  | caaccgcctc  | 540 |
| ggctacctca  | aggacgtgcc | gctgcccatc | tgccctcgcg  | tgctcaaaac  | gttggtactcg | 600 |
| gacgacgacg  | acgdtcagta | atagcacatc | gacgacgacg  | dtcgatatgt  | aatagcacgt  | 660 |
| cgctcgacgac | cgacgcgacg | cgtcgacagc | tggtctggac  | taaacccaaa  | atcctcttca  | 720 |
| cctggattac  | aaatatgtaa | ctgagaaagg | aaaggaaaac  | aaaaatgtaa  | ctgcgtggct  | 780 |
| gtaccaaaatt | ctgagtgctg | gattcttgc  |             |             |             |     |

(2) INFORMATION FOR SEQ ID NO:2806:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 207 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..207
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574265

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2806:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Ser | Ile | Pro | Ala | Thr | Thr | Phe | Ala | Val | Ile | Leu | Ser | Val | Leu |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     | 15  |     |     |     |
| Phe | Cys | Ala | Ala | Ala | Gly | Thr | Ala | Val | Asp | Asn | Asp | Leu | Pro | Asp | Tyr |
|     |     |     |     | 20  |     |     |     | 25  |     |     |     | 30  |     |     |     |
| Val | Ile | Gln | Gly | Arg | Val | Tyr | Cys | Asp | Thr | Cys | Arg | Ala | Gly | Phe | Val |
|     |     |     |     | 35  |     |     |     | 40  |     |     |     | 45  |     |     |     |
| Thr | Asn | Val | Thr | Glu | Tyr | Ile | Ala | Gly | Ala | Lys | Val | Arg | Leu | Glu | Cys |
|     |     |     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |
| Lys | His | Phe | Gly | Thr | Gly | Lys | Leu | Glu | Arg | Ser | Ile | Asp | Gly | Val | Thr |
|     |     |     |     | 65  |     |     |     | 70  |     |     |     | 75  |     |     | 80  |
| Asp | Gly | Asn | Gly | Thr | Tyr | Thr | Xaa | Glu | Leu | Lys | Asp | Ser | His | Glu | Glu |
|     |     |     |     | 85  |     |     |     | 90  |     |     |     | 95  |     |     |     |
| Asp | Ile | Cys | Glu | Val | Val | Leu | Val | Glu | Ser | Pro | Arg | Lys | Asp | Trp | Arg |
|     |     |     |     | 100 |     |     |     | 105 |     |     |     | 110 |     |     |     |
| Pro | Gly | Ala | Gly | Gly | Gln | Gly | Pro | Arg | Arg | Pro | Xaa | His | Gln | Glu |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Arg | Arg | His | Gln | Arg | Gln | Pro | Ala | Pro | Arg | Gln | Pro | Ala | Arg | Leu | Pro |
| 130 |     |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Gln | Gly | Arg | Ala | Ala | Ala | His | Leu | Arg | Leu | Ala | Ala | Gln | Thr | Val | Gly |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |     |
| Leu | Gly | Arg | Arg | Arg | Xaa | Ser | Val | Ile | Ala | His | Arg | Arg | Arg | Xaa | Ser |
|     |     |     |     | 165 |     |     |     |     |     | 170 |     |     |     | 175 |     |
| Ile | Cys | Asn | Ser | Thr | Ser | Ser | Thr | Thr | Asp | Arg | Ser | Arg | Arg | Arg | Leu |
|     |     |     |     | 180 |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Ala | Gly | Thr | Lys | Pro | Gln | Ile | Leu | Phe | Thr | Trp | Ile | Thr | Asn | Met |     |
|     |     |     |     | 195 |     |     | 200 |     |     |     |     | 205 |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2807:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 645 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..645
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574297

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2807:

|             |            |            |            |            |            |     |
|-------------|------------|------------|------------|------------|------------|-----|
| atcggtgagg  | cgagcccgga | gtggaactgt | ggaagcgttg | agcttttttc | ttctttgtct | 60  |
| tgctgcgcaa  | gaagaaggga | aacgagaggg | ggcgccgcat | ggcgaagagg | ctgctcccgt | 120 |
| cgctgaaccg  | gggtcgtggg | gagaagctgg | tgacgcccga | gaagaccgcc | ggcgccatcc | 180 |
| tcgtcccgga  | aacatccaag | cagattaggt | tgatgtcttt | cctgagactg | ttgcctcaaa | 240 |
| ggctaccocga | acttatcagg | caggtggagc | aagatgttga | gactgtaatc | cacgtttctc | 300 |
| agccgggtcc  | aataggaatt | Ggtggagcac | aaattcacag | acgcggagat | cttagagggc | 360 |
| agggctacag  | tgaagaagGg | cagtgataa  | ttggcgaa   | aattggacc  | ttgagagaaa | 420 |
| tgttagcaga  | taattggaaa | aaatataccc | ctggtgtctt | ctatcaacag | twattgnbvk | 480 |
| raatagggtg  | ccatggctgg | atgcagttgt | tgccattagt | tagatttgag | cacgatctgc | 540 |
| ttatcggggg  | ttatgttaac | tggtctaaat | gacacgtctg | ttctctttg  | tttcatgggt | 600 |
| tgaaaacgttc | atatttagag | aatgcagtaa | ttcgactccg | attcgc     |            |     |

(2) INFORMATION FOR SEQ ID NO:2808:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 157 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..157
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574298

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2808:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Lys | Arg | Leu | Leu | Pro | Ser | Leu | Asn | Arg | Val | Leu | Val | Glu | Lys |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     | 15  |     |     |     |
| Leu | Val | Gln | Pro | Lys | Lys | Thr | Ala | Gly | Ile | Leu | Val | Pro | Glu | Thr |     |
|     |     |     | 20  |     |     |     | 25  |     |     |     | 30  |     |     |     |     |
| Ser | Lys | Gln | Ile | Arg | Leu | Met | Ser | Phe | Leu | Arg | Leu | Leu | Pro | Gln | Arg |
|     |     |     | 35  |     |     | 40  |     |     |     | 45  |     |     |     |     |     |
| Leu | Pro | Gln | Leu | Ile | Arg | Gln | Val | Glu | Gln | Asp | Val | Glu | Thr | Val | Ile |
|     |     |     | 50  |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| His | Val | Leu | Gln | Pro | Gly | Pro | Ile | Gly | Ile | Gly | Gly | Ala | Gln | Ile | His |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Arg | Arg | Gly | Asp | Leu | Arg | Gly | Gln | Gly | Tyr | Ser | Glu | Lys | Arg | Gln | Trp |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     | 95  |     |     |
| Ile | Ile | Gly | Glu | Glu | Ile | Gly | Pro | Leu | Arg | Glu | Met | Leu | Ala | Asp | Lys |
|     |     |     | 100 |     |     |     | 105 |     |     |     |     | 110 |     |     |     |
| Trp | Lys | Lys | Tyr | Thr | Pro | Gly | Val | Phe | Tyr | Gln | Gln | Xaa | Leu | Xaa | Xaa |

115 120 125  
Ile Gly Cys His Gly Trp Met Gln Leu Leu Pro Leu Val Arg Phe Glu  
130 135 140  
His Asp Leu Leu Ile Gly Ser Tyr Val Asn Cys Ser Lys  
145 150 155

(2) INFORMATION FOR SEQ ID NO:2809:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..119

(D) OTHER INFORMATION: / Ceres Seq. ID 1574299

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2809:

Met Ser Phe Leu Arg Leu Leu Pro Gln Arg Leu Pro Gln Leu Ile Arg  
1 5 10 15  
Gln Val Glu Gln Asp Val Glu Thr Val Ile His Val Leu Gln Pro Gly  
20 25 30  
Pro Ile Gly Ile Gly Gly Ala Gln Ile His Arg Arg Gly Asp Leu Arg  
35 40 45  
Gly Gln Gly Tyr Ser Glu Lys Arg Gln Trp Ile Ile Gly Glu Glu Ile  
50 55 60  
Gly Pro Leu Arg Glu Met Leu Ala Asp Lys Trp Lys Lys Tyr Thr Pro  
65 70 75 80  
Gly Val Phe Tyr Gln Gln Xaa Leu Xaa Xaa Ile Gly Cys His Gly Trp  
85 90 95  
Met Gln Leu Leu Pro Leu Val Arg Phe Glu His Asp Leu Leu Ile Gly  
100 105 110  
Ser Tyr Val Asn Cys Ser Lys  
115

(2) INFORMATION FOR SEQ ID NO:2810:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 766 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -

- (B) LOCATION: 1..766

(D) OTHER INFORMATION: / Ceres Seq. ID 1574312

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2810:

agatcagcat tcaaaactagg gtttactcct gccgctccga gaaaacaaa aagcgtcast 60  
ccgcgcggctt cctccgcgcct ttctcccccgc cgcgcgcgcgc gccgctcctt cctcagcgca 120  
ggcagcgcaa gatgaagctc gtcagggttcc ttatgaagct gaacaatgag acgggtcacca 180  
tcgagctcaa gaacggcacg gttgtacacg gccacatcac cgggtgttagc ataagcatga 240  
acactcatct gaagacagtg aagctttacac tgaaaggga gaacacctgta acacttgacc 300  
acctcagcgt gcgagggaac aacatccgcct actacatcct tcccgacagc ttaaacctgg 360  
aaacottgct ggtagaggaa acccctaggg tgaagcctaa gaagccaact acaggaagac 420  
ctttggggcg tggtcgcggc cgaggctcgt gacgtggtcg gggccggggg Ccagcgtgag 480  
ctttatcgtt cccctgctgt cggctccctt gcaagacaag ttctctctac aatgtaaaac 540  
dtctttctct tgcacgcgtg gtgaaagaat gttgcactgt taccttctgt atgaaggtgg 600  
acgdaatatc tcaatgtcag tagttcttgc tgtgaaatca cgctgtctac ctggccccc 660  
tactcatgcc trctcttaggt ttactactcta gttratttgt aatgttttt ttctccccc 720  
tgaatacat gtaagctgcc gcagagcttt ggatgtctag ggttgt

(2) INFORMATION FOR SEQ ID NO:2811:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 158 amino acids

- (B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..158  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1574313  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2811:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Ile | Ser | Ile | Gln | Thr | Arg | Val | Tyr | Ser | Cys | Arg | Ser | Glu | Lys | Thr | Asn |  |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Lys | Arg | Xaa | Ser | Ala | Gly | Phe | Leu | Arg | Ala | Phe | Ser | Pro | Pro | Xaa | Pro |  |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Pro | Pro | Leu | Leu | Pro | Tyr | Ala | Arg | His | Ala | Lys | Met | Lys | Leu | Val | Arg |  |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Phe | Leu | Met | Lys | Leu | Asn | Asn | Glu | Thr | Val | Thr | Ile | Glu | Leu | Lys | Asn |  |
|     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |  |
| Gly | Thr | Val | Val | His | Gly | Thr | Ile | Thr | Gly | Val | Asp | Ile | Ser | Met | Asn |  |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     |     | 80  |  |
| Thr | His | Leu | Lys | Thr | Val | Lys | Leu | Thr | Leu | Lys | Gly | Lys | Asn | Pro | Val |  |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     | 95  |     |     |  |
| Thr | Leu | Asp | His | Leu | Ser | Val | Arg | Gly | Asn | Asn | Ile | Arg | Tyr | Tyr | Ile |  |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |
| Leu | Pro | Asp | Ser | Leu | Asn | Leu | Glu | Thr | Leu | Leu | Val | Glu | Glu | Thr | Pro |  |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |  |
| Arg | Val | Lys | Pro | Lys | Lys | Pro | Thr | Thr | Gly | Lys | Pro | Leu | Gly | Arg | Gly |  |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |  |
| Arg | Gly | Arg | Gly | Arg | Gly | Arg | Gly | Arg | Gly | Arg | Gly | Pro | Arg |     |     |  |
| 145 |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:2812:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 115 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
    (B) LOCATION: 1..115  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1574314

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2812:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Lys | Leu | Val | Arg | Phe | Leu | Met | Lys | Leu | Asn | Asn | Glu | Thr | Val | Thr |  |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     | 15  |     |     |  |
| Ile | Glu | Leu | Lys | Asn | Gly | Thr | Val | Val | His | Gly | Thr | Ile | Thr | Gly | Val |  |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Asp | Ile | Ser | Met | Asn | Thr | His | Leu | Lys | Thr | Val | Lys | Leu | Thr | Leu | Lys |  |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Gly | Lys | Asn | Pro | Val | Thr | Leu | Asp | His | Leu | Ser | Val | Arg | Gly | Asn | Asn |  |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |
| Ile | Arg | Tyr | Tyr | Ile | Leu | Pro | Asp | Ser | Leu | Asn | Leu | Glu | Thr | Leu | Leu |  |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |  |
| Val | Glu | Glu | Thr | Pro | Arg | Val | Lys | Pro | Lys | Lys | Pro | Thr | Thr | Gly | Lys |  |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |  |
| Pro | Leu | Gly | Arg | Gly | Arg | Gly | Arg | Gly | Arg | Gly | Arg | Gly | Arg | Gly | Arg |  |
|     | 100 |     |     |     |     |     | 105 |     |     |     |     |     | 110 |     |     |  |
| Gly | Pro | Arg |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|     | 115 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:2813:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 108 amino acids  
    (B) TYPE: amino acid

(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..108  
(D) OTHER INFORMATION: / Ceres Seq. ID 1574315  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2813:  
Met Lys Leu Asn Asn Glu Thr Val Thr Ile Glu Leu Lys Asn Gly Thr  
1 5 10 15  
Val Val His Gly Thr Ile Thr Gly Val Asp Ile Ser Met Asn Thr His  
20 25 30  
Leu Lys Thr Val Lys Leu Thr Leu Lys Gly Lys Asn Pro Val Thr Leu  
35 40 45  
Asp His Leu Ser Val Arg Gly Asn Asn Ile Arg Tyr Tyr Ile Leu Pro  
50 55 60  
Asp Ser Leu Asn Leu Glu Thr Leu Leu Val Glu Glu Thr Pro Arg Val  
65 70 75 80  
Lys Pro Lys Lys Pro Thr Thr Gly Lys Pro Leu Gly Arg Gly Arg Gly  
85 90 95  
Arg Gly Arg Gly Arg Gly Arg Gly Arg Gly Pro Arg  
100 105

(2) INFORMATION FOR SEQ ID NO:2814:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 533 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
(A) NAME/KEY: -  
(B) LOCATION: 1..533  
(D) OTHER INFORMATION: / Ceres Seq. ID 1574376  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2814:  
aacgaagcgtt gcttctacga gaggatatag agaggaagaa cagctcgctcc gagaccatga 60  
agagcagcccc acacctgggtg ctgattccctgt gcctccaggc cgctctgggtc atgggCgtct 120  
tcgccgctttt ggctaaaagaa aatgccctgg ttgagagcaa ggccatcgac atcaaacccgg 180  
ggcagctcaa gtgctgcacc aactgcaact tctctctctc ggggtctctac acctgcgacg 240  
acgtcaaaaaa ggactgcgac cccgtctgca agaagtcgct cgctgcctgt cagccctccct 300  
actcgggcaa caacaagtgc aggtgcacgc acaccttctt cggcatgtgc ggccccaagt 360  
gctagctaga gaggaagaac gcgcgctgct gctagctgct atagcttctgt tcttcccgct 420  
ccggccgGcc gccggcCgtt gNcatgttct acgtactgtg tgttgtgcta Ctacgtactg 480  
gcttcttctgt tgttcggttc ttgtgttct ctcgacagtg caccttgccg gcc

(2) INFORMATION FOR SEQ ID NO:2815:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 120 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..120  
(D) OTHER INFORMATION: / Ceres Seq. ID 1574377  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2815:  
Arg Ser Leu Leu Arg Glu Asp Ile Glu Arg Lys Asn Ser Ser Ser  
1 5 10 15  
Glu Thr Met Lys Ser Ser Pro His Leu Val Leu Ile Leu Cys Leu Gln  
20 25 30  
Ala Ala Leu Val Met Gly Val Phe Ala Ala Leu Ala Lys Glu Asn Ala  
35 40 45

Leu Val Glu Ser Lys Ala Ile Asp Ile Asn Pro Gly Gln Leu Lys Cys  
50 55 60  
Cys Thr Asn Cys Asn Phe Ser Phe Ser Gly Leu Tyr Thr Cys Asp Asp  
65 70 75 80  
Val Lys Lys Asp Cys Asp Pro Val Cys Lys Lys Cys Val Val Ala Val  
85 90 95  
His Ala Ser Tyr Ser Gly Asn Asn Lys Phe Arg Cys Thr Asp Thr Phe  
100 105 110

Leu Gly Met Cys Gly Pro Lys Cys  
115 120

(2) INFORMATION FOR SEQ ID NO:2816:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 102 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..102

(D) OTHER INFORMATION: / Ceres Seq. ID 1574378

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2816:

Met Lys Ser Ser Pro His Leu Val Leu Ile Leu Cys Leu Gln Ala Ala  
1 5 10 15  
Leu Val Met Gly Val Phe Ala Ala Leu Ala Lys Glu Asn Ala Leu Val  
20 25 30  
Glu Ser Lys Ala Ile Asp Ile Asn Pro Gly Gln Leu Lys Cys Cys Thr  
35 40 45  
Asn Cys Asn Phe Ser Phe Ser Gly Leu Tyr Thr Cys Asp Asp Val Lys  
50 55 60  
Lys Asp Cys Asp Pro Val Cys Lys Lys Cys Val Val Ala Val His Ala  
65 70 75 80  
Ser Tyr Ser Gly Asn Asn Lys Phe Arg Cys Thr Asp Thr Phe Leu Gly  
85 90 95  
Met Cys Gly Pro Lys Cys  
100

(2) INFORMATION FOR SEQ ID NO:2817:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 84 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..84

(D) OTHER INFORMATION: / Ceres Seq. ID 1574379

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2817:

Met Gly Val Phe Ala Ala Leu Ala Lys Glu Asn Ala Leu Val Glu Ser  
1 5 10 15  
Lys Ala Ile Asp Ile Asn Pro Gly Gln Leu Lys Cys Cys Thr Asn Cys  
20 25 30  
Asn Phe Ser Phe Ser Gly Leu Tyr Thr Cys Asp Asp Val Lys Lys Asp  
35 40 45  
Cys Asp Pro Val Cys Lys Lys Cys Val Val Ala Val His Ala Ser Tyr  
50 55 60  
Ser Gly Asn Asn Lys Phe Arg Cys Thr Asp Thr Phe Leu Gly Met Cys  
65 70 75 80  
Gly Pro Lys Cys

(2) INFORMATION FOR SEQ ID NO:2818:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 818 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..818  
(D) OTHER INFORMATION: / Ceres Seq. ID 1574380

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2818:

```
gggcccaaca cgaggctccc ggactctcca gttccttcgc tctctgttaa cccrrrgcgg 60
ccgacgaggc cggngaccac cgacggcgac gatggcgggc ggcgagggca agtccaagaa 120
acgcgcgtct tctactctct cagcgggagg agaagggggg gaacgggaaga ggcGggacaa 180
gaaggagagc aagaggagga gccgagagca caggagggat gacgatgaca gacacaagaa 240
gaaggggaaa cacatcgaca ggaacaaaag aaaagagaga gattcgaagg ataggcattc 300
caeggagaag acgagcaaga gaaaagacaa ggaacgggcc ttcaaaagaa tatccaagga 360
tgactacttt gcaaagaaca acgagttcgc taccctgggtg aaggaggaaa agggcaaaat 420
tttctcagat ttgtcttcag agtctgctcg tgatcttttc ttgaagtttg tgaacaatg 480
gaacaaaggc aagctgccat cacaatacta tgaggggatt acgagtgccc cacgatcagc 540
gcacaattgg aacatcaaag catgatacgt ttctcggttc atcgggtctt cggcttgaga 600
tgttttttgc ttctcggcgc agatttttct tatagtgtga tctagcaact gcttttaata 660
tctcgggttg ttgtatttaa gctgatgttc agaattgctg tctaaagcag gagggtagat 720
cgtgggtctc tctagtatcc agtggttaac atcaacgcta cttttccatt gatcactact 780
gtctgactct acaatgagca aacatactgt ttctgggg
```

(2) INFORMATION FOR SEQ ID NO:2819:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 187 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..187  
(D) OTHER INFORMATION: / Ceres Seq. ID 1574381

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2819:

```
Gly Pro Thr Arg Gly Ser Arg Thr Pro Gln Phe Leu Arg Ser Val
1 5 10 15
Thr Xaa Xaa Gly Arg Arg Gly Arg Xaa Pro Pro Thr Ala Thr Met Gly
 20 25 30
Gly Gly Glu Gly Lys Ser Lys Lys Arg Arg Ser Ser Thr Ser Ser Ala
 35 40 45
Glu Glu Glu Gly Gly Glu Arg Lys Arg Arg Asp Lys Lys Glu Ser Lys
 50 55 60
Arg Arg Ser Arg Asp Asp Arg Glu Asp Asp Asp Arg His Lys Lys
 65 70 75 80
Lys Gly Lys His Ile Asp Arg Asn Lys Gly Lys Glu Arg Asp Ser Lys
 85 90 95
Asp Arg His Ser Lys Glu Lys Thr Ser Lys Arg Lys Asp Lys Asp Ala
 100 105 110
Ala Phe Lys Glu Ile Ser Lys Asp Asp Tyr Phe Ala Lys Asn Asn Glu
 115 120 125
Phe Ala Thr Trp Leu Lys Glu Glu Lys Gly Lys Tyr Phe Ser Asp Leu
 130 135 140
Ser Ser Glu Ser Ala Arg Asp Leu Phe Leu Lys Phe Val Lys Gln Trp
 145 150 155 160
Asn Lys Gly Lys Leu Pro Ser Gln Tyr Tyr Glu Gly Ile Thr Ser Gly
 165 170 175
Pro Arg Ser Ala His Asn Trp Asn Ile Lys Ala
 180 185
```



(2) INFORMATION FOR SEQ ID NO:2820:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 157 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..157
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574382

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2820:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Gly | Gly | Gly | Glu | Gly | Lys | Ser | Lys | Lys | Arg | Arg | Ser | Ser | Thr | Ser |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Ser | Ala | Glu | Glu | Glu | Gly | Gly | Glu | Arg | Lys | Arg | Arg | Asp | Lys | Lys | Glu |
|     |     |     |     | 20  |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ser | Lys | Arg | Arg | Ser | Arg | Asp | Asp | Arg | Glu | Asp | Asp | Asp | Asp | Arg | His |
|     |     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |
| Lys | Lys | Lys | Gly | Lys | His | Ile | Asp | Arg | Asn | Lys | Gly | Lys | Glu | Arg | Asp |
|     |     |     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |
| Ser | Lys | Asp | Arg | His | Ser | Lys | Glu | Lys | Thr | Ser | Lys | Arg | Lys | Asp | Lys |
|     |     |     |     | 65  |     |     |     | 70  |     |     |     | 75  |     |     | 80  |
| Asp | Ala | Ala | Phe | Lys | Glu | Ile | Ser | Lys | Asp | Asp | Tyr | Phe | Ala | Lys | Asn |
|     |     |     |     | 85  |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Asn | Glu | Phe | Ala | Thr | Trp | Leu | Lys | Glu | Lys | Gly | Lys | Tyr | Phe | Ser |     |
|     |     |     |     | 100 |     |     |     | 105 |     |     |     | 110 |     |     |     |
| Asp | Leu | Ser | Ser | Glu | Ser | Ala | Arg | Asp | Leu | Phe | Leu | Lys | Phe | Val | Lys |
|     |     |     |     | 115 |     |     |     | 120 |     |     |     | 125 |     |     |     |
| Gln | Trp | Asn | Lys | Gly | Lys | Leu | Pro | Ser | Gln | Tyr | Tyr | Glu | Gly | Ile | Thr |
|     |     |     |     | 130 |     |     |     | 135 |     |     |     | 140 |     |     |     |
| Ser | Gly | Pro | Arg | Ser | Ala | His | Asn | Trp | Asn | Ile | Lys | Ala |     |     |     |
|     |     |     |     | 145 |     |     |     | 150 |     |     |     | 155 |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2821:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 696 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..696
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574386

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2821:

|             |            |            |            |             |             |     |
|-------------|------------|------------|------------|-------------|-------------|-----|
| gcattccacgc | tcgattcggc | cgttttccgc | atccacggag | ccagggcgacc | gccgcgcgctt | 60  |
| ccctaccac   | ccttgccggc | cgacgacgag | cgccaccacg | gcaggatgac  | gacgctgagg  | 120 |
| aacctcaaga  | tcaagacgct | gacgtgcaag | aggatcgtga | aggAdctcgc  | ctcgtacgag  | 180 |
| aaggagggtg  | agaaggaggc | ggccaagacc | gccgacatga | aggagaaggg  | cgctgatccc  | 240 |
| tacgacctca  | aacagcagga | gaatgttttg | gctgagtcga | ggatgatggt  | cccagactgc  | 300 |
| cacaaacgac  | ttgaaactgc | actggctgac | ttgaaagcaa | cactggctga  | actgaaggag  | 360 |
| tcaaatgagc  | aaggtgcgca | gattggagaa | gctgagagta | caatcgcaga  | agttgaagca  | 420 |
| gttgtaacgc  | cagcagaaga | ttaaactaaa | aaaactcttg | gtttgctgaa  | ctgttagcgc  | 480 |
| acatcctatt  | ttcgcatatt | gagcccttgt | gagcttatta | cgagatgttt  | gaggcgtgaa  | 540 |
| atcctgtacc  | attatcatca | cttctatcct | gaaatttgag | tttctgttcc  | caagttctaa  | 600 |
| gcgttaactgt | ttgtgtctgt | ggagagcgca | catccctggc | ttctccggga  | agttgttagt  | 660 |
| gtaaattgaa  | attaagaaaa | atggacgaat | ttgaat     |             |             |     |

(2) INFORMATION FOR SEQ ID NO:2822:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 147 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:

(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..147  
(D) OTHER INFORMATION: / Ceres Seq. ID 1574387  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2822:  
Ala Ser Thr Leu Asp Ser Ala Val Phe Arg Ile His Gly Ala Arg Arg  
1                  5                  10                  15  
Pro Pro Pro Leu Pro Tyr Ser Pro Leu Ala Gly Asp Asp Glu Arg His  
                  20                  25                  30  
His Gly Arg Met Thr Thr Leu Arg Asn Leu Lys Ile Lys Thr Ser Thr  
                  35                  40                  45  
Cys Lys Arg Ile Val Lys Xaa Leu Arg Ser Tyr Glu Lys Glu Val Glu  
                  50                  55                  60  
Lys Glu Ala Ala Lys Thr Ala Asp Met Lys Glu Lys Gly Ala Asp Pro  
65                  70                  75                  80  
Tyr Asp Leu Lys Gln Gln Glu Asn Val Leu Ala Glu Ser Arg Met Met  
                  85                  90                  95  
Val Pro Asp Cys His Lys Arg Leu Glu Thr Ala Leu Ala Asp Leu Lys  
                  100                  105                  110  
Ala Thr Leu Ala Glu Leu Lys Glu Ser Asn Glu Gln Gly Ala Glu Ile  
                  115                  120                  125  
Gly Glu Ala Glu Ser Thr Ile Ala Glu Val Glu Ala Val Val Lys Pro  
130                  135                  140  
Ala Glu Asp  
145

(2) INFORMATION FOR SEQ ID NO:2823:  
    (i) SEQUENCE CHARACTERISTICS:  
        (A) LENGTH: 77 amino acids  
        (B) TYPE: amino acid  
        (C) STRANDEDNESS:  
        (D) TOPOLOGY: linear  
    (ii) MOLECULE TYPE: peptide  
    (ix) FEATURE:  
        (A) NAME/KEY: peptide  
        (B) LOCATION: 1..77  
        (D) OTHER INFORMATION: / Ceres Seq. ID 1574388  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2823:  
Ile His Ala Arg Phe Gly Arg Phe Pro His Pro Arg Ser Gln Ala Thr  
1                  5                  10                  15  
Ala Ala Ala Ser Leu Leu Thr Leu Gly Arg Arg Arg Arg Ala Pro Pro  
                  20                  25                  30  
Arg Gln Asp Asp Asp Ala Glu Glu Pro Gln Asp Gln Asp Val Asp Val  
                  35                  40                  45  
Gln Glu Asp Arg Glu Gly Xaa Ala Leu Val Arg Glu Gly Gly Gly Glu  
                  50                  55                  60  
Gly Gly Gly Gln Asp Arg Arg His Glu Gly Glu Gly Arg  
65                  70                  75

(2) INFORMATION FOR SEQ ID NO:2824:  
    (i) SEQUENCE CHARACTERISTICS:  
        (A) LENGTH: 112 amino acids  
        (B) TYPE: amino acid  
        (C) STRANDEDNESS:  
        (D) TOPOLOGY: linear  
    (ii) MOLECULE TYPE: peptide  
    (ix) FEATURE:  
        (A) NAME/KEY: peptide  
        (B) LOCATION: 1..112  
        (D) OTHER INFORMATION: / Ceres Seq. ID 1574389  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2824:

Met Thr Thr Leu Arg Asn Leu Lys Ile Lys Thr Ser Thr Cys Lys Arg  
1 5 10 15  
Ile Val Lys Xaa Leu Arg Ser Tyr Glu Lys Glu Val Glu Lys Glu Ala  
20 25 30  
Ala Lys Thr Ala Asp Met Lys Glu Lys Gly Ala Asp Pro Tyr Asp Leu  
35 40 45  
Lys Gln Gln Glu Asn Val Leu Ala Glu Ser Arg Met Met Val Pro Asp  
50 55 60  
Cys His Lys Arg Leu Glu Thr Ala Leu Ala Asp Leu Lys Ala Thr Leu  
65 70 75 80  
Ala Glu Leu Lys Glu Ser Asn Glu Gln Gly Ala Glu Ile Gly Glu Ala  
85 90 95  
Glu Ser Thr Ile Ala Glu Val Glu Ala Val Val Lys Pro Ala Glu Asp  
100 105 110

(2) INFORMATION FOR SEQ ID NO:2825:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 560 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..560
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574403

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2825:

|            |            |            |             |             |            |     |
|------------|------------|------------|-------------|-------------|------------|-----|
| ttctttcaga | aaacgaaatc | cactcaggag | cgaggaaaga  | gggacagagg  | agggatagat | 60  |
| ccccgggctc | cacgcctcca | caaccatccg | tcccgatccc  | gaccagcttt  | gagatcgcca | 120 |
| tggcggacgg | cgcgtgctgc | accttcctgg | agatcctctt  | cgccatcatc  | ctcccccccc | 180 |
| tcggcgctct | cctccgattc | ggctgctgca | gaatagagtt  | ctgcattctgc | ctgctgctca | 240 |
| caatccttgg | ctacgtcccc | ggaatcatct | acgcgatcta  | tgtccttgtt  | gctctcgact | 300 |
| ctgaccagca | cgagaggga  | tactacaccc | ttgccttagag | catctgggtt  | tgccaggcgg | 360 |
| gcctgcacag | ttgagtcgaa | atcagttatt | tttttctcat  | gtggattgtc  | tgacatggca | 420 |
| taagcgccaa | tggttaacca | agtgttggtg | tctatatctc  | tgttacccaa  | cttgtgagct | 480 |
| ctctttattg | tgtccaggtt | attcaaAtct | gtaattgtga  | tactacaAga  | gaataagatg | 540 |
| cgcatgtatc | tctgagagct |            |             |             |            |     |

(2) INFORMATION FOR SEQ ID NO:2826:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..71
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574404

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2826:

Phe Phe Gln Lys Thr Lys Ser Thr Gln Glu Arg Gly Lys Arg Asp Arg  
1 5 10 15  
Gly Gly Ile Asp Pro Arg Ala Pro Arg Leu His Asn His Pro Ser Arg  
20 25 30  
Ser Arg Pro Ala Leu Arg Ser Arg Trp Arg Thr Ala Ala Ala Pro  
35 40 45  
Ser Trp Arg Ser Ser Ser Pro Ser Ser Ser Arg Pro Ser Ala Ser Ser  
50 55 60  
Ser Asp Ser Ala Ala Glu  
65 70

(2) INFORMATION FOR SEQ ID NO:2827:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 111 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..111  
(D) OTHER INFORMATION: / Ceres Seq. ID 1574405  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2827:  
Leu Ser Glu Asn Glu Ile His Ser Gly Ala Arg Lys Glu Gly Gln Arg  
1 5 10 15  
Arg Asp Arg Ser Pro Gly Ser Thr Pro Gln Pro Ser Val Pro Ile  
20 25 30  
Pro Thr Ser Phe Glu Ile Ala Met Ala Asp Gly Arg Cys Cys Thr Phe  
35 40 45  
Leu Glu Ile Leu Phe Ala Ile Ile Leu Pro Pro Leu Gly Val Phe Leu  
50 55 60  
Arg Phe Gly Cys Cys Arg Ile Glu Phe Cys Ile Cys Leu Leu Leu Thr  
65 70 75 80  
Ile Leu Gly Tyr Val Pro Gly Ile Ile Tyr Ala Ile Tyr Val Leu Val  
85 90 95  
Ala Leu Asp Ser Asp Gln His Glu Arg Glu Tyr Tyr Thr Leu Ala  
100 105 110

(2) INFORMATION FOR SEQ ID NO:2828:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 72 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..72  
(D) OTHER INFORMATION: / Ceres Seq. ID 1574406  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2828:  
Met Ala Asp Gly Arg Cys Cys Thr Phe Leu Glu Ile Leu Phe Ala Ile  
1 5 10 15  
Ile Leu Pro Pro Leu Gly Val Phe Leu Arg Phe Gly Cys Cys Arg Ile  
20 25 30  
Glu Phe Cys Ile Cys Leu Leu Leu Thr Ile Leu Gly Tyr Val Pro Gly  
35 40 45  
Ile Ile Tyr Ala Ile Tyr Val Leu Val Ala Leu Asp Ser Asp Gln His  
50 55 60  
Glu Arg Glu Tyr Tyr Thr Leu Ala  
65 70

(2) INFORMATION FOR SEQ ID NO:2829:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 778 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
(A) NAME/KEY: -  
(B) LOCATION: 1..778  
(D) OTHER INFORMATION: / Ceres Seq. ID 1574421  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2829:  
agcaagcaaa gattgcgccg gtgagggtgt tcgggacggc ggacttcgtg aacgctgcga 60  
gggttatggc ttgcctggag gaagttggcg tggagtacga ggtcgtcgag gtcgactacg 120

```

cgcccatgga gcacaagggc gccacgacc tcgaagaaa ccgcttcggc caaatcccag 180
cgtttcagga cggggacacg atgctctttg aatcccagc aatcgccaag tacgtgctcc 240
gcaaatactc caagtacgct caagtgcacc tgctccgtga gggcaaccgc gaggaagccg 300
coatggtaga cgtgtggacg gaggtcgagg cgcacacctc cctaccgcgc catcgccccc 360
wtyttctacg agtacgRtgg tgtacccgcg cgagcatggc acbacgccc accaggaggt 420
ggtggacagc agtgtggaga ggytcaggaa ggtcctcgac gtctacgagg cgcacctgta 480
caagaccaag cagctctatc tcgccgggga ctacttcagc ctgcgccrfs tcaaccagct 540
ccgtacacc tcaccacctc taggacacc gcnacgcgtc gctcttcgag gcgtatccctc 600
acgttaagcg ctggtgggag agagtatatg cagcccgctc gctgcagaag ctgcgccccc 660
atatggtgat caaagcctga ttgcacgtac ctttgtatca tcagattctt ccttgggggtg 720
tatatatgca aggggtacct ttcttgcaar ataaataaag arataataaa atccgatc

```

(2) INFORMATION FOR SEQ ID NO:2830:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 186 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..186
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574422

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2830:

```

Gln Ala Lys Ile Ala Pro Val Arg Val Phe Gly Thr Ala Asp Phe Val
1 5 10 15
Asn Ala Ala Arg Val Met Ala Cys Leu Glu Glu Val Gly Val Glu Tyr
20 25 30
Glu Val Val Glu Val Asp Tyr Ala Ala Met Glu His Lys Gly Ala Gln
35 40 45
His Leu Ala Arg Asn Pro Phe Gly Gln Ile Pro Ala Phe Gln Asp Gly
50 55 60
Asp Thr Met Leu Phe Glu Ser Arg Ala Ile Ala Lys Tyr Val Leu Arg
65 70 75 80
Lys Tyr Ser Lys Ser Ala Gln Val Asp Leu Leu Arg Glu Gly Asn Pro
85 90 95
Glu Glu Ala Ala Met Val Asp Val Trp Thr Glu Val Glu Ala His Thr
100 105 110
Tyr Leu Pro Gly His Arg Ala Xaa Xaa Leu Arg Val Xaa Trp Cys Thr
115 120 125
Pro Pro Ser Met Ala Xaa Arg Pro Thr Arg Arg Trp Trp Thr Arg Val
130 135 140
Trp Arg Xaa Ser Gly Arg Ser Ser Thr Ser Thr Arg Arg Thr Cys Thr
145 150 155 160
Arg Pro Ser Ser Ser Ile Ser Pro Gly Thr Thr Ser Ala Ser Pro Xaa
165 170 175
Ser Thr Thr Ser Arg Thr Pro Ser Thr Ser
180 185

```

(2) INFORMATION FOR SEQ ID NO:2831:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 165 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..165
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574423

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2831:

```

Met Ala Cys Leu Glu Glu Val Gly Val Glu Tyr Glu Val Val Glu Val
1 5 10 15

```

```

Asp Tyr Ala Ala Met Glu His Lys Gly Ala Gln His Leu Ala Arg Asn
 20 25 30
Pro Phe Gly Gln Ile Pro Ala Phe Gln Asp Gly Asp Thr Met Leu Phe
 35 40 45
Glu Ser Arg Ala Ile Ala Lys Tyr Val Leu Arg Lys Tyr Ser Lys Ser
 50 55 60
Ala Gln Val Asp Leu Leu Arg Glu Gly Asn Pro Glu Glu Ala Ala Met
 65 70 75 80
Val Asp Val Trp Thr Glu Val Glu Ala His Thr Tyr Leu Pro Gly His
 85 90 95
Arg Ala Xaa Xaa Leu Arg Val Xaa Trp Cys Thr Pro Pro Ser Met Ala
 100 105 110
Xaa Arg Pro Thr Arg Arg Trp Trp Thr Arg Val Trp Arg Xaa Ser Gly
 115 120 125
Arg Ser Ser Thr Ser Thr Arg Arg Thr Cys Thr Arg Pro Ser Ser Ser
 130 135 140
Ile Ser Pro Gly Thr Thr Ser Ala Ser Pro Xaa Ser Thr Thr Ser Arg
 145 150 155 160
Thr Pro Ser Thr Ser
 165

```

(2) INFORMATION FOR SEQ ID NO:2832:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 145 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..145

(D) OTHER INFORMATION: / Ceres Seq. ID 1574424

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2832:

```

Met Glu His Lys Gly Ala Gln His Leu Ala Arg Asn Pro Phe Gly Gln
1 5 10 15
Ile Pro Ala Phe Gln Asp Gly Asp Thr Met Leu Phe Glu Ser Arg Ala
 20 25
Ile Ala Lys Tyr Val Leu Arg Lys Tyr Ser Lys Ser Ala Gln Val Asp
 35 40 45
Leu Leu Arg Glu Gly Asn Pro Glu Glu Ala Ala Met Val Asp Val Trp
 50 55 60
Thr Glu Val Glu Ala His Thr Tyr Leu Pro Gly His Arg Ala Xaa Xaa
 65 70 75 80
Leu Arg Val Xaa Trp Cys Thr Pro Pro Ser Met Ala Xaa Arg Pro Thr
 85 90 95
Arg Arg Trp Trp Thr Arg Val Trp Arg Xaa Ser Gly Arg Ser Ser Thr
 100 105 110
Ser Thr Arg Arg Thr Cys Thr Arg Pro Ser Ser Ile Ser Pro Gly
 115 120 125
Thr Thr Ser Ala Ser Pro Xaa Ser Thr Thr Ser Arg Thr Pro Ser Thr
 130 135 140

```

Ser  
145

(2) INFORMATION FOR SEQ ID NO:2833:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 756 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..756

(D) OTHER INFORMATION: / Ceres Seq. ID 1574438

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2833:

|               |            |            |            |            |             |     |
|---------------|------------|------------|------------|------------|-------------|-----|
| aaaaaaaaactta | gccgcgtgga | cgcacaccag | caactgccct | cctcgcgcgc | gctgcctccc  | 60  |
| tccgcgcggac   | cgatctaccc | tccgcgcgca | ccatgtcgt  | gategccggg | gaggacttcc  | 120 |
| agcatatcct    | gcgtttgctg | aacaccaacg | tggatgggaa | gcagaagatc | atgttcgcca  | 180 |
| tgacctcaat    | caagggtgtc | ggcgcccgct | tctccaacat | cgctctgaag | aaggccgaca  | 240 |
| tcgacatgaa    | caagagggcc | ggcgaGctga | cgcttgatga | gctggagcgc | ctRgatgNac  | 300 |
| ggctcgtggcc   | aaccctaggc | agttcaaggt | gccggactgg | ttcctcaaca | ggaagaagga  | 360 |
| ttacaaggac    | ggcaggttct | cgcaggtcgt | ctccaacgcc | cttgatatga | agctcaaggga | 420 |
| cgaccttgag    | aggctcaaga | agatcaggaa | ccaccgtggt | ctgcgtcact | actggggcct  | 480 |
| ccgtgtccgt    | ggccagcaca | ccaagactac | tggcaggcgt | gbaaaagacc | ttggtgtctc  | 540 |
| caagaagcga    | tgagctytat | atcaccccca | caaactcttg | cgcactacc  | atgtcggttt  | 600 |
| gtgtccaaac    | agtcctgatg | aagggtttct | gttkaggcwg | tkkscstgaa | tggtgttktg  | 660 |
| ctctaggaca    | atatcgcggt | tattgaacck | taatatatcg | tgtccctggg | atgtgttttt  | 720 |
| tttttgcac     | tttataagta | atttcatttg | gatgag     |            |             |     |

(2) INFORMATION FOR SEQ ID NO:2834:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 91 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..91

(D) OTHER INFORMATION: / Ceres Seq. ID 1574439

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2834:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Lys | Asn | Leu | Ala | Ala | Trp | Thr | His | Thr | Ser | Thr | Cys | Pro | Pro | Arg | Arg |
| 1   |     | 5   |     |     |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Arg | Cys | Leu | Pro | Pro | Arg | Asp | Arg | Ser | Thr | Leu | Arg | Arg | His | His | Val |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     |     | 30  |     |
| Ala | Asp | Arg | Arg | Gly | Gly | Leu | Pro | Ala | Tyr | Pro | Ala | Phe | Ala | Glu | His |
|     |     |     | 35  |     |     |     |     | 40  |     |     |     |     |     | 45  |     |
| Gln | Arg | Gly | Trp | Glu | Ala | Glu | Asp | His | Val | Arg | His | Asp | Leu | Asn | Gln |
|     |     |     | 50  |     |     |     |     | 55  |     |     |     |     |     | 60  |     |
| Gly | Cys | Arg | Ala | Pro | Leu | Leu | Gln | His | Arg | Leu | Gln | Glu | Gly | Arg | His |
|     |     |     | 65  |     |     |     |     | 70  |     |     |     |     |     | 80  |     |
| Arg | His | Glu | Gln | Glu | Gly | Arg | Arg | Ala | Asp | Ala |     |     |     |     |     |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2835:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 105 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..105

(D) OTHER INFORMATION: / Ceres Seq. ID 1574440

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2835:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ser | Leu | Ile | Ala | Gly | Glu | Asp | Phe | Gln | His | Ile | Leu | Arg | Leu | Leu |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Asn | Thr | Asn | Val | Asp | Gly | Lys | Gln | Lys | Ile | Met | Phe | Ala | Met | Thr | Ser |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     |     | 30  |     |
| Ile | Lys | Gly | Val | Gly | Arg | Arg | Phe | Ser | Asn | Ile | Val | Cys | Lys | Lys | Ala |
|     |     |     | 35  |     |     |     |     | 40  |     |     |     |     |     | 45  |     |
| Asp | Ile | Asp | Met | Asn | Lys | Arg | Ala | Gly | Glu | Leu | Thr | Pro | Asp | Glu | Leu |
|     |     |     | 50  |     |     |     |     | 55  |     |     |     |     |     | 60  |     |
| Glu | Arg | Xaa | Asp | Xaa | Arg | Ser | Trp | Pro | Thr | Leu | Gly | Ser | Ser | Arg | Cys |

65 70 75 80  
Arg Thr Gly Ser Ser Thr Gly Arg Arg Ile Thr Arg Thr Ala Gly Ser  
85 90 95  
Arg Arg Ser Ser Pro Thr Pro Leu Ile  
100 105

(2) INFORMATION FOR SEQ ID NO:2836:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 79 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..79
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574441

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2836:

Met Phe Ala Met Thr Ser Ile Lys Gly Val Gly Arg Arg Phe Ser Asn  
1 5 10 15  
Ile Val Cys Lys Lys Ala Asp Ile Asp Met Asn Lys Arg Ala Gly Glu  
20 25 30  
Leu Thr Pro Asp Glu Leu Glu Arg Xaa Asp Xaa Arg Ser Trp Pro Thr  
35 40 45  
Leu Gly Ser Ser Arg Cys Arg Thr Gly Ser Ser Thr Gly Arg Arg Ile  
50 55 60  
Thr Arg Thr Ala Gly Ser Arg Arg Ser Ser Pro Thr Pro Leu Ile  
65 70 75

(2) INFORMATION FOR SEQ ID NO:2837:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 415 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..415
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574446

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2837:

tcaaaactaca tctcctttgg gcacgtacgc gtctgatagc tgcagtggtt ggggttggtc 60  
tcgtgtctatt cagaacacaca gtacgcgaagaa ctattcgggtg gggccgaaga tgggtgtcgct 120  
gaaggtgcaca aagcgcctcgc ccgcaagcgt ttctcaagtgt gggaaagcca aagtgttggtc 180  
tgaccccaat gaagtttagt agatctccat ggcgaactcc cgtaagactt atccgctagc 240  
tccccccctc cgattaattg ctcaactgggt tggggttgta tggatctctg ggtgaggtg 300  
atggtttatc tggtttcata tattgcatca atggctgcac tattcttttc tactatcatt 360  
ttgcagtgctc gtttacctac ggccaccatt gaaaacacta ttggctgtag ctgct

(2) INFORMATION FOR SEQ ID NO:2838:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 97 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..97
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574447

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2838:

Pro Asn Ser Ser Pro Leu Gly Thr Tyr Ala Ser Asn Ser Cys Ser Gly  
1 5 10 15  
Trp Gly Trp Leu Arg Ala Ile Gln Lys His Ser Ser Glu Asn Trp Ser



|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |  |  |  |    |  |  |  |  |    |  |  |  |  |  |    |  |  |  |  |    |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|--|--|--|----|--|--|--|--|----|--|--|--|--|--|----|--|--|--|--|----|
|     |     |     |     |     |     |     |     |     |     | 20  |     |     |     |     |     |  |  |  |  |  | 25 |  |  |  |  |    |  |  |  |  |  | 30 |  |  |  |  |    |
| Val | Gly | Pro | Lys | Met | Val | Ser | Leu | Lys | Val | Pro | Lys | Arg | Leu | Ala | Ala |  |  |  |  |  |    |  |  |  |  |    |  |  |  |  |  |    |  |  |  |  |    |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     | 35  |  |  |  |  |  |    |  |  |  |  | 40 |  |  |  |  |  |    |  |  |  |  | 45 |
| Ser | Val | Leu | Lys | Cys | Gly | Lys | Gly | Lys | Val | Trp | Leu | Asp | Pro | Asn | Glu |  |  |  |  |  |    |  |  |  |  |    |  |  |  |  |  |    |  |  |  |  |    |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     | 50  |  |  |  |  |  |    |  |  |  |  | 55 |  |  |  |  |  |    |  |  |  |  | 60 |
| Val | Ser | Glu | Ile | Ser | Met | Ala | Asn | Ser | Arg | Lys | Thr | Tyr | Pro | Leu | Ala |  |  |  |  |  |    |  |  |  |  |    |  |  |  |  |  |    |  |  |  |  |    |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     | 65  |  |  |  |  |  |    |  |  |  |  | 70 |  |  |  |  |  |    |  |  |  |  | 75 |
| Pro | Pro | Leu | Arg | Leu | Ile | Ala | His | Trp | Val | Gly | Val | Val | Trp | Ile | Ser |  |  |  |  |  |    |  |  |  |  |    |  |  |  |  |  |    |  |  |  |  |    |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     | 85  |  |  |  |  |  |    |  |  |  |  | 90 |  |  |  |  |  |    |  |  |  |  | 95 |

Gly

(2) INFORMATION FOR SEQ ID NO:2839:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 61 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..61
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574448

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2839:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Val | Ser | Leu | Lys | Val | Pro | Lys | Arg | Leu | Ala | Ala | Ser | Val | Leu | Lys |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     | 15  |     |     |
| Cys | Gly | Lys | Gly | Lys | Val | Trp | Leu | Asp | Pro | Asn | Glu | Val | Ser | Glu | Ile |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| Ser | Met | Ala | Asn | Ser | Arg | Lys | Thr | Tyr | Pro | Leu | Ala | Pro | Pro | Leu | Arg |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| Leu | Ile | Ala | His | Trp | Val | Gly | Val | Val | Trp | Ile | Ser | Gly |     |     |     |
| 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2840:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 751 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..751
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574509

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2840:

|             |            |             |            |            |             |     |
|-------------|------------|-------------|------------|------------|-------------|-----|
| aacacacgcca | aaccctaaac | accaaagccc  | cgcataataa | tacettcccc | tcccatcttt  | 60  |
| tcccctctcc  | tgccgcgcgc | gccgctcccg  | ctcccagctc | gtgttcgcgt | tcttgacagcc | 120 |
| gtcgcgcgca  | agCGctccag | agaacttccg  | tcaacatggg | gaagacacgt | ggtatgggag  | 180 |
| ccgggcgcga  | Gctcaagacc | caccgcgaGga | accagcgggt | ggctgacaag | gcatacaaga  | 240 |
| agagccattt  | gggcaatgag | tggagaagaac | ccttcgctgg | gtcatcccat | gccaaaggca  | 300 |
| ttgtctctga  | gaagatttgt | attgaggcca  | agcagcccaa | ctccgctatc | cgtaaagtgtg | 360 |
| ctcgtgttca  | gcttgttaa  | aattggcaaga | agattgctgc | cttcgtgcc  | aatgacgggt  | 420 |
| gtttgaacta  | cattgaggaa | aatgatgagg  | tcttgattgc | tggatttgt  | cgtaaagggc  | 480 |
| acgctgtgtg  | agatatctct | ggtgtccggt  | tcaaggctgt | caaggtttcc | gggtgtcttc  | 540 |
| tgttgtccct  | tttcaaggag | aagaaagaga  | agccaaagtc | ttagattgct | cttgctacca  | 600 |
| aaatcagcaa  | gcgtggagtt | gaacggggag  | ggcgtagat  | gattaagaag | aatggttgct  | 660 |
| tgctatgttt  | gcagtgcatt | cgtgcaattg  | ttaaacctaa | attttgttgg | tgaaaacgat  | 720 |
| ttcttttcag  | acttgcttct | gttgagtgcc  |            |            |             |     |

(2) INFORMATION FOR SEQ ID NO:2841:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 193 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:

(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..193  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1574510  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2841:  
His Arg Gln Thr Leu Asn Thr Lys Ala Pro His Ile Asn Thr Phe Pro  
1                  5                  10                  15  
Ser His Leu Phe Pro Ser Pro Ala Ala Ala Ala Pro Ala Pro Ser  
                  20                  25                  30  
Ser Cys Ser Ala Ser Cys Ser Arg Arg Arg Glu Ala Leu Gln Arg Thr  
                  35                  40                  45  
Ser Val Asn Met Gly Lys Thr Arg Gly Met Gly Ala Gly Arg Lys Leu  
50                  55                  60  
Lys Thr His Arg Arg Asn Gln Arg Trp Ala Asp Lys Ala Tyr Lys Lys  
65                  70                  75                  80  
Ser His Leu Gly Asn Glu Trp Lys Lys Pro Phe Ala Gly Ser Ser His  
                  85                  90                  95  
Ala Lys Gly Ile Val Leu Glu Lys Ile Gly Ile Glu Ala Lys Gln Pro  
100                  105                  110  
Asn Ser Ala Ile Arg Lys Cys Ala Arg Val Gln Leu Val Lys Asn Gly  
115                  120                  125  
Lys Lys Ile Ala Ala Phe Val Pro Asn Asp Gly Cys Leu Asn Tyr Ile  
130                  135                  140  
Glu Glu Asn Asp Glu Val Leu Ile Ala Gly Phe Gly Arg Lys Gly His  
145                  150                  155                  160  
Ala Val Gly Asp Ile Pro Gly Val Arg Phe Lys Val Val Lys Val Ser  
                  165                  170                  175  
Gly Val Ser Leu Leu Ala Leu Phe Lys Glu Lys Lys Glu Lys Pro Arg  
180                  185                  190  
Ser

(2) INFORMATION FOR SEQ ID NO:2842:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 142 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..142  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1574511  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2842:  
Met Gly Lys Thr Arg Gly Met Gly Ala Gly Arg Lys Leu Lys Thr His  
1                  5                  10                  15  
Arg Arg Asn Gln Arg Trp Ala Asp Lys Ala Tyr Lys Lys Ser His Leu  
20                  25                  30  
Gly Asn Glu Trp Lys Lys Pro Phe Ala Gly Ser Ser His Ala Lys Gly  
35                  40                  45  
Ile Val Leu Glu Lys Ile Gly Ile Glu Ala Lys Gln Pro Asn Ser Ala  
50                  55                  60  
Ile Arg Lys Cys Ala Arg Val Gln Leu Val Lys Asn Gly Lys Lys Ile  
65                  70                  75                  80  
Ala Ala Phe Val Pro Asn Asp Gly Cys Leu Asn Tyr Ile Glu Glu Asn  
85                  90                  95  
Asp Glu Val Leu Ile Ala Gly Phe Gly Arg Lys Gly His Ala Val Gly  
100                  105                  110  
Asp Ile Pro Gly Val Arg Phe Lys Val Val Lys Val Ser Gly Val Ser  
115                  120                  125

Leu Leu Ala Leu Phe Lys Glu Lys Lys Glu Lys Pro Arg Ser  
130 135 140

(2) INFORMATION FOR SEQ ID NO:2843:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 136 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..136
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574512

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2843:

```
Met Gly Ala Gly Arg Lys Leu Lys Thr His Arg Arg Asn Gln Arg Trp
1 5 10 15
Ala Asp Lys Ala Tyr Lys Lys Ser His Leu Gly Asn Glu Trp Lys Lys
20 25 30
Pro Phe Ala Gly Ser Ser His Ala Lys Gly Ile Val Leu Glu Lys Ile
35 40 45
Gly Ile Glu Ala Lys Gln Pro Asn Ser Ala Ile Arg Lys Cys Ala Arg
50 55 60
Val Gln Leu Val Lys Asn Gly Lys Lys Ile Ala Ala Phe Val Pro Asn
65 70 75 80
Asp Gly Cys Leu Asn Tyr Ile Glu Glu Asn Asp Glu Val Leu Ile Ala
85 90 95
Gly Phe Gly Arg Lys Gly His Ala Val Gly Asp Ile Pro Gly Val Arg
100 105 110
Phe Lys Val Val Lys Val Ser Gly Val Ser Leu Leu Ala Leu Phe Lys
115 120 125
Glu Lys Lys Glu Lys Pro Arg Ser
130 135
```

(2) INFORMATION FOR SEQ ID NO:2844:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 978 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..978
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574523

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2844:

```
aaaggaaact cactcccaact ttactcctat ccaactgcggc ctggacgcgt gcgagaggct 60
tgaccaagca gcagcagcag cagcagcgat ggcgcctctg aagctgtacg ggaatccgcgt 120
gtcccccaac gtgggtgcgcg tggccaccgt gctcaacgag aagggcctcg acttcgagat 180
cgtccccgtc gacctcacca ccggcgccca caagcagccc gacttctcta cctctcaacc 240
tttcggccag atccccggctc tcgtcgacgg agacgaakyc tcttcgagtc ccgcgcgcgtc 300
aacccgtata tcgccagcaa gtacgcgtca gggcacggac ctgctccccg ctgcaggcgtc 360
ggcggcgcaac tggaggtgtg gctggagggt gagtgcaccc acttctaccc gaacgcgatc 420
ccgtgggtgt tcacagctgt ctctgaggccg ctctggggcg cgcccccgag cgggcggttg 480
tggagaagca ccgcggagcag ctgcgcaagg tgctcgacgt gtacgaggcg cacttggccc 540
gcaacaagta ccCtcgcccg ggacaagttc acgctcgccg acgccaacca ccgctctacc 600
ctgctctacc tcagcaagac ccccaaggcc gggctcgctc ccgccccgcc ccacgtcaag 660
gctcgtgtgg agggcatcgc cgcccgcgcc cggttccaga agaccgtcgc cgccatcccc 720
ttgccccgcc cgccctctct ctcgggttga cctcgcttgc cgctgctgtg gtccgggatg 780
cgctcgagcc ccgagtgcaa taaaagaggg cgcactctgt gttgctcttg tgtgtgttca ttgctctttg 840
tgtgctataa cagcctgtgt aataaacact gttgctcttg tgtgtgttca ttgctctttg 900
gttggttgtt ccttgcatat cctactagtg ctgatctttt tgtgaagctt ggattggatg 960
gacgcgtttt cttgcgcg
```

(2) INFORMATION FOR SEQ ID NO:2845:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 147 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..147

(D) OTHER INFORMATION: / Ceres Seq. ID 1574524

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2845:

```
Lys Glu Thr His Ser His Phe Thr Pro Ile His Cys Gly Leu Asp Ala
1 5 10 15
Cys Glu Arg Leu Asp Gln Ala Ala Ala Ala Ala Met Ala Pro
20 25 30
Leu Lys Leu Tyr Gly Met Pro Leu Ser Pro Asn Val Val Arg Val Ala
35 40 45
Thr Val Leu Asn Glu Lys Gly Leu Asp Phe Glu Ile Val Pro Val Asp
50 55 60
Leu Thr Thr Gly Ala His Lys Gln Pro Asp Phe Leu Thr Leu Asn Pro
65 70 75 80
Phe Gly Gln Ile Pro Ala Leu Val Asp Gly Asp Glu Xaa Ser Ser Ser
85 90 95
Pro Ala Arg Ser Thr Gly Thr Ser Pro Ala Ser Thr Arg Gln Gly Thr
100 105 110
Asp Leu Leu Pro Ala Thr Ala Ser Ala Ala Asn Trp Arg Cys Gly Trp
115 120 125
Arg Trp Ser Arg Thr Thr Ser Thr Arg Thr His Arg Arg Trp Cys Ser
130 135 140
Ser Cys Ser
145
```

(2) INFORMATION FOR SEQ ID NO:2846:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 118 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..118

(D) OTHER INFORMATION: / Ceres Seq. ID 1574525

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2846:

```
Met Ala Pro Leu Lys Leu Tyr Gly Met Pro Leu Ser Pro Asn Val Val
1 5 10 15
Arg Val Ala Thr Val Leu Asn Glu Lys Gly Leu Asp Phe Glu Ile Val
20 25 30
Pro Val Asp Leu Thr Thr Gly Ala His Lys Gln Pro Asp Phe Leu Thr
35 40 45
Leu Asn Pro Phe Gly Gln Ile Pro Ala Leu Val Asp Gly Asp Glu Xaa
50 55 60
Ser Ser Ser Pro Ala Arg Ser Thr Gly Thr Ser Pro Ala Ser Thr Arg
65 70 75 80
Gln Gly Thr Asp Leu Leu Pro Ala Thr Ala Ser Ala Ala Asn Trp Arg
85 90 95
Cys Gly Trp Arg Trp Ser Arg Thr Thr Ser Thr Arg Thr His Arg Arg
100 105 110
Trp Cys Ser Ser Cys Ser
115
```

(2) INFORMATION FOR SEQ ID NO:2847:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 110 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..110  
(D) OTHER INFORMATION: / Ceres Seq. ID 1574526  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2847:  
Met Pro Leu Ser Pro Asn Val Val Arg Val Ala Thr Val Leu Asn Glu  
1 5 10 15  
Lys Gly Leu Asp Phe Glu Ile Val Pro Val Asp Leu Thr Thr Gly Ala  
20 25 30  
His Lys Gln Pro Asp Phe Leu Thr Leu Asn Pro Phe Gly Gln Ile Pro  
35 40 45  
Ala Leu Val Asp Gly Asp Glu Xaa Ser Ser Ser Pro Ala Arg Ser Thr  
50 55 60  
Gly Thr Ser Pro Ala Ser Thr Arg Gln Gly Thr Asp Leu Leu Pro Ala  
65 70 75 80  
Thr Ala Ser Ala Ala Asn Trp Arg Cys Gly Trp Arg Trp Ser Arg Thr  
85 90 95  
Thr Ser Thr Arg Thr His Arg Arg Trp Cys Ser Ser Cys Ser  
100 105 110

(2) INFORMATION FOR SEQ ID NO:2848:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 677 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
(A) NAME/KEY: -  
(B) LOCATION: 1..677  
(D) OTHER INFORMATION: / Ceres Seq. ID 1574547  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2848:  
aaccaccgtt cagaggagta ctcccggttc gagcacacta gtcttccctg cgcttgetcg 60  
ctcttctctt cccccatggc gctgctcgcc gtccaggGca tggccatgtc caccgccgcc 120  
gcggccctcc catctcaca ccacggcgcc gtctcatcct acgtctccac ctctctctac 180  
gcgtcgccag ctctccgcgc ctctcccgcc gcccgagctg cgctcgccgt cgccaccgtc 240  
ttgtcgccca cgtcactcc agttcttgac gtctactgcg ggagagggga caagaaaacg 300  
aaaaggggca aaaggttcaa ccattcatat ggcaatgcga ggccgcgcaa caagaagaag 360  
ggaactgggc ctgcgcggct cttgtctcct ccagctcctc caaggaagga tcagttcgat 420  
gatggggaga tcatttcaat cgagattgac gaggacatcc tggaaatagg ttgtccgagtt 480  
ctgccttgct ttatatttgc cctgagctta attggcctag ttgtaccaaa atcaaatatt 540  
acataattta agtaattatt tctcgccta taattatga tgggtaggct gccacacttt 600  
catttgctga gtaatgttcc tactactgac tgggttcttt attttccttt ccagctgctg 660  
agttctttac tctcttc

(2) INFORMATION FOR SEQ ID NO:2849:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 155 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..155  
(D) OTHER INFORMATION: / Ceres Seq. ID 1574548  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2849:

Asn His Arg Ser Glu Glu Tyr Ser Arg Ser Glu His Thr Ser Leu Pro  
1 5 10 15  
Cys Ala Cys Ser Leu Leu Leu Ala Pro Met Ala Leu Leu Ala Val Gln  
20 25 30  
Gly Met Ala Met Ser Thr Ala Ala Ala Leu Pro Ser His Asn His  
35 40 45  
Gly Ala Val Ser Ser Tyr Val Ser Thr Ser Tyr Ala Leu Ala Ala  
50 55 60  
Ser Ala Ala Phe Pro Arg Ala Arg Ala Ala Phe Ala Val Gly Thr Val  
65 70 75 80  
Leu Ser Ala Thr Val Thr Pro Val Leu Asp Val Tyr Cys Gly Arg Gly  
85 90 95  
Asp Lys Lys Thr Lys Arg Gly Lys Arg Phe Asn His Ser Tyr Gly Asn  
100 105 110  
Ala Arg Pro Arg Asn Lys Lys Lys Gly Thr Gly Pro Ala Arg Leu Phe  
115 120 125  
Ala Pro Pro Ala Pro Pro Arg Lys Asp Gln Phe Asp Asp Gly Glu Ile  
130 135 140  
Ile Ser Ile Glu Ile Asp Glu Asp Ile Leu Glu  
145 150 155

(2) INFORMATION FOR SEQ ID NO:2850:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 167 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..167

(D) OTHER INFORMATION: / Ceres Seq. ID 1574549

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2850:

Thr Thr Val Pro Arg Ser Thr Pro Val Pro Ser Thr Leu Val Phe Pro  
1 5 10 15  
Ala Leu Ala Arg Ser Phe Leu Pro Pro Trp Arg Cys Ser Pro Ser Arg  
20 25 30  
Ala Trp Pro Cys Pro Pro Pro Pro Arg Pro Ser His Leu Thr Thr Thr  
35 40 45  
Ala Pro Ser His Pro Thr Ser Pro Pro Pro Thr Arg Ser Gln Pro  
50 55 60  
Pro Pro Pro Ser Pro Ala Pro Glu Leu Arg Ser Pro Ser Ala Pro Ser  
65 70 75 80  
Cys Arg Pro Pro Ser Leu Gln Phe Leu Thr Ser Thr Ala Gly Glu Gly  
85 90 95  
Thr Arg Lys Arg Lys Gly Ala Lys Gly Ser Thr Ile His Met Ala Met  
100 105 110  
Arg Gly Arg Ala Thr Arg Arg Glu Leu Gly Leu Arg Gly Ser Leu  
115 120 125  
Leu Leu Gln Leu Leu Gln Gly Arg Ile Ser Ser Met Met Gly Arg Ser  
130 135 140  
Phe Gln Ser Arg Leu Thr Arg Thr Ser Trp Asn Arg Leu Ser Glu Phe  
145 150 155  
Cys Leu Ala Leu Tyr Leu Pro  
165

(2) INFORMATION FOR SEQ ID NO:2851:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 130 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..130  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1574550  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2851:  
Met Ala Leu Leu Ala Val Gln Gly Met Ala Met Ser Thr Ala Ala Ala  
1                  5                  10                  15  
Ala Leu Pro Ser His Asn His Gly Ala Val Ser Ser Tyr Val Ser Thr  
                  20                  25                  30  
Ser Ser Tyr Ala Leu Ala Ala Ser Ala Ala Phe Pro Arg Ala Arg Ala  
                  35                  40                  45  
Ala Phe Ala Val Gly Thr Val Leu Ser Ala Thr Val Thr Pro Val Leu  
50                  55                  60  
Asp Val Tyr Cys Gly Arg Gly Asp Lys Lys Thr Lys Arg Gly Lys Arg  
65                  70                  75                  80  
Phe Asn His Ser Tyr Gly Asn Ala Arg Pro Arg Asn Lys Lys Lys Gly  
                  85                  90                  95  
Thr Gly Pro Ala Arg Leu Phe Ala Pro Pro Ala Pro Pro Arg Lys Asp  
                  100                 105                 110  
Gln Phe Asp Asp Gly Glu Ile Ile Ser Ile Glu Ile Asp Glu Asp Ile  
                 115                 120                 125  
Leu Glu  
130

(2) INFORMATION FOR SEQ ID NO:2852:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 615 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..615  
(D) OTHER INFORMATION: / Ceres Seq. ID 1574572

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2852:

atccgtattc ccgtcacgcc cccaacacgc ccacaaccgc aagcagcgaa agctccccta 60  
accctctccg cgcattccgat cgcaaggaga aagagggaga tgagctacta cgggcagcag 120  
ccccccgTck gcgtcccgcc gcagcaaggc taccggggca aggacggcta cccgccacgc 180  
gggtaCccgc cggccggcta ccccccgccg gcgcagggct accctccgca Gggctaccct 240  
ccgcagtagc cgcaGccgcc gcctccacag cagcagcaga gcagcgggcc ttccctcatg 300  
gagggatgct tggtctgcct ctgctgctgc tgctctctgg acgctctgct ctgagagtgga 360  
gagggggcga cgcagcgatt cgacacggcg acaagtgaat ctactagott tctatgcgag 420  
ggagagagag agagagctgg aactggattg agcctggaaat gctatcgctc tattctagct 480  
ttgtcagagc ataattatgtc gccctagttt tttatttctc tctgtcaatg ttgacgggat 540  
cacagattgt gtgtgttattc gccctgtgga tgttccgtgt ttctgttgga attcaatcct 600  
gggatttatt gtgcc

(2) INFORMATION FOR SEQ ID NO:2853:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 117 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..117  
(D) OTHER INFORMATION: / Ceres Seq. ID 1574573

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2853:

Ile Arg Ile Pro Val Thr Pro Pro Thr Arg Pro Gln Pro Glu Ala Ala  
1                  5                  10                  15  
Lys Ala Pro Leu Thr Leu Ser Ala His Pro Ile Ala Arg Lys Lys Arg

(2) INFORMATION FOR SEQ ID NO:2854:

(A) LENGTH: 131 amino acids

(C) STRANDEDNESS:

(D) TOPOLOGY: lin

MOLECULE TYPE: peptid

(A) NAME

(B) LOCATION: 1..131

(D) OTHER INFORMATION

SEQUENCE DESCRIPTION: SEQ ID NO:2854:

[illegible]

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 84 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..84

(D) OTHER INFORMATION: / Ceres Seq. ID 1574575

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2855:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ser | Tyr | Tyr | Gly | Gln | Gln | Pro | Pro | Val | Xaa | Val | Pro | Pro | Gln | Gln |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Gly | Tyr | Pro | Gly | Lys | Asp | Gly | Tyr | Pro | Pro | Ala | Gly | Tyr | Pro | Pro | Ala |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Gly | Tyr | Pro | Pro | Pro | Ala | Gln | Gly | Tyr | Pro | Pro | Gln | Gly | Tyr | Pro | Pro |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |



Gln Tyr Ala Gln Pro Pro Pro Gln Gln Gln Gln Ser Ser Gly Pro  
50 55 60  
Ser Phe Met Glu Gly Cys Leu Ala Ala Leu Cys Cys Cys Leu Leu  
65 70 75 80  
Asp Ala Cys Phe

(2) INFORMATION FOR SEQ ID NO:2856:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 869 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..869
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574580

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2856:

|            |            |            |            |             |             |     |
|------------|------------|------------|------------|-------------|-------------|-----|
| agctagtag  | cagcgcaaca | ccaccgatca | gctatacaag | caaggtagct  | acctagtaga  | 60  |
| gtacgtagag | gccgggtctc | cagaagacga | acatgtcgtg | gagctccgac  | gagaaccaca  | 120 |
| ggttcgagca | ggcgctggca | gattacgacg | aggatactcc | aggacgctgg  | cagctcgtgr  | 180 |
| cccaggcggt | cgggcgccgc | aggacggcgg | acgacgtctg | ggcgcaactac | ctgcacctgg  | 240 |
| agggggacat | cgacgacatg | ggcgccaggg | agcgggcgaa | cgccgcgcgc  | caacagtacc  | 300 |
| gccgcaacgc | ccacgacgac | caacaccacg | acggcgccaa | cgccaacgcc  | aacgcccacg  | 360 |
| ccagccgcaa | ccatattagt | cgggcgagca | acggcgcgcg | cgccagcagc  | agtaacacta  | 420 |
| acaacattag | tagtcatcgc | gctactaaca | gcaacgacag | agccaaacgc  | ccgcagGaat  | 480 |
| gagacgcggc | cgggcaggag | agacgatgaa | ccacacaaac | tacgtactat  | cctactacca  | 540 |
| taatatgggt | gatatcgcca | cctttccgcg | tacgaacgtg | tatgctctaa  | ttaaaggaata | 600 |
| atcctagtag | tagcctatag | ccccagacta | agggcttgtt | cggttagctc  | ttaatccata  | 660 |
| tggattgaat | gggattggat | gggtttgaac | ccaaacaagt | caaaacttct  | ctcaattttt  | 720 |
| tccaattcca | tccaatccat | gtgtattggg | aataacaaaa | caagctctaa  | tgtgtattgc  | 780 |
| tctaattgtg | tgttcgtgca | tgccgcgtac | gacggacgta | cgcaagtgtg  | aaacettggg  | 840 |
| cactatttat | atgtataaag | ttatatcgc  |            |             |             |     |

(2) INFORMATION FOR SEQ ID NO:2857:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..129
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574581

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2857:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ser | Trp | Ser | Ser | Asp | Glu | Asn | His | Arg | Phe | Glu | Gln | Ala | Leu | Ala |
| 1   |     | 5   |     |     |     |     |     |     |     | 10  |     |     |     | 15  |     |
| Asp | Tyr | Asp | Glu | Asp | Thr | Pro | Gly | Arg | Trp | Gln | Leu | Xaa | Ala | Gln | Ala |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Val | Gly | Gly | Gly | Arg | Thr | Ala | Asp | Asp | Val | Trp | Arg | His | Tyr | Leu | His |
|     |     | 35  |     |     |     |     | 40  |     |     |     | 45  |     |     |     |     |
| Leu | Glu | Gly | Asp | Ile | Asp | Asp | Met | Gly | Ala | Arg | Glu | Arg | Ala | Asn | Arg |
|     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Arg | Arg | Gln | Gln | Tyr | Arg | Arg | Asn | Ala | Gln | Gln | His | Gln | His | Gln | His |
|     |     | 65  |     |     |     | 70  |     |     |     | 75  |     |     |     | 80  |     |
| Gly | Ala | Asn | Ala | Asn | Ala | Asn | Ala | His | Ala | Ser | Arg | Asn | His | Ile | Ser |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Arg | Arg | Ser | Asn | Gly | Gly | Gly | Ala | Ser | Ser | Ser | Asn | Thr | Asn | Asn | Ile |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Ser | Ser | His | Arg | Ala | Thr | Asn | Ser | Asn | Asp | Arg | Ala | Lys | Arg | Pro | Gln |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |

Glu

(2) INFORMATION FOR SEQ ID NO:2858:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 74 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..74
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574582

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2858:

```
Met Gly Ala Arg Glu Arg Ala Asn Arg Arg Arg Gln Gln Tyr Arg Arg
1 5 10 15
Asn Ala Gln Gln His Gln His Gln His Gly Ala Asn Ala Asn Ala Asn
20 25 30
Ala His Ala Ser Arg Asn His Ile Ser Arg Arg Ser Asn Gly Gly Gly
35 40 45
Ala Ser Ser Ser Asn Thr Asn Asn Ile Ser Ser His Arg Ala Thr Asn
50 55 60
Ser Asn Asp Arg Ala Lys Arg Pro Gln Glu
65 70
```

(2) INFORMATION FOR SEQ ID NO:2859:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 833 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..833
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574616

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2859:

```
ttggttcgcg gccacatcac caagctccgg gcgctgctgt acgtcgccgc ccagctgctg 60
gcgtctctcc tgcctgcgat cctctccgcg tacctcagcg gcggcatggt gaccccgatg 120
cacgcctctg gcgctggcat caacccgatg caggcgcttg tgatggaggt gatcctcacc 180
ttctcgctgc tcttgctcac ctacgccatg atcctggacc cgcggascag gtccgcaccca 240
tcggcccgct gctgacgggg ctcatagctg gcgcccaacag cctcgccggc ggcaacttca 300
cgggcgcgct catgaacccg gcgcggtcct tcggtcccgc catggccacc ggggtctgtg 360
ccaaccactg ggtctacttg atcggcccgcg tgctcgccgg gtccctggcc ggctctgtgt 420
acgagtcgct gtccatgggt aacaagacgc acgagccgct gctcaatgga gacatctgac 480
gaccgtcgcc ccccaaggca gtgagcacgg ttcatgcttg tttctgttaa aatagttcgt 540
tacctacaag catgatcatg atattgacca aggtaattaa ttagagaggg ttgctgttaa 600
atagttaccc ttggtgggatt gtgggatgta gaaattgttg ctgggctttg cttttctttt 660
ttcttttttt cttttctctc caaggaaatt tttaagaggg ctgggttctg taagagattt 720
gtttaggcta ttagttagct atatagtaga aaactagaga atgctatacg ttggacgtga 780
ttttttttca cgtatattgt gtacagatat ggtatttttt atcttccgga tgg
```

(2) INFORMATION FOR SEQ ID NO:2860:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 64 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..84
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574617

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2860:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Leu | Val | Arg | Gly | His | Ile | Thr | Lys | Leu | Arg | Ala | Leu | Leu | Tyr | Val | Ala |  |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |  |
| Ala | Gln | Leu | Leu | Ala | Ser | Ser | Leu | Ala | Cys | Ile | Leu | Leu | Arg | Tyr | Leu |  |
|     |     | 20  |     |     |     |     | 25  |     |     |     | 30  |     |     |     |     |  |
| Ser | Gly | Gly | Met | Val | Thr | Pro | Val | His | Ala | Leu | Gly | Ala | Gly | Ile | Asn |  |
|     |     | 35  |     |     |     |     | 40  |     |     |     | 45  |     |     |     |     |  |
| Pro | Met | Gln | Gly | Leu | Val | Met | Glu | Val | Ile | Leu | Thr | Phe | Ser | Leu | Leu |  |
|     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |  |
| Phe | Val | Thr | Tyr | Ala | Met | Ile | Leu | Asp | Pro | Arg | Xaa | Arg | Ser | Ala | Pro |  |
|     |     | 65  |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |  |
| Ser | Ala | Arg | Cys |     |     |     |     |     |     |     |     |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:2861:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 158 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..158
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574618

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2861:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Gly | Ser | Arg | Pro | His | His | Gln | Ala | Pro | Gly | Ala | Ala | Val | Arg | Arg | Arg |  |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     | 15  |     |     |     |  |
| Pro | Ala | Ala | Gly | Val | Leu | Pro | Arg | Leu | His | Pro | Pro | Pro | Leu | Pro | Gln |  |
|     |     | 20  |     |     |     |     | 25  |     |     |     | 30  |     |     |     |     |  |
| Arg | Arg | His | Gly | Asp | Pro | Ser | Ala | Arg | Pro | Gly | Arg | Trp | His | Gln | Pro |  |
|     |     | 35  |     |     |     |     | 40  |     |     |     | 45  |     |     |     |     |  |
| Asp | Ala | Gly | Leu | Gly | Asp | Gly | Gly | Asp | Pro | His | Leu | Leu | Ala | Ala | Leu |  |
|     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |  |
| Arg | His | Leu | Arg | His | Asp | Pro | Gly | Pro | Ala | Xaa | Gln | Val | Arg | Thr | Ile |  |
|     |     | 65  |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |  |
| Gly | Pro | Leu | Leu | Thr | Gly | Leu | Ile | Val | Gly | Ala | Asn | Ser | Leu | Ala | Gly |  |
|     |     | 85  |     |     |     |     | 90  |     |     |     | 95  |     |     |     |     |  |
| Gly | Asn | Phe | Thr | Gly | Ala | Ser | Met | Asn | Pro | Ala | Arg | Ser | Phe | Gly | Pro |  |
|     |     | 100 |     |     |     |     | 105 |     |     |     | 110 |     |     |     |     |  |
| Ala | Met | Ala | Thr | Gly | Val | Trp | Thr | Asn | His | Trp | Val | Tyr | Trp | Ile | Gly |  |
|     |     | 115 |     |     |     |     | 120 |     |     |     | 125 |     |     |     |     |  |
| Pro | Leu | Leu | Gly | Gly | Ser | Leu | Ala | Gly | Phe | Val | Tyr | Glu | Ser | Leu | Phe |  |
|     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |  |
| Met | Val | Asn | Lys | Thr | His | Glu | Pro | Leu | Leu | Asn | Gly | Asp | Ile |     |     |  |
|     |     | 145 |     |     | 150 |     |     |     | 155 |     |     |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:2862:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 538 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..538
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574619

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2862:

|            |            |            |             |            |            |     |
|------------|------------|------------|-------------|------------|------------|-----|
| atctcatca  | caggcaacaa | ggcaccacac | ctcttcttct  | tcttctctct | ctctctagca | 60  |
| cagCtagcgc | ctgtctccct | tcgctgtgta | tcattgtcttg | cagcagcggc | aagtgcgact | 120 |
| gtggctccag | ctgtctctgc | ggcagctcat | gcaactgcac  | gtcccctaac | gtggagaccg | 180 |
| ccgccgcgac | cagcatcaag | accacggtcc | tcgccgcgcc  | gaccaccaag | gccagcgccg | 240 |

ggcgcttcga ggcggccacc gagggcgcg gctgcgactg caacacctgc aactgcggca 300  
ccagctgcgg ctgctcctgc tgcagctgca actgagccgg tcaggcgatg gcgcacgaga 360  
gtcgagagga cgacgacgag tcgtataaat ataatagcgg cgtctaaata agatcctgtc 420  
aactgcaccc gccattatcg atccatggtc gtcctggggg ttcattgtca tctgtaacgt 480  
gctgcgggtc atgtccgtct cgtgccgat ttaatttta tatgcatgta ttgtgttt

(2) INFORMATION FOR SEQ ID NO:2863:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 110 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..110

(D) OTHER INFORMATION: / Ceres Seq. ID 1574620

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2863:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Pro | His | His | Arg | Gln | Gln | Gly | Thr | Thr | Pro | Leu | Leu | Leu | Leu | Pro | Pro |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Pro | Pro | Ser | Thr | Ala | Ser | Ala | Cys | Ser | Pro | Ser | Pro | Val | Ile | Met | Ser |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Cys | Ser | Ser | Gly | Lys | Cys | Asp | Cys | Gly | Ser | Ser | Cys | Ser | Cys | Gly | Ser |
|     |     | 35  |     |     |     |     | 40  |     |     |     | 45  |     |     |     |     |
| Ser | Cys | Asn | Cys | Met | Ser | Pro | Asn | Val | Glu | Thr | Ala | Ala | Ala | Ser | Ser |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Ile | Lys | Thr | Thr | Val | Leu | Ala | Ala | Pro | Thr | Thr | Lys | Ala | Ser | Ala | Gly |
|     | 65  |     |     | 70  |     |     |     |     | 75  |     |     |     |     |     | 80  |
| Gly | Phe | Glu | Ala | Ala | Thr | Glu | Gly | Gly | Gly | Cys | Asp | Cys | Asn | Thr | Cys |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Asn | Cys | Gly | Thr | Ser | Cys | Gly | Cys | Ser | Cys | Cys | Ser | Cys | Asn |     |     |
|     |     |     | 100 |     |     |     | 105 |     |     |     |     |     | 110 |     |     |

(2) INFORMATION FOR SEQ ID NO:2864:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 80 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..80

(D) OTHER INFORMATION: / Ceres Seq. ID 1574621

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2864:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ser | Cys | Ser | Ser | Gly | Lys | Cys | Asp | Cys | Gly | Ser | Ser | Cys | Ser | Cys |
| 1   |     |     |     |     | 5   |     |     |     | 10  |     |     |     | 15  |     |     |
| Gly | Ser | Ser | Cys | Asn | Cys | Met | Ser | Pro | Asn | Val | Glu | Thr | Ala | Ala | Ala |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ser | Ser | Ile | Lys | Thr | Thr | Val | Leu | Ala | Ala | Pro | Thr | Thr | Lys | Ala | Ser |
|     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| Ala | Gly | Gly | Phe | Glu | Ala | Ala | Thr | Glu | Gly | Gly | Gly | Cys | Asp | Cys | Asn |
|     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |
| Thr | Cys | Asn | Cys | Gly | Thr | Ser | Cys | Gly | Cys | Ser | Cys | Cys | Ser | Cys | Asn |
|     | 65  |     |     |     | 70  |     |     |     | 75  |     |     |     |     |     | 80  |

(2) INFORMATION FOR SEQ ID NO:2865:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..58  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1574622  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2865:  
Met Ser Pro Asn Val Glu Thr Ala Ala Ala Ser Ser Ile Lys Thr Thr  
1                  5                  10                  15  
Val Leu Ala Ala Pro Thr Thr Lys Ala Ser Ala Gly Gly Phe Glu Ala  
                  20                  25                  30  
Ala Thr Glu Gly Gly Gly Cys Asp Cys Asn Thr Cys Asn Cys Gly Thr  
                  35                  40                  45  
Ser Cys Gly Cys Ser Cys Cys Ser Cys Asn  
50                  55

(2) INFORMATION FOR SEQ ID NO:2866:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 657 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..657
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574626

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2866:

|            |             |            |            |            |            |     |
|------------|-------------|------------|------------|------------|------------|-----|
| arngccgtct | ttcttcgtta  | ctgcgcccg  | ctcccggaag | ctcgaccct  | ttacagccg  | 60  |
| cgaagaagat | gcacctgtgg  | ccatcgctcc | ggatccgcga | ctcgttcaag | cacggctacc | 120 |
| tccagaagct | ggagctcaac  | ctcggaaca  | tgaagcgcg  | gcagCGgcag | cgccagggcc | 180 |
| ggcagggaga | gagccaggag  | gaccaggag  | gccagcccg  | cgccaacggg | aagcgccgc  | 240 |
| tgctcgagga | ccgctcgcca  | tcggggctcg | tgcttgccg  | cgcgctcgag | ctgcctggg  | 300 |
| acgcccgttt | gtccctcacc  | tgctgctgct | gttgcttctg | ctgcggagCt | tgtagcgag  | 360 |
| aagaggatca | cccaactgcc  | cgctaagaag | caacttcag  | tgctgtata  | ttcatcagat | 420 |
| cacgaaaacc | agataatttg  | tggcataaat | gaattggagt | caaatagttc | aaatagtttt | 480 |
| gatcagcttt | gtacatatgg  | ttttctattc | atccttatgc | cgcccataga | tgctattgat | 540 |
| aaacgggaaa | aaggatcctt  | aatttttttg | ttggaaaccc | gtgtgttagg | tattttgggc | 600 |
| gtgtaatcag | gtcgatatctg | tatttaggat | aatctgtggg | gttgctgttt | ctcaact    |     |

(2) INFORMATION FOR SEQ ID NO:2867:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..117
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574627

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2867:

|                                                                 |  |
|-----------------------------------------------------------------|--|
| Xaa Pro Ser Phe Phe Val Thr Cys Pro Arg Ser Pro Lys Leu Glu Pro |  |
| 1                  5                  10                  15    |  |
| Phe Thr Ala Gly Glu Glu Asp Ala Pro Val Ala Ile Ala Pro Asp Pro |  |
| 20                  25                  30                      |  |
| Arg Leu Val Gln Ala Arg Leu Pro Pro Glu Ala Gly Ala Gln Pro Arg |  |
| 35                  40                  45                      |  |
| Gln His Glu Ala Arg Ala Ala Ala Pro Gly Pro Ala Gly Arg Glu     |  |
| 50                  55                  60                      |  |
| Pro Gly Gly Pro Gly Arg Pro Ala Arg Arg Gln Arg Glu Gly Ala Ala |  |
| 65                  70                  75                  80  |  |
| Ala Arg Gly Pro Leu Ala Ile Gly Val Arg Ala Cys Arg Arg Ala Arg |  |
| 85                  90                  95                      |  |

Ala Arg Leu Gly Arg Arg Leu Ala Pro His Leu Leu Leu Leu Leu Leu  
100 105 110  
Leu Leu Arg Ser Leu  
115

(2) INFORMATION FOR SEQ ID NO:2868:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 127 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..127

(D) OTHER INFORMATION: / Ceres Seq. ID 1574628

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2868:

Xaa Arg Leu Ser Ser Leu Pro Ala Pro Ala Pro Arg Ser Ser Asn Pro  
1 5 10 15  
Leu Gln Pro Ala Lys Lys Met His Leu Trp Pro Ser Leu Arg Ile Arg  
20 25 30  
Asp Ser Phe Lys His Gly Tyr Leu Gln Lys Leu Glu Leu Asn Leu Gly  
35 40 45  
Asn Met Lys Arg Ala Gln Arg Gln Arg Gln Gly Arg Gln Gly Glu Ser  
50 55 60  
Gln Glu Asp Gln Asp Gly Gln Pro Gly Gly Asn Gly Lys Ala Pro Leu  
65 70 75 80  
Leu Glu Asp Arg Ser Pro Ser Gly Ser Val Leu Ala Gly Ala Leu Glu  
85 90 95  
Leu Ala Trp Asp Ala Val Leu Leu Leu Thr Cys Cys Cys Cys Cys Phe  
100 105 110  
Cys Cys Gly Ala Cys Ser Asp Glu Glu Asp His Pro Thr Ala Arg  
115 120 125

(2) INFORMATION FOR SEQ ID NO:2869:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..105

(D) OTHER INFORMATION: / Ceres Seq. ID 1574629

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2869:

Met His Leu Trp Pro Ser Leu Arg Ile Arg Asp Ser Phe Lys His Gly  
1 5 10 15  
Tyr Leu Gln Lys Leu Glu Leu Asn Leu Gly Asn Met Lys Arg Ala Gln  
20 25 30  
Arg Gln Arg Gln Gly Arg Gln Gly Glu Ser Gln Glu Asp Gln Asp Gly  
35 40 45  
Gln Pro Gly Gly Asn Gly Lys Ala Pro Leu Leu Glu Asp Arg Ser Pro  
50 55 60  
Ser Gly Ser Val Leu Ala Gly Ala Leu Glu Leu Ala Trp Asp Ala Val  
65 70 75 80  
Leu Leu Leu Thr Cys Cys Cys Cys Cys Phe Cys Cys Gly Ala Cys Ser  
85 90 95  
Asp Glu Glu Asp His Pro Thr Ala Arg  
100 105

(2) INFORMATION FOR SEQ ID NO:2870:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 853 base pairs

- (B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
(A) NAME/KEY: -  
(B) LOCATION: 1..853  
(D) OTHER INFORMATION: / Ceres Seq. ID 1574636

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2870:

|            |            |            |             |            |             |     |
|------------|------------|------------|-------------|------------|-------------|-----|
| anactcatcc | caaaccagag | cgaagaagaa | tcgccatcac  | agcaagctac | gcgcactgaa  | 60  |
| atcctccaat | ccacaggaca | cagctctact | tcacacgttc  | gcagactcgc | acgcaccgag  | 120 |
| cggctagcga | ntcaacgaga | aatgtcgtcg | gtgaggcgca  | cagcgtgttc | gacccatttc  | 180 |
| ctgtggacct | cttcgacccc | ttcgacagca | tgttccgctc  | catcgtgccg | ccgtcgttgt  | 240 |
| cgtcgtcggc | ggcctccgag | acgcgccgct | tcgccagcgc  | ccgcctcgac | tggaaaggaa  | 300 |
| cgcccgaggc | gcaagtgttc | aaggccgacc | tcgccggcgt  | gaagaaggag | gaggtcaagg  | 360 |
| tggaggtgga | ggacggcaac | gtgctgtcta | tcagcgggca  | gcgcaacagg | gagaaggagg  | 420 |
| acaaggcgga | caagtggcac | cgctgggagc | cgagCagcgg  | ccagtctcgt | cgccgcttcc  | 480 |
| gcctgcggga | gaacggcaag | acggaggagg | tgaggggcgc  | gctggagaac | ggcgtgctca  | 540 |
| cggtcacctg | gcccaggccc | gaggtcaaga | agcccgagggt | taagagcatc | cagatctcgc  | 600 |
| tctgaagaag | acatggacgc | gaggtgaatg | gtcgcgtcgc  | gttcgcgtcg | cgccgctcgg  | 660 |
| tcttgggttt | cagcgacgcg | actcgtgtgt | gtgtgactgt  | ggttgctctg | ctttgggtatg | 720 |
| tctgtgtgtg | cgtgtgtcgt | ttcagtggtt | cgtggtcatc  | gtctgtacat | tgtgtgtgtc  | 780 |
| ggtgagctcc | cgcactcagt | gtgttgtgtt | ctgcgagtga  | ataaataaaa | acaaccagc   | 840 |
| tgctgctctg | tgt        |            |             |            |             |     |

(2) INFORMATION FOR SEQ ID NO:2871:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..113  
(D) OTHER INFORMATION: / Ceres Seq. ID 1574637

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2871:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Xaa | Leu | Ile | Pro | Asn | Gln | Ser | Glu | Glu | Ser | Pro | Ser | Gln | Gln | Ala |
| 1   |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Thr | Arg | Thr | Glu | Ile | Leu | Gln | Ser | Thr | Gly | His | Ser | Ser | Thr | Ser |
|     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Val | Arg | Arg | Leu | Ala | Arg | Thr | Glu | Arg | Leu | Ala | Xaa | Gln | Arg | Met |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |
| Ser | Leu | Val | Arg | Arg | Thr | Ala | Cys | Ser | Thr | His | Ser | Leu | Trp | Ser |
|     |     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |
| Ser | Thr | Pro | Ser | Thr | Ala | Cys | Ser | Ala | Pro | Ser | Cys | Arg | Arg | Cys |
|     |     | 65  |     |     |     |     | 70  |     |     |     | 75  |     |     | 80  |
| Arg | Arg | Arg | Arg | Pro | Pro | Arg | Pro | Pro | Pro | Ser | Pro | Ala | Pro | Ser |
|     |     |     |     | 85  |     |     |     |     |     | 90  |     |     |     | 95  |
| Thr | Gly | Arg | Arg | Arg | Pro | Arg | Arg | Thr | Cys | Ser | Arg | Pro | Thr | Pro |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |

Ala

(2) INFORMATION FOR SEQ ID NO:2872:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide

(B) LOCATION: 1..66

(D) OTHER INFORMATION: / Ceres Seq. ID 1574638

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2872:

Met Ser Leu Val Arg Arg Thr Ala Cys Ser Thr His Ser Leu Trp Thr  
1 5 10 15  
Ser Ser Thr Pro Ser Thr Ala Cys Ser Ala Pro Ser Cys Arg Arg Arg  
20 25 30  
Cys Arg Arg Arg Arg Pro Pro Arg Pro Pro Ser Pro Ala Pro Ala  
35 40 45  
Ser Thr Gly Arg Arg Arg Pro Arg Arg Thr Cys Ser Arg Pro Thr Ser  
50 55 60  
Pro Ala  
65

(2) INFORMATION FOR SEQ ID NO:2873:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 131 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..131

(D) OTHER INFORMATION: / Ceres Seq. ID 1574639

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2873:

Met Phe Arg Ser Ile Val Pro Pro Ser Leu Ser Ser Ser Ala Ala Ser  
1 5 10 15  
Glu Thr Ala Ala Phe Ala Ser Ala Arg Ile Asp Trp Lys Glu Thr Pro  
20 25 30  
Glu Ala His Val Phe Lys Ala Asp Leu Pro Gly Val Lys Lys Glu Glu  
35 40 45  
Val Lys Val Glu Val Glu Asp Gly Asn Val Leu Leu Ile Ser Gly Gln  
50 55 60  
Arg Ser Arg Glu Lys Glu Asp Lys Gly Asp Lys Trp His Arg Val Glu  
65 70 75 80  
Arg Ser Ser Gly Gln Phe Val Arg Arg Phe Arg Leu Pro Glu Asn Ala  
85 90 95  
Lys Thr Glu Glu Val Arg Ala Ala Leu Glu Asn Gly Val Leu Thr Val  
100 105 110  
Thr Val Pro Lys Ala Glu Val Lys Lys Pro Glu Val Lys Ser Ile Gln  
115 120 125  
Ile Ser Val  
130

(2) INFORMATION FOR SEQ ID NO:2874:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 962 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..962

(D) OTHER INFORMATION: / Ceres Seq. ID 1574673

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2874:

|             |             |            |            |             |            |     |
|-------------|-------------|------------|------------|-------------|------------|-----|
| aacaagcatc  | agagctcggt  | gtcacaaaac | ctgaccgatg | gcggcccggtg | gtccacagc  | 60  |
| tgctctcggtg | gtcagaacag  | gatcgcgaga | cctctcccc  | tccttttctt  | tcacagccgc | 120 |
| ggcgctcccc  | tcggcgcgctc | tgaggccggt | aggagcggtg | gtccgcggtg  | gagggtacac | 180 |
| ctgcaggctc  | cgcgccgtct  | gcgccatggg | ctccgcgccc | tcgtcgtccc  | aatccccgtc | 240 |
| gccgcacacg  | ccttcaggac  | aaacccaagg | gaaagcagat | tataaatcac  | tgagtgaaga | 300 |
| ggagtgggaag | aagcgccctga | ctgaagagca | gtattattgt | actcggcaga  | agggcactga | 360 |



|             |            |            |             |             |            |     |
|-------------|------------|------------|-------------|-------------|------------|-----|
| aagagcattc  | actggggaat | actggaatac | taaaacccca  | ggcattttac  | agtgtgtctg | 420 |
| ctgcgacacc  | cctctgtttc | agtcacaaac | caaatgtgat  | agtggtactg  | ggtggccatc | 480 |
| ctattataaa  | ccaattgggt | aaaatgtcaa | gagcaagctt  | gatattgcaa  | tcatttttat | 540 |
| gccccggacc  | gaggtgtctc | gtgcaacCtg | tgatgtctcat | ctgggggcatg | tcCTTTttcg | 600 |
| atgaacgggcc | accaccaaca | gggaagagat | actgtatcaa  | tagtgcatct  | ctgaaattga | 660 |
| agcccccaata | gtttctggat | actttagcaa | gaagtcaact  | ataacgctgg  | tcgcgcctat | 720 |
| gtaaacttcg  | gggttatgta | tataaactac | tcgagttgta  | gcataattat  | tattctcttt | 780 |
| gttatgtaat  | atatgtgttc | acaaacogat | gaaagtatga  | aacaaacagc  | cgctacttca | 840 |
| ctctgtgatt  | ctggtctaga | attaaggtgt | tgtttgggtg  | acgaattgta  | acgtaaatgg | 900 |
| caacggtaat  | ggtttgcaat | cgagtgaacg | ttgacaacgg  | taataaattt  | aaatagatct | 960 |
| tt          |            |            |             |             |            |     |

(2) INFORMATION FOR SEQ ID NO:2875:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 188 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..188
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574674

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2875:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Ala | Arg | Cys | Ser | Thr | Ala | Ala | Ser | Val | Val | Arg | Thr | Gly | Ser |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Arg | Asp | Leu | Ser | Pro | Ser | Phe | Ser | Phe | Thr | Ala | Ala | Ala | Leu | Pro | Ser |
|     |     |     | 20  |     |     |     |     |     | 25  |     |     |     | 30  |     |     |
| Ala | Arg | Leu | Arg | Pro | Val | Gly | Ala | Trp | Val | Arg | Gly | Gly | Gly | Tyr | Thr |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Cys | Arg | Leu | Arg | Ala | Val | Cys | Ala | Met | Gly | Ser | Ala | Pro | Ser | Ser | Ser |
|     |     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |
| Gln | Ser | Pro | Ser | Pro | His | Thr | Pro | Ser | Gly | Gln | Thr | Gln | Gly | Lys | Ala |
|     |     |     | 65  |     |     | 70  |     |     | 75  |     |     |     |     | 80  |     |
| Asp | Tyr | Lys | Ser | Leu | Ser | Glu | Glu | Glu | Trp | Lys | Lys | Arg | Leu | Thr | Glu |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     | 95  |     |     |
| Glu | Gln | Tyr | Tyr | Val | Thr | Arg | Gln | Lys | Gly | Thr | Glu | Arg | Ala | Phe | Thr |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Gly | Glu | Tyr | Trp | Asn | Thr | Lys | Thr | Pro | Gly | Ile | Tyr | Gln | Cys | Val | Cys |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Cys | Asp | Thr | Pro | Leu | Phe | Gln | Ser | Ser | Thr | Lys | Phe | Asp | Ser | Gly | Thr |
|     |     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |
| Gly | Trp | Pro | Ser | Tyr | Tyr | Lys | Pro | Ile | Gly | Glu | Asn | Val | Lys | Ser | Lys |
|     |     |     | 145 |     |     | 150 |     |     |     | 155 |     |     |     | 160 |     |
| Leu | Asp | Met | Ser | Ile | Ile | Phe | Met | Pro | Arg | Thr | Glu | Val | Leu | Cys | Ala |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     | 175 |     |     |
| Thr | Cys | Asp | Ala | His | Leu | Gly | His | Val | Leu | Phe | Arg |     |     |     |     |
|     |     |     | 180 |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2876:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 132 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..132
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574675

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2876:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Gly | Ser | Ala | Pro | Ser | Ser | Ser | Gln | Ser | Pro | Ser | Pro | His | Thr | Pro |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |

Ser Gly Gln Thr Gln Gly Lys Ala Asp Tyr Lys Ser Leu Ser Glu Glu  
20 25 30  
Glu Trp Lys Lys Arg Leu Thr Glu Glu Gln Tyr Tyr Val Thr Arg Gln  
35 40 45  
Lys Gly Thr Glu Arg Ala Phe Thr Gly Glu Tyr Trp Asn Thr Lys Thr  
50 55 60  
Pro Gly Ile Tyr Gln Cys Val Cys Cys Asp Thr Pro Leu Phe Gln Ser  
65 70 75 80  
Ser Thr Lys Phe Asp Ser Gly Thr Gly Trp Pro Ser Tyr Tyr Lys Pro  
85 90 95  
Ile Gly Glu Asn Val Lys Ser Lys Leu Asp Met Ser Ile Ile Phe Met  
100 105 110  
Pro Arg Thr Glu Val Leu Cys Ala Thr Cys Asp Ala His Leu Gly His  
115 120 125  
Val Leu Phe Arg  
130

(2) INFORMATION FOR SEQ ID NO:2877:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..111
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574676

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2877:

Met Leu Leu Gly Arg Arg Ala Leu Lys Glu His Ser Leu Gly Asn Thr  
1 5 10 15  
Gly Ile Leu Lys Pro Gln Ala Phe Ile Ser Val Ser Ala Ala Thr Pro  
20 25 30  
Leu Cys Phe Ser His Gln Pro Asn Leu Ile Val Val Leu Gly Gly His  
35 40 45  
Pro Ile Ile Asn Gln Leu Val Lys Met Ser Arg Ala Ser Leu Ile Cys  
50 55 60  
Gln Ser Phe Leu Cys Pro Gly Pro Arg Cys Ser Val Gln Pro Val Met  
65 70 75 80  
Leu Ile Trp Gly Met Ser Phe Phe Asp Asp Gly Pro Pro Pro Thr Gly  
85 90 95  
Lys Arg Tyr Cys Ile Asn Ser Ala Ser Leu Lys Leu Lys Pro Gln  
100 105 110

(2) INFORMATION FOR SEQ ID NO:2878:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 755 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..755
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574677

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2878:

agatctcaac gcaactaaaa cattttatct tctctatcgc tactccaaga gtacccaatc 60  
accogagccat ggccatctca gtcactgcgc tggcgcgctt gcccgcttct cggctcaaa 120  
aagcctcccg cagccgctccc gccagagggt cgtagcgttc atcgtctgcg gcccggtgcg 180  
cgcgaccgcg cggttttgtgg gcggtggcgcc cagctgcgcg cccacgcgcg cggatctcgc 240  
aaagaaggtg tccagagagca tcaagcaggc ccaggagagc tgcgcagatg acccggtgag 300  
cggcgagtg cgtggcggcgt gggacgagct ggaggagctc agcgcggcgc ccagccactt 360  
gcgcgaccgc cagaagggcg ccgaccgcct cgaggagtag tgcaaggaca accccgagGa 420

ccgcagcagtg ccCGcagcta cgaggactga accacgcgcg cgcgaggttg gatcgctgtc 480  
acttgatctta gctagGcagc ttagctcggc atgatggcga catgtgtaga cgtgcaatgg 540  
atcgggtatg atcctctgtt gattcagctct gccttggtgt ggaataaaac gaggtttgct 600  
gtttattata agtaacattt aggagctcct actgtagtct caaggcaggt gtaatcctta 660  
gaaacatttg atggtgtgct tctagccttg tagtactcga tatgtgcaat tctgtaaagt 720  
atcgcagatt ttccacctga gcattgatt gctgc

(2) INFORMATION FOR SEQ ID NO:2879:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..170

(D) OTHER INFORMATION: / Ceres Seq. ID 1574678

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2879:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asp | Leu | Asn | Ala | Thr | Lys | Thr | Phe | Tyr | Leu | Leu | Tyr | Arg | Tyr | Ser | Lys |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ser | Thr | Gln | Ser | Pro | Ser | His | Gly | His | Leu | Ser | His | Cys | Arg | Gly | Arg |
|     |     |     | 20  |     |     |     | 25  |     |     |     |     | 30  |     |     |     |
| Leu | Ala | Arg | Phe | Ser | Ala | Gln | Arg | Ser | Leu | Pro | Gln | Pro | Ser | Arg | Gln |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Arg | Val | Val | Ala | Phe | Ile | Val | Val | Arg | Pro | Val | Arg | Ala | His | Arg | Arg |
|     |     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |
| Phe | Val | Gly | Val | Ala | Ala | Ser | Ser | Pro | Pro | Thr | Pro | Pro | Asp | Leu | Ala |
|     |     |     | 65  |     |     |     | 70  |     |     |     |     | 75  |     |     | 80  |
| Lys | Lys | Val | Ser | Glu | Ser | Ile | Lys | Gln | Ala | Gln | Glu | Thr | Cys | Ala | Asp |
|     |     |     |     |     |     |     | 85  |     |     |     |     |     |     |     |     |
| Asp | Pro | Val | Ser | Gly | Glu | Cys | Val | Ala | Ala | Trp | Asp | Glu | Leu | Glu | Glu |
|     |     |     |     |     |     |     | 100 |     |     |     |     |     |     |     |     |
| Leu | Ser | Ala | Ala | Ala | Ser | His | Leu | Arg | Asp | Arg | Gln | Lys | Gly | Ala | Asp |
|     |     |     |     |     |     |     | 115 |     |     |     |     |     |     |     |     |
| Pro | Leu | Glu | Glu | Tyr | Cys | Lys | Asp | Asn | Pro | Glu | Asp | Arg | Arg | Val | Pro |
|     |     |     |     |     |     |     | 120 |     |     |     |     |     |     |     |     |
| Ala | Arg | Thr | Arg | Thr | Glu | Pro | Arg | Ala | Arg | Glu | Val | Gly | Ser | Leu | Ser |
|     |     |     |     |     |     |     | 135 |     |     |     |     |     |     |     |     |
| Leu | Asp | Leu | Ala | Arg | Gln | Leu | Ser | Ser | Ala |     |     |     |     |     |     |
|     |     |     |     |     |     |     | 150 |     |     |     |     |     |     |     |     |
|     |     |     |     |     |     |     | 165 |     |     |     |     |     |     |     | 170 |

(2) INFORMATION FOR SEQ ID NO:2880:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1114 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1114
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574693

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2880:

|            |            |            |            |             |            |     |
|------------|------------|------------|------------|-------------|------------|-----|
| aacgcccctt | tcttgcgagt | gaggccaaag | ccgagcaaac | aaaacgatat  | gccgctgcc  | 60  |
| tgaaccgaga | ccaccaccgc | tctgcctcgc | ctcgcctcac | ctcacctcat  | ctcacctcgc | 120 |
| cgactagggt | tttgtaccgc | cgtggatctc | gccgtccccg | ccatggagctg | ctgcacacgc | 180 |
| ggaacctctc | tcgcgcggca | ggctccgacc | accgggggag | accggatggg  | gactaccatc | 240 |
| gtcggggctc | gctacgaggg | cggcgctgct | ctgggcgcgc | attccaggac  | cagcactgga | 300 |
| atgtatgtag | ccaaccgtgc | ttcagacaag | attactcaac | tgacagacaa  | tgtgtatgtc | 360 |
| tgtcgtctcg | gatctgctcg | tgatacacaa | gtcatttcgg | attatgtacg  | ctatttcctc | 420 |
| caccaacaca | caatccagct | tgGacaacca | gctaccgtta | aagtgtcagc  | camctTgatt | 480 |
| aggtTgctag | cttatcagaA | caagaacatg | ttgcaagctg | gcattgattg  | tggaggatgg | 540 |

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ggacaagtac gagggaggcc aaattttctc agtccctctc ggtggaacga tcttgaagca 600
accatttgca attggaggtt caggtccagt tacctatatg ctcttcttga tcatgaatgg 660
aaagagggaag tagagtcagga agaggcagag aaatttgtgg tgaaggtagt ttcccttgct 720
atggcccggtg atggtgctag tggagggggtt gtccgcacag ttacaataaa tgcggatggc 780
gtgaagagga aactttaccg tggcgacaag ctacccctgt ggcacgacga gctggaaccc 840
cagaactcgt tgcttgatat tcttgctgct gggaaccctg atcccatggt gcagtgaaat 900
cgccctccac ttactttgtg aacttttcac tgtatctgac ttgttcttga ttatttctcc 960
ttgaactatg tcagaccaga gtaatttacg aattgtgtgt atcgacacct aataaattca 1020
tgtttagctg ggtgattggc gttttgagtt aatggttact ggtaagcggt ctactgctgt 1080
agttaagcct gtggcaagta ttcaaatatt cagt

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(2) INFORMATION FOR SEQ ID NO:2881:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 244 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..244

(D) OTHER INFORMATION: / Ceres Seq. ID 1574694

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2881:

```

Met Asp Val Ser His Ala Gly Ser Ser Val Ala Gly Glu Ala Pro Thr
1 5 10 15
Thr Gly Glu His Arg Met Gly Thr Thr Ile Val Gly Val Cys Tyr Glu
20 25 30
Gly Gly Val Val Leu Gly Ala Asp Ser Arg Thr Ser Thr Gly Met Tyr
35 40 45
Val Ala Asn Arg Ala Ser Asp Lys Ile Thr Gln Leu Thr Asp Asn Val
50 55 60
Tyr Val Cys Arg Ser Gly Ser Ala Ala Asp Thr Gln Val Ile Ser Asp
65 70 75 80
Tyr Val Arg Tyr Phe Leu His Gln His Thr Ile Gln Leu Gly Gln Pro
85 90 95
Ala Thr Val Lys Val Ala Ala Xaa Leu Ile Arg Leu Leu Ala Tyr Gln
100 105 110
Asn Lys Asn Met Leu Gln Ala Gly Met Ile Val Gly Gly Trp Gly Gln
115 120 125
Val Arg Gly Arg Pro Asn Phe Leu Ser Pro Ser Arg Trp Asn Asp Leu
130 135 140
Glu Ala Thr Ile Cys Asn Trp Arg Phe Arg Ser Ser Tyr Leu Tyr Ala
145 150 155 160
Leu Leu Asp His Glu Trp Lys Glu Gly Met Ser Gln Glu Glu Ala Glu
165 170 175
Lys Phe Val Val Lys Val Val Ser Leu Ala Met Ala Arg Asp Gly Ala
180 185 190
Ser Gly Gly Val Val Arg Thr Val Thr Ile Asn Ala Asp Gly Val Lys
195 200 205
Arg Asn Phe Tyr Pro Gly Asp Lys Leu Pro Leu Trp His Asp Glu Leu
210 215 220
Glu Pro Gln Asn Ser Leu Leu Asp Ile Leu Ala Gly Asn Pro Asp
225 230 235 240
Pro Met Val Gln

```

(2) INFORMATION FOR SEQ ID NO:2882:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 223 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..223

(D) OTHER INFORMATION: / Ceres Seq. ID 1574695

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2882:

Met Gly Thr Thr Ile Val Gly Val Cys Tyr Glu Gly Gly Val Val Leu  
1 5 10 15  
Gly Ala Asp Ser Arg Thr Ser Thr Gly Met Tyr Val Ala Asn Arg Ala  
20 25 30  
Ser Asp Lys Ile Thr Gln Leu Thr Asp Asn Val Tyr Val Cys Arg Ser  
35 40 45  
Gly Ser Ala Ala Asp Thr Gln Val Ile Ser Asp Tyr Val Arg Tyr Phe  
50 55 60  
Leu His Gln His Thr Ile Gln Leu Gly Gln Pro Ala Thr Val Lys Val  
65 70 75 80  
Ala Ala Xaa Leu Ile Arg Leu Leu Ala Tyr Gln Asn Lys Asn Met Leu  
85 90 95  
Gln Ala Gly Met Ile Val Gly Gly Trp Gly Gln Val Arg Gly Arg Pro  
100 105 110  
Asn Phe Leu Ser Pro Ser Arg Trp Asn Asp Leu Glu Ala Thr Ile Cys  
115 120 125  
Asn Trp Arg Phe Arg Ser Ser Tyr Leu Tyr Ala Leu Leu Asp His Glu  
130 135 140  
Trp Lys Glu Gly Met Ser Gln Glu Glu Ala Glu Lys Phe Val Val Lys  
145 150 155 160  
Val Val Ser Leu Ala Met Ala Arg Asp Gly Ala Ser Gly Gly Val Val  
165 170 175  
Arg Thr Val Thr Ile Asn Ala Asp Gly Val Lys Arg Asn Phe Tyr Pro  
180 185 190  
Gly Asp Lys Leu Pro Leu Trp His Asp Glu Leu Glu Pro Gln Asn Ser  
195 200 205  
Leu Leu Asp Ile Leu Ala Ala Gly Asn Pro Asp Pro Met Val Gln  
210 215 220

(2) INFORMATION FOR SEQ ID NO:2883:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 198 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..198

(D) OTHER INFORMATION: / Ceres Seq. ID 1574696

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2883:

Met Tyr Val Ala Asn Arg Ala Ser Asp Lys Ile Thr Gln Leu Thr Asp  
1 5 10 15  
Asn Val Tyr Val Cys Arg Ser Gly Ser Ala Ala Asp Thr Gln Val Ile  
20 25 30  
Ser Asp Tyr Val Arg Tyr Phe Leu His Gln His Thr Ile Gln Leu Gly  
35 40 45  
Gln Pro Ala Thr Val Lys Val Ala Ala Xaa Leu Ile Arg Leu Leu Ala  
50 55 60  
Tyr Gln Asn Lys Asn Met Leu Gln Ala Gly Met Ile Val Gly Gly Trp  
65 70 75 80  
Gly Gln Val Arg Gly Arg Pro Asn Phe Leu Ser Pro Ser Arg Trp Asn  
85 90 95  
Asp Leu Glu Ala Thr Ile Cys Asn Trp Arg Phe Arg Ser Ser Tyr Leu  
100 105 110  
Tyr Ala Leu Leu Asp His Glu Trp Lys Glu Gly Met Ser Gln Glu Glu  
115 120 125

Ala Glu Lys Phe Val Val Lys Val Val Ser Leu Ala Met Ala Arg Asp  
130 135 140  
Gly Ala Ser Gly Gly Val Val Arg Thr Val Thr Ile Asn Ala Asp Gly  
145 150 155 160  
Val Lys Arg Asn Phe Tyr Pro Gly Asp Lys Leu Pro Leu Trp His Asp  
165 170 175  
Glu Leu Glu Pro Gln Asn Ser Leu Leu Asp Ile Leu Ala Ala Gly Asn  
180 185 190  
Pro Asp Pro Met Val Gln  
195

(2) INFORMATION FOR SEQ ID NO:2884:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 762 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..762
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574701

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2884:

|             |            |             |            |            |             |     |
|-------------|------------|-------------|------------|------------|-------------|-----|
| agctttgttt  | ttgtgtgtgt | cagchvgrcg  | gtccgagcta | cgccgtggag | ctggggcgggc | 60  |
| tggaacggcaa | gacgttcaac | agggccatcg  | tgaagcacgt | cctcccgggc | ccggcgttca  | 120 |
| acctggacca  | gctcaacgcc | ctcttcgcgc  | agaacggcct | cacgcagacg | gacatgatcg  | 180 |
| cgctctcagg  | cggccacacg | atcgggggtga | cgcactgcga | caagttcgtg | cgccggatct  | 240 |
| acacgttcaa  | gcagcggctg | gcgtggaacc  | cgccgatgaa | cctggacttc | ctgcgctcgc  | 300 |
| tgccggcggt  | gtgccccctc | agctacagcc  | ccacgGcgtt | cgccatgctg | gacgtcaacca | 360 |
| gcgccggggt  | cttcgacaa  | gcctacttca  | acaacctccg | ctacaacaag | ggcctgctcg  | 420 |
| ctctcgacca  | gggtcctctt | accgaccgcc  | gtccctcgcc | cacctgcaac | ctcttcgccc  | 480 |
| ccaacgccac  | cgctctctac | gaggcattcg  | tcgcccacat | ggccaagctc | ggcaggatcg  | 540 |
| gcctcaagac  | cggcgccgac | ggcgagatac  | gccgcgtctg | cacgcgcgtc | aactaagcct  | 600 |
| gcattggctg  | cttgcctctt | gcgtgcgtgg  | gtttacttta | tttcaactct | tctttctctt  | 660 |
| gtttatatac  | gtacgtttgt | cggatggatt  | ttggtagcca | tgagatgaca | tccttgctct  | 720 |
| gagctagcgg  | acctgccccc | attgatgat   | atagattgat | cc         |             |     |

(2) INFORMATION FOR SEQ ID NO:2885:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 231 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..231
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574702

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2885:

|                                                                 |  |
|-----------------------------------------------------------------|--|
| Ala Leu Phe Leu Val Cys Ala Xaa Xaa Arg Ser Glu Leu Arg Arg Gly |  |
| 1 5 10 15                                                       |  |
| Ala Gly Ala Ala Gly Arg Gln Asp Val Gln Gln Gly His Arg Gly Ala |  |
| 20 25 30                                                        |  |
| Arg Pro Pro Gly Pro Arg Leu Gln Pro Gly Pro Ala Gln Arg Pro Leu |  |
| 35 40 45                                                        |  |
| Arg Ala Glu Arg Pro His Ala Asp Gly His Asp Arg Ala Leu Arg Arg |  |
| 50 55 60                                                        |  |
| Ala His Asp Arg Gly Asp Ala Leu Arg Gln Val Arg Ala Ala Asp Leu |  |
| 65 70 75 80                                                     |  |
| His Val Gln Ala Ala Gly Val Glu Pro Ala Asp Glu Pro Gly Leu     |  |
| 85 90 95                                                        |  |
| Pro Ala Leu Ala Ala Gly Val Pro Pro Gln Leu Gln Pro His Gly     |  |
| 100 105 110                                                     |  |

Val Arg His Ala Gly Arg His His Ala Gln Gly Leu Arg Gln Arg Leu  
115 120 125  
Leu Gln Gln Pro Pro Leu Gln Gln Gly Pro Ala Arg Leu Arg Pro Gly  
130 135 140  
Ala Leu His Arg Pro Pro Leu Pro Thr His Arg Gln Pro Leu Arg Arg  
145 150 155 160  
Gln Arg His Arg Leu Leu Arg Gly Ile Arg Arg His Gly Gln Ala  
165 170 175  
Arg Gln Asp Arg Pro Gln Asp Arg Arg Arg Arg Asp Thr Pro Arg  
180 185 190  
Leu His Arg Arg Gln Leu Ser Leu His Trp Leu Leu Ala Ala Cys Val  
195 200 205  
Arg Gly Phe His Leu Phe His Phe Phe Leu Leu Phe Ile Tyr Val  
210 215 220  
Arg Leu Ser Asp Gly Phe Trp  
225 230

(2) INFORMATION FOR SEQ ID NO:2886:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 197 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..197
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574703

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2886:

Leu Cys Phe Trp Cys Val Gln Xaa Xaa Gly Pro Ser Tyr Gly Val Glu  
1 5 10 15  
Leu Gly Arg Leu Asp Gly Lys Thr Phe Asn Arg Ala Ile Val Lys His  
20 25 30  
Val Leu Pro Gly Pro Gly Phe Asn Leu Asp Gln Leu Asn Ala Leu Phe  
35 40 45  
Ala Gln Asn Gly Leu Thr Gln Thr Asp Met Ile Ala Leu Ser Gly Ala  
50 55 60  
His Thr Ile Gly Val Thr His Cys Asp Lys Phe Val Arg Arg Ile Tyr  
65 70 75 80  
Thr Phe Lys Gln Arg Leu Ala Trp Asn Pro Pro Met Asn Leu Asp Phe  
85 90 95  
Leu Arg Ser Leu Arg Arg Val Cys Pro Leu Ser Tyr Ser Pro Thr Ala  
100 105 110  
Phe Ala Met Leu Asp Val Thr Thr Pro Arg Val Phe Asp Asn Ala Tyr  
115 120 125  
Phe Asn Asn Leu Arg Tyr Asn Lys Gly Leu Leu Ala Ser Asp Gln Val  
130 135 140  
Leu Phe Thr Asp Arg Arg Ser Arg Pro Thr Val Asn Leu Phe Ala Ala  
145 150 155 160  
Asn Ala Thr Ala Phe Tyr Glu Ala Phe Val Ala Ala Met Ala Lys Leu  
165 170 175  
Gly Arg Ile Gly Leu Lys Thr Gly Ala Asp Gly Glu Ile Arg Arg Val  
180 185 190  
Cys Thr Ala Val Asn  
195

(2) INFORMATION FOR SEQ ID NO:2887:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 140 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(A) NAME/KEY: peptide  
(B) LOCATION: 1..140  
(D) OTHER INFORMATION: / Ceres Seq. ID 1574704

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ile | Ala | Leu | Ser | Gly | Ala | His | Thr | Ile | Gly | Val | Thr | His | Cys | Asp |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Lys | Phe | Val | Arg | Arg | Ile | Tyr | Thr | Phe | Lys | Gln | Arg | Leu | Ala | Trp | Asn |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Pro | Pro | Met | Asn | Leu | Asp | Phe | Leu | Arg | Ser | Leu | Arg | Arg | Val | Cys | Pro |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Leu | Ser | Tyr | Ser | Pro | Thr | Ala | Phe | Ala | Met | Leu | Asp | Val | Thr | Thr | Pro |
|     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Arg | Val | Phe | Asp | Asn | Ala | Tyr | Phe | Asn | Asn | Leu | Arg | Tyr | Asn | Lys | Gly |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Leu | Leu | Ala | Ser | Asp | Gln | Val | Leu | Phe | Thr | Asp | Arg | Arg | Ser | Arg | Pro |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Thr | Val | Asn | Leu | Phe | Ala | Ala | Asn | Ala | Thr | Ala | Phe | Tyr | Glu | Ala | Phe |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Val | Ala | Ala | Met | Ala | Lys | Leu | Gly | Arg | Ile | Gly | Leu | Lys | Thr | Gly | Ala |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Asp | Gly | Glu | Ile | Arg | Arg | Val | Cys | Thr | Ala | Val | Asn |     |     |     |     |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |

(A) LENGTH: 736 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(D) OTHER INFORMATION: / Ceres Seq. ID 1574713

|            |            |            |            |             |             |     |
|------------|------------|------------|------------|-------------|-------------|-----|
| cccaaaatcc | tccaccacg  | accgcacatg | ggtttcgcga | ccgcattgga  | gaacctccgc  | 60  |
| gcctcccaac | ccaccacacc | accgcacgcg | tcacacgcg  | cgccatggc   | ggccagcgca  | 120 |
| agccggcgcc | tccggaggcc | cgctctcacc | aaggtccacc | agctcaggcc  | gggccaccaac | 180 |
| ggggcacacc | tcaccgtcaa | gtgtctgcag | gccaccacc  | tgcctggcgc  | cgccgcgccCa | 240 |
| ggcgacaccc | ccgcgcgcc  | atcNcggGgc | gcgcgcgac  | gccgagtgcc  | tcgtcgggga  | 300 |
| cgagacggcg | gccatcgtct | tcaccgcgc  | caacgcacaa | tgtagcttc   | tgaagcccaa  | 360 |
| tcgcagatgc | atcttcgcga | atgcGcaaa  | agacatgttc | aaatgagctaa | tgaagctctgc | 420 |
| agtgcagaca | ttggggcgga | tgttagctgt | agagccacgc | agttttcaac  | tgaaggaaga  | 480 |
| caacaacatc | tccttaaatg | atgatagatt | ggttaatgtg | ctgtagtaga  | tgtccaatcc  | 540 |
| aagcgtttct | gcccccttta | ttgttcctta | taagaaggaa | gtaccatgaa  | tgaacattct  | 600 |
| aaagcctctt | gaagcgaagt | gatgtttatt | gctcacgttg | ggtagataaa  | ggtcacaggt  | 660 |
| tgtatggctc | tgttagaact | ttggataaat | taagatgaat | tgcccttcga  | tctatgagat  | 720 |
| gtatgtccat | ctttgt     |            |            |             |             |     |

Pro Lys Tyr Ser Thr Thr Ala Pro Thr Arg Val Ser Ala Pro His Cys



|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 1   |     |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |
| Arg | Thr | Ser | Pro | Pro | Pro | Pro | Ser | Pro | His | His | Arg | Arg | Cys | Pro | Gln |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Arg | Arg | Arg | Arg | Ala | Ala | Ala | Thr | Ser | Arg | Arg | Ser | Gly | Gly | Pro | Ser |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ser | Pro | Arg | Ser | Thr | Ser | Ser | Gly | Arg | Ala | Pro | Thr | Gly | Thr | Pro | Ser |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Pro | Ser | Arg | Ser | Ser | Ala | Pro | Pro | Pro | Cys | Leu | Gly | Ala | Arg | Ala | Gln |
|     | 65  |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Ala | His | Pro | Pro | Pro | Pro | His | Xaa | Arg | Ala | Pro | Arg | Ile | Ala | Glu | Cys |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Leu | Val | Gly | Asp | Glu | Thr | Gly | Ala | Ile | Val | Phe | Thr | Ala | Arg | Asn | Asp |
|     |     |     | 100 |     |     |     | 105 |     |     |     |     |     | 110 |     |     |
| Gln | Val | Asp | Leu | Leu | Lys | Pro | Asn | Ala | Thr | Val | Ile | Leu | Arg | Asn | Ala |
|     | 115 |     |     |     |     | 120 |     |     |     |     |     | 125 |     |     |     |
| Lys | Ile | Asp | Met | Phe | Lys | Gly | Ser | Met | Arg | Leu | Ala | Val | Asp | Lys | Trp |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Gly | Arg | Ile | Glu | Ala | Val | Glu | Pro | Ala | Ser | Phe | Thr | Val | Lys | Glu | Asp |
|     | 145 |     |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |     |
| Asn | Asn | Leu | Ser | Leu | Ile | Glu | Tyr | Glu | Leu | Val | Asn | Val | Ala | Glu |     |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | 175 |     |

(2) INFORMATION FOR SEQ ID NO:2890:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 116 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..116

(D) OTHER INFORMATION: / Ceres Seq. ID 1574715

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2890:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gln | Asn | Thr | Pro | Pro | His | Pro | Leu | Gly | Phe | Pro | His | Arg | Ile | Ala |     |
| 1   |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |     |
| Glu | Pro | Arg | Arg | Leu | His | Pro | His | His | Thr | Thr | Gly | Asp | Val | His | Ser |
|     |     |     | 20  |     |     |     | 25  |     |     |     |     | 30  |     |     |     |
| Gly | Gly | Ala | Gly | Arg | Gln | Arg | Gln | Ala | Gly | Ala | Pro | Glu | Ala | Arg | Leu |
|     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| His | Gln | Gly | Arg | Pro | Ala | Gln | Ala | Gly | His | Gln | Arg | Ala | His | Pro | His |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Arg | Gln | Gly | Arg | Gln | Arg | His | Pro | Arg | Ala | Trp | Ala | Arg | Ala | Pro | Arg |
|     | 65  |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Arg | Thr | Arg | Arg | Arg | Pro | Ile | Xaa | Ala | Arg | Arg | Ala | Ser | Pro | Ser | Ala |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     | 95  |     |     |     |
| Ser | Ser | Gly | Thr | Arg | Pro | Ala | Pro | Ser | Ser | Ser | Pro | Pro | Ala | Thr | Thr |
|     |     |     | 100 |     |     |     | 105 |     |     |     |     |     | 110 |     |     |
| Lys | Leu | Thr | Cys |     |     |     |     |     |     |     |     |     |     |     |     |
|     |     |     | 115 |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2891:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 534 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..534

(D) OTHER INFORMATION: / Ceres Seq. ID 1574735

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2891:

```
aaaaccattc cccgttctcg attccaattc caaccagccc atcccccttc gagcacagcg 60
gcagagcggg ggcggaaggca agagcaaaaca gtagtagcgc cgccgcgcgt gccgtcgctg 120
tcgtgtgtgt gtgtggagag gaaagaccgg gttttgtttt ttacggetta gcgttgagca 180
gctgagatgt tgcgagcgct ggcggcgagg tgctgcgGcc actggcgGcC gggcgccgGg 240
gcggcgctct gctcaccagg aacgtcgGca tcagctacaa cctgcgcccc gccaacccgc 300
tcggctactt caaggacgtg ccgctgcccc tctgcgcctc gctgctcaag cagttggact 360
cggacgacga cgacgatcag taatagcaca tcgtcgacga ccgcagactg gctggcacta 420
aaccacaatt cctcttcacc tggattacaa atatgtaact gagaaagaaa aggaatacaa 480
aaatgtaact gcgtggctgt accaaattct gagtgctgga ttcttgctat tgctc
```

(2) INFORMATION FOR SEQ ID NO:2892:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 139 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..139

(D) OTHER INFORMATION: / Ceres Seq. ID 1574736

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2892:

```
Lys Pro Phe Pro Val Pro Asp Ser Asn Ser Asn Gln Pro Ile Pro Leu
1 5 10 15
Arg Ala His Ala Gln Ser Gly Gly Glu Gly Lys Ser Lys Gln Ser Ser
20 25 30
Arg Arg Arg Arg Arg Arg Arg Arg Val Cys Val Trp Arg Gly Lys
35 40 45
Thr Gly Phe Cys Phe Leu Arg Leu Ser Val Glu Gln Leu Arg Cys Cys
50 55 60
Glu Arg Trp Arg Arg Gly Ala Ala Ala Thr Gly Arg Arg Ala Pro Arg
65 70 75 80
Arg Arg Pro Ala His Gln Glu Arg Arg His Gln Leu Gln Pro Ala Pro
85 90 95
Arg Gln Pro Ala Arg Leu Leu Gln Gly Arg Ala Ala Ala His Leu Arg
100 105 110
Leu Ala Ala Gln Ala Val Gly Leu Gly Arg Arg Arg Ser Val Ile
115 120 125
Ala His Arg Arg Arg Pro Gln Thr Gly Trp His
130 135
```

(2) INFORMATION FOR SEQ ID NO:2893:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 91 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..91

(D) OTHER INFORMATION: / Ceres Seq. ID 1574737

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2893:

```
Met Leu Arg Ala Leu Ala Ala Arg Cys Cys Gly His Trp Pro Pro Gly
1 5 10 15
Ala Ala Ala Ala Ser Cys Ser Pro Gly Thr Ser Ala Ser Ala Thr Thr
20 25 30
Cys Ala Pro Pro Thr Arg Ser Ala Thr Ser Arg Thr Cys Arg Cys Pro
35 40 45
Ser Ala Pro Arg Cys Ser Ser Ser Trp Thr Arg Thr Thr Thr Thr Ile
50 55 60
Ser Asn Ser Thr Ser Ser Thr Thr Ala Asp Trp Leu Ala Leu Asn His
65 70 75 80
```

Lys Ser Ser Ser Pro Gly Leu Gln Ile Cys Asn  
85 90

(2) INFORMATION FOR SEQ ID NO:2894:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1185 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1185
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574738

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2894:

```
agctcgtgtac cgccggcga gcagtcggtt tgcgtcctctt ccttgattaa accttcggta 60
cccatatcca cctgctgtcc cgaccttcca gtcttctccg tagggggctc gctccataga 120
tttcgcgcga aggggcaacg gcacacccac caactgacct gaccacagag ggaaccgcag 180
atgaagatca ttccggtccc ttgcctggat gacaaactatg cctacttaat cgtggacgag 240
agcaccgaag aggcagcgcc cgttgacctt gtggaaacgg agaaggttct caaggcgccc 300
ggcgaggtcg gcgcctacgt cgactgcgtt ctacccaccc atcaccactg ggatcatgct 360
gggtggcaatg agaagatgag gctgcaggtg ccagggtata aggtatttgg aggatccctg 420
gacaatgtga aagcgtgcac tgatcaggtg gagaatggaa tgaagttgtc acttgggaag 480
gacattgaga tactatgcct acacacgcct tgccacacta aAggtcatat cagctactat 540
gttactagta aggaggtgaa gatccagcgg tcttcaccgg agataccctg ttcattgctg 600
gggtgtgggaa gttttttgag ggttctgcag agcaaatgta tcagtccctt attgttacac 660
tgggttcgct gccaaagtca acccgagttt actgtgggca tgagtacact gtgaagaacc 720
taaaattcat gctgacactg gagccagaga atgagaagac gaaacagaaa ctggaattgg 780
ctgaaaagca gcgcgaagcg aatcagccaa cagtgcctct gactatagga gatgagtttg 840
agataaatac tttcatgcgt gttgatctac cagaaataca ggccgaattc agtgtcaact 900
ctccagttga agcaatgata gaggtcagga agaccaagga taattggaga ggttgaggac 960
accatgggcc gccactagtc tgttgaaaca cgattccaaa gtgaactaat gcagaaacct 1020
tgccctgtag gtgggaatga ggtttactgc gctgaatgc ttgagaaat gtgttgttgt 1080
gaaggagaag actcctacaa taastccgcg ttaatgagta gtaacaaatc gctcctgtga 1140
acttgtggtc tgtttgccaa taataatgta cgaactgtag tgccct
```

(2) INFORMATION FOR SEQ ID NO:2895:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 177 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..177
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574739

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2895:

```
Met Lys Ile Ile Pro Val Pro Cys Leu Asp Asn Tyr Ala Tyr Leu
1 5 10 15
Ile Val Asp Glu Ser Thr Lys Lys Ala Ala Val Asp Pro Val Glu
20 25 30
Pro Glu Lys Val Leu Lys Ala Ala Gly Glu Val Gly Ala Tyr Val Asp
35 40 45
Cys Val Leu Thr Thr His His His Trp Asp His Ala Gly Gly Asn Glu
50 55 60
Lys Met Arg Leu Gln Val Pro Gly Ile Lys Val Phe Gly Gly Ser Leu
65 70 75 80
Asp Asn Val Lys Gly Cys Thr Asp Gln Val Glu Asn Gly Met Lys Leu
85 90 95
Ser Leu Gly Lys Asp Ile Glu Ile Leu Cys Leu His Thr Pro Cys His
100 105 110
Thr Lys Gly His Ile Ser Tyr Tyr Val Thr Ser Lys Glu Val Lys Ile
```

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |  |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|--|--|
|     | 115 |     |     |     |     | 120 |     |     |     |     |     | 125 |     |     |     |  |  |  |  |
| Gln | Arg | Ser | Ser | Pro | Glu | Ile | Pro | Cys | Ser | Leu | Leu | Gly | Val | Gly | Ser |  |  |  |  |
|     | 130 |     |     |     |     | 135 |     |     |     |     |     | 140 |     |     |     |  |  |  |  |
| Phe | Leu | Arg | Val | Leu | Gln | Ser | Lys | Cys | Ile | Ser | Pro | Leu | Leu | Leu | His |  |  |  |  |
|     | 145 |     |     |     | 150 |     |     |     |     |     | 155 |     |     |     | 160 |  |  |  |  |
| Trp | Val | Arg | Cys | Gln | Ser | Gln | Pro | Glu | Phe | Thr | Val | Gly | Met | Ser | Thr |  |  |  |  |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |  |  |  |  |
| Leu |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |  |  |

(2) INFORMATION FOR SEQ ID NO:2896:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 112 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..112

(D) OTHER INFORMATION: / Ceres Seq. ID 1574740

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2896:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |  |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|--|--|
| Met | Arg | Leu | Gln | Val | Pro | Gly | Ile | Lys | Val | Phe | Gly | Gly | Ser | Leu | Asp |  |  |  |  |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |  |  |  |  |
| Asn | Val | Lys | Gly | Cys | Thr | Asp | Gln | Val | Glu | Asn | Gly | Met | Lys | Leu | Ser |  |  |  |  |
|     |     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |  |  |  |  |
| Leu | Gly | Lys | Asp | Ile | Glu | Ile | Leu | Cys | Leu | His | Thr | Pro | Cys | His | Thr |  |  |  |  |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |  |  |  |
| Lys | Gly | His | Ile | Ser | Tyr | Tyr | Val | Thr | Ser | Lys | Glu | Val | Lys | Ile | Gln |  |  |  |  |
|     |     |     | 50  |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |  |  |  |
| Arg | Ser | Ser | Pro | Glu | Ile | Pro | Cys | Ser | Leu | Leu | Gly | Val | Gly | Ser | Phe |  |  |  |  |
|     |     |     | 65  |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |  |  |  |  |
| Leu | Arg | Val | Leu | Gln | Ser | Lys | Cys | Ile | Ser | Pro | Leu | Leu | Leu | His | Trp |  |  |  |  |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |  |  |  |  |
| Val | Arg | Cys | Gln | Ser | Gln | Pro | Glu | Phe | Thr | Val | Gly | Met | Ser | Thr | Leu |  |  |  |  |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     |     | 110 |     |  |  |  |  |

(2) INFORMATION FOR SEQ ID NO:2897:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 106 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..106

(D) OTHER INFORMATION: / Ceres Seq. ID 1574741

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2897:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |  |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|--|--|
| Met | Tyr | Gln | Ser | Leu | Ile | Val | Thr | Leu | Gly | Ser | Leu | Pro | Lys | Ser | Thr |  |  |  |  |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     | 15  |     |  |  |  |  |
| Arg | Val | Tyr | Cys | Gly | His | Glu | Tyr | Thr | Val | Lys | Asn | Leu | Lys | Phe | Met |  |  |  |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     |     | 30  |     |  |  |  |  |
| Leu | Thr | Leu | Glu | Pro | Glu | Asn | Glu | Lys | Thr | Lys | Gln | Lys | Leu | Glu | Trp |  |  |  |  |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |  |  |  |
| Ala | Glu | Lys | Gln | Arg | Glu | Ala | Asn | Gln | Pro | Thr | Val | Pro | Ser | Thr | Ile |  |  |  |  |
|     |     |     | 50  |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |  |  |  |
| Gly | Asp | Glu | Phe | Glu | Ile | Asn | Thr | Phe | Met | Arg | Val | Asp | Leu | Pro | Glu |  |  |  |  |
|     |     |     | 65  |     | 70  |     |     | 75  |     |     |     |     |     | 80  |     |  |  |  |  |
| Ile | Gln | Ala | Lys | Phe | Ser | Val | Asn | Ser | Pro | Val | Glu | Ala | Met | Ile | Glu |  |  |  |  |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |  |  |  |  |

Val Arg Lys Thr Lys Asp Asn Trp Arg Gly  
100 105

(2) INFORMATION FOR SEQ ID NO:2898:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 691 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..691
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574754

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2898:

|             |             |            |            |            |            |     |
|-------------|-------------|------------|------------|------------|------------|-----|
| atcactaggc  | caccaccag   | cggcgggctc | cagtcgcaac | tcgcaacaca | gtcacagagc | 60  |
| ccgcgcgccca | aagaagagac  | tcaactccag | gagacaagac | agtgagaact | gaagagaagg | 120 |
| atgggcttcg  | agaagcagat  | cctgagatcc | ggcacccggc | ccaagccgat | aaagggccag | 180 |
| aaggctcaccc | ttaactgcac  | cggctacggg | aaggatcggt | atcttccaag | aaattttgga | 240 |
| gcaccaagga  | ccctgggcag  | cagccattca | gtttcagcat | tggtcagggt | tcagtgatca | 300 |
| aaggatggga  | cgagggaatt  | atgaccatgc | aagtgggtga | agttgctcgt | atccagtgcg | 360 |
| cgccctgatta | tgccttatgga | gccggcgggt | tcccagcctg | gggaattcaa | ccaaactcag | 420 |
| tgcttgtgtT  | tcgagattga  | agtctctcag | gccacagta  | tcgcatctgt | cagctatgga | 480 |
| aacgttggcc  | atgctttctc  | agtAaatgaa | ataattccgt | gttcacctca | tgctacatac | 540 |
| agcagattgg  | tgttacgagb  | baaatcctgt | gamactttag | cattctgtaa | cogtggatgt | 600 |
| cgagtttatg  | gagttccctg  | tgtggcgcc  | caagtaagt  | tctcgtaaaa | gattgtaata | 660 |
| tgatggcttc  | cattgtga    | tgtaggcsc  | t          |            |            |     |

(2) INFORMATION FOR SEQ ID NO:2899:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..58
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574755

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2899:

|                                                                     |    |    |
|---------------------------------------------------------------------|----|----|
| Met Gly Phe Glu Lys Lys Val Thr Val His Cys Thr Gly Tyr Gly Lys Asp | 10 | 15 |
| Ile Lys Gly Glu Lys Val Thr Val His Cys Thr Gly Tyr Gly Lys Asp     | 20 | 30 |
| Arg Asp Leu Pro Arg Asn Phe Gly Ala Pro Arg Thr Leu Gly Ser Ser     | 35 | 45 |
| His Ser Val Ser Ala Leu Val Arg Val Gln                             | 50 | 55 |

(2) INFORMATION FOR SEQ ID NO:2900:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..39
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574756

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2900:

|                                                                 |   |    |    |
|-----------------------------------------------------------------|---|----|----|
| Met Thr Met Gln Val Gly Glu Val Ala Arg Ile Gln Cys Thr Pro Asp | 5 | 10 | 15 |
| Tyr Ala Tyr Gly Ala Gly Gly Phe Pro Ala Trp Gly Ile Gln Pro Asn |   |    |    |

20 25 30  
Ser Val Leu Val Phe Arg Asp  
35  
(2) INFORMATION FOR SEQ ID NO:2901:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 37 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..37  
(D) OTHER INFORMATION: / Ceres Seq. ID 1574757  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2901:  
Met Gln Val Gly Glu Val Ala Arg Ile Gln Cys Thr Pro Asp Tyr Ala  
1 5 10 15  
Tyr Gly Ala Gly Gly Phe Pro Ala Trp Gly Ile Gln Pro Asn Ser Val  
20 25 30  
Leu Val Phe Arg Asp  
35

(2) INFORMATION FOR SEQ ID NO:2902:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 600 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
(A) NAME/KEY: -  
(B) LOCATION: 1..600  
(D) OTHER INFORMATION: / Ceres Seq. ID 1574758  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2902:  
tcatacaag caaaagcaac aaggcagcag cacaagcaag aaccacacct cctcccttcg 60  
cctgtgatca tgtcgtcttg ctgcggcgcc aagtgcgggt gcggtccag ctgctccctgc 120  
ggcagcggtat gcaacggctg cggtatgtac cctgacgttg agaccgcgc caccagcagc 180  
gtcaagacca cggctctcgc cgcgccgacc accaaggcca gcgccggcgg cttccgaggcg 240  
gccaccgagg gcggcggtct cgaactgcaac acctgcaagt gcggcaccag ctgcggctgc 300  
tcctgtctga gctgcaactg agccggcccg gcccgcgcat ggcgcacgag agtcgagagg 360  
aggaggacga cgacgaggcB dtdtaaatat aatagcgccg tccagtaaat aagatcctgt 420  
caactgcacc cgcattatc catggtcgtc cgtccNtcg cctgcgtctc ctggtcctcg 480  
ggttcgtctg aactcctcgc cggcttcacg acgcgatgcc gcctccgtcg atcctgtccg 540  
tctcgtgccg grbkaatat tagatctata tgcgtgtttt tctgcgttat tactacatct 600

(2) INFORMATION FOR SEQ ID NO:2903:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 106 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..106  
(D) OTHER INFORMATION: / Ceres Seq. ID 1574759  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2903:  
Ser Ser Gln Ala Lys Ala Thr Arg Gln Gln His Lys Gln Glu Pro His  
1 5 10 15  
Leu Leu Pro Ser Pro Val Ile Met Ser Ser Cys Cys Gly Gly Lys Cys  
20 25 30  
Gly Cys Gly Ser Ser Cys Ser Cys Gly Ser Gly Cys Asn Gly Cys Gly

35 40 45  
Met Tyr Pro Asp Val Glu Thr Ala Ala Thr Ser Ser Val Lys Thr Thr  
50 55 60  
Val Leu Ala Ala Pro Thr Thr Lys Ala Ser Ala Gly Gly Phe Glu Ala  
65 70 75  
Ala Thr Glu Gly Gly Gly Cys Asp Cys Asn Thr Cys Lys Cys Gly Thr  
85 90 95  
Ser Cys Gly Cys Ser Cys Cys Ser Cys Asn  
100 105

(2) INFORMATION FOR SEQ ID NO:2904:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 83 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..83

(D) OTHER INFORMATION: / Ceres Seq. ID 1574760

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2904:

Met Ser Ser Cys Cys Gly Gly Lys Cys Gly Cys Gly Ser Ser Cys Ser  
1 5 10 15  
Cys Gly Ser Gly Cys Asn Gly Cys Gly Met Tyr Pro Asp Val Glu Thr  
20 25 30  
Ala Ala Thr Ser Ser Val Lys Thr Thr Val Leu Ala Ala Pro Thr Thr  
35 40 45  
Lys Ala Ser Ala Gly Gly Phe Glu Ala Ala Thr Glu Gly Gly Cys  
50 55 60  
Asp Cys Asn Thr Cys Lys Cys Gly Thr Ser Cys Gly Cys Ser Cys Cys  
65 70 75 80  
Ser Cys Asn

(2) INFORMATION FOR SEQ ID NO:2905:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 58 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..58

(D) OTHER INFORMATION: / Ceres Seq. ID 1574761

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2905:

Met Tyr Pro Asp Val Glu Thr Ala Ala Thr Ser Ser Val Lys Thr Thr  
1 5 10 15  
Val Leu Ala Ala Pro Thr Thr Lys Ala Ser Ala Gly Gly Phe Glu Ala  
20 25 30  
Ala Thr Glu Gly Gly Gly Cys Asp Cys Asn Thr Cys Lys Cys Gly Thr  
35 40 45  
Ser Cys Gly Cys Ser Cys Cys Ser Cys Asn  
50 55

(2) INFORMATION FOR SEQ ID NO:2906:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 842 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..842  
(D) OTHER INFORMATION: / Ceres Seq. ID 1574762

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2906:

|             |             |            |            |            |            |     |
|-------------|-------------|------------|------------|------------|------------|-----|
| ctcgaaatct  | cgcccccctg  | tcgagttgtc | catatccctt | cctctcttcc | tcgccaggcc | 60  |
| aaccgctgat  | tgttgttcag  | acagaggaag | gaaggaagga | aggaggagat | cagaagcatc | 120 |
| agccatgtcg  | aactcggcgt  | cggaatggc  | cgtttgtgac | gaatgcaaac | tcaagtcttc | 180 |
| ggaactcaag  | gcgaagagga  | gcttccgttt | catcgtgttc | aagatcaacg | agaacgtgca | 240 |
| gcaggtgggt  | gtggacaggc  | ttgggggacc | aggtgaaagc | tacgatgcgt | tcagggcctg | 300 |
| ctttcccgcc  | aacgagTgyc  | gctacgcggt | gtttgatttt | gactttgtca | ctgatgagaa | 360 |
| ctgcgaagaag | agcaagatct  | tcttcacatc | ttgggcccac | gatgcatcga | gggtgagaag | 420 |
| caagatgttg  | tacgcaagct  | ccaaggaccg | gttcaagagg | gagctogacg | gcattcaggt | 480 |
| ggagctacaa  | gcaactgagc  | cgagcgaaat | gagcatggac | atcatcaagt | cgcgagccct | 540 |
| ctgaaaacagc | cgggccatcag | ctcctgcatg | cccgtcgatt | cttcggtgtt | ggtaacggtc | 600 |
| atccggttttc | gtgtcccttgt | ttttcctgga | agcaaaagcc | ttgcgttctg | tatgagactt | 660 |
| ctgtatacca  | tttccctctc  | ctnknntttc | ccaatctctg | ccgtagtcct | gcactcctgc | 720 |
| tactgctgta  | aactagwact  | tatttgcgtg | ttgtctcgt  | ggcattgtcg | agtcgcttat | 780 |
| gtgtctatgc  | aatgctatgt  | gtgagaagcc | taatgtacct | tagcttaatc | accgaattgc | 840 |

(2) INFORMATION FOR SEQ ID NO:2907:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 180 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..180

(D) OTHER INFORMATION: / Ceres Seq. ID 1574763

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2907:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Lys | Ser | Arg | Pro | Ser | Leu | Gln | Leu | Ser | Ile | Ser | Leu | Pro | Leu | Phe |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Leu | Ala | Arg | Pro | Thr | Ala | Asp | Cys | Cys | Ser | Asp | Arg | Gly | Arg | Lys | Glu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Gly | Arg | Arg | Arg | Ser | Glu | Ala | Ser | Ala | Met | Ser | Asn | Ser | Ala | Ser | Gly |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Met | Ala | Val | Cys | Asp | Glu | Cys | Lys | Leu | Lys | Phe | Leu | Glu | Leu | Lys | Ala |
|     |     |     | 50  |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Lys | Arg | Ser | Phe | Arg | Phe | Ile | Val | Phe | Lys | Ile | Asn | Glu | Asn | Val | Gln |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Gln | Val | Val | Val | Asp | Arg | Leu | Gly | Gly | Pro | Gly | Glu | Ser | Tyr | Asp | Ala |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     | 95  |     |     |
| Phe | Arg | Ala | Cys | Phe | Pro | Ala | Asn | Glu | Xaa | Arg | Tyr | Ala | Val | Phe | Asp |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     | 110 |     |     |     |
| Phe | Asp | Phe | Val | Thr | Asp | Glu | Asn | Cys | Gln | Lys | Ser | Lys | Ile | Phe | Phe |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Ile | Ser | Trp | Ala | Pro | Asp | Ala | Ser | Arg | Val | Arg | Ser | Lys | Met | Leu | Tyr |
|     |     |     | 130 |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Ala | Ser | Ser | Lys | Asp | Arg | Phe | Lys | Arg | Glu | Leu | Asp | Gly | Ile | Gln | Val |
| 145 |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |     |
| Glu | Leu | Gln | Ala | Thr | Glu | Pro | Ser | Glu | Met | Ser | Met | Asp | Ile | Ile | Lys |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     | 175 |     |     |

Ser Arg Ala Leu  
180

(2) INFORMATION FOR SEQ ID NO:2908:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 137 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear



(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..137

(D) OTHER INFORMATION: / Ceres Seq. ID 1574764

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2908:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Arg | Asn | Leu | Ala | Pro | Arg | Cys | Ser | Cys | Pro | Tyr | Pro | Phe | Leu | Ser | Ser |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ser | Pro | Gly | Gln | Pro | Leu | Ile | Val | Val | Gln | Thr | Glu | Glu | Gly | Arg | Lys |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Glu | Gly | Gly | Asp | Gln | Lys | His | Gln | Pro | Cys | Arg | Thr | Arg | Arg | Arg | Glu |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Trp | Pro | Phe | Val | Thr | Asn | Ala | Asn | Ser | Ser | Ser | Trp | Asn | Ser | Arg | Arg |
|     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Arg | Gly | Ala | Ser | Val | Ser | Ser | Cys | Ser | Arg | Ser | Thr | Arg | Thr | Cys | Ser |
|     |     | 65  |     |     |     | 70  |     |     |     | 75  |     |     |     | 80  |     |
| Arg | Trp | Trp | Trp | Thr | Gly | Leu | Gly | Asp | Gln | Val | Lys | Ala | Thr | Met | Arg |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Ser | Gly | Pro | Ala | Phe | Pro | Pro | Thr | Ser | Xaa | Ala | Thr | Arg | Cys | Leu | Ile |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Leu | Thr | Leu | Ser | Leu | Met | Arg | Thr | Ala | Arg | Arg | Ala | Arg | Ser | Ser | Ser |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     |     | 125 |     |     |
| Ser | Leu | Gly | Pro | Gln | Met | His | Arg | Gly |     |     |     |     |     |     |     |
|     |     | 130 |     |     |     | 135 |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2909:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 139 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..139

(D) OTHER INFORMATION: / Ceres Seq. ID 1574765

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2909:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ser | Asn | Ser | Ala | Ser | Gly | Met | Ala | Val | Cys | Asp | Glu | Cys | Lys | Leu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Lys | Phe | Leu | Glu | Leu | Lys | Ala | Lys | Arg | Ser | Phe | Arg | Phe | Ile | Val | Phe |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Lys | Ile | Asn | Glu | Asn | Val | Gln | Gln | Val | Val | Val | Asp | Arg | Leu | Gly | Gly |
|     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| Pro | Gly | Glu | Ser | Tyr | Asp | Ala | Phe | Arg | Ala | Cys | Phe | Pro | Ala | Asn | Glu |
|     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Xaa | Arg | Tyr | Ala | Val | Phe | Asp | Phe | Asp | Phe | Val | Thr | Asp | Glu | Asn | Cys |
|     |     | 65  |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Gln | Lys | Ser | Lys | Ile | Phe | Phe | Ile | Ser | Trp | Ala | Pro | Asp | Ala | Ser | Arg |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Val | Arg | Ser | Lys | Met | Leu | Tyr | Ala | Ser | Ser | Lys | Asp | Arg | Phe | Lys | Arg |
|     |     |     | 100 |     |     |     | 105 |     |     |     |     |     | 110 |     |     |
| Glu | Leu | Asp | Gly | Ile | Gln | Val | Glu | Leu | Gln | Ala | Thr | Glu | Pro | Ser | Glu |
|     |     | 115 |     |     |     | 120 |     |     |     |     |     | 125 |     |     |     |
| Met | Ser | Met | Asp | Ile | Ile | Lys | Ser | Arg | Ala | Leu |     |     |     |     |     |
|     |     | 130 |     |     |     | 135 |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2910:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 672 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..672

(D) OTHER INFORMATION: / Ceres Seq. ID 1574769

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2910:

|            |            |             |            |            |            |     |
|------------|------------|-------------|------------|------------|------------|-----|
| acagccgtca | cgcacttcaa | tccagcagcc  | tctgctctgc | ctgcgtcgca | gccagtggct | 60  |
| cagcgggtgc | gcccggtgct | gtcacgtctt  | gtcctcaatc | tctctctctc | tcaatcctca | 120 |
| ctctctccgc | tctctttctc | ctccccagtc  | cccaacggtg | aggccccccg | cgtgcagccc | 180 |
| atcgacgcat | tgccgctgca | agcgcsaggac | accgagggct | agaagcgcg  | gcggtgccag | 240 |
| ggctcggcgc | tgggttgcca | atggcgaggc  | ggcttatgct | ggcgctccct | gtgctcctct | 300 |
| tctttattgt | cgtcgggcgc | ccgggattct  | tccgtgctaa | tggggaatgg | gtcacatgct | 360 |
| tctgttcagt | gcactggcac | ggtggatctg  | aagtttactt | cgggaaagat | cgtgcagctg | 420 |
| aagaacgtgc | atcatgtccc | kkctatacac  | aagaatctcg | ttagcggaac | ccttctatgt | 480 |
| agagatgggt | tcaaggtagt | tttagagctc  | aataaattag | ttgtgtccaa | gtctggacaa | 540 |
| ttttattgga | aaggctatga | ttggcgaggc  | ttgttccgct | tttcttttgt | agatttcaat | 600 |
| aataagctcg | tgaaccatat | ttgtgcta    | gttgatgatc | ttgcgagtat | ttggcattct | 660 |
| cgtttggctc | at         |             |            |            |            |     |

(2) INFORMATION FOR SEQ ID NO:2911:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 73 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..73

(D) OTHER INFORMATION: / Ceres Seq. ID 1574770

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2911:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Ala | Val | Thr | His | Phe | Asn | Pro | Ala | Ala | Leu | Pro | Ala | Ser |     |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     | 15  |     |     |
| Gln | Pro | Val | Ala | Gln | Arg | Leu | Arg | Pro | Cys | Leu | Ser | Arg | Leu | Val |
|     |     |     |     | 20  |     |     |     | 25  |     |     |     | 30  |     |     |
| Asn | Leu | Ser | Leu | Ser | Gln | Ser | Ser | Pro | Leu | Arg | Leu | Ser | Phe | Ser |
|     |     |     |     | 35  |     |     |     | 40  |     |     |     | 45  |     |     |
| Pro | Val | Pro | Asn | Gly | Glu | Ala | Pro | Ala | Val | Gln | Pro | Ile | Asp | Ala |
|     |     |     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |
| Pro | Leu | Gln | Gly | Xaa | Asp | Thr | Glu | Gly |     |     |     |     |     |     |
| 65  |     |     |     | 70  |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2912:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 112 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..112

(D) OTHER INFORMATION: / Ceres Seq. ID 1574771

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2912:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gln | Pro | Ser | Arg | Thr | Ser | Ile | Gln | Gln | Pro | Leu | Leu | Cys | Leu | Arg | Arg |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     | 15  |     |     |     |
| Ser | Gln | Trp | Leu | Ser | Gly | Cys | Ala | Arg | Ala | Cys | His | Val | Leu | Ser | Ser |
|     |     |     |     | 20  |     |     |     | 25  |     |     |     | 30  |     |     |     |
| Ile | Ser | Leu | Ser | Leu | Asn | Pro | His | Leu | Ser | Gly | Ser | Leu | Ser | Pro | Pro |
|     |     |     |     | 35  |     |     |     | 40  |     |     |     | 45  |     |     |     |
| Gln | Ser | Pro | Thr | Val | Arg | Pro | Pro | Pro | Cys | Ser | Pro | Ser | Thr | His | Cys |
|     |     |     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |
| Arg | Cys | Lys | Ala | Xaa | Thr | Pro | Arg | Ala | Arg | Ser | Gly | Gly | Gly | Ala | Arg |
| 65  |     |     |     | 70  |     |     |     | 75  |     |     |     | 80  |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | Arg | Arg | Ser | Val | Gly | Asn | Gly | Glu | Ala | Ala | Tyr | Ala | Gly | Ala | Pro |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Cys | Ala | Pro | Leu | Leu | Ile | Ala | Arg | Arg | Ala | Pro | Gly | Ile | Leu | Pro | Cys |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     |     | 110 |     |

(2) INFORMATION FOR SEQ ID NO:2913:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..111

(D) OTHER INFORMATION: / Ceres Seq. ID 1574772

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2913:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Gly | Asn | Gly | Ser | His | Ala | Ser | Val | His | Gly | Thr | Gly | Thr | Val | Asp |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Leu | Lys | Phe | Thr | Ser | Gly | Lys | Ile | Val | Gln | Leu | Lys | Asn | Val | His | His |
|     |     |     | 20  |     |     |     | 25  |     |     |     |     |     | 30  |     |     |
| Val | Xaa | Xaa | Ile | His | Lys | Asn | Leu | Val | Ser | Gly | Thr | Leu | Leu | Cys | Arg |
|     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |
| Asp | Gly | Phe | Lys | Val | Val | Leu | Glu | Ser | Asn | Lys | Leu | Val | Val | Ser | Lys |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ser | Gly | Gln | Phe | Ile | Gly | Lys | Gly | Tyr | Asp | Cys | Gly | Gly | Leu | Phe | Arg |
| 65  |     |     |     | 70  |     |     |     | 75  |     |     |     |     |     | 80  |     |
| Phe | Ser | Leu | Leu | Asp | Phe | Asn | Asn | Lys | Ser | Val | Asn | His | Ile | Cys | Ala |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Asn | Val | Asp | Asp | Leu | Ala | Ser | Ile | Trp | His | Ser | Arg | Leu | Cys | His |     |
|     |     | 100 |     |     |     |     | 105 |     |     |     |     |     | 110 |     |     |

(2) INFORMATION FOR SEQ ID NO:2914:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 588 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..588

(D) OTHER INFORMATION: / Ceres Seq. ID 1574773

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2914:

|             |             |            |            |            |             |     |
|-------------|-------------|------------|------------|------------|-------------|-----|
| aaacctactga | cgagctcgcc  | atggcctccc | tctctctgc  | cgccgtcacc | gccccttctct | 60  |
| tcgcgcgacc  | agcgccacccc | gogccgtggt | cagaaggagg | tccttcaccg | tgccgcgcctc | 120 |
| ttctccgcaag | gccaccgcga  | ccgccgcgct | ggcaatggct | gccagcgccc | tgcttgccgcg | 180 |
| cggtgccatg  | gccaggagg   | tgctgtggg  | cgcaggcgac | ggcgggctcg | tcttcgagcc  | 240 |
| cgagcagttc  | accgtcaagg  | ccggcgacac | catcTacatt | caagaacaac | gccggtcttc  | 300 |
| cgacacaagt  | ctctttcgac  | gaagacgagg | tgccgagcgg | cgtcgacacc | accaagatct  | 360 |
| cgcaggaggga | gtacctcaac  | gcgcgagcgg | agacctactc | cgtcaccctc | accgtgccgg  | 420 |
| gaacctacgg  | cttctactgc  | gagccgcata | aaggagccgg | aatggtcggc | aagatcacccg | 480 |
| tcaactaat   | aaagtagcta  | tcgatcgata | tcattcatg  | tattagctgt | tgcttctctgc | 540 |
| ttgtactcc   | gccgatctgt  | ccatctctwc | atgttttcgk | cttcacac   |             |     |

(2) INFORMATION FOR SEQ ID NO:2915:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 163 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..163

(D) OTHER INFORMATION: / Ceres Seq. ID 1574774

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2915:

```
Asn Leu Leu Thr Ser Ser Pro Trp Pro Pro Ser Pro Leu Pro Pro Ser
1 5 10 15
Pro Pro Leu Pro Ser Pro His Gln Arg His Pro Arg Arg Gly Gln Lys
20 25 30
Glu Val Leu His Arg Ala Arg Leu Ser Pro Gln Gly His Arg His Arg
35 40 45
Arg Arg Gly Asn Gly Cys Gln Arg Pro Ala Cys Arg Arg Cys His Gly
50 55 60
Pro Gly Gly Ala Ala Gly Arg Arg Arg Arg Ala Arg Leu Arg Ala
65 70 75 80
Gln Pro Val His Arg Gln Gly Arg Arg His His Leu His Ser Arg Thr
85 90 95
Thr Pro Ala Ser Arg Thr Thr Xaa Ser Ser Thr Lys Thr Arg Cys Arg
100 105 110
Ala Ala Ser Thr Pro Pro Arg Ser Arg Arg Arg Ser Thr Ser Thr Arg
115 120 125
Gln Ala Arg Pro Thr Pro Ser Pro Ser Pro Cys Arg Glu Pro Thr Ala
130 135 140
Ser Thr Ala Ser Arg Ile Lys Glu Pro Glu Trp Ser Ala Arg Ser Pro
145 150 155 160
Ser Thr Asn
```

(2) INFORMATION FOR SEQ ID NO:2916:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 161 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..161

(D) OTHER INFORMATION: / Ceres Seq. ID 1574775

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2916:

```
Pro Thr Asp Glu Leu Ala Met Ala Ser Leu Ser Ser Ala Ala Val Thr
1 5 10 15
Ala Pro Ser Phe Ala Ala Pro Ala Pro Pro Ala Pro Trp Ser Glu Gly
20 25 30
Gly Pro Ser Pro Cys Ala Pro Leu Ser Ala Arg Pro Pro Ala Pro Pro
35 40 45
Pro Trp Gln Trp Leu Pro Ala Pro Cys Leu Pro Ala Val Pro Trp Pro
50 55 60
Arg Arg Cys Cys Trp Ala Gln Ala Thr Ala Gly Ser Ser Ser Ser Pro
65 70 75 80
Ala Ser Ser Pro Ser Arg Pro Ala Thr Pro Ser Thr Phe Lys Asn Asn
85 90 95
Ala Gly Phe Pro His Asn Val Xaa Phe Asp Glu Asp Glu Val Pro Ser
100 105 110
Gly Val Asp Thr Thr Lys Ile Ser Gln Glu Glu Tyr Leu Asn Ala Pro
115 120 125
Gly Glu Thr Tyr Ser Val Thr Leu Thr Val Pro Gly Thr Tyr Gly Phe
130 135 140
Tyr Cys Glu Pro His Gln Gly Ala Gly Met Val Gly Lys Ile Thr Val
145 150 155 160
Asn
```

(2) INFORMATION FOR SEQ ID NO:2917:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 155 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..155
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574776

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2917:

```
Met Ala Ser Leu Ser Ser Ala Ala Val Thr Ala Pro Ser Phe Ala Ala
1 5 10 15
Pro Ala Pro Pro Ala Pro Trp Ser Glu Gly Gly Pro Ser Pro Cys Ala
20 25 30
Pro Leu Ser Ala Arg Pro Pro Ala Pro Pro Trp Gln Trp Leu Pro
35 40 45
Ala Pro Cys Leu Pro Ala Val Pro Trp Pro Arg Arg Cys Cys Trp Ala
50 55 60
Gln Ala Thr Ala Gly Ser Ser Ser Pro Ala Ser Ser Pro Ser Arg
65 70 75 80
Pro Ala Thr Pro Ser Thr Phe Lys Asn Asn Ala Gly Phe Pro His Asn
85 90 95
Val Xaa Phe Asp Glu Asp Glu Val Pro Ser Gly Val Asp Thr Thr Lys
100 105 110
Ile Ser Gln Glu Glu Tyr Leu Asn Ala Pro Gly Glu Thr Tyr Ser Val
115 120 125
Thr Leu Thr Val Pro Gly Thr Tyr Gly Phe Tyr Cys Glu Pro His Gln
130 135 140
Gly Ala Gly Met Val Gly Lys Ile Thr Val Asn
145 150 155
```

(2) INFORMATION FOR SEQ ID NO:2918:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 466 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..466
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574797

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2918:

```
gataaatctc tccatcagcgc agcacctagc tagcagcagc caatgacgaa gccttcgcgag 60
gtgctgttgg cggcgcctgc cgytgggagc gtggtcctgc tgcgtgtgtg cgccgcgcgcg 120
ccgcgggggag cCgacgcgcgc gacggcgtgc gacgccacgc agctgacgcc gtgcgcgcgcg 180
gccatcatca tcgggaggtc gccacgcgcg cgcgtgctgca gtaggctcaa ggagcagcag 240
ccgtgcctgt gcacgtacgc gcgcgacccc aatcttcagc gctacgtcaa ctgcgccaaac 300
ggcaagaagg ccatggccgc gtgcaagggt cccgtrccgt cgtgctagt aacttctgtt 360
tgcrcgcgcg ccgcgtacgt gtcgtgtogt gcctgtgtca gtagcagcaa gcccactgg 420
acagggacag agtatggcgt cactttctgt ttccgtacat acgtac
```

(2) INFORMATION FOR SEQ ID NO:2919:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 101 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide

(B) LOCATION: 1..101  
(D) OTHER INFORMATION: / Ceres Seq. ID 1574798  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2919:  
Met Thr Lys Pro Ser Gln Val Leu Leu Ala Ala Leu Ala Xaa Trp Ala  
1 5 10 15  
Val Val Leu Leu Leu Cys Ala Ala Ala Pro Arg Gly Ala Asp Ala  
20 25 30  
Ala Thr Ala Cys Asp Ala Thr Gln Leu Thr Pro Cys Ala Gly Ala Ile  
35 40 45  
Ile Ile Gly Arg Ser Pro Ser Ala Ala Cys Cys Ser Arg Leu Lys Glu  
50 55 60  
Gln Gln Pro Cys Leu Cys Thr Tyr Ala Arg Asp Pro Asn Leu Gln Arg  
65 70 75 80  
Tyr Val Asn Ser Pro Asn Gly Lys Lys Ala Met Ala Ala Cys Lys Val  
85 90 95  
Pro Xaa Pro Ser Cys  
100

(2) INFORMATION FOR SEQ ID NO:2920:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 743 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..743

(D) OTHER INFORMATION: / Ceres Seq. ID 1574803

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2920:

|            |            |             |            |            |             |     |
|------------|------------|-------------|------------|------------|-------------|-----|
| aggatcctct | cggcgcgagg | ctccgagttg  | ccgtctccgc | ctctctgagt | tagcgttctc  | 60  |
| caccaagagc | agcatggagt | ccgacgtgta  | cagctacggc | gtggtgtctg | tggagctgct  | 120 |
| cacgaggagg | gcggcggttg | atccctcgtt  | tcccacggc  | acggacatag | tcagctgggc  | 180 |
| gtcgtccgcc | ctgaacSggc | accgacaaaa  | tcgaggccgt | ctgcgacccg | gctctcatgt  | 240 |
| aggaagtctt | cggcacgggt | gagatggagg  | aggtgagtaa | ggctctgtca | gtggcgctgc  | 300 |
| ggtgcgcggc | cagggaggcg | agccaaagc   | ctccatgac  | gcgcgtctgt | aaggagctga  | 360 |
| cgatgcacg  | gcctgccact | ggcgcgggcc  | ggctcgtgtc | caagtccga  | caggggaaac  | 420 |
| caggatcgca | atccaacagc | agcgccctacc | ggcagtagga | tctctgactc | tgccgagctg  | 480 |
| tttggggaca | ccaactttac | tcaacttgta  | gtctctactc | tatagTacc  | ctcgttggt   | 540 |
| gtacatctgt | attggttagt | tggcaaatag  | tagttgtagt | tcaaatgaaa | cggagagatg  | 600 |
| ctggactTcg | tgctcagtgc | agtgaagcaa  | gctgcttggt | ctgaaatctg | tggactgtgtg | 660 |
| cttgctcgtg | gcttcacagg | acgggaccag  | gagagaatgg | gtattcgaaa | ttgtactaaa  | 720 |
| ggaaaaaaaa | attagatggt | ctg         |            |            |             |     |

(2) INFORMATION FOR SEQ ID NO:2921:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 92 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..92

(D) OTHER INFORMATION: / Ceres Seq. ID 1574804

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2921:

Gly Ser Ser Arg Pro Arg Ala Pro Ser Cys Arg Leu Arg Leu Ser Glu  
1 5 10 15  
Leu Ala Phe Ser Thr Lys Ser Ser Met Glu Ser Asp Val Tyr Ser Tyr  
20 25 30  
Gly Val Val Leu Leu Glu Leu Leu Thr Arg Arg Ala Ala Val Asp Pro  
35 40 45  
Ser Phe Pro Asp Gly Thr Asp Ile Val Ser Trp Ala Ser Ser Ala Leu

(2) INFORMATION FOR SEQ ID NO:2922:

- [illegible]

- ```

(2) INFORMATION FOR SEQ ID NO:2923:
      (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 73 amino acids
            (B) TYPE: amino acid
            (C) STRANDEDNESS:
            (D) TOPOLOGY: linear
      (ii) MOLECULE TYPE: peptide
      (ix) FEATURE:
            (A) NAME/KEY: peptide
            (B) LOCATION: 1..73
            (D) OTHER INFORMATION: / Ceres Seq. ID 1574806
      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2923:
Met Glu Glu Val Phe Gly Thr Val Glu Met Glu Glu Val Ser Lys Val
1                               10                               15
Leu Ser Val Ala Leu Arg Cys Ala Ala Arg Glu Ala Ser Gln Arg Pro
20                               25                               30
Ser Met Thr Ala Val Val Lys Glu Leu Thr Asp Ala Arg Pro Ala Thr
35                               40                               45
Gly Gly Gly Arg Ser Leu Ser Lys Ser Lys Gln Gly Lys Pro Gly Ser
50                               55                               60
Gln Ser Asn Ser Ser Ala Tyr Arg Gln
65                               70

```

- | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|--------|
| 2017 | 2018 | 2019 | 2020 | 2021 | 2022 | 2023 | 2024 | 2025 | 2026 | 2027 | 2028 | 2029 | 2030 | 2031 | 2032 | 2033 | 2034 | 2035 | 2036 | 2037 | 2038 | 2039 | 2040 | 2041 | 2042 | 2043 | 2044 | 2045 | 2046 | 2047 | 2048 | 2049 | 2050 | 2051 | 2052 | 2053 | 2054 | 2055 | 2056 | 2057 | 2058 | 2059 | 2060 | 2061 | 2062 | 2063 | 2064 | 2065 | 2066 | 2067 | 2068 | 2069 | 2070 | 2071 | 2072 | 2073 | 2074 | 2075 | 2076 | 2077 | 2078 | 2079 | 2080 | 2081 | 2082 | 2083 | 2084 | 2085 | 2086 | 2087 | 2088 | 2089 | 2090 | 2091 | 2092 | 2093 | 2094 | 2095 | 2096 | 2097 | 2098 | 2099 | 2100 | 2101 | 2102 | 2103 | 2104 | 2105 | 2106 | 2107 | 2108 | 2109 | 2110 | 2111 | 2112 | 2113 | 2114 | 2115 | 2116 | 2117 | 2118 | 2119 | 2120 | 2121 | 2122 | 2123 | 2124 | 2125 | 2126 | 2127 | 2128 | 2129 | 2130 | 2131 | 2132 | 2133 | 2134 | 2135 | 2136 | 2137 | 2138 | 2139 | 2140 | 2141 | 2142 | 2143 | 2144 | 2145 | 2146 | 2147 | 2148 | 2149 | 2150 | 2151 | 2152 | 2153 | 2154 | 2155 | 2156 | 2157 | 2158 | 2159 | 2160 | 2161 | 2162 | 2163 | 2164 | 2165 | 2166 | 2167 | 2168 | 2169 | 2170 | 2171 | 2172 | 2173 | 2174 | 2175 | 2176 | 2177 | 2178 | 2179 | 2180 | 2181 | 2182 | 2183 | 2184 | 2185 | 2186 | 2187 | 2188 | 2189 | 2190 | 2191 | 2192 | 2193 | 2194 | 2195 | 2196 | 2197 | 2198 | 2199 | 2200 | 2201 | 2202 | 2203 | 2204 | 2205 | 2206 | 2207 | 2208 | 2209 | 2210 | 2211 | 2212 | 2213 | 2214 | 2215 | 2216 | 2217 | 2218 | 2219 | 2220 | 2221 | 2222 | 2223 | 2224 | 2225 | 2226 | 2227 | 2228 | 2229 | 2230 | 2231 | 2232 | 2233 | 2234 | 2235 | 2236 | 2237 | 2238 | 2239 | 2240 | 2241 | 2242 | 2243 | 2244 | 2245 | 2246 | 2247 | 2248 | 2249 | 2250 | 2251 | 2252 | 2253 | 2254 | 2255 | 2256 | 2257 | 2258 | 2259 | 2260 | 2261 | 2262 | 2263 | 2264 | 2265 | 2266 | 2267 | 2268 | 2269 | 2270 | 2271 | 2272 | 2273 | 2274 | 2275 | 2276 | 2277 | 2278 | 2279 | 2280 | 2281 | 2282 | 2283 | 2284 | 2285 | 2286 | 2287 | 2288 | 2289 | 2290 | 2291 | 2292 | 2293 | 2294 | 2295 | 2296 | 2297 | 2298 | 2299 | 2300 | 2301 | 2302 | 2303 | 2304 | 2305 | 2306 | 2307 | 2308 | 2309 | 2310 | 2311 | 2312 | 2313 | 2314 | 2315 | 2316 | 2317 | 2318 | 2319 | 2320 | 2321 | 2322 | 2323 | 2324 | 2325 | 2326 | 2327 | 2328 | 2329 | 2330 | 2331 | 2332 | 2333 | 2334 | 2335 | 2336 | 2337 | 2338 | 2339 | 2340 | 2341 | 2342 | 2343 | 2344 | 2345 | 2346 | 2347 | 2348 | 2349 | 2350 | 2351 | 2352 | 2353 | 2354 | 2355 | 2356 | 2357 | 2358 | 2359 | 2360 | 2361 | 2362 | 2363 | 2364 | 2365 | 2366 | 2367 | 2368 | 2369 | 2370 | 2371 | 2372 | 2373 | 2374 | 2375 | 2376 | 2377 | 2378 | 2379 | 2380 | 2381 | 2382 | 2383 | 2384 | 2385 | 2386 | 2387 | 2388 | 2389 | 2390 | 2391 | 2392 | 2393 | 2394 | 2395 | 2396 | 2397 | 2398 | 2399 | 2400 | 2401 | 2402 | 2403 | 2404 | 2405 | 2406 | 2407 | 2408 | 2409 | 2410 | 2411 | 2412 | 2413 | 2414 | 2415 | 2416 | 2417 | 2418 | 2419 | 2420 | 2421 | 2422 | 2423 | 2424 | 2425</ |
|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|--------|

a aaaacttgcg tgcgaagaag ctccagaacag aagccatcaa aagcggagcgt gcgagagcgg 60
agagagagag tgaRgggaggg cgcgcagcgc gagtcctttc ttcctcctgc atctgcgcgt 120
gtttccgaca ggaagtgtttc cagcaggagc gagtacgacc gtgggggtgaa caccttctct 180
ccggagggggc ggctgtttcca ggtcgagtac gccatcgagg ccatcaagtt gggatccact 240
gcgatcggtt tgaagacaaa ggaatggtgtt gtctcgcgcg ttgagaaaag tdtgacctca 300
ccactgctgg aaccaagcag tdtggaaaaa ataattgaaa ttgatgagca cataggctgt 360
gccatgagtg gacttatgtc tgatgctaga acactagtgg aacatgctcg tdtggaact 420
cagaatcata ggttctcata cggagagcca atgactgtag aatcttcgac acaagctatc 480
tgtgacttag ctctgcgttt tggcgaaggt gacgaagagt caatgtcacg gccatttggg 540
gtctctctcc taattgctgg acatgatgag aatggacctc gc

(2) INFORMATION FOR SEQ ID NO:2925:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 194 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..194

(D) OTHER INFORMATION: / Ceres Seq. ID 1574815

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2925:

Lys Thr Ser Phe Ala Arg Ser Ser Glu Gln Lys Pro Ser Lys Ala Arg
1 5 10 15
Leu Arg Glu Arg Arg Glu Arg Val Xaa Gly Gly Ala Asp Ala Glu Ser
20 25 30
Phe Leu His Pro Ala Ser Ala Ala Val Ser Asp Arg Met Phe Leu Thr
35 40 45
Arg Thr Glu Tyr Asp Arg Gly Val Asn Thr Phe Ser Pro Glu Gly Arg
50 55 60
Leu Phe Gln Val Glu Tyr Ala Ile Glu Ala Ile Lys Leu Gly Ser Thr
65 70 75 80
Ala Ile Gly Leu Lys Thr Lys Asp Gly Val Val Leu Ala Val Glu Lys
85 90 95
Arg Val Thr Ser Pro Leu Leu Glu Pro Ser Ser Val Glu Lys Ile Met
100 105 110
Glu Ile Asp Glu His Ile Gly Cys Ala Met Ser Gly Leu Ile Ala Asp
115 120 125
Ala Arg Thr Leu Val Glu His Ala Arg Val Glu Thr Gln Asn His Arg
130 135 140
Phe Ser Tyr Gly Glu Pro Met Thr Val Glu Ser Ser Thr Gln Ala Ile
145 150 155 160
Cys Asp Leu Ala Leu Arg Phe Gly Glu Gly Asp Glu Glu Ser Met Ser
165 170 175
Arg Pro Phe Gly Val Ser Leu Leu Ile Ala Gly His Asp Glu Asn Gly
180 185 190
Pro Ser

(2) INFORMATION FOR SEQ ID NO:2926:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 150 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..150

(D) OTHER INFORMATION: / Ceres Seq. ID 1574816

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2926:

Met Phe Leu Thr Arg Thr Glu Tyr Asp Arg Gly Val Asn Thr Phe Ser

1	5	10	15
Pro Glu Gly Arg Leu Phe Gln Val Glu Tyr Ala Ile Glu Ala Ile Lys			
20	25	30	
Leu Gly Ser Thr Ala Ile Gly Leu Lys Thr Lys Asp Gly Val Val Leu			
35	40	45	
Ala Val Glu Lys Arg Val Thr Ser Pro Leu Leu Glu Pro Ser Ser Val			
50	55	60	
Glu Lys Ile Met Glu Ile Asp Glu His Ile Gly Cys Ala Met Ser Gly			
65	70	75	80
Leu Ile Ala Asp Ala Arg Thr Leu Val Glu His Ala Arg Val Glu Thr			
85	90	95	
Gln Asn His Arg Phe Ser Tyr Gly Glu Pro Met Thr Val Glu Ser Ser			
100	105	110	
Thr Gln Ala Ile Cys Asp Leu Ala Leu Arg Phe Gly Glu Gly Asp Glu			
115	120	125	
Glu Ser Met Ser Arg Pro Phe Gly Val Ser Leu Ile Ala Gly His			
130	135	140	
Asp Glu Asn Gly Pro Ser			
145	150		

(2) INFORMATION FOR SEQ ID NO:2927:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 905 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..905
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574817

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2927:

aaaccctttc gatctgtctca actaccaaac tctgtctctc cctgcttccg tcaocgcgaga	60
gcactccact ccCacgcgaa Accctagcag tgggttctccc tcgggggcccc gctaagcagc	120
ttggttccaa gctgtagaag catctccgat cccatccgcg gcgggttgag gccatcagct	180
ccggtttctg cagccggatt tgggatccgc gagatgtctt ggctcgcgcc cgaacgacatc	240
ctcctctcca cctccctcgc cggcttcttg gacaagaaac ttattgtctc gctaagagat	300
ggacggaaac tgcttggcac cctctgctca ttgtatcagt ttgcaaatgt tgttcttcag	360
ggtgctgtgt aacgagtgat tgtgggggaa caatatttgt atgttctctt tgggtctgac	420
gtaatccggg gagagaacct tgttttaatc ggagaattgg atcgcgaaaa ggatgaactc	480
ctctctcaca tgacctgtgt ttcagaagca gaaataagaa aggcgtgaaa ggcagaacgc	540
gaagccagag atctgaaagg gacgatgagg aaacggatgg agttctcgga ctctcgattaa	600
caccgtcaac Ygcggcgctt gccgctcccc attgtggcgg aatctttagt ggcggcctgt	660
gtgcataaca tgccctgtga ccgcgcgcgc gcaccttgga ttgctggagg gtttagcgaa	720
cagtttcttt ttaactagca gtgctgtttt atactctcgt gccacacagac cctttTgagc	780
gcctctgat acagctttgt caccactctg atcattgcct cgatgaatt tatatacctg	840
acgttttgga ttggatctgc gccaaaaacgc catttctatg gagagagtct ctactcttat	900

(2) INFORMATION FOR SEQ ID NO:2928:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 128 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..128
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574818

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2928:

Met Ser Trp Ser Ala Pro Asp Asp Ile Leu Leu Ser Thr Ser Leu Ala	
1	10 15

Gly Phe Leu Asp Lys Lys Leu Ile Val Leu Leu Arg Asp Gly Arg Lys
20 25 30
Leu Leu Gly Thr Leu Cys Ser Phe Asp Gln Phe Ala Asn Val Val Leu
35 40 45
Gln Gly Ala Cys Glu Arg Val Ile Val Gly Glu Gln Tyr Cys Asp Val
50 55 60
Pro Leu Gly Leu Tyr Val Ile Arg Gly Glu Asn Val Val Leu Ile Gly
65 70 75 80
Glu Leu Asp Arg Glu Lys Asp Glu Leu Pro Ala His Met Thr Cys Val
85 90 95
Ser Glu Ala Glu Ile Arg Lys Ala Glu Lys Ala Glu Arg Glu Ala Arg
100 105 110
Asp Leu Lys Gly Thr Met Arg Lys Arg Met Glu Phe Leu Asp Phe Asp
115 120 125

(2) INFORMATION FOR SEQ ID NO:2929:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 666 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..666
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574819

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2929:

gtaacgaggc atcgacactg acagagtcca cggcaccggt tgtttaccac caaccatccg 60
gcccttcccc gaccCatggc ggccggcacc cctcgctggt ggccgctcct cctgcagctc 120
gcaatcgccc ttggcatcct gctcgcdgcg gccgaggctt ggacggggga gatccgcggc 180
cgcgctgctt cgcagctctg cggcgacgca gccatcggcc cgaggagcca cgccctcgaa 240
ggtgcggagg ttgctgtcct ctgcacacaa aaatctggtg aggttatcaa ctatcaagcc 300
ttcacaaact ccaaggcgct gtatactgtc gccgagacta tgcggagagag cgacaggtgg 360
gactcgtgct tggcgaggcc tatgagcagc ttccatctac attgcacacg gcggggtgat 420
gctcactctg ggggtgaagt cacttacaac aaatcgtctg ggaacccaca cacgtcaag 480
cctttcctct acaagccggc caccatccct ctgtattgta gttaaacaac acatcttgct 540
ggaacgcaga agatagaaca tacaggaaga aaatatgtat tcgtgccccc actccatata 600
taagtaaaaa cttttgatgt aaatcaaaaga ttacgctgtc tatgggagct gttctagtgt 660
ctggtc

(2) INFORMATION FOR SEQ ID NO:2930:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 92 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..92
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574820

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2930:

Asn Glu Ala Ser Thr Leu Thr Glu Ser Thr Ala Arg Leu Val Tyr His
1 5 10 15
Gln Pro Ser Gly Pro Ser Pro Thr His Gly Gly Gly Thr Pro Ser Leu
20 25 30
Val Ala Ala Pro Pro Ala Ala Arg Asn Arg Pro Trp His Pro Ala Arg
35 40 45
Xaa Gly Arg Gly Leu Asp Gly Gly Asp Pro Arg Pro Arg Arg Leu Arg
50 55 60
Arg Leu Arg Arg Arg Ser His Arg Pro Gly Gly Pro Arg Pro Arg Arg

65 70 75 80
Cys Gly Gly Cys Cys Pro Leu His His Lys Ile Trp
85 90

(2) INFORMATION FOR SEQ ID NO:2931:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 149 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..149
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574821

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2931:

```
Met Ala Ala Ala Pro Pro Arg Trp Trp Pro Leu Leu Leu Gln Leu Ala
1      5      10      15
Ile Ala Leu Gly Ile Leu Leu Xaa Ala Ala Glu Ala Trp Thr Gly Glu
20     25     30
Ile Arg Gly Arg Val Val Cys Asp Val Cys Gly Asp Ala Ala Ile Gly
35     40     45
Pro Glu Asp His Ala Leu Glu Gly Ala Glu Val Ala Val Leu Cys Ile
50     55     60
Thr Lys Ser Gly Glu Val Ile Asn Tyr Gln Ala Phe Thr Asn Ser Lys
65     70     75     80
Gly Val Tyr Thr Val Ala Glu Thr Met Pro Glu Ser Asp Arg Trp Asp
85     90     95
Ser Cys Leu Ala Arg Pro Met Ser Ser Phe His Leu His Cys Thr Arg
100    105    110
Arg Gly Asp Ala His Ser Gly Val Lys Phe Thr Tyr Asn Lys Ser Ser
115    120    125
Gly Asn Pro His Thr Val Lys Pro Phe Leu Tyr Lys Pro Ala Thr Ile
130    135    140
Pro Leu Tyr Cys Ser
145
```

(2) INFORMATION FOR SEQ ID NO:2932:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 816 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..816
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574838

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2932:

```
aaaattccatt ccaaatccgc agtccgcaga cgagagtggg agcggggcac agacaggagaag 60
aagaagccaat ggcgcgtgtcc Ctctccctcg cgcgcccocgc gccCtccgcc gtttccgcgcg 120
gcgcaggagc caggaagcta cccgcagcca gcctcgcatt cccggcgaaa tctcttctcg 180
gcgcgcgcgt ggcgcgccacc cgggcctccg tgcgctgcgc gctccgcgcg aaGccggcca 240
ctctcaccac ctgcctcgag gtgcgtgcgc cggggaagaa gggctacaag atgaagacgc 300
acaagcgctc ggcgaacggt tccgggtgac ggggaggggc aagatcgtcg gccggtgcgc 360
cgggaagcag cacttgctcg ccaagaagaa caccaagcgc aagaagagcg tctcgaagat 420
ggtgcaagtc aacaagagtg actacgacaa tgttacgggt gcactgccct acctcaagat 480
gaataggaaa gcaaaactgag agctacgtgg tcttcaaaaa atcataagtt ttggttccac 540
caaatgttaa tttttgtgat ctccactgt atttccttct caaaaaatact gaggcatcat 600
ttcaaaagca gcaaaaaaaca acctcctggta tcaacagtat agcgatattt cagaataggg 660
tgcaactgctt gctatagttg ttatttagtc gcaaatatgt gcaagtaaga gtggcaactg 720
agccattagc tctctttagg atatggccag cagatcgtgt atatggctgt gcaagacact 780
gttttgccac attttatata tagactgcac tgttttg
```

(2) INFORMATION FOR SEQ ID NO:2933:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 97 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..97
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574839

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2933:

Lys Phe His Ser Lys Ser Ala Val Arg Arg Arg Glu Trp Lys Arg Gly
1 5 10 15
Thr Asp Arg Lys Arg Ser Gln Trp Arg Cys Pro Ser Pro Ser Arg Ala
20 25 30
Pro Arg Pro Ser Pro Phe Pro Pro Ala Gln Glu Pro Gly Ser Tyr Pro
35 40 45
Gln Pro Ala Ser His Ser Arg Arg Asn Pro Ser Ser Ala Arg Arg Trp
50 55 60
Pro Pro Pro Arg Pro Pro Ser Arg Arg Arg Ser Arg Ala Ser Arg Pro
65 70 75 80
Pro Pro Pro Pro Arg Ser Arg Ser Ser Arg Arg Gly Arg Arg Ala Thr
85 90 95
Arg

(2) INFORMATION FOR SEQ ID NO:2934:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 165 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..165
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574840

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2934:

Asn Ser Ile Pro Asn Pro Gln Ser Ala Asp Glu Ser Gly Ser Gly Ala
1 5 10 15
Gln Thr Gly Arg Glu Ala Asn Gly Ala Val Pro Leu Pro Arg Ala Pro
20 25 30
Arg Ala Pro Arg Arg Phe Arg Arg Arg Ser Gln Glu Ala Thr Arg
35 40 45
Ser Gln Pro Arg Ile Pro Gly Glu Ile Leu Leu Arg Arg Ala Ala Gly
50 55 60
Arg His Arg Gly Leu Arg Arg Val Ala Ala Pro Ala Gln Ala Gly His
65 70 75 80
Leu His His Leu Ala Arg Gly Arg Arg Gly Gly Glu Glu Gly Leu Gln
85 90 95
Asp Glu Asp Ala Gln Gly Val Gly Glu Arg Phe Arg Val Thr Gly Arg
100 105 110
Gly Lys Ile Val Arg Arg Cys Ala Gly Lys Gln His Leu Leu Ala Lys
115 120 125
Lys Asn Thr Lys Arg Lys Lys Arg Leu Ser Lys Met Val Gln Val Asn
130 135 140
Lys Ser Asp Tyr Asp Asn Val Thr Gly Ala Leu Pro Tyr Leu Lys Val
145 150 155 160
Asn Arg Lys Ala Asn
165

(2) INFORMATION FOR SEQ ID NO:2935:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 108 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..108
(D) OTHER INFORMATION: / Ceres Seq. ID 1574841
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2935:
Ile Pro Phe Gln Ile Arg Ser Pro Gln Thr Arg Val Glu Ala Gly His
1 5 10 15
Arg Gln Glu Glu Lys Pro Met Ala Leu Ser Leu Ser Leu Ala Arg Pro
20 25 30
Ala Pro Leu Ala Val Ser Ala Gly Ala Arg Lys Leu Pro Ala
35 40 45
Ala Ser Leu Ala Phe Pro Ala Lys Ser Phe Phe Gly Ala Pro Leu Ala
50 55 60
Ala Thr Ala Ala Ser Val Ala Ser Pro Leu Pro Arg Lys Pro Ala Thr
65 70 75 80
Ser Thr Thr Ser Leu Glu Val Val Ala Ala Gly Lys Lys Gly Tyr Lys
85 90 95
Met Lys Thr His Lys Ala Ser Ala Asn Gly Ser Gly
100 105

(2) INFORMATION FOR SEQ ID NO:2936:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 743 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..743
(D) OTHER INFORMATION: / Ceres Seq. ID 1574842

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2936:

acaggcgaaaa aaaaaaactg ttgttagcgc tgacgtgcgt raggagctcg gactcggagc 60
gaatcgaaaaa ggcgaaaaact cagtgtctcg agtttctctg gwnccnaggc gatggctggg 120
aaggggaggga aagcgttgct cgccgcgaag actacggcgg ccaagtcgcc cgagaaggac 180
aagggggaaga aggccccaat ctcaagctcc tcccgcgccg gctccagatt ccctgttggg 240
cgtatccacc gtcagctgaa gcaaaaggact caggcaaatg gtccgcttgg tgccaccgca 300
gcgctctaact cgcgtgccat cctggagtag ttgactgccg aggttctKgg agctggcgaa 360
tgctagcaag gatctgaagk tgaagcgtat cacccttcgc catttgcaac tagccattcg 420
tgagagcgag gagctggaca cctcatcaa gggcaccatc gcaggcggag gtgtcatccc 480
gcacattcac aagtccctga tcaacaagtc ctccaaggag tgaagactag gggatgtgca 540
tctttagttt aaactagact tctgtgcgct cctcggcgag tccttgcgat cctgtaggtt 600
ttagttgagc tgtcaggttg gtgctctctc gtgtaacgct tgccctggta tgcttcatca 660
gttatttggt tattgtgttt gtgttgagtt gttaacttca ggggtgcгаа cctggatgct 720
tatttagtta tgtgactact gct

(2) INFORMATION FOR SEQ ID NO:2937:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 124 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..124
(D) OTHER INFORMATION: / Ceres Seq. ID 1574843

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2937:

Arg	Arg	Lys	Lys	Lys	Leu	Phe	Val	Ser	Val	Thr	Cys	Xaa	Arg	Ser	Leu
1			5						10					15	
Glu	Ser	Asp	Gly	Ile	Glu	Lys	Ala	Lys	Thr	Gln	Cys	Leu	Glu	Phe	Pro
			20					25					30		
Arg	Xaa	Xaa	Gly	Asp	Gly	Trp	Glu	Gly	Arg	Glu	Arg	Leu	Ala	Arg	Arg
		35				40						45			
Glu	Asp	Trp	Gly	Gly	Gln	Val	Arg	Arg	Glu	Gly	Gln	Gly	Glu	Glu	Gly
	50				55					60					
Pro	Asn	Leu	Thr	Leu	Leu	Pro	Arg	Arg	Pro	Pro	Val	Pro	Cys	Trp	Ala
	65			70					75					80	
Tyr	Pro	Pro	Ser	Ala	Glu	Ala	Lys	Asp	Ser	Gly	Lys	Trp	Ser	Arg	Trp
			85					90					95		
Cys	His	Arg	Ser	Arg	Leu	Leu	Arg	Cys	His	Pro	Gly	Val	Leu	Asp	Cys
			100					105					110		
Arg	Gly	Ser	Xaa	Ser	Trp	Arg	Met	Leu	Ala	Arg	Ile				
		115				120									

(2) INFORMATION FOR SEQ ID NO:2938:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 84 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..84

(D) OTHER INFORMATION: / Ceres Seq. ID 1574844

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2938:

Met	Ala	Gly	Lys	Gly	Gly	Lys	Gly	Leu	Leu	Ala	Ala	Lys	Thr	Thr	Ala
1			5					10						15	
Ala	Lys	Ser	Ala	Glu	Lys	Asp	Lys	Gly	Lys	Lys	Ala	Pro	Ile	Ser	Arg
			20					25					30		
Ser	Ser	Arg	Ala	Gly	Leu	Gln	Phe	Pro	Val	Gly	Arg	Ile	His	Arg	Gln
		35				40						45			
Leu	Lys	Gln	Arg	Thr	Gln	Ala	Asn	Gly	Arg	Val	Gly	Ala	Thr	Ala	Ala
	50				55					60					
Val	Tyr	Ser	Ala	Ala	Ile	Leu	Glu	Tyr	Leu	Thr	Ala	Glu	Val	Xaa	Gly
	65			70					75					80	
Ala	Gly	Glu	Cys												

(2) INFORMATION FOR SEQ ID NO:2939:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 739 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..739

(D) OTHER INFORMATION: / Ceres Seq. ID 1574849

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2939:

atgttctctgtg	gcaaacacac	acacacacac	acacacacac	acacacacac	acacacacac	60
acacatogTt	ttgtctgttc	aacaaagctc	tacacgggaa	gacaggctgc	ttctttcttg	120
cagtcctctg	tccagaagcc	tgaagaatg	gcgtcaccca	acgtcacatt	ccttgccctc	180
ttcgtggccc	tcgcactatc	ggcgcttcac	accgacgcag	cggcgccggt	cagaaacctt	240
gcacataggt	agcgacacat	ggtgcgtggc	caagccgtgc	acgcaggagg	cggcgctgcg	300
gggcaacctg	gagttcgcc	gctccgagag	cgactcggcg	gccatccagg	gcaccggcgt	360
gcgccagacc	cgacagcctg	ctgtcgcggg	cgctcggtgc	catgaacgcc	tactaccagg	420
ccggggggag	gaactcgttg	aactgcttct	tcaacggcac	cggcataatc	accatcactg	480

acccacgct tggcacctgc aaatatgctt gacacgacgg gctgctctgc tgctgctgtg 540
ctcaacggac gatgaataag gctgtatggg aatgatgcat cttttccttc tctttgtttt 600
gttattgtgt ctgtgtgagt gacagggag tatccttgca gaaccaacca gtatcatgtc 660
tgagcactgt agagagaatt tccgtgcttt tatttccaa atacagtctt actccaggcc 720
agtggctgga ggggagttt

(2) INFORMATION FOR SEQ ID NO:2940:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 82 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..82
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574850

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2940:

Met	Phe	Ser	Gly	Lys	His	Thr	His	Thr	His	Thr	His	Thr	His	Thr	His
1			5					10					15		
Thr	His	Thr	His	Thr	His	Arg	Phe	Ala	Val	Ala	Thr	Lys	Leu	Tyr	Thr
			20					25					30		
Gly	Arg	Gln	Ala	Ala	Ser	Phe	Leu	Gln	Ser	Leu	Val	Gln	Lys	Pro	Glu
			35					40					45		
Glu	Met	Ala	Ser	Pro	Asn	Val	Thr	Phe	Leu	Ala	Phe	Phe	Val	Ala	Leu
			50					55					60		
Ala	Leu	Ser	Ala	Leu	His	Thr	Asp	Ala	Ala	Ala	Val	Arg	Asn	Leu	
			65			70				75			80		
Ala	Xaa														

(2) INFORMATION FOR SEQ ID NO:2941:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 159 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..159
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574852

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2941:

Cys	Ser	Leu	Ala	Asn	Thr	His	Thr	His	Thr	His	Thr	His	Thr	His	Thr
1				5					10					15	
His	Thr	His	Thr	His	Ile	Val	Leu	Leu	Leu	Gln	Gln	Ser	Ser	Thr	Arg
				20					25					30	
Glu	Asp	Arg	Leu	Leu	Leu	Ser	Cys	Ser	Leu	Trp	Ser	Arg	Ser	Leu	Lys
				35					40					45	
Lys	Trp	Arg	His	Pro	Thr	Ser	His	Ser	Leu	Pro	Ser	Ser	Trp	Pro	Ser
				50					55					60	
His	Tyr	Arg	Arg	Phe	Thr	Pro	Thr	Gln	Arg	Arg	Arg	Ser	Glu	Thr	Leu
				70					75					80	
His	Xaa	Arg	Ser	Asp	Thr	Trp	Cys	Val	Ala	Lys	Pro	Ser	Thr	Gln	Glu
				85					90					95	
Ala	Ala	Leu	Arg	Gly	Asn	Leu	Glu	Phe	Ala	Cys	Ser	Glu	Ser	Asp	Cys
				100					105					110	
Gly	Ala	Ile	Gln	Gly	Thr	Gly	Val	Arg	Pro	Ala	Arg	Gln	Pro	Ala	Val
				115					120					125	
Ala	Gly	Val	Gly	Gly	His	Glu	Arg	Leu	Leu	Pro	Gly	Pro	Gly	Glu	Glu
				130					135					140	
Leu	Val	Glu	Leu	Leu	Leu	Gln	Arg	His	Arg	His	Asn	His	His	His	
				145					150					155	

(2) INFORMATION FOR SEQ ID NO:2942:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1132 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1132
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574853

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2942:

agctcaccgc	cacctccacg	ctcgaagctc	ctcccgaaacc	ggccgcacatcg	tcgccatggc	60
agccgcgcgt	tctgcaagct	ccgtgaagga	agtgtgcgcg	tctccctcga	cctccgcctc	120
cgagccccct	Cccccctttc	gatggcaacca	ccaggttgta	cgtggccctat	ccttgcccggt	180
tcgcgcagcg	cttggattgc	tagaaactac	aagggctctgc	aggacaagat	taagatagtt	240
gcacatgcac	tcgctgacag	gccagcgtgg	tacaaggaga	aggtttatcc	agaaaaacaag	300
gtgcctcttc	tagagcacga	caaccagggtg	aaaggagaga	gcttggtattt	ggttaagtac	360
atcgacaaca	acttcgaagg	tccatcgttg	ctccccgagg	atcatgcaaa	gcagcagttc	420
gctgaggagc	tgctcggata	cactgacgca	tccaacaaag	cattttactc	atgtttagtc	480
gacagggaag	atgtgtctga	ggaagccgtt	gctgccttgg	acaaaataga	agacgccctg	540
gggaaattca	acgacggccc	gttcttccct	ggccagttca	gtctggtgga	cgttgcgat	600
gtaccggtca	tcgagaggtt	tcagatactc	tattccaata	taaaagaacta	tgacatcaca	660
aaggggcagc	ccagcccttca	gaattcctac	gaggaaagtga	acaagatcga	tcggtacaca	720
cagactaaac	tggaaccgca	gtttttgctt	gagcaaacaa	agaagccggt	tggtgattgct	780
taaaagcctgt	gaccaaggag	gagactttgc	ccagaagcac	cagcgtagta	gatcgagact	840
cgtttttagta	ggttgtgtgc	ttggtatata	cgctcgtgtc	tcaataaaggc	atggccttct	900
ttaatggctg	tgcttctgaa	aataaataaa	ctagttgtcc	aggtattatc	gttgcttttg	960
tgacgtgtcg	atgtcactgt	atatatatga	atgggtggga	aaGaatatgc	gatgtgcagt	1020
gtgttctgtg	caaatatttc	cgagatgaag	gatacgtatc	catgtagaca	ttcatatatt	1080
gctcatattg	tgacacggcg	catgaagac	atggtttcgg	ccctaccac	gc	

(2) INFORMATION FOR SEQ ID NO:2943:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 260 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..260
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574854

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2943:

Ser	Ser	Pro	Pro	Pro	Pro	Arg	Ser	Lys	Leu	Leu	Pro	Asn	Arg	Pro	His	
1				5					10						15	
Arg	Arg	His	Gly	Ser	Arg	Arg	Phe	Cys	Lys	Leu	Arg	Glu	Gly	Ser	Ala	
			20					25					30			
Ala	Val	Ser	Pro	Asp	Leu	Arg	Leu	Arg	Ala	Pro	Ser	Pro	Phe	Ser	Met	
		35					40				45					
Ala	Pro	Pro	Gly	Cys	Thr	Trp	Pro	Ile	Phe	Ala	Arg	Ser	Arg	Ser	Ala	
		50				55					60					
Trp	Ile	Ala	Arg	Asn	Tyr	Lys	Gly	Leu	Gln	Asp	Lys	Ile	Lys	Ile	Val	
	65				70				75						80	
Ala	Ile	Asp	Leu	Ala	Asp	Arg	Pro	Ala	Trp	Tyr	Lys	Glu	Lys	Val	Tyr	
			85						90					95		
Pro	Glu	Asn	Lys	Val	Pro	Ser	Leu	Glu	His	Asp	Asn	Gln	Val	Lys	Gly	
			100					105					110			
Glu	Ser	Leu	Asp	Leu	Val	Lys	Tyr	Ile	Asp	Asn	Asn	Phe	Glu	Gly	Pro	
		115					120					125				
Ser	Leu	Leu	Pro	Glu	Asp	His	Ala	Lys	Gln	Gln	Phe	Ala	Glu	Glu	Leu	
	130						135					140				

Leu Gly Tyr Thr Asp Ala Phe Asn Lys Ala Phe Tyr Ser Cys Leu Val
145 150 155 160
Asp Arg Glu Asp Val Ser Glu Glu Ala Val Ala Ala Leu Asp Lys Ile
165 170 175
Glu Asp Ala Leu Gly Lys Phe Asn Asp Gly Pro Phe Phe Leu Gly Gln
180 185 190
Phe Ser Leu Val Asp Val Ala Tyr Val Pro Phe Ile Glu Arg Phe Gln
195 200 205
Ile Leu Tyr Ser Asn Ile Lys Asn Tyr Asp Ile Thr Lys Gly Arg Pro
210 215 220
Ser Leu Gln Lys Phe Ile Glu Glu Val Asn Lys Ile Asp Ala Tyr Thr
225 230 235 240
Gln Thr Lys Leu Asp Pro Gln Phe Leu Leu Glu Gln Thr Lys Lys Arg
245 250 255
Leu Gly Ile Ala
260

(2) INFORMATION FOR SEQ ID NO:2944:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 213 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..213

(D) OTHER INFORMATION: / Ceres Seq. ID 1574855

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2944:

Met Ala Pro Pro Gly Cys Thr Trp Pro Ile Phe Ala Arg Ser Arg Ser
1 5 10 15
Ala Trp Ile Ala Arg Asn Tyr Lys Gly Leu Gln Asp Lys Ile Lys Ile
20 25 30
Val Ala Ile Asp Leu Ala Asp Arg Pro Ala Trp Tyr Lys Glu Lys Val
35 40 45
Tyr Pro Glu Asn Lys Val Pro Ser Leu Glu His Asp Asn Gln Val Lys
50 55 60
Gly Glu Ser Leu Asp Leu Val Lys Tyr Ile Asp Asn Asn Phe Glu Gly
65 70 75 80
Pro Ser Leu Leu Pro Glu Asp His Ala Lys Gln Phe Ala Glu Glu
85 90 95
Leu Leu Gly Tyr Thr Asp Ala Phe Asn Lys Ala Phe Tyr Ser Cys Leu
100 105 110
Val Asp Arg Glu Asp Val Ser Glu Glu Ala Val Ala Leu Asp Lys
115 120 125
Ile Glu Asp Ala Leu Gly Lys Phe Asn Asp Gly Pro Phe Phe Leu Gly
130 135 140
Gln Phe Ser Leu Val Asp Val Ala Tyr Val Pro Phe Ile Glu Arg Phe
145 150 155 160
Gln Ile Leu Tyr Ser Asn Ile Lys Asn Tyr Asp Ile Thr Lys Gly Arg
165 170 175
Pro Ser Leu Gln Lys Phe Ile Glu Glu Val Asn Lys Ile Asp Ala Tyr
180 185 190
Thr Gln Thr Lys Leu Asp Pro Gln Phe Leu Leu Glu Gln Thr Lys Lys
195 200 205
Arg Leu Gly Ile Ala
210

(2) INFORMATION FOR SEQ ID NO:2945:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 747 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

- (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..747
(D) OTHER INFORMATION: / Ceres Seq. ID 1574868

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2945:

aaaaaaccaa	aagcagaggg	gaaagtgcg	tcggctctga	ctctggggca	cttggtgcac	60
gaccgcgtct	ctctctgcaa	ctgcaactgc	aacgcaccaa	gaaactgcgc	gcgatcgatc	120
ggggaaggag	ataaacatgg	tgcaacggaa	gctggargtc	ctcctcgctc	ccgccaaggg	180
actcgaggag	accgatttcc	tcaataacat	ggacccttcc	gtgatcetta	cctgcgcgac	240
ccaagacgag	aaaagcagcg	tcgcaaatgg	agcaggaagc	gagcccgaat	ggaacgagac	300
cttcgtcttc	accgtcttcc	acgacacccc	gcagctgcac	ctcaagatca	tggaacgagc	360
cctcaccaac	gacgatttgc	tcggcgaagc	aaacctcccc	ctggaggccg	tggttcaggc	420
aggcagcctt	cccccgccg	ttcacccggt	cgccaaggag	gagaagtact	gcggagaggt	480
caagctcgct	cacttcaact	ccagcagcgg	aaactgcgcg	ccttgatgac	aacgaggagg	540
ggcgcgctta	cagcagctgg	agttgatcta	tctgccatgg	gatgcatgca	tcatatatat	600
ccaccaagag	aagcagaggt	aattaatata	tctactcaag	agaagaatca	gtgttgctgt	660
tatgcgaccc	tctatctatc	tatatatatg	tgcttaattt	gtcataacga	ctgccaatat	720
aaaataaact	attcagagtt	gtttgcc				

(2) INFORMATION FOR SEQ ID NO:2946:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..129
(D) OTHER INFORMATION: / Ceres Seq. ID 1574869

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2946:

Met	Val	His	Gly	Lys	Leu	Xaa	Val	Leu	Leu	Val	Ser	Ala	Lys	Gly	Leu
1			5						10				15		
Glu	Asp	Thr	Asp	Phe	Leu	Asn	Asn	Met	Asp	Pro	Phe	Val	Ile	Leu	Thr
			20					25					30		
Cys	Arg	Thr	Gln	Glu	Gln	Lys	Ser	Ser	Val	Ala	Asn	Gly	Ala	Gly	Ser
			35				40					45			
Glu	Pro	Glu	Trp	Asn	Glu	Thr	Phe	Val	Phe	Thr	Val	Ser	Asp	Asp	Thr
			50			55					60				
Pro	Gln	Leu	His	Leu	Lys	Ile	Met	Asp	Ser	Asp	Leu	Thr	Asn	Asp	Asp
65			70					75					80		
Phe	Val	Gly	Glu	Ala	Thr	Ile	Pro	Leu	Glu	Ala	Val	Phe	Gln	Glu	Gly
			85					90					95		
Ser	Leu	Pro	Pro	Ala	Val	His	Pro	Val	Val	Lys	Glu	Glu	Lys	Tyr	Cys
			100				105						110		
Gly	Glu	Val	Lys	Leu	Ala	His	Leu	His	Ser	Ser	Ser	Gly	Asn	Ser	Pro
			115				120						125		

Pro

(2) INFORMATION FOR SEQ ID NO:2947:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..105
(D) OTHER INFORMATION: / Ceres Seq. ID 1574870

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2947:

Met	Asp	Pro	Phe	Val	Ile	Leu	Thr	Cys	Arg	Thr	Gln	Glu	Gln	Lys	Ser
1			5						10					15	
Ser	Val	Ala	Asn	Gly	Ala	Gly	Ser	Glu	Pro	Glu	Trp	Asn	Glu	Thr	Phe
			20					25					30		
Val	Phe	Thr	Val	Ser	Asp	Asp	Thr	Pro	Gln	Leu	His	Leu	Lys	Ile	Met
			35				40					45			
Asp	Ser	Asp	Leu	Thr	Asn	Asp	Asp	Phe	Val	Gly	Glu	Ala	Thr	Ile	Pro
			50			55					60				
Leu	Glu	Ala	Val	Phe	Gln	Glu	Gly	Ser	Leu	Pro	Pro	Ala	Val	His	Pro
				70						75				80	
Val	Val	Lys	Glu	Glu	Lys	Tyr	Cys	Gly	Glu	Val	Lys	Leu	Ala	His	Leu
			85						90					95	
His	Ser	Ser	Ser	Gly	Asn	Ser	Pro	Pro							
			100				105								

(2) INFORMATION FOR SEQ ID NO:2948:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 113 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..113

(D) OTHER INFORMATION: / Ceres Seq. ID 1574871

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2948:

Met	Glu	Arg	Asp	Leu	Arg	Leu	His	Arg	Leu	Arg	Arg	His	Pro	Ala	Ala
1			5						10					15	
Ala	Pro	Gln	Asp	His	Gly	Gln	Arg	Pro	His	Gln	Arg	Arg	Phe	Arg	Arg
			20					25					30		
Arg	Ser	Asn	His	Pro	Pro	Gly	Gly	Arg	Val	Ser	Gly	Arg	Gln	Pro	Ser
			35				40					45			
Pro	Gly	Gly	Ser	Pro	Gly	Arg	Gln	Gly	Gly	Glu	Val	Leu	Arg	Arg	Gly
			50			55					60				
Gln	Ala	Arg	Ser	Pro	Ser	Leu	Gln	Gln	Arg	Lys	Leu	Ala	Ala	Leu	Met
			65			70				75				80	
Thr	Thr	Arg	Arg	Gly	Arg	Leu	Thr	Ala	Ala	Gly	Val	Asp	Leu	Ser	Ala
			85					90						95	
Met	Gly	Cys	Met	His	His	Ile	Tyr	Pro	Pro	Arg	Glu	Glu	Arg	Ile	Ile
			100					105						110	
Asn															

(2) INFORMATION FOR SEQ ID NO:2949:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 935 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..935

(D) OTHER INFORMATION: / Ceres Seq. ID 1574880

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2949:

agt	tta	tggg	ctg	gaat	ggg	cgc	tca	aac	tgg	ccc	ggt	tta	cgt	gaatt	ttr	gcg	ggg	gct	gc	60
cg	ct	ggg	gat	c	gag	ac	gtg	tgg	ctg	caca	gcg	ac	gtc	ctcg	trg	gag	cgrg	cgg	gc	120
cag	gc	cag	ag	gtt	tc	gtc	ccg	aac	cc	tagt	tct	cc	acac	gc	ctg	cg	cca	tgg	cc	180
cg	gc	gc	gc	ctc	gc	cc	ctgc	agc	gc	cca	gtg	cct	gc	gc	gc	aac	cc	cttc	tct	240
gc	at	gg	ctc	gc	ta	acc	gc	a	gc	ttg	ag	gt	cat	ctc	ca	ac	g	act	att	300
gaa	ag	cagg	c	gag	gt	gtg	ta	ag	gt	gg	gc	gc	tgg	cc	act	tc	gc	ca	acc	360

gatgctcgca gtccccgaacc tggacaaaatt cgccatacta atccgagagc agcgcaagCt 420
ctatcaaacgc gaagaggagg tccgcggtgaa acaagtcacg gagaagaatg atgatgcacg 480
gtacacaggaa gaagaatatga agcagtagca aacggcagca aagcggctag ataacgcact 540
ctctgggtgtg aggagggttca tctcgactgg aaacgagctg cgtactccgt taacaaaaaga 600
cgaaaattgtt tccgagggtgg cgaggcgagc caacatcaac atccatccgg agaacctgca 660
tctgcagtcga cctttggcgt cgctcggcga atttgagttg cccctccggg taccgcagaa 720
cataccgtgc ccagaaggtta agctccagtg gactctgaag gtgaagatca ggagaaaaatg 780
agcgacaggaa ctgggggaagt ttcttttggc ccccccacaa ctggtgtatg gtacccaaacc 840
attgttagct ccgaacaat ggtaccaaac catgtgttat gcaagtttag ctccgaaaaa 900
tttttttctg atgtataata aaagagtaag gttgc

(2) INFORMATION FOR SEQ ID NO:2950:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 203 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..203

(D) OTHER INFORMATION: / Ceres Seq. ID 1574881

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2950:

Met Ala Ala Ala Arg Ala Ala Leu Arg Leu Gln Arg Gln Cys Leu Ala
1 5 10 15
Ala Asn Pro Phe Leu Phe Ser Gly His Gly Leu Arg Tyr Arg Lys Leu
20 25 30
Glu Val Ile Leu Thr Thr Thr Ile Asp Lys Leu Gly Lys Ala Gly Glu
35 40 45
Val Val Lys Val Ala Pro Gly His Phe Arg Asn His Leu Met Pro Lys
50 55 60
Met Leu Ala Val Pro Asn Leu Asp Lys Phe Ala Ile Leu Ile Arg Glu
65 70 75 80
Gln Arg Lys Leu Tyr Gln Arg Glu Glu Glu Val Ala Val Lys Gln Val
85 90 95
Thr Glu Lys Asp Asp Asp Ala Arg Leu Gln Glu Glu Arg Met Lys Gln
100 105 110
Tyr Gln Thr Ala Ala Lys Arg Leu Asp Asn Ala Leu Leu Val Leu Arg
115 120 125
Arg Phe Ile Ser Thr Gly Asn Glu Leu Arg Thr Pro Val Thr Lys Asp
130 135 140
Glu Ile Val Ser Glu Val Ala Arg Gln Leu Asn Ile Asn Ile His Pro
145 150 155 160
Glu Asn Leu His Leu Gln Ser Pro Leu Ala Ser Leu Gly Glu Phe Glu
165 170 175
Leu Pro Leu Arg Leu Pro Gln Asn Ile Pro Cys Pro Glu Gly Lys Leu
180 185 190
Gln Trp Thr Leu Lys Val Lys Ile Arg Arg Lys
195 200

(2) INFORMATION FOR SEQ ID NO:2951:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 142 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..142

(D) OTHER INFORMATION: / Ceres Seq. ID 1574882

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2951:

Met Pro Lys Met Leu Ala Val Pro Asn Leu Asp Lys Phe Ala Ile Leu

1	5	10	15
Ile Arg Glu	Gln Arg Lys Leu Tyr	Gln Arg Glu Glu Glu Val Ala Val	
20	25	30	
Lys Gln Val Thr	Glu Lys Asp Asp Asp Ala Arg Leu Gln Glu Glu Arg		
35	40	45	
Met Lys Gln Tyr	Gln Thr Ala Ala Lys Arg Leu Asp Asn Ala Leu Leu		
50	55	60	
Val Leu Arg Arg Phe	Ile Ser Thr Gly Asn Glu Leu Arg Thr Pro Val		
65	70	75	80
Thr Lys Asp Glu	Ile Val Ser Glu Val Ala Arg Gln Leu Asn Ile Asn		
85	90	95	
Ile His Pro Glu	Asn Leu His Leu Gln Ser Pro Leu Ala Ser Leu Gly		
100	105	110	
Glu Phe Glu Leu	Pro Leu Arg Leu Pro Gln Asn Ile Pro Cys Pro Glu		
115	120	125	
Gly Lys Leu Gln Trp	Thr Leu Lys Val Lys Ile Arg Arg Lys		
130	135	140	

(2) INFORMATION FOR SEQ ID NO:2952:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 139 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..139

(D) OTHER INFORMATION: / Ceres Seq. ID 1574883

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2952:

Met Leu Ala Val	Pro Asn Leu Asp Lys Phe Ala Ile Leu Ile Arg Glu
1	5
Gln Arg Lys Leu Tyr	Gln Arg Glu Glu Val Ala Val Lys Gln Val
20	25
Thr Glu Lys Asp Asp	Asp Ala Arg Leu Gln Glu Glu Arg Met Lys Gln
35	40
Tyr Gln Thr Ala Ala	Lys Arg Leu Asp Asn Ala Leu Leu Val Leu Arg
50	55
Arg Phe Ile Ser Thr	Gly Asn Glu Leu Arg Thr Pro Val Thr Lys Asp
65	70
Glu Ile Val Ser Glu	Val Ala Arg Gln Leu Asn Ile Asn Ile His Pro
85	90
Glu Asn Leu His Leu	Gln Ser Pro Leu Ala Ser Leu Gly Glu Phe Glu
100	105
Leu Pro Leu Arg Leu	Pro Gln Asn Ile Pro Cys Pro Glu Gly Lys Leu
115	120
Gln Trp Thr Leu Lys	Val Lys Ile Arg Arg Lys
130	135

(2) INFORMATION FOR SEQ ID NO:2953:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 938 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..938

(D) OTHER INFORMATION: / Ceres Seq. ID 1574896

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2953:

gcacgagagtc caggacatcaa ggcccagaa aaaagtccga acgcatctct tctttctact
tctttgtaac ccaagacgaa ctggtgaac tctttctcct cgcgcasacc ggagcacaat

60

120

caaggattcc	agtcacgctc	tgccaatgga	gtgcgttttg	ggcttggttg	gccgcgactt	180
cgcggtggtg	gccggcgaca	cctccgcgtg	gcagagtatc	ctcgtccaca	agactgacga	240
ggacaaagta	atggtctctg	actcgcacaa	gctgttgggc	gcttcarggg	agcctggtga	300
cgcggtgcag	ttttacggag	tcatacagaa	gaacctccac	ctgtaccagt	tcgcacaacac	360
catcccgctg	tcaaccgcgc	Ctgccgccaa	cttcacacgc	ggcgagctcg	ccacagccct	420
tcgtaagaat	ccatacatgg	tcaatgttat	tctcggtggt	tacgataagg	atggtggcgc	480
ctcactgtac	tacatcgact	acattgcgac	cttcgacaag	atcgacaagg	gcgcttttgg	540
gtacggatcg	tatttctgcc	tgctctgat	ggacaagctg	taccgcccgc	acatgaccgt	600
tgaggaascg	gtagacctcg	ttgataagtg	cattaaggag	atccggctgc	ggctggttgt	660
ggcgccocag	aactctgtga	tcaagatcgt	cgacaaggac	ggggccaggg	agtacgcgag	720
gcgtgaactc	gtcggcgaca	gtgcacctcg	tgaagctgca	gctacggttg	cgcctgagg	780
catgaaactt	gtttgtgtta	gttgtttgtt	tctcagcgag	gctactatgt	aatcaaatgg	840
atactggtgg	gggtcccaac	gctgtttttt	aatcaatitt	agccccagaca	tgtaattctg	900
ttcttgact	aattcatgtc	ttcgccgagt	acaagttg			

(2) INFORMATION FOR SEQ ID NO:2954:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 210 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..210

(D) OTHER INFORMATION: / Ceres Seq. ID 1574897

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2954:

Met	Glu	Cys	Val	Leu	Gly	Leu	Val	Gly	Arg	Asp	Phe	Ala	Val	Ala
1			5						10				15	
Ala	Asp	Thr	Ser	Ala	Val	Gln	Ser	Ile	Leu	Val	His	Lys	Thr	Asp
			20					25					30	
Asp	Lys	Val	Met	Val	Leu	Asp	Ser	His	Lys	Leu	Leu	Gly	Ala	Ser
			35					40				45		Xaa
Glu	Pro	Gly	Asp	Arg	Val	Gln	Phe	Thr	Glu	Phe	Ile	Gln	Lys	Asn
			50				55				60			Leu
His	Leu	Tyr	Gln	Phe	Arg	Asn	Thr	Ile	Pro	Leu	Ser	Thr	Ala	Ala
			65			70			75				80	
Ala	Asn	Phe	Thr	Arg	Gly	Glu	Leu	Ala	Thr	Ala	Leu	Arg	Lys	Asn
			85					90					95	Pro
Tyr	Met	Val	Asn	Val	Ile	Leu	Gly	Gly	Tyr	Asp	Lys	Asp	Val	Gly
			100				105						110	Ala
Ser	Leu	Tyr	Tyr	Ile	Asp	Tyr	Ile	Ala	Thr	Leu	His	Lys	Ile	Asp
			115				120					125		Lys
Gly	Ala	Phe	Gly	Tyr	Gly	Ser	Tyr	Phe	Cys	Leu	Ser	Leu	Met	Asp
			130				135					140		Lys
Leu	Tyr	Arg	Pro	Asp	Met	Thr	Val	Glu	Glu	Xaa	Val	Asp	Leu	Val
			145			150				155			160	Asp
Lys	Cys	Ile	Lys	Glu	Ile	Arg	Leu	Arg	Leu	Val	Val	Ala	Pro	Glu
			165						170				175	Asn
Phe	Val	Ile	Lys	Ile	Val	Asp	Lys	Asp	Gly	Ala	Arg	Glu	Tyr	Ala
			180					185					190	Arg
Arg	Glu	Leu	Val	Gly	Asp	Ser	Ala	Pro	Ala	Glu	Ala	Ala	Ala	Thr
			195				200						205	Val
Ala	Ala													

(2) INFORMATION FOR SEQ ID NO:2955:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 175 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..175

(D) OTHER INFORMATION: / Ceres Seq. ID 1574898

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2955:

```
Met Val Leu Asp Ser His Lys Leu Leu Gly Ala Ser Xaa Glu Pro Gly
1      5      10      15
Asp Arg Val Gln Phe Thr Glu Phe Ile Gln Lys Asn Leu His Leu Tyr
20      25      30
Gln Phe Arg Asn Thr Ile Pro Leu Ser Thr Ala Ala Ala Asn Phe
35      40      45
Thr Arg Gly Glu Leu Ala Thr Ala Leu Arg Lys Asn Pro Tyr Met Val
50      55      60
Asn Val Ile Leu Gly Gly Tyr Asp Lys Asp Val Gly Ala Ser Leu Tyr
65      70      75
Tyr Ile Asp Tyr Ile Ala Thr Leu His Lys Ile Asp Lys Gly Ala Phe
85      90      95
Gly Tyr Gly Ser Tyr Phe Cys Leu Ser Leu Met Asp Lys Leu Tyr Arg
100     105     110
Pro Asp Met Thr Val Glu Glu Xaa Val Asp Leu Val Asp Lys Cys Ile
115     120     125
Lys Glu Ile Arg Leu Arg Leu Val Val Ala Pro Gln Asn Phe Val Ile
130     135     140
Lys Ile Val Asp Lys Asp Gly Ala Arg Glu Tyr Ala Arg Arg Glu Leu
145     150     155
Val Gly Asp Ser Ala Pro Ala Glu Ala Ala Thr Val Ala Ala
165     170     175
```

(2) INFORMATION FOR SEQ ID NO:2956:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 113 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..113

(D) OTHER INFORMATION: / Ceres Seq. ID 1574899

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2956:

```
Met Val Asn Val Ile Leu Gly Gly Tyr Asp Lys Asp Val Gly Ala Ser
1      5      10      15
Leu Tyr Tyr Ile Asp Tyr Ile Ala Thr Leu His Lys Ile Asp Lys Gly
20      25      30
Ala Phe Gly Tyr Gly Ser Tyr Phe Cys Leu Ser Leu Met Asp Lys Leu
35      40      45
Tyr Arg Pro Asp Met Thr Val Glu Glu Xaa Val Asp Leu Val Asp Lys
50      55      60
Cys Ile Lys Glu Ile Arg Leu Arg Leu Val Val Ala Pro Gln Asn Phe
65      70      75
Val Ile Lys Ile Val Asp Lys Asp Gly Ala Arg Glu Tyr Ala Arg Arg
85      90      95
Glu Leu Val Gly Asp Ser Ala Pro Ala Glu Ala Ala Ala Thr Val Ala
100     105     110
Ala
```

(2) INFORMATION FOR SEQ ID NO:2957:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 907 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..907

(D) OTHER INFORMATION: / Ceres Seq. ID 1574910

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2957:

atccatccaa	ctcttcataa	caggcgacct	gagagcagag	cagacagaga	gcgttctggc	60
agccgtttcg	gasttgaaac	tctgcaacca	ccaacagcta	aactaaaagc	agcrgcggac	120
ggcgcgcggt	actggacagc	cgccgcagca	tggtctacgc	ggcgcasagc	aggggtgacca	180
gcaccgacgc	agggctgcaga	aggtgatggt	ggctgtagac	gagagcgagt	gcagccggca	240
cgcgctggag	tgggcgctgc	ggaacctggc	gcccacgctg	gccccaccgc	tactggtgct	300
caaccgtcag	cgcacttcc	cgctcggata	cgctcctgc	gcgcaccctc		360
gggcaccgtc	cctccgggtg	ctccggagct	catcaggctc	atgcaggagc	agcagaggga	420
gctccacgag	gagctcctcg	acaaggccag	ggccatctgc	gccgagcacg	gggttctggt	480
agaggcaatt	gtcagggtgc	gagatgcmaa	ggagggtgata	tgtagaagtg	ctgagaagaa	540
aaatgtcgat	ctgctgggtc	ttggaaacca	cagtcgtggg	ccaatacaga	gggtgttctc	600
tgggagcgct	agtaactact	gtgtacatca	ttctaagtgt	ccagttcttg	tggtgaagaa	660
ccaaggctga	tgaaggattc	aactccagc	tgctagtctc	aatcatgttc	gggtatttgt	720
caacgtattt	gtaattgtga	gtacttgctt	tagccaaacg	cattggccaa	taaaagtact	780
tgctttgctt	cttggaaagg	ccgaggctgg	actggaggag	agttcttttt	ctttttcttt	840
ttcttcgtca	gtgtgccttc	gctccggaat	ggcagagttg	taaataagaa	ctacgaacct	900

tggtgcgc

(2) INFORMATION FOR SEQ ID NO:2958:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 154 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..154

(D) OTHER INFORMATION: / Ceres Seq. ID 1574911

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2958:

Met	Val	Ala	Val	Asp	Glu	Ser	Glu	Cys	Ser	Arg	His	Ala	Leu	Glu	Trp
1				5					10					15	
Ala	Leu	Arg	Asn	Leu	Ala	Pro	Thr	Leu	Ala	Pro	Pro	Leu	Leu	Val	Leu
				20				25					30		
Thr	Val	Gln	Pro	His	Phe	Pro	Leu	Gly	Tyr	Val	Ser	Ala	Ala	Ser	Phe
		35					40				45				
Gly	Ala	Pro	Leu	Gly	Thr	Val	Pro	Val	Ala	Pro	Gly	Leu	Ile	Arg	
		50			55				60						
Ser	Met	Gln	Glu	Gln	Arg	Glu	Leu	Thr	Gln	Glu	Leu	Leu	Asp	Lys	
		65			70				75				80		
Ala	Arg	Ala	Ile	Cys	Ala	Glu	His	Gly	Val	Ala	Val	Glu	Ala	Ile	Val
			85					90					95		
Glu	Val	Gly	Asp	Ala	Lys	Glu	Val	Ile	Cys	Glu	Val	Ala	Glu	Lys	Lys
			100					105					110		
Asn	Val	Asp	Leu	Leu	Val	Leu	Gly	Ser	His	Ser	Arg	Gly	Pro	Ile	Gln
		115					120					125			
Arg	Leu	Phe	Leu	Gly	Ser	Val	Ser	Asn	Tyr	Cys	Val	His	His	Ser	Lys
		130				135						140			
Cys	Pro	Val	Leu	Val	Val	Lys	Asn	Gln	Gly						
		145				150									

(2) INFORMATION FOR SEQ ID NO:2959:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 89 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..89

(D) OTHER INFORMATION: / Ceres Seq. ID 1574912

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2959:

```
Met Gln Gln Gln Gln Arg Glu Leu Thr Gln Gln Leu Leu Asp Lys Ala
1           5           10           15
Arg Ala Ile Cys Ala Glu His Gly Val Ala Val Glu Ala Ile Val Glu
20           25           30
Val Gly Asp Ala Lys Glu Val Ile Cys Glu Val Ala Glu Lys Lys Asn
35           40           45
Val Asp Leu Leu Val Leu Gly Ser His Ser Arg Gly Pro Ile Gln Arg
50           55           60
Leu Phe Leu Gly Ser Val Ser Asn Tyr Cys Val His His Ser Lys Cys
65           70           75           80
Pro Val Leu Val Val Lys Asn Gln Gly
85
```

(2) INFORMATION FOR SEQ ID NO:2960:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 846 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..846

(D) OTHER INFORMATION: / Ceres Seq. ID 1574947

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2960:

```
gccatcggttc cctcctctgc acccccccac ctccgacatc ctgcctcgca gcagaccctc 60
ctctggtgcg cgtgcgccac cgcgagatg tcgaagaaaa tcgtggtgaa gctgcacctg 120
caggacaaca aggacaagca gaaggccatg aaggctgtct cgcgctcac cggcctgcac 180
gagatatccg cggacatggc gtcgcacaag atgacggtgg ccgcatggtt ggaccccgct 240
agcgtgttga gcaagctgcg caaggcgctg tggtcggcga ccategatc cgtcggccct 300
gccaccgcgc cgccgcgcgc gccgcaccaa ctgtcacctg cgctatggcc cgtatcaagg 360
tgacacgagc tcggggggaag agcaagacgg acctgcaggc gcaGctcaag gagctgaagt 420
ctgagctctc cctcctccgc gtaGccaagg tcaccggcgg cgacccaac aagctctcca 480
agatcaaggc ggtgcgcacc tcgatcgcgc gcgtgtctac agtgcctcgc cagaagcaga 540
agtcggcggt gcgggaggcg tacaagaaga agaacctgct cccctcgac ctccgcccta 600
agaagaccgc tgccatccgc cgccgtctga ccaagcacca gctttctctg aagaccgaga 660
gggaaagaaa gcgtgagaag tacttcccca tgaggaahta tgctatcaag gcctaggcta 720
gaactgtgag atgctgtgct tagcatatca tcggctgtgt ttttaattttt ggtttgatg 780
gacatttgtt gaagtacgat gtattcctct gtttccatat aaatggctag attggtttga 840
ctggct
```

(2) INFORMATION FOR SEQ ID NO:2961:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 138 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..138

(D) OTHER INFORMATION: / Ceres Seq. ID 1574948

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2961:

```
Ala Ile Val Pro Ser Ser Ala Pro Pro Ile Leu Gly His Pro Arg Leu
1           5           10           15
Gln Gln Thr Leu Leu Trp Cys Ala Cys Ala Thr Gly Glu Met Ser Lys
20           25           30
Lys Ile Val Val Lys Leu His Leu Asp Asn Lys Asp Lys Gln Lys
```

	35		40		45	
Ala Met Lys	Ala Val	Ser Ala	Leu Thr	Gly Ile	Asp Glu	Ile Ser Ala
50		55		60		
Asp Met Ala	Ser His	Lys Met	Thr Val	Val Gly	Met Val	Asp Pro Val
65		70		75		80
Ser Val Val	Ser Lys	Leu Arg	Lys Ala	Ser Trp	Ser Ala	Thr Ile Glu
	85			90		95
Ser Val Gly	Pro Ala	Thr Ala	Ala Ala	Ala Pro	Pro His	Gln Leu Ser
	100			105		110
Pro Ser Leu	Trp Pro	Val Ser	Arg Cys	Thr Ser	Ser Gly	Arg Ala
	115		120		125	
Arg Arg Thr	Cys Arg	Arg Arg	Ser Ser	Arg Ser		
130		135				

(2) INFORMATION FOR SEQ ID NO:2962:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 237 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..237
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574949

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2962:

His Arg Ser	Leu Leu	Cys Thr	Pro His	Pro Arg	Thr Ser	Ser Ser	Pro Ala
1		5		10		15	
Ala Asp Pro	Pro Leu	Val Arg	Val Arg	His Arg	Arg Asp	Val Glu	Glu
	20		25		30		
Asn Arg Gly	Glu Ala	Ala Pro	Ala Gly	Gln Gln	Gly Gln	Ala Glu	Gly
	35		40		45		
His Glu Gly	Cys Leu	Gly Ala	His Arg	His Arg	Arg Asp	Ile Arg	Gly
	50		55		60		
His Gly Val	Ala Gln	Asp Asp	Gly Gly	Arg His	Gly Gly	Pro Arg	Glu
	65		70		75		80
Arg Gly Glu	Gln Ala	Ala Gln	Gly Val	Val Val	Gly Asp	His Arg	Val
	85		90		95		
Arg Arg Pro	Cys His	Arg Arg	Arg Arg	Pro Ala	Ala Ser	Thr Val	Thr
	100		105		110		
Val Ala Met	Ala Arg	Ile Lys	Val His	Glu Leu	Arg Gly	Lys Ser	Lys
	115		120		125		
Thr Asp Leu	Gln Ala	Gln Leu	Lys Glu	Leu Lys	Ser Glu	Leu Ser	Leu
	130		135		140		
Leu Arg Val	Ala Lys	Val Thr	Gly Gly	Ala Pro	Asn Lys	Leu Ser	Lys
	145		150		155		160
Ile Lys Val	Val Arg	Thr Ser	Ile Ala	Arg Val	Leu Thr	Val Ile	Ser
	165		170		175		
Gln Lys Gln	Lys Ser	Ala Leu	Arg Glu	Ala Tyr	Lys Lys	Lys Asn	Leu
	180		185		190		
Leu Pro Leu	Asp Leu	Arg Pro	Lys Lys	Thr Arg	Ala Ile	Arg Arg	Arg
	195		200		205		
Leu Thr Lys	His Gln	Leu Ser	Leu Lys	Thr Glu	Arg Glu	Lys Lys	Arg
	210		215		220		
Glu Lys Tyr	Phe Pro	Met Arg	Lys Tyr	Ala Ile	Lys Ala		
	225		230		235		

(2) INFORMATION FOR SEQ ID NO:2963:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 123 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..123
 (D) OTHER INFORMATION: / Ceres Seq. ID 1574950
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2963:
Met Ala Arg Ile Lys Val His Glu Leu Arg Gly Lys Ser Lys Thr Asp
1 5 10 15
Leu Gln Ala Gln Leu Lys Glu Leu Lys Ser Glu Leu Ser Leu Leu Arg
 20 25 30
Val Ala Lys Val Thr Gly Gly Ala Pro Asn Lys Leu Ser Lys Ile Lys
 35 40 45
Val Val Arg Thr Ser Ile Ala Arg Val Leu Thr Val Ile Ser Gln Lys
 50 55 60
Gln Lys Ser Ala Leu Arg Glu Ala Tyr Lys Lys Lys Asn Leu Leu Pro
65 70 75 80
Leu Asp Leu Arg Pro Lys Lys Thr Arg Ala Ile Arg Arg Arg Leu Thr
 85 90 95
Lys His Gln Leu Ser Leu Lys Thr Glu Arg Glu Lys Lys Arg Glu Lys
 100 105 110
Tyr Phe Pro Met Arg Lys Tyr Ala Ile Lys Ala
 115 120
(2) INFORMATION FOR SEQ ID NO:2964:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1052 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: DNA (genomic)
 (ix) FEATURE:
 (A) NAME/KEY: -
 (B) LOCATION: 1..1052
 (D) OTHER INFORMATION: / Ceres Seq. ID 1574981
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2964:
taagaatgat gtgatcaaat ttgtccaaga gaacaatttt cattctgggt tctttgatgg 60
aactgaaaac aacatggtag ctgatgccta tgaattgaag gtgcgtcttg aacacatcat 120
tgaaaggata gccttgattt ctgatgctgc aaatacagaa cgacctcttc ttgttgtcaa 180
caacttgctc ataggtgggg ctctggctgc aaggtctaag tacaccctac agcatttggg 240
cattaccact gtactctgtt tgtgttcaaa tgagattggt caatccgatt cccaatttcc 300
cgatcttttt gaatacaaga acttttcaat tagcgatgat gatgatgcaa acatcagtga 360
tctttttgag gaagcatcac acttcattga tcatgtggat catgttgggg gcaaggttct 420
agttcattgc tttgaaggga aaagtgggag tgcccacagtc gtacttgctt atctttatgt 480
tagagagggc tttactcttg caaaagcctg gaacttactg aagaagatca accgtcgagc 540
gcaGccaaac aagggttcgc aaaggctctc ctggcccttg acaagaggct gcattggcaag 600
gtatctatgg actggcaaca caagcggcca gaaatgaagg ttgtgtccat ctgcagcaag 660
aatgttggtc taagtacgag ttcaactaac ctgcacctgc agaagggcaca caagcgtcta 720
ctctcgaggc gtgtcgacag cgccatgacc atgaagatcc aaaaaatcgat cgagtcactc 780
cagatcagcc gaggaggaag cctgagcccg tcccagaagc tgaccaaggt gttagcaaat 840
gagctgagct tctgatctgt tttcctgtac tatagatgag gcaatgtact tggctcacat 900
tgtaataact tgtactatca gactgaactt gtgaactgtag gtttagttca cagccctata 960
tgattagcac acgaatgttc aggtgtgaag ggtgcaacac taaagaatgt tcaggtcttt 1020
tatttgttgc ctgcagtatg cagttttctt ct
(2) INFORMATION FOR SEQ ID NO:2965:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 211 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide

(B) LOCATION: 1..211

(D) OTHER INFORMATION: / Ceres Seq. ID 1574982

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2965:

Lys Asn Asp Val Ile Lys Phe Cys Gln Glu Asn Asn Phe His Ser Gly
1 5 10 15
Phe Phe Asp Gly Thr Glu Asn Asn Met Val Ala Asp Ala Tyr Glu Leu
20 25 30
Lys Val Arg Leu Glu His Ile Ile Glu Arg Ile Ala Leu Ile Ser Asp
35 40 45
Ala Ala Asn Thr Glu Arg Pro Ser Leu Val Val Asn Asn Leu Phe Ile
50 55 60
Gly Gly Ala Leu Ala Ala Arg Ser Lys Tyr Thr Leu Gln His Leu Gly
65 70 75 80
Ile Thr His Val Leu Cys Leu Cys Ser Asn Glu Ile Gly Gln Ser Asp
85 90 95
Ser Gln Phe Pro Asp Leu Phe Glu Tyr Lys Asn Phe Ser Ile Ser Asp
100 105 110
Asp Asp Asp Ala Asn Ile Ser Asp Leu Phe Glu Glu Ala Ser Asp Phe
115 120 125
Ile Asp His Val Asp His Val Gly Gly Lys Val Leu Val His Cys Phe
130 135 140
Glu Gly Lys Ser Arg Ser Ala Thr Val Val Leu Ala Tyr Leu Met Leu
145 150 155 160
Arg Glu Gly Phe Thr Leu Ala Lys Ala Trp Asn Leu Leu Lys Lys Val
165 170 175
His Arg Arg Ala Gln Pro Asn Asp Gly Ser Gln Arg Leu Ser Trp Pro
180 185 190
Leu Thr Arg Gly Cys Met Ala Arg Tyr Leu Trp Thr Gly Asn Thr Ser
195 200 205
Gly Gln Lys
210

(2) INFORMATION FOR SEQ ID NO:2966:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 187 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..187

(D) OTHER INFORMATION: / Ceres Seq. ID 1574983

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2966:

Met Val Ala Asp Ala Tyr Glu Leu Lys Val Arg Leu Glu His Ile Ile
1 5 10 15
Glu Arg Ile Ala Leu Ile Ser Asp Ala Ala Asn Thr Glu Arg Pro Ser
20 25 30
Leu Val Val Asn Asn Leu Phe Ile Gly Gly Ala Leu Ala Arg Ser
35 40 45
Lys Tyr Thr Leu Gln His Leu Gly Ile Thr His Val Leu Cys Leu Cys
50 55 60
Ser Asn Glu Ile Gly Gln Ser Asp Ser Gln Phe Pro Asp Leu Phe Glu
65 70 75 80
Tyr Lys Asn Phe Ser Ile Ser Asp Asp Asp Ala Asn Ile Ser Asp
85 90 95
Leu Phe Glu Glu Ala Ser Asp Phe Ile Asp His Val Asp His Val Gly
100 105 110
Gly Lys Val Leu Val His Cys Phe Glu Gly Lys Ser Arg Ser Ala Thr
115 120 125
Val Val Leu Ala Tyr Leu Met Leu Arg Glu Gly Phe Thr Leu Ala Lys
130 135 140

Ala Trp Asn Leu Leu Lys Lys Val His Arg Arg Ala Gln Pro Asn Asp
145 150 155 160
Gly Ser Gln Arg Leu Ser Trp Pro Leu Thr Arg Gly Cys Met Ala Arg
165 170 175
Tyr Leu Trp Thr Gly Asn Thr Ser Gly Gln Lys
180 185

(2) INFORMATION FOR SEQ ID NO:2967:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 948 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..948
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574984

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2967:

ctycgtgcc	ctctctgvt	ctctcgcatc	cttctttact	gcccgagagt	tctgactagc	60
cacatccagt	caagcagtaa	aggcgaccca	tggaggcggc	ggcgagagaat	aaggaggccg	120
agcaggagga	gcagcagcta	ccgcacggcg	agaaggataa	cgcgcccggc	gccgcccagg	180
aagacgaagg	ggattccggag	gagaccggag	gccgcaaccg	cgacctcaag	tccggccttc	240
accccttag	gcacaaactc	gtgctctggt	acactgcgcg	gacgcctgga	gcgaggtcgc	300
agtcgtacga	ggacaacatc	aagaagatca	tcgatttcag	cacagtcgaa	tcgttctggg	360
tttgcactag	ccaccttggt	cgcccttctt	ccctgcccag	ccccactgac	cttcatctct	420
tcaaggatgg	catccgtccc	ctctgggagg	atctctcaaa	ccagaatggt	ggcaagtgga	480
taattagatt	caaaaaagca	gtttcaggct	gattttggga	ggatttggtg	ctagtggtag	540
taggcgacca	gcttgagtat	agcgatgatg	tctgtggtgt	tgtgcttagt	gtccgtttca	600
atgaagacat	tctgagcgtc	tggaaacggg	acgcacacaga	ccatcaggct	gtgatggcat	660
tgagggtatc	tatacaagagg	cacctcaagc	tgccgcacag	ctatctgatg	gagtacaaac	720
cccatgatst	tcgcggcggt	acaactogtc	ctacagggaac	acatgggtga	gaggatagat	780
aaacctcatg	atactcggga	gcttcaactgc	gacggttctg	aagcaaaagag	actcttttat	840
gtaccaagaa	cgcagacat	tatgcaatgt	agtactacta	ctactactac	tcaaaagccc	900
ctacaatgtg	acgcgcaaca	attttactat	ctaatgtgtt	ttttttgc		

(2) INFORMATION FOR SEQ ID NO:2968:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 160 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..160
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574985

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2968:

Xaa Arg Xaa Pro Pro Xaa Leu Leu Ala Ile Leu Leu Tyr Cys Pro Arg	
1 5 10 15	
Val Leu Thr Ser His Ile Gln Ser Ser Ser Lys Gly Ala Pro Trp Arg	
20 25 30	
Arg Arg Arg Arg Ile Arg Arg Pro Ser Arg Arg Ser Ser Tyr Arg	
35 40 45	
Thr Arg Arg Arg Ile Thr Arg Pro Pro Pro Arg Lys Thr Lys Arg	
50 55 60	
Ile Arg Arg Arg Pro Ser Ala Ala Thr Ala Thr Ser Ser Pro Ala Phe	
65 70 75 80	
Thr Pro Leu Gly Thr Asn Ser Cys Ser Gly Thr Leu Ala Gly Arg Leu	
85 90 95	
Glu Arg Gly Arg Ser Arg Thr Arg Thr Thr Ser Arg Arg Ser Ser Ile	
100 105 110	
Ser Ala Gln Ser Asn Arg Ser Gly Phe Ala Thr Ala Thr Leu Arg Ala	

115	120	125
Leu Leu Pro Cys Arg Ala Pro Leu Thr Phe Ile Ser Ser Arg Met Ala		
130	135	140
Ser Val Pro Ser Gly Arg Ile Leu Gln Thr Arg Met Val Ala Ser Gly		
145	150	155
		160

(2) INFORMATION FOR SEQ ID NO:2969:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 226 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..226
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574986

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2969:

Met	Glu	Ala	Ala	Ala	Glu	Asn	Lys	Glu	Ala	Glu	Gln	Glu	Glu	Gln	Gln
1			5					10						15	
Leu	Pro	His	Ala	Gln	Lys	Asp	Asn	Ala	Pro	Ala	Ala	Ala	Glu	Glu	Asp
			20				25						30		
Glu	Ala	Asp	Ser	Glu	Glu	Thr	Glu	Arg	Arg	Asn	Arg	Asp	Leu	Lys	Ser
		35				40						45			
Gly	Leu	His	Pro	Leu	Arg	His	Lys	Leu	Val	Leu	Trp	Tyr	Thr	Arg	Arg
	50				55					60					
Thr	Pro	Gly	Ala	Arg	Ser	Gln	Ser	Tyr	Glu	Asp	Asn	Ile	Lys	Lys	Ile
65				70				75						80	
Ile	Asp	Phe	Ser	Thr	Val	Glu	Ser	Phe	Trp	Val	Cys	Tyr	Cys	His	Leu
			85					90						95	
Ala	Arg	Pro	Ser	Leu	Pro	Ser	Pro	Thr	Asp	Leu	His	Leu	Phe	Lys	
		100				105						110			
Asp	Gly	Ile	Arg	Pro	Leu	Trp	Glu	Asp	Pro	Ala	Asn	Gln	Asn	Gly	Gly
	115					120						125			
Lys	Trp	Ile	Ile	Arg	Phe	Lys	Lys	Ala	Val	Ser	Gly	Arg	Phe	Trp	Glu
	130					135						140			
Asp	Leu	Val	Leu	Val	Val	Gly	Asp	Gln	Leu	Glu	Tyr	Ser	Asp	Asp	
145			150					155						160	
Val	Cys	Gly	Val	Val	Leu	Ser	Val	Arg	Phe	Asn	Glu	Asp	Ile	Leu	Ser
			165					170						175	
Val	Trp	Asn	Arg	Asn	Ala	Ser	Asp	His	Gln	Ala	Val	Met	Ala	Leu	Arg
			180					185						190	
Asp	Ser	Ile	Lys	Arg	His	Leu	Lys	Leu	Pro	His	Ser	Tyr	Leu	Met	Glu
	195					200						205			
Tyr	Lys	Pro	His	Asp	Xaa	Arg	Gly	Val	Thr	Thr	Arg	Pro	Thr	Gly	Thr
	210					215					220				
His	Gly														
225															

(2) INFORMATION FOR SEQ ID NO:2970:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 965 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..965
- (D) OTHER INFORMATION: / Ceres Seq. ID 1574999

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2970:

agaccagcaa	tcaacattca	agccatggca	ctgttcaagt	gcattgtgcat	cttcttagtc	60
togctttcac	tcgcctccac	cttcaccaat	gcccaggaag	aatcttcaca	tgggactctc	120
ccaccgttcc	cttgcattcc	agggccagca	cgcccccgcg	ggttgccacc	ttgcccgcgc	180
gcaccaaccc	agtgctacac	gtcgtgtgct	ggaatgatgc	cgtgcgcgga	cttctcacc	240
cacaacgagg	tgccaccgat	gcccaccacg	gtcgcctgtt	gtGgatggte	tcaggtgact	300
cgtaaccaac	cggtccatct	gtctatgcca	tatcgtcaac	ggtaacatca	acaagctcct	360
accggcgccc	atgataccgc	tgccgatggt	ggcgctcccc	cgctttttgt	ttgtccgctt	420
cccacgagcc	atacttgcgc	gggtgatcag	agggcatttg	ccaccgatga	accctccgcg	480
tcacaccag	gcataccgct	cgggaaccac	atctacatcg	ccagcagcat	caccatcgga	540
atcaccacca	gcagcatcgc	caccagaatc	gcgctcgaca	ccaccaccag	agtcgctcga	600
ctacaccgcc	gacaccagca	gcagcaccac	cgaaatcacc	gtctgatcca	ccaccagcta	660
cgtaaccagca	atcatcatct	gatccaccgt	cgaccaccag	agctacacca	acggcgactc	720
catcccccac	atcttaatac	cgaagaatat	ttcaaaagca	gtagttagtt	agtcгааааа	780
gatatgcgtt	ttaggattct	agttgatatg	cgtccattat	tttgttcac	tcgaatgcag	840
tagtgtgtta	gctatgtagt	tgcataccta	tcataactaa	gtctattaga	agtatctcta	900
ataatattta	ggatctgtca	tcaataaaat	gtatgcaaca	atacgaatat	tgtattattt	960

(2) INFORMATION FOR SEQ ID NO:2971:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 114 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..114

(D) OTHER INFORMATION: / Ceres Seq. ID 1575000

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2971:

Arg	Pro	Ala	Ile	Asn	Ile	Gln	Ala	Met	Ala	Leu	Phe	Lys	Cys	Met	Cys
1			5					10						15	
Ile	Phe	Leu	Val	Ser	Leu	Leu	Leu	Ala	Leu	Thr	Phe	Thr	Asn	Ala	Gln
			20					25					30		
Glu	Glu	Ser	Ser	His	Arg	Thr	Leu	Pro	Pro	Phe	Pro	Cys	Ile	Pro	Gly
			35				40					45			
Gln	Pro	Arg	Pro	Pro	Arg	Leu	Pro	Pro	Cys	Pro	Pro	Ala	Pro	Thr	Glu
			50				55					60			
Cys	Tyr	Thr	Ser	Leu	Ser	Gly	Met	Met	Pro	Cys	Ala	Asp	Phe	Leu	Thr
65				70					75					80	
His	Asn	Glu	Val	Pro	Pro	Met	Pro	Pro	Thr	Val	Ala	Cys	Cys	Gly	Tyr
			85						90					95	
Ser	Gln	Val	Thr	Arg	His	Gln	Arg	Val	His	Leu	Ser	Met	Pro	Tyr	Arg
			100					105					110		
Gln	Arg														

(2) INFORMATION FOR SEQ ID NO:2972:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 123 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..123

(D) OTHER INFORMATION: / Ceres Seq. ID 1575001

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2972:

Thr	Ser	Asn	Gln	His	Ser	Ser	His	Gly	Thr	Val	Gln	Val	His	Val	His
1			5					10					15		
Leu	Leu	Ser	Leu	Ala	Ser	Thr	Arg	Pro	His	Leu	His	Gln	Cys	Pro	Gly
			20					25					30		

Arg Ile Phe Thr Ser Asp Ser Pro Thr Val Pro Leu His Pro Arg Pro
35 40 45
Ala Thr Ala Pro Ala Val Ala Thr Leu Pro Ala Gly Thr Asn Arg Val
50 55 60
Leu His Val Ala Val Gly Asn Asp Ala Val Arg Gly Leu Pro His Pro
65 70 75 80
Gln Arg Gly Ala Thr Asp Ala Thr His Gly Arg Leu Leu Trp Met Val
85 90 95
Ser Gly His Ser Ser Pro Thr Arg Pro Ser Val Tyr Ala Ile Ser Ser
100 105 110
Thr Val Thr Ser Thr Ser Ser Thr Arg Arg Pro
115 120

(2) INFORMATION FOR SEQ ID NO:2973:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 106 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..106
- (D) OTHER INFORMATION: / Ceres Seq. ID 1575002

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2973:

Met Ala Leu Phe Lys Cys Met Cys Ile Phe Leu Val Ser Leu Leu Leu
1 5 10 15
Ala Leu Thr Phe Thr Asn Ala Gln Glu Glu Ser Ser His Arg Thr Leu
20 25 30
Pro Pro Phe Pro Cys Ile Pro Gly Gln Pro Arg Pro Pro Arg Leu Pro
35 40 45
Pro Cys Pro Pro Ala Pro Thr Glu Cys Tyr Thr Ser Leu Ser Gly Met
50 55 60
Met Pro Cys Ala Asp Phe Leu Thr His Asn Glu Val Pro Pro Met Pro
65 70 75 80
Pro Thr Val Ala Cys Cys Gly Trp Ser Gln Val Thr Arg His Gln Arg
85 90 95
Val His Leu Ser Met Pro Tyr Arg Gln Arg
100 105

(2) INFORMATION FOR SEQ ID NO:2974:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 660 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..660
- (D) OTHER INFORMATION: / Ceres Seq. ID 1575003

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2974:

aagaagaact	cggtgcgggt	catcctgcc	aacctggagg	tgaagtctgt	cgaccccgac	60
acgggcccgt	cgctgcccac	gaacaacgcc	ggggagatct	cgctccggag	tcaggccgtg	120
atgcagggct	actacaggaa	gaaggaggag	acggagcgca	ccatcgatgc	caagggggtg	180
ctccataccg	gcgacgtcgg	ctacatcgac	gacgacggcg	acgtgttcat	cgtcgaccgg	240
atcaaggagc	tcatacaagta	caagggcctc	caggtcgctc	ctgcccgagct	ggaggccatt	300
ctcctgtccc	accgctcggt	ccaagatgcg	gccgtcttcg	gcctgcggga	cgaggaggct	360
ggcgagatcc	cggtgtcggt	cggtgtcgcg	cggtgtggcg	cgctcgagag	cgaaCGgaN	420
catcatggcg	tacgtggcgg	gccgcgtggc	gtcgtacaag	aagctccggc	tgctgcagtt	480
cggtgacgtc	atccacaagt	cggtgtcagg	caagatcctg	cggcggcagc	tcgggggacga	540
gttcgttagc	aggacccaaa	cggcggcagc	ctagctctag	cgagagctag	acagtccaat	600
atgccagtta	catacttaca	ttgcacacgt	acatcaaacg	aataaatgtc	aagctattct	660

(2) INFORMATION FOR SEQ ID NO:2975:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 182 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..182
- (D) OTHER INFORMATION: / Ceres Seq. ID 1575004

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2975:

Lys Lys Asn Ser Val Gly Phe Ile Leu Pro Asn Leu Glu Val Lys Phe
1 5 10 15
Val Asp Pro Asp Thr Gly Arg Ser Leu Pro Lys Asn Thr Pro Gly Glu
20 25 30
Ile Cys Val Arg Ser Gln Ala Val Met Gln Gly Tyr Tyr Arg Lys Lys
35 40 45
Glu Glu Thr Glu Arg Thr Ile Asp Ala Lys Gly Trp Leu His Thr Gly
50 55 60
Asp Val Gly Tyr Ile Asp Asp Asp Gly Asp Val Phe Ile Val Asp Arg
65 70 75 80
Ile Lys Glu Leu Ile Lys Tyr Lys Gly Phe Gln Val Ala Pro Ala Glu
85 90 95
Leu Glu Ala Ile Leu Leu Ser His Pro Ser Val Gln Asp Ala Ala Val
100 105 110
Phe Gly Leu Pro Asp Glu Glu Ala Gly Glu Ile Pro Val Ser Cys Val
115 120 125
Val Arg Arg Cys Gly Ala Ser Glu Ser Glu Ala Xaa His His Gly Val
130 135 140
Arg Gly Gly Pro Arg Gly Val Val Gln Glu Ala Pro Ala Ala Val
145 150 155 160
Arg Gly Arg His Pro Gln Val Gly Val Arg Gln Asp Pro Ala Ala Ala
165 170 175
Ala Pro Gly Arg Val Arg
180

(2) INFORMATION FOR SEQ ID NO:2976:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 195 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..195
- (D) OTHER INFORMATION: / Ceres Seq. ID 1575005

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2976:

Glu Glu Leu Gly Arg Val His Pro Ala Gln Pro Gly Gly Glu Val Arg
1 5 10 15
Arg Pro Arg His Gly Pro Val Ala Ala Gln Glu His Ala Arg Gly Asp
20 25 30
Leu Arg Pro Glu Ser Gly Arg Asp Ala Gly Leu Leu Gln Glu Glu Gly
35 40 45
Gly Asp Gly Ala His His Arg Cys Gln Gly Val Ala Pro Tyr Arg Arg
50 55 60
Arg Arg Leu His Arg Arg Arg Arg Arg Val His Arg Arg Pro Asp
65 70 75 80
Gln Gly Ala His Gln Val Gln Gly Leu Pro Gly Arg Ser Cys Arg Ala
85 90 95

Gly Gly His Ser Pro Val Pro Pro Val Gly Pro Arg Cys Gly Arg Leu
100 105 110
Arg Pro Ala Gly Arg Gly Trp Arg Asp Pro Gly Val Val Arg Gly
115 120 125
Ala Ala Val Trp Arg Val Gly Glu Arg Ser Gly Xaa Ser Trp Arg Thr
130 135 140
Trp Arg Ala Ala Trp Arg Arg Thr Arg Ser Ser Gly Cys Cys Ser Ser
145 150 155 160
Trp Thr Ser Ser Thr Ser Arg Cys Gln Ala Arg Ser Cys Gly Gly Ser
165 170 175
Ser Gly Thr Ser Ser Leu Ala Gly Pro Lys Arg Arg Gln Pro Ser Ser
180 185 190
Ser Glu Ser
195

(2) INFORMATION FOR SEQ ID NO:2977:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 142 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..142

(D) OTHER INFORMATION: / Ceres Seq. ID 1575006

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2977:

Met Gln Gly Tyr Tyr Arg Lys Lys Glu Glu Thr Glu Arg Thr Ile Asp
1 5 10 15
Ala Lys Gly Trp Leu His Thr Gly Asp Val Gly Tyr Ile Asp Asp Asp
20 25 30
Gly Asp Val Phe Ile Val Asp Arg Ile Lys Glu Leu Ile Lys Tyr Lys
35 40 45
Gly Phe Gln Val Ala Pro Ala Glu Leu Glu Ala Ile Leu Leu Ser His
50 55 60
Pro Ser Val Gln Asp Ala Ala Val Phe Gly Leu Pro Asp Glu Glu Ala
65 70 75 80
Gly Glu Ile Pro Val Ser Cys Val Val Arg Arg Cys Gly Ala Ser Glu
85 90 95
Ser Glu Ala Xaa His His Gly Val Arg Gly Gly Pro Arg Gly Val Val
100 105 110
Gln Glu Ala Pro Ala Ala Val Arg Gly Arg His Pro Gln Val Gly
115 120 125
Val Arg Gln Asp Pro Ala Ala Ala Pro Gly Arg Val Arg
130 135 140

(2) INFORMATION FOR SEQ ID NO:2978:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 487 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -

(B) LOCATION: 1..487

(D) OTHER INFORMATION: / Ceres Seq. ID 1575013

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2978:

gactccacgc	cgccagtcac	gaccacgccg	cgctccgcgc	tggaaccctt	tagccgagcg	60
gagCaaggga	agaaatgggg	aagggtacgg	gcagcttcgg	caagcggccg	aacaagacgc	120
acacgctctg	catccgctgc	ggccgcgcga	gcttccacct	ccagaagagc	acctgctctt	180
ctgcgggcta	ccccgccgcc	cgcatccgca	agtataactg	gagtggtgaa	gccatcaggc	240
gtaagacaac	tggtaccgga	aggatgaggt	acatgcgaca	cgttcctcgc	cgtttcaaga	300

gcaacttcag agaagggact gaggtgccc caaagaaggg tgtgtgtgct gccaaactaag 360
tgtggtcttg ctgcatcaaa gaagtgtgac aacttgagac ttttgattg aattgtactt 420
ctgaactctt tagccataa tactatgctt gaattaattt cagacgcctt ggagaggtat 480
gatatgt

(2) INFORMATION FOR SEQ ID NO:2979:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 75 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..75

(D) OTHER INFORMATION: / Ceres Seq. ID 1575014

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2979:

Asp Ser Thr Pro Pro Val Thr Thr Thr Pro Arg Leu Arg Leu Glu Pro
1 5 10 15
Phe Ser Arg Ala Glu Gln Gly Lys Lys Trp Gly Arg Val Arg Ala Ala
20 25 30
Ser Ala Ser Ala Gly Thr Arg Arg Thr Arg Ser Ala Ser Ala Ala Ala
35 40 45
Ala Ala Ala Ser Thr Ser Arg Arg Ala Pro Ala Pro Ala Ala Thr
50 55 60
Pro Pro Pro Ala Ser Ala Ser Ile Thr Gly Val
65 70 75

(2) INFORMATION FOR SEQ ID NO:2980:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 71 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..71

(D) OTHER INFORMATION: / Ceres Seq. ID 1575015

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2980:

Thr Pro Arg Arg Gln Ser Arg Pro Arg Arg Ala Ser Ala Trp Asn Pro
1 5 10 15
Leu Ala Glu Arg Ser Lys Gly Arg Asn Gly Glu Gly Tyr Gly Gln Leu
20 25 30
Arg Gln Ala Pro Glu Gln Asp Ala His Ala Leu His Pro Leu Arg Pro
35 40 45
Pro Gln Leu Pro Pro Pro Glu Glu His Leu Leu Leu Arg Leu Pro
50 55 60
Arg Arg Pro His Pro Gln Val
65 70

(2) INFORMATION FOR SEQ ID NO:2981:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 94 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..94

(D) OTHER INFORMATION: / Ceres Seq. ID 1575016

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2981:

Met Gly Lys Gly Thr Gly Ser Phe Gly Lys Arg Arg Asn Lys Thr His

1	5	10	15
Thr Leu Cys Ile Arg Cys Gly Arg Arg Ser Phe His Leu Gln Lys Ser			
	20	25	30
Thr Cys Ser Ser Cys Gly Tyr Pro Ala Ala Arg Ile Arg Lys Tyr Asn			
	35	40	45
Trp Ser Val Lys Ala Ile Arg Arg Lys Thr Thr Gly Thr Gly Arg Met			
	50	55	60
Arg Tyr Met Arg His Val Pro Arg Arg Phe Lys Ser Asn Phe Arg Glu			
	65	70	75
Gly Thr Glu Ala Ala Pro Lys Lys Gly Val Ala Ala Asn			
	85	90	

(2) INFORMATION FOR SEQ ID NO:2982:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 670 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..670
- (D) OTHER INFORMATION: / Ceres Seq. ID 1575017

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2982:

gagcctcgaa	ccctaacc	caccacgtaa	ctccttgaa	ttaccgaaat	gccactcttc	60
ttctccaaat	tgcaccatt	ggtccccgc	gtccgcgcgc	ttccatcgc	cgcgccgaca	120
gccggcgang	sgaccctaag	ctgtctcgaa	tgcgggatga	gtcctctgc	ctatcccccg	180
ccgagctgga	cgactatg	gcgctcctgc	gCctcaagct	ccgcctgtgc	ctcactctca	240
gcgcagbent	Tggagcctct	ccggcccgagg	ccggggagcgc	cgcggtgcga	gcgtggagg	300
Cgcgcgcgc	kgtgaagacg	gcgtctcgact	tgaagatcga	gaagtacgag	gccgcgcgcga	360
agattaaagat	catcaaggag	gtgcgcgcga	tgacggacct	gggtctgaag	gaggcgaagg	420
agctcgtaga	gaaggcgccc	atagtgtgtgc	gcgcgggggtt	gcctaaagag	gagggccgagg	480
cgctcgcgcg	taagctcaag	gccgcgcggtg	ccgctgttgc	actcgagtga	tccacacgaag	540
gtgtgcgcctc	tttttttttt	gttctctagtg	ttcttagacg	atgcaacgta	tctttgcgcc	600
ttaatttgtt	tgtaatggaa	ttcaatagat	tggtataggg	tataaagagg	atgcaacgtc	660
taagaacact						

(2) INFORMATION FOR SEQ ID NO:2983:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 175 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..175
- (D) OTHER INFORMATION: / Ceres Seq. ID 1575018

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2983:

Ala Ser Asn Pro Asn Pro His His Val Thr Pro Trp Asn Tyr Arg Asn							
	5	10	15				
Ala Thr Leu Leu Leu Gln Ile Arg Thr Ile Gly Pro Pro Arg Pro Pro							
	20	25	30				
Pro Phe His Arg Arg Gly Asp Ser Arg Arg Xaa Asp Pro Lys Leu Ser							
	35	40	45				
Arg Ile Ala Asp Glu Leu Leu Ala Leu Ser Pro Ala Glu Leu Asp Asp							
	50	55	60				
Tyr Ala Ala Leu Leu Arg Leu Lys Leu Arg Leu Ser Leu Thr Ser Ser							
	65	70	75				
Ala Xaa Xaa Gly Ala Ser Pro Ala Gly Ala Gly Asp Ala Ala Ala Ala							
	85	90	95				
Ala Val Glu Ala Ala Ala Xaa Val Lys Thr Ala Phe Asp Leu Lys Ile							
	100	105	110				

Glu Lys Tyr Glu Ala Ala Ala Lys Ile Lys Ile Ile Lys Glu Val Arg
115 120 125
Ala Met Thr Asp Leu Gly Leu Lys Glu Ala Lys Glu Leu Val Glu Lys
130 135 140
Ala Pro Ile Val Val Arg Ala Gly Leu Pro Lys Glu Glu Ala Glu Ala
145 150 155 160
Leu Ala Ala Lys Leu Lys Ala Ala Gly Ala Val Ala Leu Glu
165 170 175

(2) INFORMATION FOR SEQ ID NO:2984:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 88 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..88
- (D) OTHER INFORMATION: / Ceres Seq. ID 1575019

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2984:

Met Pro Leu Phe Phe Ser Lys Phe Ala Pro Leu Val Pro Arg Val Arg
1 5 10 15
Arg Leu Ser Ile Ala Ala Ala Thr Ala Gly Xaa Xaa Thr Leu Ser Cys
20 25 30
Leu Glu Ser Arg Met Ser Ser Ser Pro Tyr Pro Pro Pro Ser Trp Thr
35 40 45
Thr Met Arg Arg Ser Cys Ala Ser Ser Ser Ala Cys Arg Ser Pro Pro
50 55 60
Ala Gln Xaa Leu Glu Pro Leu Arg Pro Gly Pro Gly Thr Pro Arg Leu
65 70 75 80
Gln Pro Trp Arg Pro Pro Arg Xaa
85

(2) INFORMATION FOR SEQ ID NO:2985:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1109 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1109
- (D) OTHER INFORMATION: / Ceres Seq. ID 1575027

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2985:

gttcggttcc ttctcgtacc gagccgagg tagccagcca accgcccagc cakycacaa 60
cgatgaagcg cttcttccag ccagtgccca aggaacggct ccggtccaa aagcgggctag 120
cggngtgctg ctgaaccggg cgacggcccc acatcagcgc gtgcccgccac cgGccgctgg 180
cggggatgta gaggggaggg ccaccaggga gccgttccaa ttctcgacgt ggaacgccc aa 240
cagcctgcct ctcgccgatga agagcgactg gccctgtttc tcgcagctcg tcgcccgcc 300
tgaccgccag gtcatttggt tccaggaagt gcggatgcgc gcagctgggt ccaaaagggct 360
acctaaaaac cccagtgtaac taaaagatga cacaagcttg tcacggggatg aaaagcaggt 420
agttctacgt gctttgtcag cttcaccttt caaagactac cgtgtctggt ggtctctttc 480
agattcaaaa tatgctggga castatgttt ataaagaaaa agtttgagcc taagaaggtg 540
tctttcaact tggatagaac atcttctaag catgaagcgc atgggcgtgt tataattgcg 600
gaatttgat cattctcttt tactgaacac ttattctcca acaattggat ggaaggaggga 660
ggaaaatgca tttaaaagaa gacgtaagt ggacaagagg atgctagaat ttgttcaaca 720
cgtggataaa cccttaactc ggtgtgggga cttgaatgtc agtcatgaag aatcgacgt 780
cagccatcct gattttctta gcagcgctaa gctgaatgga tacacccac ccaataaaga 840
ggactgtgga cagccagatg tcaccccagc agagagacgg cgttttggca acatattatt 900
ccaaggaaa cgtgtagatg cttacaggga cctgcacaaa gaaaaggaca tagacggtgg 960
cttctcttg tccggtcatc caattggcaa gtaccgagga aagagaatga ggtatcgacta 1020

cttcctgtgt tcggaacagt taaaggacag aatgatttca tgtgaaatgc atggccgtgg 1080
cattgaattg gatggatttt atggaagt

(2) INFORMATION FOR SEQ ID NO:2986:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..170
- (D) OTHER INFORMATION: / Ceres Seq. ID 1575028

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2986:

Phe	Gly	Ser	Phe	Ser	Tyr	Arg	Ala	Ala	Gly	Ser	Gln	Pro	Thr	Ala	Asp	
1				5					10					15		
Ala	Xaa	Thr	Ser	Asp	Glu	Ala	Leu	Leu	Pro	Ala	Ser	Ala	Gln	Gly	Arg	
			20					25					30			
Leu	Pro	Val	Gln	Glu	Ala	Ala	Ser	Xaa	Val	Leu	Leu	Asn	Arg	Ala	Thr	
		35					40					45				
Ala	Pro	His	Gln	Pro	Val	Pro	Pro	Ala	Pro	Gly	Gly	Asp	Val	Glu		
		50				55				60						
Gly	Arg	Pro	Thr	Glu	Glu	Pro	Phe	Lys	Phe	Leu	Thr	Trp	Asn	Ala	Asn	
		65			70					75				80		
Ser	Leu	Leu	Leu	Arg	Met	Lys	Ser	Asp	Trp	Pro	Ala	Phe	Ser	Gln	Leu	
			85						90					95		
Val	Ala	Arg	Leu	Asp	Pro	Asp	Val	Ile	Cys	Val	Gln	Glu	Val	Arg	Met	
			100					105					110			
Pro	Ala	Ala	Gly	Ser	Lys	Gly	Ala	Pro	Lys	Asn	Pro	Ser	Glu	Leu	Lys	
			115				120					125				
Asp	Asp	Thr	Ser	Leu	Ser	Arg	Asp	Glu	Lys	Gln	Val	Val	Leu	Arg	Ala	
		130					135				140					
Leu	Ser	Ala	Ser	Pro	Phe	Lys	Asp	Tyr	Arg	Val	Trp	Trp	Ser	Leu	Ser	
		145			150					155				160		
Asp	Ser	Lys	Tyr	Ala	Gly	Thr	Xaa	Cys	Leu							
				165					170							

(2) INFORMATION FOR SEQ ID NO:2987:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 85 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..85
- (D) OTHER INFORMATION: / Ceres Seq. ID 1575029

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2987:

Met	Lys	Ser	Asp	Trp	Pro	Ala	Phe	Ser	Gln	Leu	Val	Ala	Arg	Leu	Asp	
1				5					10					15		
Pro	Asp	Val	Ile	Cys	Val	Gln	Glu	Val	Arg	Met	Pro	Ala	Ala	Gly	Ser	
			20					25						30		
Lys	Gly	Ala	Pro	Lys	Asn	Pro	Ser	Glu	Leu	Lys	Asp	Asp	Thr	Ser	Leu	
		35					40					45				
Ser	Arg	Asp	Glu	Lys	Gln	Val	Val	Leu	Arg	Ala	Leu	Ser	Ala	Ser	Pro	
		50				55					60					
Phe	Lys	Asp	Tyr	Arg	Val	Trp	Trp	Ser	Leu	Ser	Asp	Ser	Lys	Tyr	Ala	
		65			70					75				80		
Gly	Thr	Xaa	Cys	Leu												
				85												

(2) INFORMATION FOR SEQ ID NO:2988:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 136 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..136
(D) OTHER INFORMATION: / Ceres Seq. ID 1575030
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2988:
Met Leu Glu Phe Val Gln His Val Asp Lys Pro Leu Ile Trp Cys Gly
1 5 10 15
Asp Leu Asn Val Ser His Glu Glu Ile Asp Val Ser His Pro Asp Phe
20 25 30
Phe Ser Ser Ala Lys Leu Asn Gly Tyr Thr Pro Pro Asn Lys Glu Asp
35 40 45
Cys Gly Gln Pro Gly Phe Thr Pro Ala Glu Arg Arg Phe Gly Asn
50 55 60
Ile Leu Phe Gln Gly Lys Leu Val Asp Ala Tyr Arg His Leu His Lys
65 70 75 80
Glu Lys Asp Ile Asp Gly Gly Phe Ser Trp Ser Gly His Pro Ile Gly
85 90 95
Lys Tyr Arg Gly Lys Arg Met Arg Ile Asp Tyr Phe Leu Val Ser Glu
100 105 110
Gln Leu Lys Asp Arg Ile Val Ser Cys Glu Met His Gly Arg Gly Ile
115 120 125
Glu Leu Asp Gly Phe Tyr Gly Ser
130 135
(2) INFORMATION FOR SEQ ID NO:2989:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 316 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..316
(D) OTHER INFORMATION: / Ceres Seq. ID 1575038
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2989:
atctctcact caaccgcgcg cgaagCacac gagatagagc tgctagaggc tagagcagta 60
gagctagaag aggaggacaa caaccatgga tgcgcggcg gcgcgcgcgc gcagggggaga 120
tacgaagaag aagaagatgc ttgccaccct ggtgggctgc aactacgcgc gcacgcgcgta 180
cgagctgcag ggctgcatca acgacgtcca cgcctgcgc gccgtactcc tcgcccgctt 240
cggCttcgcg cctgcgcagc tcaccgtgct caccgcacgc cagcacgggc gcggcggcgcg 300
cgcggcgcgtg ctcccg
(2) INFORMATION FOR SEQ ID NO:2990:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 105 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..105
(D) OTHER INFORMATION: / Ceres Seq. ID 1575039
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2990:
Ile Ser His Ser Thr Ala Arg Glu Ala His Glu Ile Glu Leu Leu Glu
1 5 10 15

Ala Arg Ala Val Glu Leu Glu Glu Glu Asp Asn Asn His Gly Cys Gly
20 25 30
Gly Gly Gly Gly Glu Gly Arg Tyr Glu Glu Glu Glu Asp Ala Cys
35 40 45
His Pro Gly Gly Leu Gln Leu Arg Arg His Ala Val Arg Ala Ala Gly
50 55 60
Leu His Gln Arg Arg Pro Arg His Ala Arg Pro Pro Arg Pro Leu
65 70 75 80
Arg Leu Arg Ala Cys Arg Arg His Arg Ala His Arg Arg Pro Ala Arg
85 90 95
Ala Arg Arg Arg Arg Arg Ala Pro
100 105

(2) INFORMATION FOR SEQ ID NO:2991:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 77 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide
(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..77
(D) OTHER INFORMATION: / Ceres Seq. ID 1575040

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2991:

Met Asp Ala Ala Ala Ala Ala Ala Arg Gly Asp Thr Lys Lys Lys
1 5 10 15
Lys Met Leu Ala Thr Leu Val Gly Cys Asn Tyr Ala Gly Thr Pro Tyr
20 25 30
Glu Leu Gln Gly Cys Ile Asn Asp Val His Ala Met Arg Ala Val Leu
35 40 45
Leu Ala Arg Phe Gly Phe Ala Pro Ala Asp Val Thr Val Leu Thr Asp
50 55 60
Asp Gln His Gly Arg Gly Gly Gly Gly Val Leu Pro
65 70 75

(2) INFORMATION FOR SEQ ID NO:2992:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 75 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide
(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..75
(D) OTHER INFORMATION: / Ceres Seq. ID 1575041

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2992:

Met Arg Arg Arg Arg Arg Arg Arg Gly Glu Ile Arg Arg Arg Arg
1 5 10 15
Cys Leu Pro Pro Trp Trp Ala Ala Thr Thr Pro Ala Arg Arg Thr Ser
20 25 30
Cys Arg Ala Ala Ser Thr Thr Ser Thr Pro Cys Ala Pro Ser Ser Ser
35 40 45
Pro Ala Ser Ala Ser Arg Leu Pro Thr Ser Pro Cys Ser Pro Thr Thr
50 55 60
Ser Thr Gly Ala Ala Ala Ala Ala Cys Ser
65 70 75

(2) INFORMATION FOR SEQ ID NO:2993:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 928 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single

- (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:

(A) NAME/KEY: -
(B) LOCATION: 1..928
(D) OTHER INFORMATION: / Ceres Seq. ID 1575056

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2993:

agggccttgc	attttttctc	cgcgtttg	tcctccgatt	acgttccctc	gctactcgct	60
agtcgccact	tctcccggtg	cccccccg	tctctcttct	cgttgcgacg	actcggcgat	120
ccctgcgcgc	ccccgtctcc	cgcctccgc	cgcagggtgc	ccagggtgtc	gcggggccct	180
tcgcggcgca	tgagcaccac	acaggagggt	actgagaact	acgcaaatcc	taagacatgc	240
ttcttccatg	ttctcttcaa	ggcatcgcga	ttggcggtct	acatactgtc	caactgttct	300
gtgaacaact	tcgtcatcat	ctttgtcatc	actgtgctcc	tcgcagcact	tgactctctg	360
gtcgtgaaga	atgtcagcgg	aaggatactg	gttggcgctg	gggtgtggaa	tgagattaac	420
gatgaggggg	agagtgtctg	gaagtttgag	tgccttgatg	gagagctccc	tggttaggat	480
gaataagaag	gactcatggc	tgctctgggt	gactctatat	ttgactcgcg	ctgcactggat	540
tatacttggg	atattctcgc	tcacacagact	tcaagctgat	tacottctcg	ttgttggagt	600
ttgcttgagc	ctcagcattg	caaatawat	kgstrwcwsc	rwwtgcawtm	wagatkcsc	660
gaagaacatc	caggattgga	caaggaaatg	actctatca	ggtagtgtca	gacgcactct	720
gcagtcagca	tttggtgtct	gaacaataac	ctatgacctt	gttatcagtg	tagtgctgta	780
taattttcac	ataacatgat	tggttactag	agtgcgctcg	tttttttttt	tggtggctat	840
gtgcactctg	ctaggcagag	tcggaagaac	atcttcagag	ccgtgtatca	actcgatgta	900
taatgcagtt	tgaataaaat	ctctcttt				

(2) INFORMATION FOR SEQ ID NO:2994:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 158 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1..158
(D) OTHER INFORMATION: / Ceres Seq. ID 1575057

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2994:

Arg	Ala	Leu	His	Phe	Phe	Leu	Arg	Phe	Ala	Phe	Pro	Asp	Tyr	Val	Pro
1			5						10				15		
Ser	Leu	Leu	Ala	Ser	Arg	His	Phe	Ser	Arg	Cys	Pro	Pro	Ala	Ser	Leu
			20					25					30		
Phe	Ser	Leu	Arg	Arg	Leu	Gly	Asp	Pro	Cys	Arg	Pro	Pro	Ser	Pro	Ala
			35				40					45			
Pro	Arg	Arg	Gln	Val	Pro	Arg	Leu	Ser	Pro	Gly	Pro	Ser	Pro	Ala	Met
			50				55				60				
Ser	Thr	Gln	Gln	Glu	Val	Thr	Glu	Asn	Tyr	Ala	Asn	Pro	Lys	Thr	Cys
65					70				75						80
Phe	Phe	His	Val	Leu	Phe	Lys	Ala	Ser	Ala	Leu	Ala	Phe	Tyr	Ile	Leu
			85				90						95		
Ser	Thr	Leu	Phe	Val	Asn	Asn	Phe	Val	Ile	Phe	Val	Ile	Thr	Val	
			100				105						110		
Leu	Leu	Ala	Ala	Leu	Asp	Phe	Trp	Val	Val	Lys	Asn	Val	Ser	Gly	Arg
			115				120					125			
Ile	Leu	Val	Gly	Leu	Arg	Trp	Trp	Asn	Glu	Ile	Asn	Asp	Glu	Gly	Glu
			130				135					140			
Ser	Val	Trp	Lys	Phe	Glu	Cys	Leu	Asp	Gly	Glu	Ser	Pro	Gly		
145					150					155					

(2) INFORMATION FOR SEQ ID NO:2995:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 123 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..123
 (D) OTHER INFORMATION: / Ceres Seq. ID 1575058
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2995:
Met Ser Ala Glu Gly Tyr Trp Leu Gly Cys Gly Gly Gly Met Arg Leu
1 5 10 15
Thr Met Arg Glu Arg Val Ser Gly Ser Leu Ser Ala Leu Met Glu Ser
 20 25 30
Pro Leu Ala Arg Met Asn Lys Lys Asp Ser Trp Leu Phe Trp Trp Thr
 35 40 45
Leu Tyr Leu Thr Ala Ala Ala Trp Ile Ile Leu Gly Ile Phe Ser Leu
50 55 60
Ile Arg Leu Gln Ala Asp Tyr Leu Leu Val Val Gly Val Cys Leu Ser
65 70 75 80
Leu Ser Ile Ala Asn Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa Asp Xaa
 85 90 95
Lys Lys Asn Ile Gln Asp Trp Thr Arg Asn Ala Leu Leu Ser Gly Ser
100 105 110
Val Arg Ser His Leu Gln Ser Ala Phe Gly Val
115 120

(2) INFORMATION FOR SEQ ID NO:2996:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 110 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..110
 (D) OTHER INFORMATION: / Ceres Seq. ID 1575059
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2996:
Met Arg Leu Thr Met Arg Glu Arg Val Ser Gly Ser Leu Ser Ala Leu
1 5 10 15
Met Glu Ser Pro Leu Ala Arg Met Asn Lys Lys Asp Ser Trp Leu Phe
 20 25 30
Trp Trp Thr Leu Tyr Leu Thr Ala Ala Ala Trp Ile Ile Leu Gly Ile
 35 40 45
Phe Ser Leu Ile Arg Leu Gln Ala Asp Tyr Leu Leu Val Val Gly Val
50 55 60
Cys Leu Ser Leu Ser Ile Ala Asn Xaa Xaa Xaa Xaa Xaa Cys Xaa
65 70 75 80
Xaa Asp Xaa Lys Lys Asn Ile Gln Asp Trp Thr Arg Asn Ala Leu Leu
 85 90 95
Ser Gly Ser Val Arg Ser His Leu Gln Ser Ala Phe Gly Val
100 105 110

(2) INFORMATION FOR SEQ ID NO:2997:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 887 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: DNA (genomic)
 (ix) FEATURE:
 (A) NAME/KEY: -
 (B) LOCATION: 1..887
 (D) OTHER INFORMATION: / Ceres Seq. ID 1575067
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2997:
ataaataact tatgaggcca aactaaagar ggcagggcag gcgaatcgaa ggaaaagtag

tcaggagagg cgtttccctc gcaatcgacc atcacagatc aaatcgctgc aactagctag 120
ggtttcgctg cctcatctct cgtcgatcca tcatggcggt ccgaggggcga aaacaagagg 180
atgatcacgc tcaggagctc cgacttagag gacttcgagg tggaggaagc ggtggccatg 240
gagtcgcaga ctctccgcga catgatcgag gacgactgcd ccgacaaagg catcccgctc 300
cccaacgtca actccaggat cctctctaa gtcacgaGg tactgcaaca gtacagctcca 360
cgccgcccgc aaaccgcgtg actccgctgc ctccgagggc ggcgaggacc tcaagagctg 420
ggacgcgaag tctgtcaagg tggaccaGgc tacgctcttc gacctcatcc tgggtgccaa 480
ctatctgaac atcaagggat tgctggacct gacctgccag acggttgctg acatgatcaa 540
gggcaagact ccggaggaga tccgcaagac attcagcatc aagaacgact tcaccaagaa 600
ggaggaggat gagatcgcca tggagaacca gtgggccttc gactgattgt tctcttctct 660
tccctgggtga tgggtgggtg tcttttacia gaacagatgg atgtctgcac tgcactctac 720
aatgctagt c tatctactta cgaataagta gtgaataagt agtataatg tctgtatggt 780
tgtatccctt tttgatttgg atgtatgtca agctgggtgg tgctagtctg tctgtctgga 840
ctgtttacta gttaatatct cataatacat atataaagt ggaatctt

(2) INFORMATION FOR SEQ ID NO:2998:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 75 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..75

(D) OTHER INFORMATION: / Ceres Seq. ID 1575068

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2998:

Met Ala Ser Glu Gly Glu Asn Lys Arg Met Ile Thr Leu Arg Ser Ser
1 5 10 15
Asp Leu Glu Glu Phe Glu Val Glu Glu Ala Val Ala Met Glu Ser Gln
20 25 30
Thr Leu Arg His Met Ile Glu Asp Asp Cys Xaa Asp Asn Gly Ile Pro
35 40 45
Leu Pro Asn Val Asn Ser Arg Ile Leu Ser Lys Val Ile Glu Val Leu
50 55 60
Gln Gln Ser Arg Pro Arg Arg Arg Gln Thr Arg
65 70 75

(2) INFORMATION FOR SEQ ID NO:2999:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..66

(D) OTHER INFORMATION: / Ceres Seq. ID 1575069

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2999:

Met Ile Thr Leu Arg Ser Ser Asp Leu Glu Glu Phe Glu Val Glu Glu
1 5 10 15
Ala Val Ala Met Glu Ser Gln Thr Leu Arg His Met Ile Glu Asp Asp
20 25 30
Cys Xaa Asp Asn Gly Ile Pro Leu Pro Asn Val Asn Ser Arg Ile Leu
35 40 45
Ser Lys Val Ile Glu Val Leu Gln Gln Ser Arg Pro Arg Arg Arg Gln
50 55 60
Thr Arg
65

(2) INFORMATION FOR SEQ ID NO:3000:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 amino acids

(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..47
(D) OTHER INFORMATION: / Ceres Seq. ID 1575070
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3000:
Met Glu Ser Gln Thr Leu Arg His Met Ile Glu Asp Asp Cys Xaa Asp
1 5 10 15
Asn Gly Ile Pro Leu Pro Asn Val Asn Ser Arg Ile Leu Ser Lys Val
20 25 30
Ile Glu Val Leu Gln Gln Ser Arg Pro Arg Arg Arg Gln Thr Arg
35 40 45

(2) INFORMATION FOR SEQ ID NO:3001:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 723 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..723

(D) OTHER INFORMATION: / Ceres Seq. ID 1575105

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3001:

gcgggtttgcm ggcactvrca ggargagaga ccganarcrc ggcgcaggarg gcgtcgagca 60
ctgavgwqcn ghircggcgg cgccgagctg gacggaggag gggaccacaa gaagcggcgg 120
ctgaccgacg agcaggtaga gatgctggar ctgagcttcc gggaggagcg gaagctggag 180
accggccgga aggtgcacct ggccgcccag ctccggctcg accccaagca ggtcgcgcgtc 240
tggttcacga accgcggcgc ccgccacaag agcaagctgc tcgaggagga gttcgcccaag 300
ctcaagcagg cacacgacgc cgccatcctc cacaatgcc accttgagaa cgaggtgatg 360
agRgctgaag gacaagctgg tgctcgccga ggaggagGct gacgcgttcc agatccgcgg 420
gcaaccacgc ggtctccggt gacggcggag acgtcatggc ccgtgccgtc tgcagcggga 480
gcccagctc atcgttctcg actggcact gccagcagcc cggaggaggc ggccggcggc 540
gcgatcact gggggacgac gacctgctc atgttctga ctatgcctac gctgacagca 600
gcgtggctga gtggtttagc ctgtatggac tgatgtaatc gatggtatgg tatgccatcg 660
tcgtcggcag attaattcta gctagctact catcgtagcg tgctattgct gtgsgaatt 720
gct

(2) INFORMATION FOR SEQ ID NO:3002:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 133 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..133

(D) OTHER INFORMATION: / Ceres Seq. ID 1575106

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3002:

Ala Val Cys Xaa His Xaa Gln Xaa Glu Arg Pro Xaa Xaa Arg Arg Arg
1 5 10 15
Xaa Arg Arg Ala Ala Xaa Xaa Xaa Xaa Gly Gly Gly Glu Leu Asp Gly
20 25 30
Gly Gly Asp His Lys Lys Arg Arg Leu Thr Asp Glu Gln Val Glu Met
35 40 45
Leu Xaa Leu Ser Phe Arg Glu Glu Arg Lys Leu Glu Thr Gly Arg Lys
50 55 60
Val His Leu Ala Ala Glu Leu Gly Leu Asp Pro Lys Gln Val Ala Val

65 70 75 80
Trp Phe Gln Asn Arg Arg Ala Arg His Lys Ser Lys Leu Leu Glu Glu
85 90 95
Glu Phe Ala Lys Leu Lys Gln Ala His Asp Ala Ala Ile Leu His Lys
100 105 110
Cys His Leu Glu Asn Glu Val Met Xaa Ala Glu Gly Gln Ala Gly Ala
115 120 125
Arg Arg Gly Gly Gly
130

(2) INFORMATION FOR SEQ ID NO:3003:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 114 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..114
(D) OTHER INFORMATION: / Ceres Seq. ID 1575107

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3003:

Gly Leu Xaa Ala Xaa Xaa Gly Xaa Glu Thr Xaa Xaa Xaa Ala Gln Xaa
1 5 10 15
Ala Ser Ser Ser Xaa Xaa Xaa Xaa Arg Arg Arg Arg Ala Gly Arg Arg
20 25 30
Arg Gly Pro Gln Glu Ala Ala Ala Asp Arg Arg Ala Gly Arg Asp Ala
35 40 45
Gly Xaa Glu Leu Pro Gly Gly Ala Glu Ala Gly Asp Arg Pro Glu Gly
50 55 60
Ala Pro Gly Arg Arg Ala Arg Ala Arg Pro Gln Ala Gly Arg Arg Leu
65 70 75 80
Val Pro Glu Pro Pro Arg Pro Pro Gln Glu Gln Ala Ala Arg Gly Gly
85 90 95
Val Arg Gln Ala Gln Ala Gly Thr Arg Arg Arg His Pro Pro Gln Met
100 105 110
Pro Pro

(2) INFORMATION FOR SEQ ID NO:3004:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 86 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..86
(D) OTHER INFORMATION: / Ceres Seq. ID 1575108

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3004:

Met Leu Xaa Leu Ser Phe Arg Glu Glu Arg Lys Leu Glu Thr Gly Arg
1 5 10 15
Lys Val His Leu Ala Ala Glu Leu Gly Leu Asp Pro Lys Gln Val Ala
20 25 30
Val Trp Phe Gln Asn Arg Arg Ala Arg His Lys Ser Lys Leu Leu Glu
35 40 45
Glu Glu Phe Ala Lys Leu Lys Gln Ala His Asp Ala Ala Ile Leu His
50 55 60
Lys Cys His Leu Glu Asn Glu Val Met Xaa Ala Glu Gly Gln Ala Gly
65 70 75 80
Ala Arg Arg Gly Gly Gly
85

(2) INFORMATION FOR SEQ ID NO:3005:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 770 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

```
(ix) FEATURE:
```

- (A) NAME/KEY: -
(B) LOCATION: 1..770
(D) OTHER INFORMATION: / Ceres Seq. ID 1575124

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3005:

aatctccagat	cgtgttttgg	cggaaagaga	cagacacgca	aacgagagga	ctcgagagag	60
attccgcgcg	caccacgcgc	ctagatcgag	cgcgcgcagt	cgcgcagatc	ctctcgccgc	120
cttcccaagg	ccaacctctgg	ccttccccct	tctctccctt	ctttgtotata	tcgtcccgagc	180
ctgtccctcg	ccgcacgtcg	caccaaagggc	gtctccgcga	gggcctcttc	ctctctctca	240
tcacgcgact	ctctctctgg	ttcggcgatg	gaggatttcg	tcagaagaac	ggtggccgat	300
aaccocggtg	tcattctact	taagctcatg	tgctcatatt	ccatggaggt	gaagtcacga	360
ttcaagcgat	tcggtgtgca	ggccacgctc	atcgagctcg	caactctcgg	aaagtcaagt	420
ccacaactac	aaaaaggtatt	agaaagagtc	actggacagt	ctactctgtc	taacgttttt	480
atcgtgtgaa	aattccctgtg	acgctgcaca	gataccgtga	agctgtgtac	gaacggggga	540
gtcgactgac	atgctctcgg	actcggatatt	caacattgac	aactcatgac	aagctatgtt	600
ctcgaaagat	tgggcgagacg	ttggcgacga	ctgattgtag	ttctcttttt	taacctgtgc	660
gtgacacaac	actgtgtgtca	ttttcacatt	ttcgtttgtg	actccgataa	aatcattgaa	720
tattgacacc	gtatatatgc	aatttctctg	aaaaagaaag	gaaccagctc		

(2) INFORMATION FOR SEQ ID NO:3006:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 182 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..182
(D) OTHER INFORMATION: / Ceres Seq. ID 1575125

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3006:

[illegible]

(2) INFORMATION FOR SEQ ID NO:3007:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 154 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..154
- (D) OTHER INFORMATION: / Ceres Seq. ID 1575126

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3007:

```
Met Pro Pro Pro Gln Ser Gly Met Thr Leu Cys Arg Leu Pro Lys Ala
1      5      10      15
Thr Leu Gly Leu Pro Leu Ser Leu Pro Ser Leu Leu Tyr Arg Pro Ser
20      25      30
Leu Ser Leu Ala Ala Arg Arg Thr Lys Ala Val Ser Ala Arg Ala Ser
35      40      45
Ser Ser Ser Pro Ser Pro Asp Ser Ser Phe Gly Ser Arg Met Glu Asp
50      55      60
Ser Val Lys Lys Thr Val Ala Asp Asn Pro Val Val Ile Tyr Ser Lys
65      70      75      80
Ser Trp Cys Ser Tyr Ser Met Glu Val Lys Ser Leu Phe Lys Arg Ile
85      90      95
Gly Val Gln Pro His Val Ile Glu Leu Asp Asn Leu Gly Ala Gln Gly
100      105      110
Pro Gln Leu Gln Lys Val Leu Glu Arg Leu Thr Gly Gln Ser Thr Val
115      120      125
Pro Asn Val Phe Ile Gly Gly Lys His Val Gly Arg Cys Thr Asp Thr
130      135      140
Val Lys Ala Val Ser Gln Gly Gly Ala Ser
145      150
```

(2) INFORMATION FOR SEQ ID NO:3008:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 147 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..147
- (D) OTHER INFORMATION: / Ceres Seq. ID 1575127

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3008:

```
Met Thr Leu Cys Arg Leu Pro Lys Ala Thr Leu Gly Leu Pro Leu Ser
1      5      10      15
Leu Pro Ser Leu Leu Tyr Arg Pro Ser Leu Ser Leu Ala Ala Arg Arg
20      25      30
Thr Lys Ala Val Ser Ala Arg Ala Ser Ser Ser Ser Pro Ser Pro Asp
35      40      45
Ser Ser Phe Gly Ser Arg Met Glu Asp Ser Val Lys Lys Thr Val Ala
50      55      60
Asp Asn Pro Val Val Ile Tyr Ser Lys Ser Trp Cys Ser Tyr Ser Met
65      70      75      80
Glu Val Lys Ser Leu Phe Lys Arg Ile Gly Val Gln Pro His Val Ile
85      90      95
Glu Leu Asp Asn Leu Gly Ala Gln Gly Pro Gln Leu Gln Lys Val Leu
100      105      110
Glu Arg Leu Thr Gly Gln Ser Thr Val Pro Asn Val Phe Ile Gly Gly
115      120      125
Lys His Val Gly Arg Cys Thr Asp Thr Val Lys Ala Val Ser Gln Gly
```

130 135 140
Gly Ala Ser
145

(2) INFORMATION FOR SEQ ID NO:3009:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 685 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..685

(D) OTHER INFORMATION: / Ceres Seq. ID 1575143

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3009:

ccatatcatg	ctccaggacg	cagcgaccgg	tattatttat	gtgctgggtt	agctagtcac	60
cattatagca	aacttagcta	gctagctacc	tgcctataat	ggagcgggag	caggagttgg	120
accttgagct	caccctcctc	ccctccgacct	gggctacgca	ggaagaggcg	cccggtctct	180
tcctctgcac	gtactgcggc	cgcaagttct	gcacctccca	ggcgctcggc	ggccaccaga	240
acgcgcacaa	gtacgagcgc	gccctagcca	agcgcccgcc	ggacatcgcc	gctgccttgc	300
gtaagCacgg	tggtcccggtg	acgcgcgctg	gccagttcca	cgccggggcc	agccccagcg	360
ccaggggcac	tgccggagtc	gctggatctg	aacgacctga	tgctgggagg	gagaggccac	420
tgccgggtgga	cgagctgcaa	ggtgctccgg	cgccctggca	atctggcgcc	cCtgcctcac	480
caggtcgagc	gcacagagga	gctggatttg	tcctctggcc	tggtattatt	gcgtttctcc	540
gatccatgat	ccacttccat	ctccttggtc	ttgcgtattt	aaattgctat	atacatgcac	600
gtatatataa	tggtgattgt	ttctctcccc	agaggccaga	gcgcccttaa	attcgctcagt	660
gtgtgctact	tgacggttac	tggtc				

(2) INFORMATION FOR SEQ ID NO:3010:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 183 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..183

(D) OTHER INFORMATION: / Ceres Seq. ID 1575144

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3010:

Met	Glu	Arg	Glu	Gln	Glu	Leu	Asp	Leu	Glu	Leu	Thr	Leu	Leu	Pro	Ser
1			5					10				15			
Ala	Trp	Ala	Thr	Gln	Glu	Glu	Ala	Pro	Gly	Phe	Phe	Leu	Cys	Thr	Tyr
			20					25					30		
Cys	Gly	Arg	Lys	Phe	Cys	Thr	Ser	Gln	Ala	Leu	Gly	Gly	His	Gln	Asn
			35					40				45			
Ala	His	Lys	Tyr	Glu	Arg	Ala	Leu	Ala	Lys	Arg	Arg	Arg	Asp	Ile	Ala
			50					55				60			
Ala	Ala	Leu	Arg	Lys	His	Gly	Val	Pro	Val	Thr	Arg	Ala	Gly	Gln	Phe
			65					70				75			80
His	Ala	Gly	Ala	Ser	Pro	Ser	Ala	Arg	Ala	Thr	Ala	Gly	Val	Ala	Gly
			85					90					95		
Ser	Glu	Arg	Pro	Asp	Glu	Gly	Arg	Glu	Arg	Pro	Val	Ala	Val	Asp	Glu
			100					105					110		
Leu	Gln	Gly	Ala	Pro	Ala	Pro	Trp	Gln	Ser	Gly	Gly	Pro	Ala	Pro	Pro
			115					120				125			
Gly	Arg	Ala	His	Arg	Gly	Ala	Gly	Phe	Val	Pro	Arg	Pro	Val	Ile	Ile
			130					135				140			
Ala	Phe	Ser	Arg	Ser	Met	Tyr	His	Phe	His	Leu	Gly	Phe	Ala	Tyr	
			145					150				155			160
Leu	Asn	Cys	Tyr	Ile	His	Ala	Cys	Ile	Tyr	Asn	Val	Ile	Ala	Phe	Leu
			165					170							175

Pro Gln Arg Pro Glu Arg Leu
180

(2) INFORMATION FOR SEQ ID NO:3011:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 788 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..788
(D) OTHER INFORMATION: / Ceres Seq. ID 1575163

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3011:

atctccgaaa	aaaaaacgcg	aacgcagAAC	gccgccggcc	cgctcgtgac	tctgtgttcc	60
cttcctccac	ttgccttctg	gttcgtgatt	cgtgatttcc	ccgccggaaa	gccgagggag	120
agggagcgat	atgggggttcg	tccgagacac	gatggagtcg	atccgcctcca	tgcagatCcg	180
ccaagtgtc	atgcagatca	tcagcctcgg	tatgattgtt	acctctgcgt	taatatcatg	240
gaagggtttg	atagtttttca	cggggagcga	gtcaccagtt	gtagtgtgtc	tctcgggtag	300
catggagcct	ggatttataa	gggggtgatat	cctgtttttg	catatgagca	aagatcccat	360
tcgcacagga	gaaatagttg	ttttcaatat	cgatggctcg	gagattccaa	ttgtccaccg	420
agtgattaa	gtccatgaac	gtcaggacac	tcagaaagtg	gacatcctca	ccaaaggtga	480
caataatttt	ggggatgacc	gactattata	tgacatggc	cagctttggc	tccagcaaca	540
ccacattatg	gggcgtgcgg	tgggctaact	tccatagtgt	ggctgggtta	caattatcat	600
gactgagaaa	ccatttatta	agtaacctgt	gattggcgca	ctgggcttgc	tggtcataac	660
gtcgaaagat	tagtcatgtc	aaacttcagg	gccatgtaga	tttgtctctt	atggcgcaac	720
agcagagatc	actggctttg	tggcgtttga	gagatgcgcg	tatgttgccg	catgtatcaa	780
acgagrag						

(2) INFORMATION FOR SEQ ID NO:3012:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 180 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..180
(D) OTHER INFORMATION: / Ceres Seq. ID 1575164

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3012:

Met	Gly	Phe	Val	Gly	Asp	Thr	Met	Glu	Ser	Ile	Arg	Ser	Met	Gln	Ile
1				5				10					15		
Arg	Gln	Val	Leu	Met	Gln	Ile	Ile	Ser	Leu	Gly	Met	Ile	Val	Thr	Ser
			20					25					30		
Ala	Leu	Ile	Ile	Trp	Lys	Gly	Leu	Ile	Val	Phe	Thr	Gly	Ser	Glu	Ser
			35					40					45		
Pro	Val	Val	Val	Val	Leu	Ser	Gly	Ser	Met	Glu	Pro	Gly	Phe	Lys	Arg
			50					55					60		
Gly	Asp	Ile	Leu	Phe	Leu	His	Met	Ser	Lys	Asp	Pro	Ile	Arg	Thr	Gly
			65					70					75		80
Glu	Ile	Val	Val	Phe	Asn	Ile	Asp	Gly	Arg	Glu	Ile	Pro	Ile	Val	His
			85					90					95		
Arg	Val	Ile	Lys	Val	His	Glu	Arg	Gln	Asp	Thr	Ala	Glu	Val	Asp	Ile
			100					105					110		
Leu	Thr	Lys	Gly	Asp	Asn	Asn	Phe	Gly	Asp	Asp	Arg	Leu	Leu	Tyr	Ala
			115					120					125		
His	Gly	Gln	Leu	Trp	Leu	Gln	Gln	His	His	Ile	Met	Gly	Arg	Ala	Val
			130					135					140		
Gly	Tyr	Leu	Pro	Tyr	Val	Gly	Trp	Val	Thr	Ile	Ile	Met	Thr	Glu	Lys
			145					150					155		160
Pro	Phe	Ile	Lys	Tyr	Leu	Leu	Ile	Gly	Ala	Leu	Gly	Leu	Leu	Val	Ile

```

(2) INFORMATION FOR SEQ ID NO:3014:
  (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 167 amino acids
      (B) TYPE: amino acid
      (C) STRANDEDNESS:
      (D) TOPOLOGY: linear
  (ii) MOLECULE TYPE: peptide
  (ix) FEATURE:
      (A) NAME/KEY: peptide
      (B) LOCATION: 1..167
      (D) OTHER INFORMATION: / Ceres Seq. ID 1575166
  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3014:
Met  Gln  Ile  Arg  Gln  Val  Leu  Met  Gln  Ile  Ile  Ser  Leu  Gly  Met  Ile
1      5      10      15
Val  Thr  Ser  Ala  Leu  Ile  Ile  Trp  Lys  Gly  Leu  Ile  Val  Phe  Thr  Gly
      20      25      30
Ser  Glu  Ser  Pro  Val  Val  Val  Leu  Ser  Gly  Ser  Met  Glu  Pro  Gly
      35      40      45
Phe  Lys  Arg  Gly  Asp  Ile  Leu  Phe  Leu  His  Met  Ser  Lys  Asp  Pro  Ile
      50      55      60
Arg  Thr  Gly  Glu  Ile  Val  Val  Phe  Asn  Ile  Asp  Gly  Arg  Glu  Ile  Pro
65      70      75      80
Ile  Val  His  Arg  Val  Ile  Lys  Val  His  Glu  Arg  Gln  Asp  Thr  Ala  Glu
      85      90      95

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Val Asp Ile Leu Thr Lys Gly Asp Asn Asn Phe Gly Asp Asp Arg Leu
100 105 110
Leu Tyr Ala His Gly Gln Leu Trp Leu Gln Gln His His Ile Met Gly
115 120 125
Arg Ala Val Gly Tyr Leu Pro Tyr Val Gly Trp Val Thr Ile Ile Met
130 135 140
Thr Glu Lys Pro Phe Ile Lys Tyr Leu Leu Ile Gly Ala Leu Gly Leu
145 150 155 160
Leu Val Ile Thr Ser Lys Asp
165

(2) INFORMATION FOR SEQ ID NO:3015:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 961 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..961

(D) OTHER INFORMATION: / Ceres Seq. ID 1575181

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3015:

acgtacgtat agnmcggcgg gaacgcgtac carghgcgg crgggcggcg ggacgggtcc 60
gtgtcgccgc cgtcgccacac cagcaacctg ccgcccgca cgcccaacct cgccgacstca 120
cgcatgattt cggcaccaca ggcctgacgc agaaggagat ggtctatctg tcgggcgcgc 180
acaccatcgg ctctctgcac tgcagctnnt tcarcggcgc gctgtcgggg tcggccacga 240
cgccrgccgg cgacgacccc accatggacc ccgcgtacgt rgcgcastgn gncrcggcag 300
tcgccgcagg gncngacccc gctcgtgccc atgGaCtaac tctcccccac gcctctcgac 360
gaggGcttct acaagggcgt catggccaac cggggcctgc tgtcctcgga ccaggcgctg 420
ctcagcgaca agaacacccg cgtgcaggtc gtcacctacg ccaacgaccc ggccaccttc 480
caggcccgat tcgccccccc catggtcaag atgggctcgc tcggcgctgt caccggcacc 540
agcggcaagg tcagggccaa ctgcagagtc gcctgattca tctcatcatc tcgtgtggag 600
ttgtagattc attatattga ttgatttga ccggacgacg tcgacgggat gctacatggc 660
ctstttcgca attgtatgta tgcctgtact tgcgcgtgta tgggtttcgc tgtgcaaat 720
ttcgtttgct cccccgattg attgaggcgt gtgtgcgtgt gtgtctcttc tgaatctgaa 780
tggaataatc ttaacctgag ctaaaactgc tcgtgtacta ccaaatagtt gcttcaaat 840
acgatggatt ttatttcaaa ctatcacttc caaacacgca caaatatgta tccaatcaac 900
tagggatcgg agaaactggt ttgtaaaggg aattttataa acacaagcta ttcagacatg 960
t

(2) INFORMATION FOR SEQ ID NO:3016:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 247 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..247

(D) OTHER INFORMATION: / Ceres Seq. ID 1575182

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3016:

Arg Thr Tyr Xaa Xaa Ala Gly Thr Arg Thr Xaa Xaa Arg Xaa Gly Gly
1 5 10 15
Gly Thr Gly Pro Cys Arg Ala Arg Arg Thr Pro Ala Thr Cys Arg Arg
20 25 30
Arg Arg Pro Thr Ser Arg Xaa His Ala Asp Leu Arg His Gln Gly Pro
35 40 45
Asp Ala Glu Gly Asp Gly His Pro Val Gly Arg Ala His His Arg Leu
50 55 60
Leu Ala Leu Gln Xaa Xaa Xaa Arg Pro Ala Val Gly Val Gly His Asp
65 70 75 80

Gly	Xaa	Arg	Ala	Gly	Pro	Asp	His	Gly	Pro	Arg	Val	Arg	Xaa	Ala	Xaa		
				85					90					95			
Xaa	Xaa	Gly	Ser	Ala	Arg	Arg	Xaa	Xaa	Thr	Arg	Ser	Cys	Pro	Trp	Thr		
				100					105				110				
Thr	Ser	Pro	Pro	Thr	Pro	Ser	Thr	Arg	Ala	Ser	Thr	Arg	Ala	Ser	Trp		
				115					120				125				
Pro	Thr	Gly	Ala	Cys	Cys	Pro	Arg	Thr	Arg	Arg	Cys	Ser	Ala	Thr	Arg		
				130					135				140				
Thr	Pro	Pro	Cys	Arg	Ser	Ser	Pro	Thr	Pro	Thr	Thr	Arg	Pro	Pro	Ser		
				145					150				155		160		
Arg	Pro	Thr	Ser	Pro	Pro	Pro	Trp	Ser	Arg	Trp	Ala	Pro	Ser	Ala	Cys		
				165					170					175			
Ser	Pro	Ala	Pro	Ala	Ala	Arg	Ser	Gly	Pro	Thr	Ala	Glu	Ser	Pro	Asp		
				180					185				190				
Ser	Ser	Ser	Ser	Leu	Val	Trp	Ser	Cys	Arg	Phe	Ile	Ile	Leu	Ile	Asp		
				195				200				205					
Leu	Asp	Arg	Thr	Thr	Ser	Thr	Gly	Cys	Tyr	Met	Ala	Xaa	Cys	Ala	Ile		
				210				215				220					
Val	Cys	Met	Pro	Val	Leu	Ala	Arg	Val	Trp	Val	Ser	Leu	Cys	Lys	Phe		
				225				230				235			240		
Ser	Leu	Ser	Pro	Pro	Ile	Asp											
				245													

(2) INFORMATION FOR SEQ ID NO:3017:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 205 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..205

(D) OTHER INFORMATION: / Ceres Seq. ID 1575183

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3017:

Val	Arg	Ile	Xaa	Xaa	Arg	Glu	Arg	Val	Pro	Xaa	Ala	Gly	Xaa	Ala	Ala		
1				5					10				15				
Gly	Arg	Val	Arg	Val	Ala	Arg	Val	Gly	His	Gln	Gln	Pro	Ala	Ala	Ala		
				20				25				30					
Asp	Gly	Gln	Arg	Arg	Ala	Xaa	Thr	Gln	Ile	Phe	Gly	Thr	Lys	Gly	Leu		
				35			40					45					
Thr	Gln	Lys	Glu	Met	Val	Ile	Leu	Ser	Gly	Ala	His	Thr	Ile	Gly	Ser		
				50			55			60							
Ser	His	Cys	Ser	Xaa	Phe	Xaa	Gly	Arg	Leu	Ser	Gly	Ser	Ala	Thr	Thr		
				65			70			75				80			
Xaa	Gly	Gly	Gln	Asp	Pro	Thr	Met	Asp	Pro	Ala	Tyr	Xaa	Ala	Xaa	Xaa		
				85				90					95				
Xaa	Xaa	Ala	Val	Pro	Ala	Gly	Xaa	Xaa	Pro	Ala	Arg	Ala	His	Gly	Leu		
				100				105					110				
Arg	Leu	Pro	Gln	Arg	Leu	Arg	Arg	Gly	Leu	Leu	Gln	Gly	Arg	His	Gly		
				115			120					125					
Gln	Pro	Gly	Pro	Ala	Val	Leu	Gly	Pro	Gly	Ala	Ala	Gln	Arg	Gln	Glu		
				130			135					140					
His	Arg	Arg	Ala	Gly	Arg	His	Leu	Arg	Gln	Arg	Pro	Gly	His	Leu	Pro		
				145			150				155				160		
Gly	Arg	Leu	Arg	Arg	Arg	His	Gly	Gln	Asp	Gly	Leu	Arg	Arg	Arg	Ala		
				165				170						175			
His	Arg	His	Gln	Arg	Gln	Gly	Gln	Gly	Gln	Leu	Gln	Ser	Arg	Leu	Ile		
				180				185						190			
His	Arg	His	His	Ser	Cys	Gly	Val	Val	Asp	Ser	Leu	Tyr					
				195			200					205					

(2) INFORMATION FOR SEQ ID NO:3018:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 153 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..153
- (D) OTHER INFORMATION: / Ceres Seq. ID 1575184

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3018:

Met Val Ile Leu Ser Gly Ala His Thr Ile Gly Ser Ser His Cys Ser
1 5 10 15
Xaa Phe Xaa Gly Arg Leu Ser Gly Ser Ala Thr Thr Xaa Gly Gly Gln
20 25 30
Asp Pro Thr Met Asp Pro Ala Tyr Xaa Ala Xaa Xaa Xaa Ala Val
35 40 45
Pro Ala Gly Xaa Xaa Pro Ala Arg Ala His Gly Leu Arg Leu Pro Gln
50 55 60
Arg Leu Arg Arg Gly Leu Leu Gln Gly Arg His Gly Gln Pro Gly Pro
65 70 75 80
Ala Val Leu Gly Pro Gly Ala Ala Gln Arg Gln Glu His Arg Arg Ala
85 90 95
Gly Arg His Leu Arg Gln Arg Pro Gly His Leu Pro Gly Arg Leu Arg
100 105 110
Arg Arg His Gly Gln Asp Gly Leu Arg Arg Arg Ala His Arg His Gln
115 120 125
Arg Gln Gly Gln Gly Gln Leu Gln Ser Arg Leu Ile His Arg His His
130 135 140
Ser Cys Gly Val Val Asp Ser Leu Tyr
145 150

(2) INFORMATION FOR SEQ ID NO:3019:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 424 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..424
- (D) OTHER INFORMATION: / Ceres Seq. ID 1575191

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3019:

atcacatttcg actctcaacy cccaaggctc cttttttttt ctgcgatctgg aagcncgcga 60
gtagcagcca tggacgtgag cggagcaggc ggtaaggcga agaaggcgcg ggcggggcgcg 120
aaggccggcg ggcgcagcaa gaagctgggtg tcgcggtcct ccaggcgccg gccccgctcg 180
tctctggtc ccagccgagc caccatctcc gccaaattaa gcccatgttg catggtatgt 240
cttggtagac atgcatgaag tagtagagag caacggtcaa cttactcctt atattcccat 300
aataataaaa tacttagagg tacttacttc aaaaaaagaa ggatctcatg actgtaacgg 360
aagtacatt ttctcttgag ttggggtgta acataaaccc agcaccaaaag ctatttgcga 420
tctc

(2) INFORMATION FOR SEQ ID NO:3020:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 85 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..85

(D) OTHER INFORMATION: / Ceres Seq. ID 1575192

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3020:

Ile	His	Phe	Asp	Ser	Gln	Xaa	Pro	Arg	Ser	Leu	Phe	Phe	Ser	Arg	Ser
1			5				10						15		
Gly	Ser	Xaa	Ala	Val	Ala	Ala	Met	Asp	Val	Ser	Gly	Ala	Gly	Gly	Lys
			20				25					30			
Ala	Lys	Lys	Gly	Ala	Ala	Gly	Arg	Lys	Ala	Gly	Gly	Pro	Thr	Lys	Lys
			35				40					45			
Ser	Val	Ser	Arg	Ser	Ser	Arg	Ala	Gly	Pro	Ala	Cys	Ser	Trp	Ser	Gln
			50				55				60				
Pro	Asp	Ala	Thr	Ile	Ser	Ala	Lys	Leu	Ser	Pro	Cys	Cys	Met	Asp	Ala
					70					75				80	
Leu	Gly	Thr	His	Ala											

(2) INFORMATION FOR SEQ ID NO:3021:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 62 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..62

(D) OTHER INFORMATION: / Ceres Seq. ID 1575193

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3021:

Met	Asp	Val	Ser	Gly	Ala	Gly	Gly	Lys	Ala	Lys	Lys	Gly	Ala	Ala	Gly
1			5				10						15		
Arg	Lys	Ala	Gly	Gly	Pro	Thr	Lys	Lys	Ser	Val	Ser	Arg	Ser	Ser	Arg
			20				25					30			
Ala	Gly	Pro	Ala	Cys	Ser	Trp	Ser	Gln	Pro	Asp	Ala	Thr	Ile	Ser	Ala
			35				40					45			
Lys	Leu	Ser	Pro	Cys	Cys	Met	Asp	Ala	Leu	Gly	Thr	His	Ala		
			50				55				60				

(2) INFORMATION FOR SEQ ID NO:3022:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 47 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..47

(D) OTHER INFORMATION: / Ceres Seq. ID 1575194

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3022:

Met	Leu	Leu	Val	His	Met	His	Glu	Val	Val	Glu	Ser	Asn	Gly	Gln	Leu
1			5				10						15		
Thr	Pro	Tyr	Ile	Pro	Ile	Ile	Lys	Tyr	Leu	Gly	Val	Leu	Thr	Ser	
			20				25				30				
Lys	Lys	Glu	Gly	Ser	His	Asp	Cys	Asn	Arg	Ser	Asp	Ile	Phe	Ser	
			35				40				45				

(2) INFORMATION FOR SEQ ID NO:3023:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 631 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..631

(D) OTHER INFORMATION: / Ceres Seq. ID 1575195

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3023:

tgcttaagggt	tcttgacaag	gagaaacgcc	aggcacattg	tgctgatgtt	ggatctcact	60
tgttggagcgg	tctaaaatcg	cttcaggaca	agcacgaaat	tataggtgat	gttagaggaa	120
ggggactgat	gcttgggggtg	gaactcggtta	cggacagaaa	ggagaagacc	cctgccaagt	180
cagaaacat	tgaactgttt	gagaagctca	gagatctcgg	ggtactagtt	ggaaaggcgg	240
gtctgcattg	taacgtcttc	agaataaaaac	caccgatgtg	cttttcgaag	gacgatgcag	300
actctctgtg	ggactccatg	gactacgcaa	tgtaaggctt	ctgaaggaaac	atgctctgag	360
ttgacaattgt	gtctgcgtgg	aaacaacact	tcctgcaccc	gcaagatgca	tgccctgaaa	420
tgaactgaa	agpgagatga	tttaatgggc	atgctccccc	ggtggtatgt	tggtgttatg	480
gtgaagtgtta	atagtccccc	tccccggaat	aaattgatga	aaggggacag	aacgtcttgc	540
ccaggtctgtg	aactgtttgt	agaagaactg	cagttaataa	atagaatagc	gagcaagcaa	600

gcgtgatc aatctgcata cgtcCatttt c

(2) INFORMATION FOR SEQ ID NO:3024:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 113 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..113

(D) OTHER INFORMATION: / Ceres Seq. ID 1575196

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3024:

Leu	Lys	Val	Leu	Asp	Lys	Glu	Lys	Arg	Gln	Ala	His	Cys	Ala	Asp	Val	
1		5						10						15		
Gly	Ser	His	Leu	Leu	Glu	Arg	Leu	Lys	Ser	Leu	Gln	Asp	Lys	His	Glu	
		20					25					30				
Ile	Ile	Gly	Asp	Val	Arg	Gly	Arg	Gly	Leu	Met	Leu	Gly	Val	Glu	Leu	
		35					40					45				
Val	Thr	Asp	Arg	Lys	Glu	Lys	Thr	Pro	Ala	Lys	Ser	Glu	Thr	Ile	Glu	
		50				55					60					
Leu	Phe	Glu	Lys	Leu	Arg	Asp	Leu	Gly	Val	Leu	Val	Gly	Lys	Gly	Gly	
		65				70					75			80		
Leu	His	Gly	Asn	Val	Phe	Arg	Ile	Lys	Pro	Pro	Met	Cys	Phe	Ser	Lys	
			85						90			95				
Asp	Asp	Ala	Asp	Phe	Leu	Val	Asp	Ser	Met	Asp	Tyr	Ala	Met	Ser	Arg	
			100					105				110				
Leu																

(2) INFORMATION FOR SEQ ID NO:3025:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 71 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..71

(D) OTHER INFORMATION: / Ceres Seq. ID 1575197

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3025:

Met	Leu	Gly	Val	Glu	Leu	Val	Thr	Asp	Arg	Lys	Glu	Lys	Thr	Pro	Ala	
1		5						10					15			
Lys	Ser	Glu	Thr	Ile	Glu	Leu	Phe	Glu	Lys	Leu	Arg	Asp	Leu	Gly	Val	
		20					25					30				
Leu	Val	Gly	Lys	Gly	Gly	Leu	His	Gly	Asn	Val	Phe	Arg	Ile	Lys	Pro	
		35				40					45					
Pro	Met	Cys	Phe	Ser	Lys	Asp	Asp	Ala	Asp	Phe	Leu	Val	Asp	Ser	Met	

50
Asp Tyr Ala Met Ser Arg Leu
65 70

60

(2) INFORMATION FOR SEQ ID NO:3026:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 595 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..595

(D) OTHER INFORMATION: / Ceres Seq. ID 1575202

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3026:

atatatttgc	ccatttgg	ggttttcgtg	aagttcgtct	tgtaacaag	gagtcacagac	60
atcctgggtg	agatccacat	gtgttggtgt	tcgtcgattt	tgacaaccct	gctcaggcta	120
caattgctct	ggaagcatta	caaggttata	agtttgacga	acacgagcgt	gattcagccc	180
atttgcgtct	gcaattctca	cgctttcccg	gtccaaggtc	agctgggtgg	cctcgcggtta	240
ggcgtaaaga	cgtgcgggacc	tcgtggttgc	cgaacctatc	gtttatacga	gcgatccaac	300
tacgggGggc	taacgcttcg	atatgcgctg	aatttcgggg	cggtggtgtt	ttagggttcg	360
tcagctcatt	tcgtgaatgc	gtgaaaggga	caatgcaata	agtgatattc	tgccatatgt	420
tattagatgc	cgtataatgt	gttaggcgat	gaaagtattt	cgacatactg	tatctgctgc	480
cttagctatt	gtggtctact	gtaacttcat	taccttgctt	cacatccgag	acaatttgag	540
tttgttatca	tgtggattat	ctgttttgaa	aatgaaact	agatgatgtt	agcct	

(2) INFORMATION FOR SEQ ID NO:3027:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..117

(D) OTHER INFORMATION: / Ceres Seq. ID 1575203

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3027:

Ile	Tyr	Phe	Ala	His	Leu	Leu	Val	Phe	Val	Lys	Phe	Val	Leu	Ser	Thr
1	5						10						15		
Arg	Ser	Pro	Asp	Ile	Leu	Val	Glu	Ile	His	Met	Cys	Cys	Val	Ser	Ser
	20						25						30		
Ile	Leu	Thr	Thr	Leu	Leu	Arg	Leu	Gln	Leu	Leu	Trp	Lys	His	Tyr	Lys
	35						40						45		
Val	Ile	Ser	Leu	Thr	Asn	Thr	Ser	Val	Ile	Gln	Pro	Ile	Cys	Val	Cys
	50						55						60		
Asn	Ser	His	Ala	Phe	Pro	Val	Gln	Gly	Gln	Leu	Val	Gly	Leu	Ala	Val
65							70						75		
Gly	Val	Lys	Thr	Cys	Gly	Pro	Arg	Gly	Cys	Arg	Thr	Tyr	Arg	Leu	Tyr
							85						90		
Glu	Arg	Ser	Asn	Tyr	Gly	Gly	Leu	Thr	Leu	Arg	Tyr	Ala	Leu	Asn	Phe
							100						105		
Gly	Ala	Val	Ala	Phe									110		
															115

(2) INFORMATION FOR SEQ ID NO:3028:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 81 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..81
(D) OTHER INFORMATION: / Ceres Seq. ID 1575204

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3028:

Ile	Phe	Arg	Pro	Phe	Val	Gly	Phe	Arg	Glu	Val	Arg	Leu	Val	Asn	Lys
1			5					10					15		
Glu	Ser	Arg	His	Pro	Gly	Gly	Asp	Pro	His	Val	Leu	Cys	Phe	Val	Asp
			20				25					30			
Phe	Asp	Asn	Pro	Ala	Gln	Ala	Thr	Ile	Ala	Leu	Glu	Ala	Leu	Gln	Gly
		35					40					45			
Tyr	Lys	Phe	Asp	Glu	His	Glu	Arg	Asp	Ser	Ala	His	Leu	Arg	Leu	Gln
	50					55				60					
Phe	Ser	Arg	Phe	Pro	Gly	Pro	Arg	Ser	Ala	Gly	Pro	Arg	Gly	Arg	
				70						75				80	
Arg															

(2) INFORMATION FOR SEQ ID NO:3029:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 91 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..91

(D) OTHER INFORMATION: / Ceres Seq. ID 1575205

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3029:

Met	Cys	Cys	Val	Ser	Ser	Ile	Leu	Thr	Thr	Leu	Leu	Arg	Leu	Gln	Leu
1			5					10					15		
Leu	Trp	Lys	His	Tyr	Lys	Val	Ile	Ser	Leu	Thr	Asn	Thr	Ser	Val	Ile
			20					25					30		
Gln	Pro	Ile	Cys	Val	Cys	Asn	Ser	His	Ala	Phe	Pro	Val	Gln	Gly	Gln
		35					40					45			
Leu	Val	Gly	Leu	Ala	Val	Gly	Val	Lys	Thr	Cys	Gly	Pro	Arg	Gly	Cys
		50				55				60					
Arg	Thr	Tyr	Arg	Leu	Tyr	Glu	Arg	Ser	Asn	Tyr	Gly	Gly	Leu	Thr	Leu
				70						75				80	
Arg	Tyr	Ala	Leu	Asn	Phe	Gly	Ala	Val	Ala	Phe					
				85					90						

(2) INFORMATION FOR SEQ ID NO:3030:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 688 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..688

(D) OTHER INFORMATION: / Ceres Seq. ID 1575210

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3030:

gaaccgcatcc	ggttttaaaag	atccgctact	agtgtcacccg	gcaacgtgtc	gacgcggtcg	60
tgctcgtgtgt	gttctctggtg	aggaagcgaa	ccctgcctgc	ctgcttgctt	gccgggcaag	120
aagtgaagac	agcgtgghgg	tgccgaagcgc	accggaccga	ggatggctac	aagaaggaac	180
gtrgcgcgcga	gcgttactgc	ccaccagcct	gcgtrggcgg	ccgtggcgag	gagatggag	240
ggcgtgtgcgc	gctacttcaag	cgacaaggcc	tccggcaggg	tgctcagcga	rgaggagcgc	300
gcgcgcgcaga	acgtctacat	acagaagatg	gawcaggaba	agctggagaa	actnawgang	360
aaggadgaca	agggccaagcc	cgadgcggcc	aagadggccc	cgccgcgcgc	agrvgsacac	420
gaagaatggt	gaggaggctc	atccgagctg	atcatgcgca	aaatcggaac	agtgctccgc	480
tgaatcggtg	gatgctgtac	tactgatgac	acgtagatgc	aaatagacgc	cgctgctacta	540

ctctgctttg caactctgct cgtcgtgtcg tgtgtgatcc catccctgtc actgtttgta 600
acttcgcttg tagctagcga cggttttgcc ttgtcccttg tcggtgcaaa tgtaattggag 660
tggaggcgtc cttagacgtc ttcatgt

(2) INFORMATION FOR SEQ ID NO:3031:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 149 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..149

(D) OTHER INFORMATION: / Ceres Seq. ID 1575211

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3031:

Asn Arg Ser Gly Leu Lys Asp Pro Leu Leu Val Ser Pro Ala Thr Cys
1 5 10 15
Arg Arg Gly Arg Val Val Cys Val Pro Gly Glu Glu Ala Asn Pro Ala
20 25 30
Cys Leu Leu Ala Cys Arg Ala Arg Ser Glu Asn Ser Val Xaa Val Arg
35 40 45
Lys Arg Pro Asp Arg Gly Trp Leu Gln Glu Gly Pro Xaa Arg Arg Ala
50 55 60
Leu Leu Pro Thr Ser Leu Arg Xaa Arg Pro Trp Arg Gly Gly Trp Arg
65 70 75 80
Ala Cys Arg Ala Thr Ser Ala Thr Arg Pro Pro Ala Gly Cys Ser Ala
85 90 95
Xaa Arg Ser Ala Pro Pro Arg Thr Ser Thr Tyr Arg Arg Trp Xaa Arg
100 105 110
Xaa Ser Trp Arg Asn Xaa Xaa Xaa Arg Xaa Thr Arg Pro Arg Pro Xaa
115 120 125
Arg Pro Arg Xaa Pro Arg Arg Arg Gln Xaa Xaa Thr Lys Asn Gly Glu
130 135 140
Glu Ala His Pro Ser
145

(2) INFORMATION FOR SEQ ID NO:3032:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 89 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..89

(D) OTHER INFORMATION: / Ceres Seq. ID 1575212

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3032:

Met Ala Thr Arg Arg Thr Xaa Ala Ala Ser Val Thr Ala His Gln Pro
1 5 10 15
Ala Xaa Ala Ala Val Ala Arg Arg Met Glu Gly Val Ser Arg Tyr Phe
20 25 30
Ser Asp Lys Ala Ser Gly Arg Val Leu Ser Xaa Glu Glu Arg Ala Ala
35 40 45
Glu Asn Val Tyr Ile Gln Lys Met Xaa Gln Xaa Lys Leu Glu Lys Xaa
50 55 60
Xaa Xaa Lys Xaa Asp Lys Ala Lys Ala Xaa Ala Ala Lys Xaa Ala Ala
65 70 75 80
Pro Pro Pro Xaa Xaa His Glu Glu Trp
85

(2) INFORMATION FOR SEQ ID NO:3033:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 555 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..555
(D) OTHER INFORMATION: / Ceres Seq. ID 1575217
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3033:
aaccacactgc agaggaccgc cgctgcgcgc tatcattcgt ttctggagac ccttctagcc 60
ccgcgcgcac cacaccacca ccaccaatgg caggactcgg atcaaggcc ctcgcgcgtg 120
tcgcgcgtct ggccgcgcgc gtccctctcag tgkctccgc gcccgaggcg cccgcgcgca 180
gcccgctctN ccgCgcgcgc cgcgcgcgcgc cgckcttcgc cgcggccctc gtgcgcctct 240
ccgcgcgcctt cctctctgcgc gccgtccgcgc actgagccga tggggccctt ccaccgcgcg 300
cgccgcgcgc tagactctatt tattggagtg gtattcagta gtactggtag tagggagatt 360
ttctcggttg tgctgtgtgc tcgtgcgcatt ttggtcggat ctggtgtcct tgggtgggtg 420
agggtttgta ccgcgtcgtg gtgtcgggtg tgtgactga ttctgatccc ctgttagata 480
ctctgctatc tcgcgcgtgat cgtgagtgat gattcgcgtc gttgtgctact gatacatat 540
tgttccttat tgggt

(2) INFORMATION FOR SEQ ID NO:3034:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 158 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..158
(D) OTHER INFORMATION: / Ceres Seq. ID 1575218
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3034:
Asn His Leu Gln Arg Thr Arg Ala Arg Arg Tyr His Ser Phe Leu Glu
1 5 10 15
Thr Leu Leu Ala Pro Pro Pro Pro His His His His Gln Trp Gln Asp
20 25 30
Ser Asp Gln Arg Pro Ser Pro Trp Ser Pro Ser Trp Arg Pro Ser Ser
35 40 45
Ser Gln Xaa Pro Pro Arg Pro Arg Arg Pro Arg Pro Ala Pro Ser Xaa
50 55 60
Ala Ala Ala Xaa Arg Arg Arg Xaa Ser Pro Arg Pro Ser Ser Pro Pro
65 70 75 80
Pro Pro Pro Ser Ser Ser Pro Pro Ser Ala Thr Glu Pro Met Gly Pro
85 90 95
Phe His Arg Arg Arg Arg Leu Asp Leu Phe Ile Gly Val Val Phe
100 105 110
Ser Ser Thr Gly Thr Arg Glu Ile Ser Ser Leu Val Ser Cys Arg Arg
115 120 125
Arg Ile Leu Val Gly Ser Gly Val Leu Gly Gly Trp Arg Val Cys Thr
130 135 140
Ala Ser Trp Cys Arg Leu Cys Asp Leu Ile Leu Ile Pro Leu
145 150 155

(2) INFORMATION FOR SEQ ID NO:3035:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 90 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide

(B) LOCATION: 1..90

(D) OTHER INFORMATION: / Ceres Seq. ID 1575219

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3035:

```
Pro Pro Ala Glu Asp Pro Arg Ser Pro Leu Ser Phe Val Ser Gly Asp
1      5      10      15
Pro Ser Ser Pro Ala Ala Thr Thr Pro Pro Pro Met Ala Gly Leu
20      25      30
Gly Ser Lys Ala Leu Ala Val Val Ala Val Leu Ala Ala Val Val Leu
35      40      45
Ser Val Xaa Ser Ala Ala Glu Ala Pro Ala Pro Ser Pro Val Xaa Arg
50      55      60
Arg Arg Xaa Ala Ser Ala Xaa Phe Ala Ala Ala Leu Val Ala Ser Ser
65      70      75      80
Ala Ala Phe Leu Phe Ala Ala Val Arg His
85      90
```

(2) INFORMATION FOR SEQ ID NO:3036:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 614 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..614

(D) OTHER INFORMATION: / Ceres Seq. ID 1575232

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3036:

```
accacacac atcacaccca gctgccattg ccctctactg acctgtgacc tccgcatttc      60
caaacagccc gagcgagcga gctagcagag cggNcggcag gcacctccct cctcaaggaa      120
catggcccgc accgagcagt tggcagtagt ggcggcggcc gtgtggccct tgggtgcgcg      180
ggcgctcagc gccccaacgc cggtaacgcc gccagcatcc cctccaagtg cggcgctcagc      240
atcccctaca ccatcagcac ctcccacgcac tgctccaggg tgaactgaac cctaaacgcac      300
gacgacggcg ccggcgccgc cctgaagacg atccatctct atcccgcgtg cgtcgcgctg      360
gcggtttcga cgtcatgac catatctacc taoccatgat cagcacttgc atgtctacta      420
ctactactga ataaaaaac tctccgcgca cgtctctctt gtgtctgtgt gtgtgagaga      480
gagaggagag ccggccatgt ccttttggct gtttggttta tttttgagtt catcggtct      540
ttattttatt ccatgtacc agtaccacac ttgtaccatg catgttcctt atgataacac      600
cacccttttt ttgt
```

(2) INFORMATION FOR SEQ ID NO:3037:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 53 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..53

(D) OTHER INFORMATION: / Ceres Seq. ID 1575233

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3037:

```
Met Ala Arg Thr Gln Gln Leu Ala Val Val Ala Ala Val Val Ala
1      5      10      15
Leu Val Pro Pro Ala Ser Ala Ala Ser Thr Pro Val Thr Pro Pro Ala
20      25      30
Ser Pro Pro Ser Ala Ala Ser Ala Ser Pro Thr Pro Ser Ala Pro Pro
35      40      45
Pro Thr Ala Pro Gly
50
```

(2) INFORMATION FOR SEQ ID NO:3038:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 39 amino acids

(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..39
 (D) OTHER INFORMATION: / Ceres Seq. ID 1575234
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3038:
Met Ser Phe Trp Leu Phe Gly Leu Phe Leu Ser Ser Cys Gly Leu Tyr
1 5 10 15
Leu Phe Pro Cys Thr Gln Tyr Pro Pro Cys Thr Met His Val Pro Tyr
 20 25 30
Asp Thr Leu Thr Ser Phe Cys
 35
(2) INFORMATION FOR SEQ ID NO:3039:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 615 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
 (A) NAME/KEY: -
 (B) LOCATION: 1..615
 (D) OTHER INFORMATION: / Ceres Seq. ID 1575235
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3039:
gcaaacccgcg tctcgcgcga agaatacgcga ttcccccctc ccgcacccca acccccgtcg 60
gagagagaga tggcatcggg ggGcggagat gcagcccccctc gcgcgcggcg ggtaccgcbg 120
cgcgccggag atgaaggaga aggtggaggc gtcggtggtg gacctggagg ccggcacccg 180
ggagacgctg taccgcggga tctcgcgcgg ggagagcgcc ctccgatggg gcttcgtccg 240
caaggtctac ggcattctcg tgcgcagctg ctctcacc caagccgtctc cgccctcacc 300
gttctccacc ccaccctcaa cgccacgctc tccgactccc cgggctctgc gctcgtgctc 360
gcccctctgc ccttcattct gatgatccca ttgtatcatt atcagcacaa gaaccacac 420
aatttgcttt tctctgggtc gtccacggtg tgcttgagct tcagcatcgg tgtggtgtg 480
gctaacaccc aagggaataa cgttctggag gctttagtgc tcacggctgg cgtggtgggt 540
tctctgagcg gtatgccttc tgggcgtcaa agaagggcaa ggaattggg tacctggggc 600
ctatcctgtc ttccg
(2) INFORMATION FOR SEQ ID NO:3040:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 205 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..205
 (D) OTHER INFORMATION: / Ceres Seq. ID 1575236
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3040:
Ala Asn Arg Val Ser Arg Glu Glu Ser Ala Phe Pro Leu Pro Arg Thr
1 5 10 15
Gln Pro Pro Ser Glu Arg Glu Met Ala Ser Val Gly Gly Asp Ala Ala
 20 25 30
Pro Arg Ala Gly Gly Val Pro Xaa Arg Ala Gly Asp Glu Gly Glu Gly
 35 40 45
Gly Gly Val Gly Gly Gly Pro Gly Gly Arg His Arg Gly Asp Ala Val
 50 55 60
Pro Gly Asp Leu Ala Arg Gly Glu Arg Pro Pro Met Gly Leu Arg Pro
65 70 75 80
Gln Gly Leu Arg His Pro Arg Ala Gln Leu Leu Thr Thr Ala Val

85 90 95
Ser Ala Leu Thr Val Leu His Pro Thr Leu Asn Ala Thr Leu Ser Asp
100 105 110
Ser Pro Gly Leu Ala Leu Val Leu Ala Val Leu Pro Phe Ile Leu Met
115 120 125
Ile Pro Leu Tyr His Tyr Gln His Lys His Pro His Asn Phe Val Phe
130 135 140
Leu Gly Leu Phe Thr Leu Cys Leu Ser Phe Ser Ile Gly Val Ala Cys
145 150 155 160
Ala Asn Thr Gln Gly Lys Ile Val Leu Glu Ala Leu Val Leu Thr Ala
165 170 175
Gly Val Val Val Ser Leu Xaa Arg Met Pro Ser Gly Arg Gln Arg Arg
180 185 190
Ala Arg Asn Ser Gly Thr Trp Gly Leu Ser Cys Leu Pro
195 200 205

(2) INFORMATION FOR SEQ ID NO:3041:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 182 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..182
- (D) OTHER INFORMATION: / Ceres Seq. ID 1575237

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3041:

Met Ala Ser Val Gly Gly Asp Ala Ala Pro Arg Ala Gly Gly Val Pro
1 5 10 15
Xaa Arg Ala Gly Asp Glu Gly Glu Gly Gly Val Gly Gly Pro
20 25 30
Gly Gly Arg His Arg Gly Asp Ala Val Pro Gly Asp Leu Ala Arg Gly
35 40 45
Glu Arg Pro Pro Met Gly Leu Arg Pro Gln Gly Leu Arg His Pro Arg
50 55 60
Ala Gln Leu Leu Leu Thr Thr Ala Val Ser Ala Leu Thr Val Leu His
65 70 75 80
Pro Thr Leu Asn Ala Thr Leu Ser Asp Ser Pro Gly Leu Ala Leu Val
85 90 95
Leu Ala Val Leu Pro Phe Ile Leu Met Ile Pro Leu Tyr His Tyr Gln
100 105 110
His Lys His Pro His Asn Phe Val Phe Leu Gly Leu Phe Thr Leu Cys
115 120 125
Leu Ser Phe Ser Ile Gly Val Ala Cys Ala Asn Thr Gln Gly Lys Ile
130 135 140
Val Leu Glu Ala Leu Val Leu Thr Ala Gly Val Val Val Ser Leu Xaa
145 150 155 160
Arg Met Pro Ser Gly Arg Gln Arg Arg Ala Arg Asn Ser Gly Thr Trp
165 170 175
Gly Leu Ser Cys Leu Pro
180

(2) INFORMATION FOR SEQ ID NO:3042:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 130 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..130

(D) OTHER INFORMATION: / Ceres Seq. ID 1575238

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3042:

Met Gly Leu Arg Pro Gln Gly Leu Arg His Pro Arg Ala Gln Leu Leu
1 5 10 15
Leu Thr Thr Ala Val Ser Ala Leu Thr Val Leu His Pro Thr Leu Asn
20 25 30
Ala Thr Leu Ser Asp Ser Pro Gly Leu Ala Leu Val Leu Ala Val Leu
35 40 45
Pro Phe Ile Leu Met Ile Pro Leu Tyr His Tyr Gln His Lys His Pro
50 55 60
His Asn Phe Val Phe Leu Gly Leu Phe Thr Leu Cys Leu Ser Phe Ser
65 70 75 80
Ile Gly Val Ala Cys Ala Asn Thr Gln Gly Lys Ile Val Leu Glu Ala
85 90 95
Leu Val Leu Thr Ala Gly Val Val Val Ser Leu Xaa Arg Met Pro Ser
100 105 110
Gly Arg Gln Arg Arg Ala Arg Asn Ser Gly Thr Trp Gly Leu Ser Cys
115 120 125
Leu Pro
130

(2) INFORMATION FOR SEQ ID NO:3043:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 519 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..519

(D) OTHER INFORMATION: / Ceres Seq. ID 1575243

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3043:

cagascagaa ascagccgca gccccagccc ccacaagacg aggcacaacat ggcgctagaa 60
gcagccacccg ccccccgcgc actctctcgcc gcgtgcctcg tctctgtggt cctcgggcggc 120
ggcaccggccc cgtcgtcggt gCtgcgcggc gccggggggc agcccgccgag gggagccgga 180
tccaggatac gtcattgtatc cggcatgggg ccccgccctc cactaatcgt cgtcgttcga 240
ggcgacgac gacgCtccgc cgccaacgac ggogagtgcc acatgcctat gctctcgtgt 300
gggcccogta cgttatttag cgctactagt actagggaaa gtgtacgtgt gatgtgtgtc 360
actcagtgct gattgatcaa tgatgctcat ttctgagcag acccaggaat gctgagtcca 420
gagagcagag cgtNtgttct acaagtgcac cgaggaataa agtgacaga aatgttgctg 480
ggttcacgtg cctctcgtgt aataaaatgg acatcttcg

(2) INFORMATION FOR SEQ ID NO:3044:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 165 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..165

(D) OTHER INFORMATION: / Ceres Seq. ID 1575244

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3044:

Gln Xaa Arg Xaa Gln Pro Gln Pro Gln Pro Gln Asp Glu Ala Thr
1 5 10 15
Met Ala Leu Glu Ala Ala Thr Ala Pro Arg Ala Leu Leu Ala Cys
20 25 30
Leu Val Leu Val Leu Gly Gly Thr Gly Pro Ser Ser Val Leu
35 40 45
Arg Gly Ala Gly Ala Gln Ala Gly Arg Gly Ala Gly Ser Arg Ile Arg
50 55 60

His Val Ser Gly Met Gly Pro Arg Arg Pro Leu Ile Val Val Val Arg
65 70 75 80
Gly Arg Arg Arg Arg Ser Ala Ala Asn Asp Gly Glu Cys His Met Pro
85 90 95
Met Leu Ser Cys Gly Pro Arg Thr Leu Leu Ser Ala Thr Ser Thr Arg
100 105 110
Glu Ser Val Arg Val Met Cys Val Thr Gln Cys Arg Leu Ile Asn Asp
115 120 125
Ala His Phe Arg Ala Asp Pro Gly Met Leu Ser Ala Glu Ser Arg Ala
130 135 140
Xaa Val Leu Gln Val His Arg Gly Ile Lys Trp Thr Glu Met Leu Ala
145 150 155 160
Gly Ser Arg Ala Phe
165

(2) INFORMATION FOR SEQ ID NO:3045:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 108 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..108
- (D) OTHER INFORMATION: / Ceres Seq. ID 1575245

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3045:

Xaa Gln Lys Xaa Ala Ala Ala Pro Ala Pro Thr Arg Arg Gly Asn Asn
1 5 10 15
Gly Ala Arg Ser Ser His Arg Pro Pro Arg Thr Pro Arg Arg Val Pro
20 25 30
Arg Pro Ala Gly Pro Arg Arg Arg His Arg Pro Val Val Gly Ala Ala
35 40 45
Arg Arg Arg Gly Ala Gly Arg Gln Gly Ser Arg Ile Gln Asp Thr Ser
50 55 60
Cys Ile Arg His Gly Ala Pro Pro Ser Thr Asn Arg Arg Arg Ser Arg
65 70 75 80
Ala Thr Thr Thr Leu Arg Arg Gln Arg Arg Arg Val Pro His Ala Tyr
85 90 95
Ala Leu Val Trp Ala Pro Tyr Val Ile Glu Arg Tyr
100 105

(2) INFORMATION FOR SEQ ID NO:3046:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 149 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..149
- (D) OTHER INFORMATION: / Ceres Seq. ID 1575246

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3046:

Met Ala Leu Glu Ala Ala Thr Ala Pro Arg Ala Leu Leu Ala Ala Cys
1 5 10 15
Leu Val Leu Leu Val Leu Gly Gly Gly Thr Gly Pro Ser Ser Val Leu
20 25 30
Arg Gly Ala Gly Ala Gln Ala Gly Arg Gly Ala Gly Ser Arg Ile Arg
35 40 45
His Val Ser Gly Met Gly Pro Arg Arg Pro Leu Ile Val Val Val Arg
50 55 60
Gly Arg Arg Arg Arg Ser Ala Ala Asn Asp Gly Glu Cys His Met Pro

(2) INFORMATION FOR SEO ID NO:3047:

(A) LENGTH: 945 base pairs

- (A) LENGTH: 945 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..945
(D) OTHER INFORMATION: / Ceres Seq. ID 1575336

ataaaccttt	tcaatgctc	agccgcgcgc	gcgcgcgctt	cttgctcttc	ctcgacgcgc	60
gcgcgcctt	tcttcgcgt	atccgcctgc	tccgcctctt	cgccacgcgc	gcggcggcgc	120
tacgctcgc	gatttcacgc	agccggtcas	gcgttcccc	cccgctcttc	ccagatggc	180
tcgcgcctc	gcctccggtc	ctccgcacac	cgccggcgta	ccctgcatcc	accatgaact	240
ctgtcagac	tgagttgtg	accccgctga	ggagggtcat	ggacacgcaa	aggatttcaa	300
ccgctttctg	cagacaaatc	cgagtttgc	gctctactgt	ttttctcttc	gacctcgatc	360
acaaggggtg	catggaatat	gagatgaAac	ctcaaaattc	aaagagggag	ttacgacggc	420
aaggtgttag	ttccaaatag	gctctgggaat	tcctgtgtgt	gccacggcgc	atactctgtg	480
cgaaagttgt	acaagtccct	gtcgaaaaaa	ttttaaggaa	ttgactatca	gtaacctgtt	540
ttactgttg	aactggtggc	atgtttgacc	agagggtaat	tgggcctaa	gatttgccaa	600
agccacgct	gtggcacgcg	atagctgtcc	ataatgacta	cttaagtgct	tatgtgtctc	660
acaagctgtg	gaagaaatcg	cacagacagt	tcaacatcaa	gaatgacttc	acctcgagg	720
agaaggaagc	gatccgagag	gagaaaccagt	gggccttcgt	gtaaggagtg	ctggtgatca	780
ttgatgccta	agtttctgtg	gtgtactact	tatgtctact	tattgtgttc	ctaaagtcta	840
taagtatttt	gggagtcact	ttgtctgcga	atgtctgcgc	taagaaattat	gtgtgcaatg	900
ctcgtattt	aactttattc	catgaagaac	vtcatctctc	acccc		

(2) INFORMATION FOR SEQ ID NO:3048:

(A) LENGTH: 253 amino acids

- (B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

```
{ix} FEATURE:
```

- (A) NAME/KEY: peptide
(B) LOCATION: 1..253
(D) OTHER INFORMATION: / Ceres Seq. ID 1575337

1	Lys	Pro	Phe	His	Cys	Ser	Ser	Arg	Arg	Arg	Arg	Phe	Phe	Val	Phe
				5					10					15	
Leu	Ala	Ala	Pro	Pro	Leu	His	Leu	Pro	Leu	Ile	Arg	Ser	Leu	Pro	Pro
			20					25					30		
Leu	Ala	Thr	Gln	Ala	Ala	Ala	Leu	Arg	Pro	Val	Ile	Ser	Ala	Thr	Ala
		35					40					45			
Ser	Xaa	Leu	Pro	Leu	Pro	Ser	Leu	Pro	Ser	Arg	Leu	Ala	Pro	Ser	Pro
	50					55					60				
Pro	Val	Leu	Arg	Thr	Pro	Ala	Gly	Asp	Pro	Ala	Ser	Thr	Met	Thr	Gly
65				70					75						80

Val	Ser	Thr	Gly	Leu	Leu	Thr	Gly	Leu	Arg	Arg	Val	Met	Glu	Gln	Gln	
				85					90					95		
Arg	Ile	Ser	Thr	Ala	Phe	Cys	Arg	Gln	Ser	Arg	Val	Ser	Ser	Ser	Thr	
				100				105					110			
Val	Ser	Phe	Ser	Asp	Leu	Asp	Glu	Lys	Gly	Asp	Met	Glu	Tyr	Asp	Asp	
				115				120				125				
Asn	Ser	Pro	Asn	Ser	Lys	Arg	Glu	Leu	Arg	Pro	Gln	Gly	Val	Asp	Pro	
				130			135				140					
Asn	Lys	Gly	Trp	Glu	Phe	Arg	Gly	Val	His	Arg	Ala	Ile	Ile	Cys	Gly	
				145			150			155				160		
Lys	Val	Gly	Gln	Val	Pro	Val	Gln	Lys	Ile	Leu	Arg	Asn	Gly	His	Thr	
				165				170						175		
Val	Thr	Val	Phe	Thr	Val	Gly	Thr	Gly	Gly	Met	Phe	Asp	Gln	Arg	Val	
				180				185					190			
Ile	Gly	Pro	Lys	Asp	Leu	Pro	Lys	Pro	Ala	Gln	Trp	His	Arg	Ile	Ala	
				195			200				205					
Val	His	Asn	Asp	Tyr	Leu	Ser	Ala	Tyr	Ala	Val	Gln	Lys	Leu	Val	Lys	
				210			215				220					
Asn	Ser	His	Glu	Thr	Phe	Asn	Ile	Lys	Asn	Asp	Phe	Thr	Pro	Glu	Glu	
				225			230			235				240		
Glu	Glu	Glu	Ile	Arg	Arg	Glu	Asn	Gln	Trp	Ala	Phe	Glu				
				245				250								

(2) INFORMATION FOR SEQ ID NO:3049:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 176 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..176

(D) OTHER INFORMATION: / Ceres Seq. ID 1575338

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3049:

Met	Thr	Gly	Val	Ser	Thr	Gly	Leu	Leu	Thr	Gly	Leu	Arg	Arg	Val	Met	
1				5					10					15		
Glu	Gln	Gln	Arg	Ile	Ser	Thr	Ala	Phe	Cys	Arg	Gln	Ser	Arg	Val	Ser	
				20				25					30			
Ser	Ser	Thr	Val	Ser	Phe	Ser	Asp	Leu	Asp	Glu	Lys	Gly	Asp	Met	Glu	
				35			40					45				
Tyr	Asp	Asp	Asn	Ser	Pro	Asn	Ser	Lys	Arg	Glu	Leu	Arg	Pro	Gln	Gly	
				50			55				60					
Val	Asp	Pro	Asn	Lys	Gly	Trp	Glu	Phe	Arg	Gly	Val	His	Arg	Ala	Ile	
				65			70			75				80		
Ile	Cys	Gly	Lys	Val	Gly	Gln	Val	Pro	Val	Gln	Lys	Ile	Leu	Arg	Asn	
				85					90				95			
Gly	His	Thr	Val	Thr	Val	Phe	Thr	Val	Gly	Thr	Gly	Gly	Met	Phe	Asp	
				100				105					110			
Gln	Arg	Val	Ile	Gly	Pro	Lys	Asp	Leu	Pro	Lys	Pro	Ala	Gln	Trp	His	
				115			120					125				
Arg	Ile	Ala	Val	His	Asn	Asp	Tyr	Leu	Ser	Ala	Tyr	Ala	Val	Gln	Lys	
				130			135				140					
Leu	Val	Lys	Asn	Ser	His	Glu	Thr	Phe	Asn	Ile	Lys	Asn	Asp	Phe	Thr	
				145			150			155				160		
Pro	Glu	Glu	Glu	Glu	Glu	Ile	Arg	Arg	Glu	Asn	Gln	Trp	Ala	Phe	Glu	
				165					170					175		

(2) INFORMATION FOR SEQ ID NO:3050:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 161 amino acids

- (B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..161
 (D) OTHER INFORMATION: / Ceres Seq. ID 1575339
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3050:

Met	Glu	Gln	Gln	Arg	Ile	Ser	Thr	Ala	Phe	Cys	Arg	Gln	Ser	Arg	Val
1			5						10					15	
Ser	Ser	Ser	Thr	Val	Ser	Phe	Ser	Asp	Leu	Asp	Glu	Lys	Gly	Asp	Met
			20					25					30		
Glu	Tyr	Asp	Asp	Asn	Ser	Pro	Asn	Ser	Lys	Arg	Glu	Leu	Arg	Pro	Gln
		35					40				45				
Gly	Val	Asp	Pro	Asn	Lys	Gly	Trp	Glu	Phe	Arg	Gly	Val	His	Arg	Ala
	50					55					60				
Ile	Ile	Cys	Gly	Lys	Val	Gly	Gln	Val	Pro	Val	Gln	Lys	Ile	Leu	Arg
65				70				75					80		
Asn	Gly	His	Thr	Val	Thr	Val	Phe	Thr	Val	Gly	Thr	Gly	Gly	Met	Phe
			85					90					95		
Asp	Gln	Arg	Val	Ile	Gly	Pro	Lys	Asp	Leu	Pro	Lys	Pro	Ala	Gln	Trp
			100				105						110		
His	Arg	Ile	Ala	Val	His	Asn	Asp	Tyr	Leu	Ser	Ala	Tyr	Ala	Val	Gln
		115				120					125				
Lys	Leu	Val	Lys	Asn	Ser	His	Glu	Thr	Phe	Asn	Ile	Lys	Asn	Asp	Phe
		130				135					140				
Thr	Pro	Glu	Glu	Glu	Glu	Glu	Ile	Arg	Arg	Glu	Asn	Gln	Trp	Ala	Phe
				150					155					160	
Glu															

(2) INFORMATION FOR SEQ ID NO:3051:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 762 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:

- (A) NAME/KEY: -
 (B) LOCATION: 1..762
 (D) OTHER INFORMATION: / Ceres Seq. ID 1575343

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3051:

acaagtcctts	agcgaaacctc	gccactcgccc	caactccgctc	ccaaaagaaga	agaagacgacg	60
gacgacagca	argtgccgcgc	gtcacgagat	ycgtccgagg	tgaccatgtc	taccgcctaag	120
anaagacgtc	ccaggaaaac	caacggctcc	acgtcgctgt	cgctcgccgc	gatgcgtcgg	180
acgacgagcc	tgtmggagmt	cgcgcggcmg	cggatctct	ccgggaggcc	caagamcgcg	240
gcggcgaggg	ggcatcgcggt	ggcagggcca	gggacgcggt	ggggcgccga	gataacgatg	300
acgcactcgg	cggactctct	ccccgccatg	gagacggcag	ccttctctaa	ggCctgcggg	360
atctgcaaac	gcgcgctcgg	ccccggccgt	gacaccttca	tctacatggg	tgagggtggcc	420
ttctgcagcc	aggagtktag	gcagcagcag	atgaacctcg	acgagctcat	ggagaagaag	480
tgctccactc	cggctggcgg	cggcggtggt	ggcgtcgcg	cgcgcgcgcg	tgggtgcctca	540
gatoagcccg	gcaagagcag	caccgtatcg	gccgcctagc	atcgccagag	gggttaataac	600
aacgaagaaa	aattttggag	ccctggtggc	gtaggcccca	aaaacgcagc	agtttccatc	660
agcctatgta	tatcctgtat	ttctggagtc	actgtgtgtg	tatatgtgtg	ggaaggggaa	720
ggatgtaggg	attccaactg	ggggcatggt	ttgcaatgca	tc		

(2) INFORMATION FOR SEQ ID NO:3052:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 192 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:

- (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..192
 (D) OTHER INFORMATION: / Ceres Seq. ID 1575344

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3052:

Thr Ser Pro Xaa Arg Thr Ser Pro Leu Ala His Ser Ala Pro Lys Glu
1 5 10 15
Glu Glu Asp Asp Asp Ser Xaa Val Pro Pro Ser Arg Asp Xaa Ser
20 25 30
Glu Val Thr Met Ser Thr Pro Thr Xaa Lys Arg Pro Arg Lys Thr Asn
35 40 45
Gly Ser Thr Ser Ser Ser Ser Ser Ala Met Arg Arg Thr Thr Ser Leu
50 55 60
Xaa Xaa Leu Ala Pro Xaa Pro Asp Leu Ser Gly Arg Pro Lys Xaa Arg
65 70 75 80
Ala Ala Arg Gly His Ala Val Ala Gly Pro Gly Thr Ala Trp Gly Ala
85 90 95
Glu Ile Thr Met Thr His Ser Ala Asp Phe Leu Pro Ala Met Glu Thr
100 105 110
Ala Ala Phe Leu Lys Ala Cys Gly Ile Cys Asn Arg Arg Leu Gly Pro
115 120 125
Gly Arg Asp Thr Phe Ile Tyr Met Gly Glu Val Ala Phe Cys Ser Gln
130 135 140
Glu Xaa Arg Gln Gln Gln Met Asn Leu Asp Glu Leu Met Glu Lys Lys
145 150 155 160
Cys Ser Thr Pro Ala Gly Gly Gly Gly Gly Val Gly Gly Gly Gly
165 170 175
Gly Gly Gly Ser Asp Gln Pro Gly Lys Ser Ser Thr Val Ala Ala Ala
180 185 190

(2) INFORMATION FOR SEQ ID NO:3053:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 157 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..157
 (D) OTHER INFORMATION: / Ceres Seq. ID 1575345

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3053:

Met Ser Thr Pro Thr Xaa Lys Arg Pro Arg Lys Thr Asn Gly Ser Thr
1 5 10 15
Ser Ser Ser Ser Ser Ala Met Arg Arg Thr Thr Ser Leu Xaa Xaa Leu
20 25 30
Ala Pro Xaa Pro Asp Leu Ser Gly Arg Pro Lys Xaa Arg Ala Ala Arg
35 40 45
Gly His Ala Val Ala Gly Pro Gly Thr Ala Trp Gly Ala Glu Ile Thr
50 55 60
Met Thr His Ser Ala Asp Phe Leu Pro Ala Met Glu Thr Ala Ala Phe
65 70 75 80
Leu Lys Ala Cys Gly Ile Cys Asn Arg Arg Leu Gly Pro Gly Arg Asp
85 90 95
Thr Phe Ile Tyr Met Gly Glu Val Ala Phe Cys Ser Gln Glu Xaa Arg
100 105 110
Gln Gln Gln Met Asn Leu Asp Glu Leu Met Glu Lys Lys Cys Ser Thr
115 120 125

Pro Ala Gly Gly Gly Gly Gly Gly Val Gly Gly Gly Gly Gly Gly Gly
130 135 140
Ser Asp Gln Pro Gly Lys Ser Ser Thr Val Ala Ala Ala
145 150 155

(2) INFORMATION FOR SEQ ID NO:3054:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 135 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..135
- (D) OTHER INFORMATION: / Ceres Seq. ID 1575346

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3054:

Met	Arg	Arg	Thr	Thr	Ser	Leu	Xaa	Xaa	Leu	Ala	Pro	Xaa	Pro	Asp	Leu
1				5					10				15		
Ser	Gly	Arg	Pro	Lys	Xaa	Arg	Ala	Ala	Arg	Gly	His	Ala	Val	Ala	Gly
			20					25				30			
Pro	Gly	Thr	Ala	Trp	Gly	Ala	Glu	Ile	Thr	Met	Thr	His	Ser	Ala	Asp
			35				40					45			
Phe	Leu	Pro	Ala	Met	Glu	Thr	Ala	Ala	Phe	Leu	Lys	Ala	Cys	Gly	Ile
	50					55					60				
Cys	Asn	Arg	Arg	Leu	Gly	Pro	Gly	Arg	Asp	Thr	Phe	Ile	Tyr	Met	Gly
	65					70			75				80		
Glu	Val	Ala	Phe	Cys	Ser	Gln	Glu	Xaa	Arg	Gln	Gln	Gln	Met	Asn	Leu
			85					90					95		
Asp	Glu	Leu	Met	Glu	Lys	Lys	Cys	Ser	Thr	Pro	Ala	Gly	Gly	Gly	Gly
			100					105				110			
Gly	Gly	Val	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Ser	Asp	Gln	Pro	Gly	Lys
			115				120								
Ser	Ser	Thr	Val	Ala	Ala	Ala									
	130					135									

(2) INFORMATION FOR SEQ ID NO:3055:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 699 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..699
- (D) OTHER INFORMATION: / Ceres Seq. ID 1575351

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3055:

accatacact	gcagctcaaa	cacagaagcg	ccccagaag	cagcagcgca	ggagcgagcg	60
atcgctatgg	ctcagggaa	aggcagtgcg	acgcgggggc	tgcgcctcg	cgccctactc	120
gccgcgcgtt	tctctctct	ctctggcgtc	gcgcagcgcg	ccaccacag	ggctcagctg	180
tccttcaacg	cggacagctg	gtccaaaggg	aagagcttcC	gtgccggcga	cgctcctcag	240
ttcaactacg	accctccgt	gcacaacgtg	gtggccgtgg	acgcgcggcg	ctacaacggc	300
tgcgcggccct	cgggcaagtc	gtacggctcc	gggagcgacc	gcatacagct	cgcccccgcc	360
accagctact	tcactctcag	ccctcaacagg	cactgcggga	tggggatgaa	gatggctcgt	420
aatgccagct	gagcaacgag	cttatatgtt	agtactgcaa	aaatatatgg	gctagtgtgt	480
gtccgataga	tcgtgcaaga	actcaatcgt	gtggcatact	cgtaccgtgt	gttcgatgga	540
cacggttcac	gtgttggtga	tgcattgcgac	tgctgttagg	tcaggcatga	tgtacgtgtg	600
gctgtggcgg	tgtagtaaaa	gcgtcctgca	gctttgttgt	tactttgttc	gatcggaagca	660
gcggtctctt	ttgtttgttc	atcaataaca	tccttcatt			

(2) INFORMATION FOR SEQ ID NO:3056:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 143 amino acids

- (B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..143
(D) OTHER INFORMATION: / Ceres Seq. ID 1575352

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3056:

Thr	His	His	Cys	Ser	Ser	Asn	Thr	Glu	Ala	Pro	Gln	Glu	Ala	Ala	Ala
1			5					10						15	
Gln	Glu	Arg	Ala	Ile	Ala	Met	Ala	Gln	Gly	Arg	Gly	Ser	Ala	Thr	Arg
			20					25					30		
Gly	Leu	Ala	Leu	Gly	Ala	Leu	Leu	Ala	Ala	Ala	Phe	Leu	Leu	Leu	Leu
			35				40					45			
Gly	Val	Ala	Asp	Ala	Ala	Thr	His	Arg	Val	Asp	Trp	Ser	Phe	Asn	Ala
			50				55				60				
Asp	Ser	Trp	Ser	Lys	Gly	Lys	Ser	Phe	Arg	Ala	Gly	Asp	Val	Leu	Glu
65				70				75						80	
Phe	Asn	Tyr	Asp	Pro	Ser	Val	His	Asn	Val	Val	Ala	Val	Asp	Ala	Gly
			85					90					95		
Gly	Tyr	Asn	Gly	Cys	Arg	Pro	Ser	Gly	Thr	Ser	Tyr	Gly	Ser	Gly	Ser
			100					105					110		
Asp	Arg	Ile	Thr	Leu	Gly	Pro	Gly	Thr	Ser	Tyr	Phe	Ile	Cys	Ser	Leu
			115				120					125			
Asn	Arg	His	Cys	Gly	Met	Gly	Met	Lys	Met	Val	Val	Asn	Ala	Ser	
			130				135					140			

(2) INFORMATION FOR SEQ ID NO:3057:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 135 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..135
(D) OTHER INFORMATION: / Ceres Seq. ID 1575353

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3057:

Pro	Ile	Thr	Ala	Ala	Gln	Thr	Gln	Lys	Arg	Pro	Lys	Lys	Gln	Gln	Arg
1				5				10					15		
Arg	Ser	Glu	Arg	Ser	Leu	Trp	Leu	Arg	Glu	Glu	Ala	Val	Arg	Arg	Gly
			20					25				30			
Gly	Leu	Pro	Ser	Ala	Pro	Tyr	Ser	Pro	Pro	Leu	Ser	Ser	Ser	Ser	Ser
			35				40					45			
Ala	Ser	Pro	Thr	Arg	Pro	Pro	Thr	Gly	Ser	Thr	Gly	Pro	Ser	Thr	Arg
			50				55				60				
Thr	Ala	Gly	Pro	Arg	Ala	Arg	Ala	Ser	Val	Pro	Ala	Thr	Ser	Ser	Ser
65				70				75					80		
Ser	Thr	Thr	Thr	Pro	Pro	Cys	Thr	Thr	Trp	Pro	Trp	Thr	Pro	Ala	
				85				90					95		
Ala	Thr	Thr	Ala	Ala	Gly	Pro	Pro	Ala	Arg	Arg	Thr	Ala	Pro	Gly	Ala
			100					105				110			
Thr	Ala	Ser	Arg	Ser	Ala	Pro	Ala	Pro	Ala	Thr	Ser	Ser	Ala	Ala	Ser
			115				120					125			
Thr	Gly	Thr	Ala	Gly	Trp	Gly									
			130			135									

(2) INFORMATION FOR SEQ ID NO:3058:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 149 amino acids
(B) TYPE: amino acid

- (C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..149
(D) OTHER INFORMATION: / Ceres Seq. ID 1575354
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3058:

Pro Ser Leu Gln Leu Lys His Arg Ser Ala Pro Arg Ser Ser Ser Ala
1 5 10 15
Gly Ala Ser Asp Arg Tyr Gly Ser Gly Lys Arg Gln Cys Asp Ala Gly
20 25 30
Ala Cys Pro Arg Arg Pro Thr Arg Arg Phe Pro Pro Pro Pro Arg
35 40 45
Arg Arg Arg Arg Gly His Pro Gln Gly Arg Leu Val Leu Gln Arg Gly
50 55 60
Gln Leu Val Gln Gly Gln Glu Leu Pro Cys Arg Arg Arg Pro Arg Val
65 70 75 80
Gln Leu Arg Pro Leu Arg Ala Gln Arg Gly Gly Arg Gly Arg Arg Arg
85 90 95
Leu Gln Arg Leu Pro Ala Leu Arg His Val Val Arg Leu Arg Glu Arg
100 105 110
Pro His His Ala Arg Pro Arg His Gln Leu Leu His Leu Gln Pro Gln
115 120 125
Gln Ala Leu Arg Asp Gly Asp Glu Asp Gly Arg Gln Cys Gln Leu Ser
130 135 140
Thr Thr Leu Ile Cys
145

- (2) INFORMATION FOR SEQ ID NO:3059:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 685 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..685
(D) OTHER INFORMATION: / Ceres Seq. ID 1575361

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3059:

gacgatgtct cttgccgcgg cgtaaccctt cgctccatt cccgcgcgca tcgcgcgtca 60
ggctccttgc gcggcattcc tgtccatccg cttaggtrgc gcgacggcga cgcggttgcg 120
tggactggcg gtgcctctgc agccagcggga gckwcgcgcc gcggcgatgg tcaagatggc 180
gaagaggggg caggagctgg aggatattcc ggccatgacg acggaacaga tgggaagarga 240
ccttgtagac ctcaaggggg agcttttctt gctccgcctt aaGcgctcgg cgcgccagga 300
gttcaagaac agcgagttca gcgcgatcg caagaggatt gctcgtatgc taaccgtgaa 360
aagagagcgg gaaattgaac aaaggaatcaa taaaagattg tctaggaagc ttgataggaa 420
atggaagcag agcatctggt tcagaccacc accatctcta agggggaaca aagaggagta 480
gaaagcgcga aaaagagggc aatgtgcaaa agtcgtttca tgcgagtgtt gcaggaaggt 540
cccttcatga tttaaccctt tattgcgttg ttatgtattc catgtttaca ttttgcataag 600
cattgtctat tgaatctgaa tttaagttgt tagtctcttc tgtaaatttc gacttattta 660
aatttacctt tctatctgtg ttatc

- (2) INFORMATION FOR SEQ ID NO:3060:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 159 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide

(B) LOCATION: 1..159

(D) OTHER INFORMATION: / Ceres Seq. ID 1575362

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3060:

Thr Met Ser Leu Ala Ala Ala Ser Pro Leu Ala Ser Ile Pro Arg Gly
1 5 10 15
Ile Ala Ala Gln Ala Pro Cys Ala Ala Phe Leu Ser Ile Arg Leu Gly
20 25 30
Xaa Ala Thr Ala Thr Arg Phe Ala Gly Leu Ala Val Ala Ser Gln Pro
35 40 45
Ala Glu Xaa Arg Ala Ala Ala Met Val Thr Met Ala Lys Arg Glu Gln
50 55 60
Glu Leu Glu Glu Ile Arg Ala Met Thr Thr Glu Gln Met Glu Xaa Glu
65 70 75 80
Val Val Asp Leu Lys Gly Glu Leu Phe Leu Leu Arg Leu Lys Arg Ser
85 90 95
Ala Arg Gln Glu Phe Lys Asn Ser Glu Phe Ser Arg Met Arg Lys Arg
100 105 110
Ile Ala Arg Met Leu Thr Val Lys Arg Glu Arg Glu Ile Glu Gln Gly
115 120 125
Ile Asn Lys Arg Leu Ser Arg Lys Leu Asp Arg Lys Trp Lys Gln Ser
130 135 140
Ile Val Val Arg Pro Pro Ser Leu Arg Gly Asn Lys Glu Glu
145 150 155

(2) INFORMATION FOR SEQ ID NO:3061:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 158 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..158

(D) OTHER INFORMATION: / Ceres Seq. ID 1575363

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3061:

Met Ser Leu Ala Ala Ala Ser Pro Leu Ala Ser Ile Pro Arg Gly Ile
1 5 10 15
Ala Ala Gln Ala Pro Cys Ala Ala Phe Leu Ser Ile Arg Leu Gly Xaa
20 25 30
Ala Thr Ala Thr Arg Phe Ala Gly Leu Ala Val Ala Ser Gln Pro Ala
35 40 45
Glu Xaa Arg Ala Ala Ala Met Val Thr Met Ala Lys Arg Glu Gln Glu
50 55 60
Leu Glu Glu Ile Arg Ala Met Thr Thr Glu Gln Met Glu Xaa Glu Val
65 70 75 80
Val Asp Leu Lys Gly Glu Leu Phe Leu Leu Arg Leu Lys Arg Ser Ala
85 90 95
Arg Gln Glu Phe Lys Asn Ser Glu Phe Ser Arg Met Arg Lys Arg Ile
100 105 110
Ala Arg Met Leu Thr Val Lys Arg Glu Arg Glu Ile Glu Gln Gly Ile
115 120 125
Asn Lys Arg Leu Ser Arg Lys Leu Asp Arg Lys Trp Lys Gln Ser Ile
130 135 140
Val Val Arg Pro Pro Pro Ser Leu Arg Gly Asn Lys Glu Glu
145 150 155

(2) INFORMATION FOR SEQ ID NO:3062:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 104 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide
(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..104

(D) OTHER INFORMATION: / Ceres Seq. ID 1575364

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3062:

Met	Val	Thr	Met	Ala	Lys	Arg	Glu	Gln	Glu	Leu	Glu	Glu	Ile	Arg	Ala		
1			5					10					15				
Met	Thr	Thr	Glu	Gln	Met	Glu	Xaa	Glu	Val	Val	Asp	Leu	Lys	Gly	Glu		
			20					25				30					
Leu	Phe	Leu	Leu	Arg	Leu	Lys	Arg	Ser	Ala	Arg	Gln	Glu	Phe	Lys	Asn		
			35					40				45					
Ser	Glu	Phe	Ser	Arg	Met	Arg	Lys	Arg	Ile	Ala	Arg	Met	Leu	Thr	Val		
			50					55				60					
Lys	Arg	Glu	Arg	Glu	Ile	Glu	Gln	Gly	Ile	Asn	Lys	Arg	Leu	Ser	Arg		
			65					70				75			80		
Lys	Leu	Asp	Arg	Lys	Trp	Lys	Gln	Ser	Ile	Val	Val	Arg	Pro	Pro	Pro		
				85				90					95				
Ser	Leu	Arg	Gly	Asn	Lys	Glu	Glu										
				100													

(2) INFORMATION FOR SEQ ID NO:3063:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 794 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..794

(D) OTHER INFORMATION: / Ceres Seq. ID 1575386

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3063:

cagaaggggg	caaagctcgc	ggcctcgcgt	cgcgcgcgtc	gttcgcgtcc	aacgcggcga	60
cscaaaggct	ggcgtccccc	ggcttctctc	tcacctcac	cccttccct	cgmcacaacca	120
caggaaagaag	cgagcagggc	atcgagtttt	ctcgatgat	ggcatcgcg	cctgcggatt	180
ccctacgggtg	cgcggcgtgc	ggcgcgcgcc	tgaacctgtc	ggcggcgac	ctgtaccogg	240
cggacttcta	cttcgaggcc	gggaacaagg	gcacgctgtc	cttctcgtgg	gtggacgagt	300
cgcgcctcgtg	gttcgcgcgc	gaggacgcga	tcgcgccctt	cttcgagacc	ctcaactact	360
ggggcatcca	ggggaagcgc	acgcgcatca	gctgcgnacc	tgcggccaac	tgtctggcca	420
skctacgaag	acggtctcgc	ggccatgcag	ggcaccgcgc	agttcgggat	ggggcccgag	480
caggctcatcc	cgcgcgcgcc	caggtaccgc	ttcaagatca	aggccatcgc	gcgccagctcc	540
tcggcacctg	cgcgcgcgcg	ctatgaaaag	tgatgtccca	tagatttctt	catctgggtg	600
cgtgtcctgt	gtgctgtcgt	tgtctgggtt	cgtgacttcc	tgtaaattac	gtagcttccct	660
gcaatttcgc	tctgtcgttg	ttttctttag	aaacagtggt	tttgaatagg	catgcgactg	720
aaactatgat	tgaataggca	tgcgacttct	aaatatcaca	caagacagaa	gatataaata	780
aaaaactatg	attg					

(2) INFORMATION FOR SEQ ID NO:3064:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 193 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..193

(D) OTHER INFORMATION: / Ceres Seq. ID 1575387

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3064:

Arg	Arg	Gly	Gln	Ser	Ser	Arg	Pro	Arg	Val	Ala	Pro	Val	Val	Pro	Val		
1			5					10				15					
Gln	Arg	Gly	Asp	Xaa	Lys	Ala	Ala	Val	Pro	Gly	Leu	Pro	Pro	Pro	Pro		

	20		25		30	
His Pro Phe Pro Ser Xaa Asn His Arg Lys Lys Arg Ala Gly His Arg	35	40	45			
Val Phe Ser Ile Asp Gly Ile Gly Ala Cys Arg Phe Leu Arg Val Arg	50	55	60			
Gly Val Arg Arg Ala Pro Glu Pro Val Gly Gly Ala Pro Val Pro Gly	65	70	75	80		
Gly Leu Leu Leu Arg Gly Arg Glu Gln Gly His Ala Val Leu Leu Val	85	90	95			
Gly Gly Arg Val Ala Pro Ala Val Arg Ala Arg Gly Pro His Pro Pro	100	105	110			
Leu Leu Arg Asp Pro Gln Leu Leu Gly His Pro Ala Glu Ala His Ala	115	120	125			
His Gln Leu Xaa Thr Cys Gly His Leu Leu Gly Xaa Xaa Thr Thr Thr	130	135	140			
Val Arg Arg Pro Cys Arg Ala Pro Ala Ser Ser Gly Trp Gly Pro Ala	145	150	155	160		
Arg Ser Ser Arg Ala Ala Pro Gly Thr Ala Ser Arg Ser Arg Pro Ser	165	170	175			
Pro Pro Ala Pro Arg His Leu Pro Pro Pro Met Lys Ser Asp Ala	180	185	190			

Pro

(2) INFORMATION FOR SEQ ID NO:3065:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 187 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..187

(D) OTHER INFORMATION: / Ceres Seq. ID 1575388

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3065:

Glu Gly Gly Lys Ala Arg Gly Leu Ala Ser Arg Arg Ser Phe Arg Ser	1	5	10	15
Asn Ala Ala Xaa Gln Arg Leu Pro Ser Pro Gly Phe Leu Leu Pro Leu	20	25	30	
Thr Pro Ser Pro Xaa Gln Thr Thr Gly Arg Ser Glu Gln Gly Ile Glu	35	40	45	
Phe Ser Arg Ser Met Ala Ser Ala Pro Ala Asp Ser Tyr Gly Cys Ala	50	55	60	
Ala Cys Gly Ala Pro Leu Asn Leu Ser Ala Ala His Leu Tyr Pro Ala	65	70	75	80
Asp Phe Tyr Phe Glu Ala Gly Asn Lys Gly Thr Leu Ser Phe Ser Trp	85	90	95	
Val Asp Glu Ser Arg Leu Arg Phe Ala Pro Glu Asp Arg Ile Arg Pro	100	105	110	
Phe Phe Glu Thr Leu Asn Tyr Trp Gly Ile Gln Arg Lys Arg Thr Arg	115	120	125	
Ile Ser Cys Xaa Pro Ala Ala Thr Cys Leu Ala Xaa Leu Arg Arg Arg	130	135	140	
Ser Ala Gly His Ala Gly His Arg Pro Val Arg Asp Gly Ala Gln Pro	145	150	155	160
Gly His Pro Ala Pro Pro Gln Val Pro Leu Gln Asp Gln Gly His Arg	165	170	175	
Arg Gln Leu Leu Gly Thr Cys Arg Arg Arg Leu	180	185		

(2) INFORMATION FOR SEQ ID NO:3066:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 135 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..135
(D) OTHER INFORMATION: / Ceres Seq. ID 1575389
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3066:

Met Ala Ser Ala Pro Ala Asp Ser Tyr Gly Cys Ala Ala Cys Gly Ala
1 5 10 15
Pro Leu Asn Leu Ser Ala Ala His Leu Tyr Pro Ala Asp Phe Tyr Phe
20 25 30
Glu Ala Gly Asn Lys Gly Thr Leu Ser Phe Ser Trp Val Asp Glu Ser
35 40 45
Arg Leu Arg Phe Ala Pro Glu Asp Arg Ile Arg Pro Phe Phe Glu Thr
50 55 60
Leu Asn Tyr Trp Gly Ile Gln Arg Lys Arg Thr Arg Ile Ser Cys Xaa
65 70 75 80
Pro Ala Ala Thr Cys Leu Ala Xaa Leu Arg Arg Arg Ser Ala Gly His
85 90 95
Ala Gly His Arg Pro Val Arg Asp Gly Ala Gln Pro Gly His Pro Ala
100 105 110
Pro Pro Gln Val Pro Leu Gln Asp Gln Gly His Arg Arg Gln Leu Leu
115 120 125
Gly Thr Cys Arg Arg Arg Leu
130 135

(2) INFORMATION FOR SEQ ID NO:3067:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 836 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..836
(D) OTHER INFORMATION: / Ceres Seq. ID 1575402

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3067:

atccgatccg agccatattta aacagacgca tgcacgcngc gccggccgga ggcgcacggcg 60
gcggcgccct cctgcggacc cagcttcgcg ctattagcta gcttgctgca gcagcgtacg 120
tgcttttctg tegtccctgcc ggtcgccatg accttcccg cgggttgcta ctgctacggcg 180
gtgcgcggcc cggctggcgc gctgctcaag ctctccacg ccgcgctgct cgtgttcgtg 240
ctgctcctct ccttctctcg cctctacgag ttctcctacg accccgagga tcacgcgcca 300
ccagccatca acggcgcccg cccagggcca gagcgcggtga agcggcgccct cccgctcgtc 360
gagttcctgg agctggtgta ttctgctgct tcacgcgtcg cgggggtggg ggcggaGCcg 420
acgtgcggcg tgtgctctga gtggcttgag gccaaaggac aggtgcggcg gctgggcaac 480
tgcacccacc cgttccacac gcgctgcctc gacgcgtgga tcgacctggg cgaggtgacg 540
tgcccgcttt gccgttccca cctgctgcg ccgcggcgcg ccggcctact cagcatggca 600
cggtctggct agtcgcgcgt ccttggttcc ctctatccct taattgccag tacgatacgt 660
gccctgtcac agccgtgcct ggcttcaggc cagcgcgcgcg cggtctggtac gcgcacagat 720
gccactgggg actggtgcgg gatgggggca gaccatgaga ccaaccgtga actaggacga 780
ctgtctatgt aaagaatttt ttccgctcaa tggatggggc caagccaaat tactwg

(2) INFORMATION FOR SEQ ID NO:3068:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 154 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..154
(D) OTHER INFORMATION: / Ceres Seq. ID 1575403

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3068:

Met	Thr	Phe	Pro	Leu	Val	Cys	Tyr	Cys	Tyr	Ala	Val	Pro	Arg	Pro	Val
1				5					10					15	
Ala	Ala	Leu	Leu	Lys	Leu	Leu	His	Ala	Ala	Val	Leu	Val	Phe	Val	Leu
				20				25					30		
Leu	Leu	Ser	Phe	Leu	Gly	Leu	Tyr	Glu	Phe	Ser	Tyr	Asp	Pro	Glu	Asp
				35			40					45			
His	Ala	Pro	Pro	Ala	Ile	Asn	Gly	Gly	Arg	Pro	Arg	Pro	Glu	Ala	Val
				50		55				60					
Lys	Arg	Arg	Leu	Pro	Leu	Val	Glu	Phe	Leu	Glu	Leu	Val	Asp	Ser	Ser
				65		70			75					80	
Ser	Ser	Pro	Ser	Ser	Gly	Val	Gly	Ala	Glu	Pro	Thr	Cys	Arg	Val	Cys
				85				90					95		
Leu	Glu	Trp	Leu	Glu	Ala	Lys	Asp	Glu	Val	Arg	Arg	Leu	Gly	Asn	Cys
				100				105					110		
Thr	His	Ala	Phe	His	Thr	Arg	Cys	Ile	Asp	Arg	Trp	Ile	Asp	Leu	Gly
				115			120					125			
Glu	Val	Thr	Cys	Pro	Leu	Cys	Arg	Ser	His	Leu	Leu	Pro	Arg	Arg	Arg
				130			135					140			
Ala	Gly	Leu	Leu	Ser	Met	Ala	Arg	Leu	Gly						
145					150										

(2) INFORMATION FOR SEQ ID NO:3069:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 674 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..674
(D) OTHER INFORMATION: / Ceres Seq. ID 1575404

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3069:

catcaacaat	gatgcctcta	aggtgaactc	tcattggtcca	catcagagtt	ctgggtccac	60
ttgtctatgg	gagaaaaaatg	agcctccagt	caatctacc	cgctacaact	tgtccgcatt	120
tgcataaaca	ctaaatgagt	taacaccaga	gctcgaggag	aagctgccac	cgacggattc	180
aaggctgaga	ccagatcaac	ggcacctgga	gaatggggag	tacgagaag	ccaatgctga	240
aaaactgcgc	ctcgagacac	agcaacggat	ggcaaggag	atgcaggaga	gtggctggaa	300
accaagatgg	ttccaaagg	acagcgagga	tggaaactac	cgctacgtcg	gaggttactg	360
ggaggcaagg	gagcagagaa	catgggtcgg	ctgcaatgac	atatttggt	actgtctatg	420
cagccagaag	ctcccaccat	ccgctctcta	cacgagctga	agtatatagg	ggtgggtaag	480
gccggaagg	catgttcagt	agttgtgtac	atcgcattaa	ccagaggggt	ttctctctgt	540
ttctgWttdg	tgttaagctg	tgagctaaaca	tgttttttct	gtcaattgtc	acattgaagc	600
caaggacatc	caagcataac	ccaacctttt	gtcgatacta	ggatacttat	gagagatcct	660
gtggacatta	ttgc					

(2) INFORMATION FOR SEQ ID NO:3070:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 152 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..152
(D) OTHER INFORMATION: / Ceres Seq. ID 1575405

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3070:

Ile Asn Asn Asp Ala Ser Lys Val Asn Ser His Gly Pro His Gln Ser
1 5 10 15
Ser Gly Ser Thr Leu Leu Trp Glu Lys Asn Glu Pro Pro Val Asn Pro
20 25 30
Thr Arg Tyr Asn Leu Ser Ala Phe Ala Ile Thr Leu Asn Glu Leu Thr
35 40 45
Pro Glu Leu Glu Glu Lys Leu Pro Pro Thr Asp Ser Arg Leu Arg Pro
50 55 60
Asp Gln Arg His Leu Glu Asn Gly Glu Tyr Glu Lys Ala Asn Ala Glu
65 70 75 80
Lys Leu Arg Leu Glu Thr Gln Gln Arg Met Ala Arg Lys Met Gln Glu
85 90 95
Ser Gly Trp Lys Pro Arg Trp Phe Gln Arg Asp Ser Glu Asp Gly Thr
100 105 110
Tyr Arg Tyr Val Gly Gly Tyr Trp Glu Ala Arg Glu Gln Arg Thr Trp
115 120 125
Val Gly Cys Asn Asp Ile Phe Gly Asn Leu Ser Ser Ser Gln Lys Leu
130 135 140
Pro Pro Ser Ala Leu Tyr Thr Ser
145 150

(2) INFORMATION FOR SEQ ID NO:3071:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 88 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..88
- (D) OTHER INFORMATION: / Ceres Seq. ID 1575406

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3071:

Met Gly Ser Thr Arg Arg Pro Met Leu Lys Asn Cys Ala Ser Arg His
1 5 10 15
Ser Asn Gly Trp Gln Gly Arg Cys Arg Arg Val Ala Gly Asn Gln Asp
20 25 30
Gly Ser Lys Gly Thr Ala Arg Met Glu Arg Thr Ala Thr Ser Glu Val
35 40 45
Thr Gly Arg Gln Gly Ser Arg Glu His Gly Ser Ala Ala Met Thr Tyr
50 55 60
Leu Val Thr Cys Leu Ala Ala Arg Ser Ser His His Pro Leu Ser Thr
65 70 75 80
Arg Ala Glu Val Tyr Arg Gly Gly
85

(2) INFORMATION FOR SEQ ID NO:3072:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 81 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..81
- (D) OTHER INFORMATION: / Ceres Seq. ID 1575407

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3072:

Met Leu Lys Asn Cys Ala Ser Arg His Ser Asn Gly Trp Gln Gly Arg
1 5 10 15
Cys Arg Arg Val Ala Gly Asn Gln Asp Gly Ser Lys Gly Thr Ala Arg
20 25 30
Met Glu Arg Thr Ala Thr Ser Glu Val Thr Gly Arg Gln Gly Ser Arg

	35		40		45	
Glu	His	Gly	Ser	Ala	Ala	Met
50					55	
Arg	Ser	Ser	His	His	Pro	Leu
65				70		
Gly						

(2) INFORMATION FOR SEQ ID NO:3073:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 521 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..521
- (D) OTHER INFORMATION: / Ceres Seq. ID 1575428

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3073:

cggttatctc	ttcttccact	gctctccaac	caCttcgtcc	tcgcccggctc	gcaactcctt	60
gatggcgccc	acggcgagtc	tcactaccac	tgctccctcc	cctccagctc	tcctcaaaagc	120
atcagctcct	ttgttatctc	cttttcgccc	cgctcccgcc	cactgcaaga	acctgtgcac	180
caagaccaag	gccacagaaa	atgatcagtc	tgctaaaaag	catcagaagg	tgaagagcat	240
tctttgcacg	gactgcgaag	gaaatggggc	aatcacatgc	accaaaatgtg	aagggaaatgg	300
ggtaaatctc	gttgactatt	tgaaggccg	atttaaagct	ggatctttat	gctgtgtgtc	360
agaattgtgt	cggcagggtg	ctaataaagg	cttctgtgtg	ggaaagaatt	ggatccacgg	420
gcagctttta	gtcatttgtt	tggaggcatt	ggattcattg	gagggtcgat	ttgtgattgt	480
aatcacgatt	aatgtaatgg	attggaaatt	cggaaggggc	c		

(2) INFORMATION FOR SEQ ID NO:3074:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 173 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..173
- (D) OTHER INFORMATION: / Ceres Seq. ID 1575429

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3074:

Val	Tyr	Leu	Phe	Phe	His	Cys	Leu	Pro	Thr	Thr	Ser	Ser	Pro	Ala
1			5						10				15	
Arg	Asn	Ser	Leu	Met	Ala	Ala	Thr	Ala	Ser	Leu	Thr	Thr	Thr	Ala
			20					25					30	
Ser	Pro	Pro	Ala	Leu	Leu	Lys	Ala	Ser	Ala	Pro	Leu	Leu	Ile	Ser
			35				40					45		
Arg	Pro	Val	Ser	Arg	His	Cys	Lys	Asn	Leu	Cys	Ile	Lys	Thr	Lys
			50			55				60				
Thr	Glu	Asn	Asp	Gln	Ser	Ala	Lys	Lys	His	Gln	Lys	Val	Lys	Ser
			65			70			75				80	
Leu	Cys	Gln	Asp	Cys	Glu	Gly	Asn	Gly	Ala	Ile	Thr	Cys	Thr	Lys
			85				90						95	
Glu	Gly	Asn	Gly	Val	Asn	Ser	Val	Asp	Tyr	Phe	Glu	Gly	Arg	Phe
			100					105					110	
Ala	Gly	Ser	Leu	Cys	Trp	Leu	Ser	Glu	Leu	Val	Arg	Gln	Val	Ser
			115				120						125	
Lys	Gly	Phe	Leu	Leu	Gly	Lys	Asn	Trp	Ile	His	Gly	Gln	Leu	Leu
			130				135						140	
Ile	Cys	Leu	Glu	Ala	Leu	Asp	Ser	Leu	Glu	Gly	Arg	Phe	Val	Ile
			145				150			155			160	
Ile	Thr	Ile	Asn	Val	Met	Asp	Trp	Lys	Phe	Gly	Arg	Gly		

165

170

(2) INFORMATION FOR SEQ ID NO:3075:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 153 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..153

(D) OTHER INFORMATION: / Ceres Seq. ID 1575430

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3075:

Met	Ala	Ala	Thr	Ala	Ser	Leu	Thr	Thr	Thr	Ala	Pro	Ser	Pro	Pro	Ala
1				5						10				15	
Leu	Leu	Lys	Ala	Ser	Ala	Pro	Leu	Leu	Ile	Ser	Phe	Arg	Pro	Val	Ser
				20					25				30		
Arg	His	Cys	Lys	Asn	Leu	Cys	Ile	Lys	Thr	Lys	Ala	Thr	Glu	Asn	Asp
				35				40				45			
Gln	Ser	Ala	Lys	Lys	His	Gln	Lys	Val	Lys	Ser	Ile	Leu	Cys	Gln	Asp
				50				55				60			
Cys	Glu	Gly	Asn	Gly	Ala	Ile	Thr	Cys	Thr	Lys	Cys	Glu	Gly	Asn	Gly
				65				70				75			80
Val	Asn	Ser	Val	Asp	Tyr	Phe	Glu	Gly	Arg	Phe	Lys	Ala	Gly	Ser	Leu
				85					90				95		
Cys	Trp	Leu	Ser	Glu	Leu	Val	Arg	Gln	Val	Ser	Asn	Lys	Gly	Phe	Leu
				100					105				110		
Leu	Gly	Lys	Asn	Trp	Ile	His	Gly	Gln	Leu	Leu	Val	Ile	Cys	Leu	Glu
				115				120				125			
Ala	Leu	Asp	Ser	Leu	Glu	Gly	Arg	Phe	Val	Ile	Val	Ile	Thr	Ile	Asn
				130				135				140			
Val	Met	Asp	Trp	Lys	Phe	Gly	Arg	Gly							
				145				150							

(2) INFORMATION FOR SEQ ID NO:3076:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 854 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..854

(D) OTHER INFORMATION: / Ceres Seq. ID 1575435

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3076:

gtagaggtct	tttactaaca	gggaaaggga	agggatggcc	acagcgcgcc	tgctccggtg	60
cgctctctcc	accttccttt	tcagcacctg	caccaccaat	ccgttgccgt	cgtrctcccc	120
tctcgtccgc	mgccagcacc	cccgcgcgcg	catggccacg	gactcctccg	ccgcctcgtt	180
ccagaaagtc	cagatccagg	gcgaggacac	cacttttgat	gcttatgttg	ttggcaaaaga	240
aaatgctcct	ggaaattgtg	ttttgcaaga	atagtgrrcg	cggtggtgac	caaggggccac	300
gacgagggga	tgaaggcrgc	ggcgcgcctg	ctggaggagt	tcgggctccc	gccggggctg	360
ctgcgcgtgg	aggaagtkac	ggaggtgggg	ttcgtgcggg	ccaccggcta	cttctggctc	420
gcgcacGcga	agaaggtgga	gcaccggttc	cgcaagatcg	gcaagcaggt	gagctacgac	480
gtcgagatcg	ccggctacgt	ccggcccaagg	ggcatcaggga	ggctcaaggg	ggtcaaggcc	540
aaggagctcg	tgctctggcc	gcccgctcac	gagatggccg	tcgacgacga	cccgcccaac	600
ggcaagatcc	acttcaagag	ctcgcgcggc	gtcaccaaga	ccttccccgt	tgannbcttc	660
gccgcgcggc	agtagccacc	cacgcgtacc	atcttatatt	atcactataa	taatacacata	720
tacaccatta	tatatggcgc	atatatatag	tattaattaa	tctcttgtgt	tactaacctta	780
tatatatggt	atgtgtgtac	ttgcttttgc	aatcctgatg	atgatgaaga	acgtaaacctc	840
tagttttttt	cctg					

(2) INFORMATION FOR SEQ ID NO:3077:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 216 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide

- (B) LOCATION: 1..216

- (D) OTHER INFORMATION: / Ceres Seq. ID 1575436

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3077:

Arg Gly Leu Leu Leu Thr Gly Lys Gly Lys Gly Trp Pro Gln Arg Ala
1 5 10 15
Cys Ser Val Ala Pro Pro Pro Ser Phe Ser Ala Pro Ala Pro Pro
20 25 30
Ile Arg Cys Ala Arg Xaa Pro Leu Ser Ser Xaa Ala Ser Thr Pro Ala
35 40 45
Pro Pro Trp Pro Arg Thr Pro Pro Pro Arg Ser Arg Arg Ser Arg
50 55 60
Ser Ser Ala Arg Thr Pro Leu Leu Met Leu Met Leu Leu Ala Lys Lys
65 70 75 80
Met Leu Leu Glu Leu Trp Phe Cys Lys Asn Ser Xaa Arg Gly Gly Asp
85 90 95
Gln Gly Pro Arg Arg Gly Asp Glu Gly Xaa Gly Gly Ala Ala Gly Gly
100 105 110
Val Arg Ala Pro Ala Gly Ala Ala Ala Gly Gly Arg Xaa Gly Gly
115 120 125
Gly Val Arg Ala Gly His Arg Leu Leu Leu Ala Arg Ala Ala Gln Glu
130 135 140
Gly Gly Ala Pro Val Pro Gln Asp Arg Gln Ala Gly Glu Leu Arg Arg
145 150 155 160
Arg Asp Arg Arg Leu Arg Pro Ala Gln Gly His Gln Glu Ala Gln Gly
165 170 175
Gly Gln Gly Gln Gly Ala Arg Ala Leu Ala Ala Arg Pro Arg Asp Gly
180 185 190
Arg Arg Arg Arg Pro Ala His Arg Gln Asp Pro Leu Gln Glu Pro Arg
195 200 205
Arg Arg His Gln Asp Leu Pro Arg
210 215

(2) INFORMATION FOR SEQ ID NO:3078:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 144 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide

- (B) LOCATION: 1..144

- (D) OTHER INFORMATION: / Ceres Seq. ID 1575437

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3078:

Met Leu Met Leu Leu Ala Lys Lys Met Leu Leu Glu Leu Trp Phe Cys
1 5 10 15
Lys Asn Ser Xaa Arg Gly Gly Asp Gln Gly Pro Arg Arg Gly Asp Glu
20 25 30
Gly Xaa Gly Gly Ala Ala Gly Gly Val Arg Ala Pro Ala Gly Ala Ala
35 40 45
Ala Ala Gly Gly Arg Xaa Gly Gly Gly Val Arg Ala Gly His Arg Leu
50 55 60
Leu Leu Ala Arg Ala Ala Gln Glu Gly Gly Ala Pro Val Pro Gln Asp
65 70 75 80

Arg Gln Ala Gly Glu Leu Arg Arg Arg Asp Arg Arg Leu Arg Pro Ala
85 90 95
Gln Gly His Gln Glu Ala Gln Gly Gly Gln Gly Gln Ala Arg Ala
100 105 110
Leu Ala Ala Arg Pro Arg Asp Gly Arg Arg Arg Pro Ala His Arg
115 120 125
Gln Asp Pro Leu Gln Glu Pro Arg Arg Arg His Gln Asp Leu Pro Arg
130 135 140

(2) INFORMATION FOR SEQ ID NO:3079:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 142 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..142

(D) OTHER INFORMATION: / Ceres Seq. ID 1575438

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3079:

Met Leu Leu Ala Lys Lys Met Leu Leu Glu Leu Trp Phe Cys Lys Asn
1 5 10 15
Ser Xaa Arg Gly Gly Asp Gln Gly Pro Arg Arg Gly Asp Glu Gly Xaa
20 25 30
Gly Gly Ala Ala Gly Gly Val Arg Ala Pro Ala Gly Ala Ala Ala Ala
35 40 45
Gly Gly Arg Xaa Gly Gly Val Arg Ala Gly His Arg Leu Leu Leu
50 55 60
Ala Arg Ala Ala Gln Glu Gly Gly Ala Pro Val Pro Gln Asp Arg Gln
65 70 75 80
Ala Gly Glu Leu Arg Arg Arg Asp Arg Arg Leu Arg Pro Ala Gln Gly
85 90 95
His Gln Glu Ala Gln Gly Gly Gln Gly Gln Gly Ala Arg Ala Leu Ala
100 105 110
Ala Arg Pro Arg Asp Gly Arg Arg Arg Arg Pro Ala His Arg Gln Asp
115 120 125
Pro Leu Gln Glu Pro Arg Arg Arg His Gln Asp Leu Pro Arg
130 135 140

(2) INFORMATION FOR SEQ ID NO:3080:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 826 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..826

(D) OTHER INFORMATION: / Ceres Seq. ID 1575439

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3080:

gcagataaca accagcaatg gtcacgactg ccgtcgccgc gccgtgccgc 60
cagctcggaa agcccaagcg gtaactgtgg ccacaaccac agcactacct cccaccctca 120
ctagaaggca gctcctcgcc cgggtcgcca ccggctccac cctcccacgc gccgcgcct 180
cagctcgccg ccccaggttc cccgagatgc cgggtccggc cggcgtgaag gccctggacc 240
ttcgggaagg ttcgggagag atcccgccgc ttggcgacca ggttcgggtt cactattatg 300
ggagattagc agcgaaGcaa ggaatggcgt tggattcgac gtatgatcac aaggacgaga 360
ccggcgatcc catgccgttt gtcttcaccc ttgggtccgg caaggttata cctggcattg 420
aagcagcagt gaagtccatg agagtggcgc gtcttcgcgc agtgatcatt ccaccatcgc 480
agggatacca aaacacgtca caagaaccgg ttcttcctaa tttctttgat cggcagaggc 540

tggtcaccac tatattcaac ccgacgcgcc tcgcaaatgg cgagggttcc actctcggca 600
cacttatctt cgacatcgag ctaatcaaca ttaggcaacg ttcataactg ttctgctcca 660
tactcttggt tctaaaaagt tggtccgtgc aagaatctgg ttatgottta agtaactgtc 720
agcgctcttc ggccaatccc caattacata ttgtaatgca tactgatcgc tgacagacga 780
tatatgaaga aaaatcaatt gaatgcggat ttgattccgt tggttct

(2) INFORMATION FOR SEQ ID NO:3081:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 209 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..209

(D) OTHER INFORMATION: / Ceres Seq. ID 1575440

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3081:

Met	Val	Thr	Thr	Ala	Val	Ala	Ala	Val	Ala	Gly	Ala	Val	Pro	Pro	Ala
1			5					10					15		
Arg	Lys	Ala	Gln	Ala	Val	Thr	Val	Ala	Thr	Thr	Thr	Ala	Leu	Pro	Pro
			20				25						30		
Thr	Leu	Thr	Arg	Arg	Gln	Leu	Leu	Ala	Ala	Val	Ala	Thr	Gly	Ser	Thr
			35				40					45			
Leu	Pro	Thr	Ala	Ala	Ala	Ser	Ala	Ala	Ala	Pro	Arg	Phe	Ala	Glu	Ile
			50				55					60			
Pro	Gly	Ser	Gly	Gly	Val	Lys	Ala	Leu	Asp	Leu	Arg	Glu	Gly	Ser	Gly
			65				70					75			80
Glu	Ile	Pro	Ala	Val	Gly	Asp	Gln	Val	Ala	Val	His	Tyr	Tyr	Gly	Arg
			85						90				95		
Leu	Ala	Ala	Lys	Gln	Gly	Trp	Arg	Phe	Asp	Ser	Thr	Tyr	Asp	His	Lys
			100					105					110		
Asp	Glu	Thr	Gly	Asp	Pro	Met	Pro	Phe	Val	Phe	Thr	Leu	Gly	Ser	Gly
			115				120						125		
Lys	Val	Ile	Pro	Gly	Met	Glu	Ala	Ala	Val	Lys	Ser	Met	Arg	Val	Gly
			130				135					140			
Gly	Leu	Arg	Arg	Val	Ile	Pro	Pro	Ser	Gln	Gly	Tyr	Gln	Asn	Thr	
			145				150					155		160	
Ser	Gln	Glu	Pro	Val	Pro	Pro	Asn	Phe	Phe	Asp	Arg	Gln	Arg	Leu	Phe
			165					170					175		
Thr	Thr	Ile	Phe	Asn	Pro	Thr	Arg	Leu	Ala	Asn	Gly	Glu	Gly	Ser	Thr
			180				185						190		
Leu	Gly	Thr	Leu	Ile	Phe	Asp	Ile	Glu	Leu	Ile	Asn	Ile	Arg	Gln	Arg
			195				200					205			
Ser															

(2) INFORMATION FOR SEQ ID NO:3082:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 529 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..529

(D) OTHER INFORMATION: / Ceres Seq. ID 1575441

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3082:

ctcgtctcca	ctgctctgct	gctcctcgca	ccgcgcgcgc	cgccgcgcga	gcgcagtaat	60
gGcttcgcgc	cggtgtctcc	ggaacgcggg	ctcccggcgc	ctctctctct	acctactct	120
ccgcgcgcgt	gcgatatatg	tactctctgc	gctaccgcgt	gcgcgcgcgc	cgccgcgcgc	180
gccggNccca	gccgcaccg	acggccggga	ccctctgggc	gaggtctatg	gccaccttca	240

cgcgacagaa gccocatgtg aatgtcggca ccattgggca cgtcgatcac ggcaaaacca 300
ctctcactgc tgcattacc aaggtcctgg ccgaggcagg gaaggccaaa gccgttggtt 360
tcgacgagat cgacaaggct ccggaggaga aagccagagg aatcaccatt gcgacagCtc 420
acgtcgagta tgagacggct aaaaggcatt atgtccacgt tgattgtcca ggtcacgcag 480
attatgtcaa gaacatgac actggagctg ctcagcgttt cctgtgttc

(2) INFORMATION FOR SEQ ID NO:3083:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 143 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..143
- (D) OTHER INFORMATION: / Ceres Seq. ID 1575442

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3083:

Ser Ser Pro Leu Leu Cys Cys Ser Ser His Arg Arg Arg Arg Arg Arg
1 5 10 15
Ser Asp Val Met Ala Ser Ala Ala Val Leu Arg Asn Ala Gly Ser Arg
20 25 30
Arg Leu Phe Ser Tyr Pro Thr Leu Arg Ala Ala Ala Ile Tyr Val Pro
35 40 45
Ser Ala Leu Pro Asp Ala Pro Ala Ala Ala Ala Pro Xaa Pro Ala
50 55 60
Ala Thr Asp Gly Arg Asp Pro Leu Gly Glu Val Tyr Gly His Leu His
65 70 75 80
Ala His Glu Ala Pro Cys Glu Cys Arg His His Trp Ala Arg Arg Ser
85 90 95
Arg Gln Asn His Ser His Cys Cys His Tyr Gln Gly Pro Gly Arg Gly
100 105 110
Arg Glu Gly Gln Ser Arg Cys Phe Arg Arg Asp Arg Gln Gly Ser Gly
115 120 125
Gly Glu Ser Gln Arg Asn His His Cys Asp Ser Ser Arg Arg Val
130 135 140

(2) INFORMATION FOR SEQ ID NO:3084:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 124 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..124
- (D) OTHER INFORMATION: / Ceres Seq. ID 1575443

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3084:

Met Ala Ser Ala Ala Val Leu Arg Asn Ala Gly Ser Arg Arg Leu Phe
1 5 10 15
Ser Tyr Pro Thr Leu Arg Ala Ala Ala Ile Tyr Val Pro Ser Ala Leu
20 25 30
Pro Asp Ala Pro Ala Ala Ala Ala Pro Xaa Pro Ala Ala Thr Asp
35 40 45
Gly Arg Asp Pro Leu Gly Glu Val Tyr Gly His Leu His Ala His Glu
50 55 60
Ala Pro Cys Glu Cys Arg His His Trp Ala Arg Ser Arg Gln Asn
65 70 75 80
His Ser His Cys Cys His Tyr Gln Gly Pro Gly Arg Gly Arg Glu Gly
85 90 95
Gln Ser Arg Cys Phe Arg Arg Asp Arg Gln Gly Ser Gly Gly Glu Ser
100 105 110

Gln Arg Asn His His Cys Asp Ser Ser Arg Arg Val
115 120

(2) INFORMATION FOR SEQ ID NO:3085:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 130 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..130

(D) OTHER INFORMATION: / Ceres Seq. ID 1575444

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3085:

Met	Tyr	Leu	Leu	Arg	Tyr	Pro	Met	Arg	Pro	Arg	Arg	Arg	Gln	Arg	Arg
1									10				15		
Xaa	Gln	Pro	Pro	Pro	Thr	Ala	Gly	Thr	Leu	Trp	Ala	Arg	Ser	Met	Ala
									25				30		
Thr	Phe	Thr	Arg	Thr	Lys	Pro	His	Val	Asn	Val	Gly	Thr	Ile	Gly	His
									40				45		
Val	Asp	His	Gly	Lys	Thr	Thr	Leu	Thr	Ala	Ala	Ile	Thr	Lys	Val	Leu
									55				60		
Ala	Glu	Ala	Gly	Lys	Ala	Lys	Ala	Val	Ala	Phe	Asp	Glu	Ile	Asp	Lys
									70				75		
Ala	Pro	Glu	Glu	Lys	Ala	Arg	Gly	Ile	Thr	Ile	Ala	Thr	Ala	His	Val
									90				95		
Glu	Tyr	Glu	Thr	Ala	Lys	Arg	His	Tyr	Ala	His	Val	Asp	Cys	Pro	Gly
									105				110		
His	Ala	Asp	Tyr	Val	Lys	Asn	Met	Ile	Thr	Gly	Ala	Ala	Gln	Arg	Phe
									120				125		

Leu Cys
130

(2) INFORMATION FOR SEQ ID NO:3086:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 632 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..632

(D) OTHER INFORMATION: / Ceres Seq. ID 1575460

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3086:

atttctctc	ccactcccaa	ccaaaccgctc	gctaactatc	actagtgcgc	gtgtgggtggt	60
cgctgctcata	tcctctcgctc	ctgcctcgcag	cgcccgatcg	cccatagcct	gctggcctgc	120
tctgctagcc	atggaccggt	ccaagtcgta	cgcgggcggg	cgcatgcaga	tcgagccgta	180
ctacggcgccg	ggcggcgggc	gaggaggagg	cgcgggggcg	gacttcgggt	cctactccta	240
cagcgccggc	gggacggggc	cgctgctcta	ctgcataaac	cagtcacagt	acggaggccc	300
ggggggcggt	gaggaggagg	tgaagcagag	caagtcgaag	cgcggtggc	tggcggaacc	360
ggacatggac	cgcaagcgcc	cgctggtggc	cgtacaaggc	gtacggcggt	gagggaaggg	420
tgaagggtc	cctccgaag	agcttcagggt	gggtcaagga	ccgtacacgc	gacctgtgtc	480
acggttggtc	ctgatccta	gagcacgcac	accacgcgc	tcctggtgtg	tgtttgtgtc	540
ctcgtagatg	ttgttcatcc	ttcctggtga	tgtgaaacca	accagtagag	tgtatgtatt	600
catgagatgt	gtgactcaag	aggtgtgttc	ag			

(2) INFORMATION FOR SEQ ID NO:3087:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 181 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..181

(D) OTHER INFORMATION: / Ceres Seq. ID 1575461

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3087:

Phe Leu Leu Pro Leu Pro Thr Lys Pro Ser Leu Thr Ile Thr Ser Arg
1 5 10 15
Arg Val Val Val Val Val Ile Ser Leu Ala Ser Ala Ser Thr Ala Arg
20 25 30
Ser Pro Ile Ala Cys Trp Pro Ala Leu Leu Ala Met Asp Arg Ser Lys
35 40 45
Ser Tyr Ala Gly Gly Arg Met Gln Ile Glu Pro Tyr Tyr Gly Gly Gly
50 55 60
Gly Gly Gly Gly Gly Gly Ala Arg Ala Asp Phe Arg Ser Tyr Ser Tyr
65 70 75 80
Ser Ala Gly Gly Thr Gly Pro Ser Ser Tyr Ser Tyr Asn Gln Tyr Glu
85 90 95
Tyr Gly Gly Pro Gly Ala Gly Glu Glu Glu Val Lys Gln Ser Lys Ser
100 105 110
Lys Arg Arg Trp Leu Ala Asp Pro Asp Met Asp Arg Lys Arg Pro Arg
115 120 125
Gly Gly Val Gln Gly Val Arg Arg Gly Gly Gln Gly Glu Gly Leu Pro
130 135 140
Pro Gln Glu Leu Gln Val Gly Gln Gly Pro Leu Pro Arg Pro Arg Leu
145 150 155 160
Arg Leu Val Leu Ile Leu Arg Ala Arg Thr Pro Pro Leu Ser Met Val
165 170 175
Val Val Trp Leu Ser
180

(2) INFORMATION FOR SEQ ID NO:3088:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 138 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..138

(D) OTHER INFORMATION: / Ceres Seq. ID 1575462

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3088:

Met Asp Arg Ser Lys Ser Tyr Ala Gly Gly Arg Met Gln Ile Glu Pro
1 5 10 15
Tyr Tyr Gly Gly Gly Gly Gly Gly Gly Ala Arg Ala Asp Phe
20 25 30
Arg Ser Tyr Ser Tyr Ser Ala Gly Gly Thr Gly Pro Ser Ser Tyr Ser
35 40 45
Tyr Asn Gln Tyr Glu Tyr Gly Gly Pro Gly Ala Gly Glu Glu Glu Val
50 55 60
Lys Gln Ser Lys Ser Lys Arg Arg Trp Leu Ala Asp Pro Asp Met Asp
65 70 75 80
Arg Lys Arg Pro Arg Gly Gly Val Gln Gly Val Arg Arg Gly Gly Gln
85 90 95
Gly Glu Gly Leu Pro Pro Gln Glu Leu Gln Val Gly Gln Gly Pro Leu
100 105 110
Pro Arg Pro Arg Leu Arg Leu Val Leu Ile Leu Arg Ala Arg Thr Pro
115 120 125
Pro Leu Ser Met Val Val Val Trp Leu Ser
130 135

(2) INFORMATION FOR SEQ ID NO:3089:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 127 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..127
 (D) OTHER INFORMATION: / Ceres Seq. ID 1575463
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3089:
Met Gln Ile Glu Pro Tyr Tyr Gly Gly Gly Gly Gly Gly Gly Gly
1 5 10 15
Ala Arg Ala Asp Phe Arg Ser Tyr Ser Tyr Ser Ala Gly Gly Thr Gly
 20 25 30
Pro Ser Ser Tyr Ser Tyr Asn Gln Tyr Glu Tyr Gly Gly Pro Gly Ala
 35 40 45
Gly Glu Glu Glu Val Lys Gln Ser Lys Ser Lys Arg Arg Trp Leu Ala
 50 55 60
Asp Pro Asp Met Asp Arg Lys Arg Pro Arg Gly Gly Val Gln Gly Val
65 70 75 80
Arg Arg Gly Gly Gln Gly Glu Gly Leu Pro Pro Gln Glu Leu Gln Val
 85 90 95
Gly Gln Gly Pro Leu Pro Arg Pro Arg Leu Arg Leu Val Leu Ile Leu
 100 105 110
Arg Ala Arg Thr Pro Pro Leu Ser Met Val Val Val Trp Leu Ser
 115 120 125

(2) INFORMATION FOR SEQ ID NO:3090:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 745 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -
(B) LOCATION: 1..745
(D) OTHER INFORMATION: / Ceres Seq. ID 1575488

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3090:

aaaaattcca agagatgaac atcttgttga gtcaactgtg ttgctgcatt cttattctag 60
gcattctacgc tccgacatcc gccacatcag acaatcctcc tctgcaggat gtagtccccca 120
tggtctcccca gggcgagcgg cgagagttgt ccatgaacgg gtctcctctgc aagcatccga 180
gcaccatcct ggcgctccgac ttcaagactc tgatgctaaa ccacgcccga gacctggaca 240
gcatagcctc ggctgctcgt gacgatgggt accgctgcgg agttcccagg cctgaacacc 300
ctgggcctgt cgatggcgcg caccgacatc gCccctacg ggtggtgtct ccgcactccc 360
caccgcgggg cgtcgagagt gatgttcgta cacgggtgcca gcgtggtggc cggttctctg 420
gacacccagg gcaggctgtt ccagaagcgt ctcggtgagg gagaggtggt cgtcttcccc 480
cgcggcttgc ttactactgt catgaactac ggtttcgccc tcgcgacggc gttctcctgt 540
ctgaacagcc agaaaccccg cgtggctcgt gtgcgccacg ccatgttttt tgcgagtgag 600
tcggacgtag tcgaaggtct aatggccagg atgctcaagt ttggagagat ggaggtgact 660
agtgaacaaca acatcactgc tggtttccca tgggcattct gatctgagta ggtgcaattc 720
aagatcgttg gtggtttaag ttccc

(2) INFORMATION FOR SEQ ID NO:3091:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 151 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..151

(D) OTHER INFORMATION: / Ceres Seq. ID 1575489

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3091:

Lys Phe Gln Glu Met Asn Ile Leu Leu Ser His Leu Cys Cys Cys Ile
1 5 10 15
Leu Ile Leu Gly Ile Tyr Ala Pro Thr Ser Ala Thr Ser Asp Asn Pro
20 25 30
Pro Leu Gln Asp Val Cys Pro Met Ala Pro Gln Gly Glu Arg Arg Glu
35 40 45
Leu Ser Met Asn Gly Phe Leu Cys Lys His Pro Ser Thr Ile Leu Ala
50 55 60
Ser Asp Phe Lys Thr Leu Met Leu Asn His Ala Gly Asp Leu Asp Ser
65 70 75 80
Ile Ala Ser Val Val Gly Glu His Gly Asp Arg Cys Arg Val Pro Arg
85 90 95
Pro Glu His Pro Gly Pro Val Asp Gly Ala His Arg His Arg Pro Leu
100 105 110
Arg Gly Gly Ala Pro Ala Leu Pro Pro Ala Gly Val Gly Asp Asp Val
115 120 125
Arg Thr Arg Trp Gln Arg Gly Gly Arg Leu Pro Gly His Arg Gly Gln
130 135 140
Ala Val Pro Glu Ala Ser Arg
145 150

(2) INFORMATION FOR SEQ ID NO:3092:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 147 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..147

(D) OTHER INFORMATION: / Ceres Seq. ID 1575490

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3092:

Met Asn Ile Leu Leu Ser His Leu Cys Cys Cys Ile Leu Ile Leu Gly
1 5 10 15
Ile Tyr Ala Pro Thr Ser Ala Thr Ser Asp Asn Pro Pro Leu Gln Asp
20 25 30
Val Cys Pro Met Ala Pro Gln Gly Glu Arg Arg Glu Leu Ser Met Asn
35 40 45
Gly Phe Leu Cys Lys His Pro Ser Thr Ile Leu Ala Ser Asp Phe Lys
50 55 60
Thr Leu Met Leu Asn His Ala Gly Asp Leu Asp Ser Ile Ala Ser Val
65 70 75 80
Val Gly Glu His Gly Asp Arg Cys Arg Val Pro Arg Pro Glu His Pro
85 90 95
Gly Pro Val Asp Gly Ala His Arg His Arg Pro Leu Arg Gly Gly Ala
100 105 110
Pro Ala Leu Pro Pro Ala Gly Val Gly Asp Asp Val Arg Thr Arg Trp
115 120 125
Gln Arg Gly Gly Arg Leu Pro Gly His Arg Gly Gln Ala Val Pro Glu
130 135 140
Ala Ser Arg
145

(2) INFORMATION FOR SEQ ID NO:3093:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 145 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..145
(D) OTHER INFORMATION: / Ceres Seq. ID 1575491

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3093:

Met	Val	Thr	Ala	Ala	Glu	Phe	Pro	Gly	Leu	Asn	Thr	Leu	Gly	Leu	Ser
1		5						10				15			
Met	Ala	Arg	Thr	Asp	Ile	Ala	Pro	Thr	Gly	Val	Val	Leu	Pro	His	Ser
		20					25					30			
His	Pro	Arg	Ala	Ser	Glu	Met	Met	Phe	Val	His	Gly	Gly	Ser	Val	Val
		35					40					45			
Ala	Gly	Phe	Leu	Asp	Thr	Glu	Gly	Arg	Leu	Phe	Gln	Lys	Arg	Leu	Gly
		50					55				60				
Glu	Gly	Glu	Val	Phe	Val	Phe	Pro	Arg	Gly	Leu	Leu	His	Tyr	Val	Met
		65					70				75			80	
Asn	Tyr	Gly	Phe	Gly	Leu	Ala	Thr	Ala	Phe	Ser	Val	Leu	Asn	Ser	Gln
							85			90				95	
Asn	Pro	Gly	Val	Val	Gly	Val	Ala	His	Ala	Met	Phe	Phe	Ala	Ser	Glu
							100			105			110		
Ser	Asp	Val	Val	Glu	Gly	Leu	Met	Ala	Arg	Met	Leu	Lys	Phe	Gly	Glu
		115					120					125			
Met	Glu	Val	Thr	Ser	Asp	Asn	Asn	Ile	Thr	Ala	Gly	Phe	Pro	Trp	Ala
		130					135					140			

Phe
145

(2) INFORMATION FOR SEQ ID NO:3094:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1105 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..1105
(D) OTHER INFORMATION: / Ceres Seq. ID 1575492

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3094:

agaaggaaga	ggctgaccgc	ctgcaagagg	agaggcacca	tttgaagag	agtactcgga	60
aaaagcttct	ggagatggag	cttgcaattt	ctagggcaaa	tgctcagctg	gagaaagcac	120
aagcttctgc	tcgcagacgt	gaggttgaga	atgcacaa	cacgtttacg	atggaagctg	180
caaagcganc	atgcagcaga	gtcagcaaca	aattattcag	agcttttaaa	gaaagacgag	240
aacagccgta	aaaggtctca	gcgttgggaa	ctgatagag	ccctattaca	agaggaactt	300
gcagcacaaa	agagcagggt	atttcgggtt	caagaacaac	tcacgcatgc	taaagaacta	360
aaggtatcaag	tgccaggcaag	gtggaaacaa	gaggaggctg	caaagactga	ggcaattgcc	420
cttgtaacct	cagtgaggaa	agagagaggg	caaattgaga	ctccatgag	gtcagaagag	480
aatttctctg	atctcaagc	agcgaatgac	gcacaaagat	acaagagtga	gatccgtgtc	540
cttgagcagc	gtattgcgca	Gctgaagggt	tcattggact	cttcaagggt	tgctgcccc	600
aagtggggag	gcagacaata	atccatgca	ttgcatcttt	ctgaaggagg	aaagaacac	660
aatgcccaga	ttttgtccaa	cacagcagta	ccccaaagtc	tcgattttga	cgatatacag	720
cgcgaccagg	agtgctcgtat	gtgcttgagc	gaggagatgt	ccgtgggtgt	ctccctctgc	780
gcccaccagg	tcgtctgtgc	caaatgcagc	gacctccatg	agaagcaagg	gatgaaggaa	840
tgccctctgt	gcggggcccc	catccagcgc	agggtgcgag	ccgcctctgc	cggttgctag	900
atttcacata	tactatttgg	attttacttt	tcttcttttt	ttcactttga	ttgtcagct	960
taagttgatg	gaagatttga	gagaataato	aggtggtgtg	agtggttgaa	actgtgcaca	1020
taatacatcg	ttaaacacca	aaacaagccc	agcagacagt	gggtactggt	ttggtttggt	1080
atatggctat	accggttgct	ctctgt				

(2) INFORMATION FOR SEQ ID NO:3095:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 299 amino acids
(B) TYPE: amino acid

- (C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..299
(D) OTHER INFORMATION: / Ceres Seq. ID 1575493
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3095:

Arg Arg Lys Arg Leu Thr Ala Cys Lys Arg Arg Gly Thr Ile Trp Lys
1 5 10 15
Arg Val Leu Gly Lys Ser Phe Trp Arg Trp Ser Leu Gln Phe Leu Gly
20 25 30
Gln Met Leu Ser Trp Arg Lys Gln Lys Leu Leu Leu Ala Asp Val Arg
35 40 45
Leu Arg Met His Asn Ser Arg Tyr Arg Trp Lys Leu Gln Ser Xaa His
50 55 60
Ala Ala Glu Ser Ala Thr Asn Ile Ser Glu Leu Leu Lys Lys Asp Glu
65 70 75 80
Asn Ser Arg Lys Arg Ser Gln Arg Trp Glu Ser Asp Arg Ala Leu Leu
85 90 95
Gln Glu Glu Leu Ala Ala Gln Lys Ser Arg Leu Phe Arg Val Gln Glu
100 105 110
Gln Leu Gln His Ala Lys Glu Leu Lys Asp Gln Val Gln Ala Arg Trp
115 120 125
Lys Gln Glu Glu Ala Ala Lys Thr Glu Ala Ile Ala Leu Val Thr Ser
130 135 140
Val Arg Lys Glu Arg Gly Gln Ile Glu Thr Ser Met Arg Ser Glu Glu
145 150 155 160
Asn Leu Leu His Leu Lys Ala Ala Asn Asp Ala Gln Arg Tyr Lys Ser
165 170 175
Glu Ile Arg Val Leu Glu Gln Arg Ile Ala Gln Leu Lys Val Ser Leu
180 185 190
Asp Ser Ser Arg Val Ala Ala Pro Lys Trp Gly Ala Asp Asn Lys Ser
195 200 205
Tyr Ala Leu His Leu Ser Glu Gly Arg Lys Asn Asn Asn Ala Gln Val
210 215 220
Leu Ser Asn Thr Ala Val Pro Gln Gly Leu Asp Phe Asp Asp Ile Gln
225 230 235 240
Arg Asp Arg Glu Cys Val Met Cys Leu Ser Glu Glu Met Ser Val Val
245 250 255
Phe Leu Pro Cys Ala His Gln Val Val Cys Ala Lys Cys Ser Asp Leu
260 265 270
His Glu Lys Gln Gly Met Lys Glu Cys Pro Ser Cys Arg Ala Pro Ile
275 280 285
Gln Arg Arg Val Arg Ala Arg Pro Ala Gly Cys
290 295

- (2) INFORMATION FOR SEQ ID NO:3096:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 266 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..266
(D) OTHER INFORMATION: / Ceres Seq. ID 1575494
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3096:

Met Leu Ser Trp Arg Lys Gln Lys Leu Leu Leu Ala Asp Val Arg Leu
1 5 10 15
Arg Met His Asn Ser Arg Tyr Arg Trp Lys Leu Gln Ser Xaa His Ala

20 25 30
Ala Glu Ser Ala Thr Asn Ile Ser Glu Leu Leu Lys Lys Asp Glu Asn
35 40 45
Ser Arg Lys Arg Ser Gln Arg Trp Glu Ser Asp Arg Ala Leu Leu Gln
50 55 60
Glu Glu Leu Ala Ala Gln Lys Ser Arg Leu Phe Arg Val Gln Glu Gln
65 70 75 80
Leu Gln His Ala Lys Glu Leu Lys Asp Gln Val Gln Ala Arg Trp Lys
85 90 95
Gln Glu Glu Ala Ala Lys Thr Glu Ala Ile Ala Leu Val Thr Ser Val
100 105 110
Arg Lys Glu Arg Gly Gln Ile Glu Thr Ser Met Arg Ser Glu Glu Asn
115 120 125
Leu Leu His Leu Lys Ala Ala Asn Asp Ala Gln Arg Tyr Lys Ser Glu
130 135 140
Ile Arg Val Leu Glu Gln Arg Ile Ala Gln Leu Lys Val Ser Leu Asp
145 150 155 160
Ser Ser Arg Val Ala Ala Pro Lys Trp Gly Ala Asp Asn Lys Ser Tyr
165 170 175
Ala Leu His Leu Ser Glu Gly Arg Lys Asn Asn Asn Ala Gln Val Leu
180 185 190
Ser Asn Thr Ala Val Pro Gln Gly Leu Asp Phe Asp Asp Ile Gln Arg
195 200 205
Asp Arg Glu Cys Val Met Cys Leu Ser Glu Glu Met Ser Val Val Phe
210 215 220
Leu Pro Cys Ala His Gln Val Val Cys Ala Lys Cys Ser Asp Leu His
225 230 235 240
Glu Lys Gln Gly Met Lys Glu Cys Pro Ser Cys Arg Ala Pro Ile Gln
245 250 255
Arg Arg Val Arg Ala Arg Pro Ala Gly Cys
260 265

(2) INFORMATION FOR SEQ ID NO:3097:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 249 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..249
- (D) OTHER INFORMATION: / Ceres Seq. ID 1575495

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3097:

Met His Asn Ser Arg Tyr Arg Trp Lys Leu Gln Ser Xaa His Ala Ala
1 5 10 15
Glu Ser Ala Thr Asn Ile Ser Glu Leu Leu Lys Lys Asp Glu Asn Ser
20 25 30
Arg Lys Arg Ser Gln Arg Trp Glu Ser Asp Arg Ala Leu Leu Gln Glu
35 40 45
Glu Leu Ala Ala Gln Lys Ser Arg Leu Phe Arg Val Gln Glu Gln Leu
50 55 60
Gln His Ala Lys Glu Leu Lys Asp Gln Val Gln Ala Arg Trp Lys Gln
65 70 75 80
Glu Glu Ala Ala Lys Thr Glu Ala Ile Ala Leu Val Thr Ser Val Arg
85 90 95
Lys Glu Arg Gly Gln Ile Glu Thr Ser Met Arg Ser Glu Glu Asn Leu
100 105 110
Leu His Leu Lys Ala Ala Asn Asp Ala Gln Arg Tyr Lys Ser Glu Ile
115 120 125
Arg Val Leu Glu Gln Arg Ile Ala Gln Leu Lys Val Ser Leu Asp Ser
130 135 140

Ser Arg Val Ala Ala Pro Lys Trp Gly Ala Asp Asn Lys Ser Tyr Ala
145 150 155 160
Leu His Leu Ser Glu Gly Arg Lys Asn Asn Ala Gln Val Leu Ser
165 170 175
Asn Thr Ala Val Pro Gln Gly Leu Asp Phe Asp Asp Ile Gln Arg Asp
180 185 190
Arg Glu Cys Val Met Cys Leu Ser Glu Glu Met Ser Val Val Phe Leu
195 200 205
Pro Cys Ala His Gln Val Val Cys Ala Lys Cys Ser Asp Leu His Glu
210 215 220 235
Lys Gln Gly Met Lys Glu Cys Pro Ser Cys Arg Ala Pro Ile Gln Arg
225 230 240
Arg Val Arg Ala Arg Pro Ala Gly Cys
245

(2) INFORMATION FOR SEQ ID NO:3098:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 780 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..780
- (D) OTHER INFORMATION: / Ceres Seq. ID 1575496

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3098:

agcgagagta	gcggctgctg	atgattctgc	ctttwcttct	ccctccctca	cctgctctct	60
ctctctctcc	ctttcttttc	cgcgcgagcg	gtgacgacga	ccgcgcgass	ccgcgcgactc	120
ctactctgat	cagggtgcctc	ggccttcgtc	gtgctctcgc	ccgcgcaacga	gtatagacgg	180
gcgcgcgatg	ccaccttcga	gctgtaccgg	aggtccacca	tcggcatgtg	cctcaccgag	240
acgtcgcagc	agatggtctc	caacggcacc	ytacgcccgg	agctcgttat	ccagggtctc	300
gtccagttcg	acaagtcctat	gacggatgct	ctggagaacc	aagtgaagag	caaggttact	360
gtcaagggtc	acctgcacac	ctacaggttc	tgtgacaacg	tgtggacctt	catcttgaca	420
gacgcaagct	tcaagaatga	ggaggccacg	gagcagggtg	gcaagggtga	gattgtggca	480
tgtgattcca	aattgctcgg	acaataggcc	tgtgtacctc	cgagggtcaag	gaagggaagct	540
ttnaagtgcg	gcgaggcggg	gtctgtctgc	gcgtcaGctg	tacacgccta	ggctaccogc	600
aggcggggtc	tgctcgcgtc	agctgtacac	gcctagggtac	cgcccgaaacg	gcatttcatt	660
tgctctcttc	gtactgtatg	tgatctcttc	tttttccctc	tgatatacaat	ctgctgcagc	720
tataccggcc	aagagtatgg	catggtatgg	cgccaggcag	ccgcaaaact	gtttttacct	780

(2) INFORMATION FOR SEQ ID NO:3099:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 106 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..106
- (D) OTHER INFORMATION: / Ceres Seq. ID 1575497

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3099:

Met	Ala	Thr	Phe	Glu	Leu	Tyr	Arg	Arg	Ser	Thr	Ile	Gly	Met	Cys	Leu
1		5						10					15		
Thr	Glu	Thr	Leu	Asp	Glu	Met	Val	Ser	Asn	Gly	Thr	Xaa	Ser	Pro	Glu
			20					25					30		
Leu	Ala	Ile	Gln	Val	Leu	Val	Gln	Phe	Asp	Lys	Ser	Met	Thr	Asp	Ala
		35					40					45			
Leu	Glu	Asn	Gln	Val	Lys	Ser	Lys	Val	Thr	Val	Lys	Gly	His	Leu	His
		50				55						60			
Thr	Thr	Arg	Phe	Cys	Asp	Asn	Val	Trp	Thr	Phe	Ile	Leu	Thr	Asp	Ala

(2) INFORMATION FOR SEQ ID NO:3100:

(i) SEQUENCE CHARACTERISTICS:

(i) SEQUENCE CHARACTERISTICS:

(ii) MOLECULE TYPE: peptide

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(ix) FEATURE:
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(D) OTHER INFORMATION: / Ceres Seq. ID 1575498

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3100:

(2) INFORMATION FOR SEO ID NO:3101:

(i) SEQUENCE CHARACTERISTICS:

(ii) MOLECULE TYPE: peptide

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(ix) FEATURE:
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(D) OTHER INFORMATION: / Ceres Seq. ID 1575499

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3101:

(2) INFORMATION FOR SEQ ID NO:3102:

(1) SEQUENCE CHARACTERISTICS:

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -
(B) LOCATION: 1..728
(D) OTHER INFORMATION: / Ceres Seq. ID 1575556

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3102:

aaagtgactg	aaaagtcccg	catgtttctc	tgccctccgt	ccgccgcgcg	aacaaccatt	60
tcctttctta	gcgcgcgcct	cgatccccc	cccaggagcta	cagaaccagt	tcattccaggc	120
gcgaatggcg	gcggcgagga	gcctgtctct	gaggcacctc	cgcttgccgg	cgcccccgtc	180
agcggcgctc	gtgaggccga	cggcgctcgt	gcattgaggcc	ctgtgggggg	agcgggtggat	240
gtcttcggag	gatgccaagg	gccttttctc	ggacaagagc	gaggtcactg	aacgcattcat	300
caaggtcgtc	aagagcttcc	cgaagatcga	tgacccctcc	aaggtgacac	cagatgcccac	360
tttcaagaat	gatcttggcc	tagacagttt	ggatgcagtg	gaggttgtca	tccgctcgga	420
agaggaaattc	agattcgaga	tacctgacaa	tgaaGgctga	caagattgac	tcggctcaag	480
ttgcagttga	cttcattgcc	tcacaccgcc	aagcgaaatg	ataaagatgc	gttgctctggt	540
atagcaaaag	tatatcgta	ttaattctct	tttatgaaga	aagttcagtt	tgaagatgta	600
cactaccgtg	cccatttggg	tacttctgct	gatgctactg	tcctttttgg	aacgaatttt	660
gctactgtgg	attgtctgca	ctaaataaaa	tgtttgaaac	tgagaaggaa	cttggatgcc	720
gtttggtt						

(2) INFORMATION FOR SEQ ID NO:3103:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 71 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1..71
(D) OTHER INFORMATION: / Ceres Seq. ID 1575557

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3103:

Lys	Val	Thr	Glu	Lys	Ser	Arg	Met	Phe	Ser	Cys	Leu	Arg	Ser	Ala	Ala
1				5						10				15	
Ala	Thr	Thr	Ile	Ser	Phe	Ser	Ser	Arg	Arg	Leu	Arg	Ser	Pro	Pro	Glu
				20				25					30		
Ala	Thr	Glu	Pro	Val	His	Pro	Gly	Ala	Asn	Gly	Gly	Gly	Glu	Glu	Pro
		35					40						45		
Ala	Ser	Glu	Ala	Pro	Pro	Leu	Gly	Gly	Gly	Pro	Val	Ser	Gly	Val	Arg
		50				55					60				
Glu	Ala	Asp	Gly	Val	Val	Ala									
65				70											

(2) INFORMATION FOR SEQ ID NO:3104:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 111 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1..111
(D) OTHER INFORMATION: / Ceres Seq. ID 1575558

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3104:

Met	Ala	Ala	Ala	Arg	Ser	Leu	Leu	Leu	Arg	His	Leu	Arg	Leu	Ala	Ala
1				5					10					15	
Ala	Pro	Ser	Ala	Ala	Ser	Val	Arg	Pro	Thr	Ala	Ser	Leu	His	Glu	Ala
				20					25				30		
Leu	Trp	Gly	Gln	Arg	Trp	Met	Ser	Ser	Glu	Asp	Ala	Lys	Gly	Ser	Phe
		35				40						45			
Leu	Asp	Lys	Ser	Glu	Val	Thr	Glu	Arg	Ile	Ile	Lys	Val	Val	Lys	Ser
		50				55					60				
Phe	Pro	Lys	Ile	Asp	Asp	Pro	Ser	Lys	Val	Thr	Pro	Asp	Ala	His	Phe
65				70					75					80	

Lys Asn Asp Leu Gly Leu Asp Ser Leu Asp Ala Val Glu Val Val Met
85 90 95
Ala Leu Glu Glu Glu Phe Arg Phe Glu Ile Pro Asp Asn Glu Gly
100 105 110

- (2) INFORMATION FOR SEQ ID NO:3105:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 73 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..73

(D) OTHER INFORMATION: / Ceres Seq. ID 1575559

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3105:

Met Ser Ser Glu Asp Ala Lys Gly Ser Phe Leu Asp Lys Ser Glu Val
1 5 10 15
Thr Glu Arg Ile Ile Lys Val Val Lys Ser Phe Pro Lys Ile Asp Asp
20 25 30
Pro Ser Lys Val Thr Pro Asp Ala His Phe Lys Asn Asp Leu Gly Leu
35 40 45
Asp Ser Leu Asp Ala Val Glu Val Val Met Ala Leu Glu Glu Phe
50 55 60
Arg Phe Glu Ile Pro Asp Asn Glu Gly
65 70

- (2) INFORMATION FOR SEQ ID NO:3106:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 546 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..546

(D) OTHER INFORMATION: / Ceres Seq. ID 1575573

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3106:

tacatcgagc acgacggcga cgtgttcac gtggaccgca tcaaggagct catcaagtac 60
aagggtcttc aggtcgcccc tgccagagctg gaggccatcc tgcgtgtcca cccgtccgtc 120
gaggaCgcgc cgcgtctcgg gctgcgggac gaggagggcg gcgaggtccc ggcgtgtgtc 180
gtggtgcggc gacgtggcgc gccggagagc gaggcggaca tgatggcgta cgtggcgggg 240
cgcgttgctg cgtacaagaa gctccggctG ctgcgcttcg tggacggcat ccccaagtcg 300
gtgtccggca agatccctcg gaggcagctc agggacgagt tcRgtcaaga agacggcagc 360
agcgtaataa tgcacatcat cctgtggggtg gctgcttgat tataccagtg caagctcctg 420
cattgcggcc ttgatgaaga caataataca attagggtag agtcagatgt tccaggctag 480
tgatacaatt gttgtttctg caaaaggtag tcccaactag tgcataataca ttggcattgt 540
ggacct

- (2) INFORMATION FOR SEQ ID NO:3107:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 132 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..132

(D) OTHER INFORMATION: / Ceres Seq. ID 1575574

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3107:

Tyr Ile Asp Asp Asp Gly Asp Val Phe Ile Val Asp Arg Ile Lys Glu

1 5 10 15
Leu Ile Lys Tyr Lys Gly Phe Gln Val Ala Pro Ala Glu Leu Glu Ala
20 25 30
Ile Leu Leu Ser His Pro Ser Val Glu Asp Ala Ala Val Phe Gly Leu
35 40 45
Pro Asp Glu Glu Ala Gly Glu Val Pro Ala Ser Cys Val Val Arg Arg
50 55 60
Arg Gly Ala Pro Glu Ser Glu Ala Asp Met Met Ala Tyr Val Ala Gly
65 70 75 80
Arg Val Ala Ser Tyr Lys Lys Leu Arg Leu Leu Arg Phe Val Asp Ala
85 90 95
Ile Pro Lys Ser Val Ser Gly Lys Ile Leu Arg Arg Gln Leu Arg Asp
100 105 110
Glu Phe Xaa Gln Glu Asp Gly Ser Ser Val Ile Met His Ile Ile Leu
115 120 125
Trp Val Ala Ala
130

(2) INFORMATION FOR SEQ ID NO:3108:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 73 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..73
- (D) OTHER INFORMATION: / Ceres Seq. ID 1575575

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3108:

Thr Ser Thr Thr Thr Ala Thr Cys Ser Ser Trp Thr Ala Ser Arg Ser
1 5 10 15
Ser Ser Ser Thr Arg Ala Ser Arg Ser Pro Leu Pro Ser Trp Arg Pro
20 25 30
Ser Cys Cys Leu Thr Arg Pro Ser Arg Thr Pro Pro Ser Ser Gly Cys
35 40 45
Arg Thr Arg Arg Pro Ala Arg Ser Arg Arg Arg Ala Trp Cys Gly Asp
50 55 60
Val Ala Arg Arg Arg Ala Arg Arg Thr
65 70

(2) INFORMATION FOR SEQ ID NO:3109:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 143 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..143
- (D) OTHER INFORMATION: / Ceres Seq. ID 1575576

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3109:

His Arg Arg Arg Arg Arg Val His Arg Gly Pro His Gln Gly Ala
1 5 10 15
His Gln Val Gln Gly Leu Pro Gly Arg Pro Cys Arg Ala Gly Gly His
20 25 30
Pro Ala Val Ser Pro Val Arg Arg Gly Arg Arg Leu Arg Ala Ala
35 40 45
Gly Arg Gly Gly Arg Arg Gly Pro Gly Val Val Arg Gly Ala Ala Thr
50 55 60
Trp Arg Ala Gly Glu Arg Gly Gly His Asp Gly Val Arg Gly Gly Ala
65 70 75 80

Arg Cys Val Val Gln Glu Ala Pro Ala Ala Ala Leu Arg Gly Arg His
85 90 95
Pro Gln Val Gly Val Arg Gln Asp Pro Ala Glu Ala Ala Gln Gly Arg
100 105 110
Val Xaa Ser Arg Arg Arg Gln Gln Arg Asn Asn Ala His His Pro Val
115 120 125
Gly Gly Cys Leu Ile Ile Pro Val Gln Asp Pro Ala Phe Ala Thr
130 135 140

(2) INFORMATION FOR SEQ ID NO:3110:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 883 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..883

(D) OTHER INFORMATION: / Ceres Seq. ID 1575588

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3110:

gtccaccctt	cggggtcacc	ggcttctgct	ttcttgtctac	gccaccgcgc	ctctcgtcta	60
tttatggagt	ccccgatcc	atgaagccgg	ggcaggccga	gagttgtcaa	ggacgacgtc	120
tgcgcggcagt	gctcctgctc	ctctctctcc	ttcttggcgc	ccgcgcggagc	ttgggttagt	180
tagtgtctct	ttcttcgcga	gacctgtgag	aggagccatc	atcatggccg	ctgttgagac	240
tgtttgctct	aaggtttgcta	tgtcatgcga	gggctgcgc	ggggcgggtca	gaagagtgct	300
ctccaagatg	gaaggagttg	aaaccttcga	catagacctc	aaggagcaga	aggtgacagt	360
caaaagcaat	gtcaagcctg	aggacgtctt	ccagacggtt	tccaagtccg	ggaagaggac	420
ctcgtactgg	gaGggcgaaG	Ccagggcccc	ggacgctgcg	gcggtccag	aagccgaagc	480
agctccacag	accgcggcag	aagcgctccc	tgctgctgct	ccgcgcggcg	cagagatcac	540
cccagccaaa	stgacgcctg	atcgctcacg	tattattcac	tcacatgtga	tgctgcggtt	600
gcgactccta	aaaccttaaa	ctagaaaatg	ctggggattg	agtttgcaat	gcactcgtgtt	660
cttgccggctg	tagcaagtga	ctataagaat	aatggaataa	acgatgacca	actggcggtat	720
gtttataata	aagcaaatgg	tgatgtgtgt	gagatgcac	acgttagggt	agaaagtgac	780
gatgtgtatg	ctggtgtgtg	tggtgagcct	cagatttttc	aaatgaatgc	ttctgtcgcg	840
gagtcacagc	cacaacgatg	cgtgcacaa	gcgtgggaatt	att		

(2) INFORMATION FOR SEQ ID NO:3111:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 223 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..223

(D) OTHER INFORMATION: / Ceres Seq. ID 1575589

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3111:

Ser Thr Phe Arg Gly His Arg Leu Leu Leu Ser Cys Tyr Ala Thr Ala	5	10	15
Pro Leu Val Tyr Leu Trp Ser Pro Pro Ile His Glu Ala Gly Ala Gly	20	25	30
Arg Glu Leu Ser Arg Thr Thr Ser Ala Gly Ser Ala Pro Ala Pro Pro	35	40	45
Pro Pro Ser Trp Pro Pro Arg Glu Leu Gly Leu Val Ser Val Ser Ser	50	55	60
Ser Arg Arg Pro Val Arg Gly Ala Ile Ile Met Ala Ala Val Glu Thr	65	70	75
Val Val Leu Lys Val Ala Met Ser Cys Glu Gly Cys Ala Gly Ala Val	85	90	95
Arg Arg Val Leu Ser Lys Met Glu Gly Val Glu Thr Phe Asp Ile Asp	100	105	110

Leu Lys Glu Gln Lys Val Thr Val Lys Gly Asn Val Lys Pro Glu Asp
115 120 125
Val Phe Gln Thr Val Ser Lys Ser Gly Lys Arg Thr Ser Tyr Trp Glu
130 135 140
Gly Glu Ala Thr Ala Pro Asp Ala Ala Ala Pro Glu Ala Glu Ala
145 150 155 160
Ala Pro Ser Thr Ala Ala Glu Ala Pro Pro Ala Ala Ala Pro Ala Ala
165 170 175
Pro Glu Ile Thr Pro Ala Lys Xaa Thr Pro Asp Arg His Ala Ile Ile
180 185 190
His Ser His Val Met Leu Arg Leu Arg Leu Leu Asn Leu Lys Ser Arg
195 200 205
Asn Ser Trp Gly Leu Ser Leu His Cys Ile Val Phe Leu Pro Val
210 215 220

(2) INFORMATION FOR SEQ ID NO:3112:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 149 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..149

(D) OTHER INFORMATION: / Ceres Seq. ID 1575590

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3112:

Met Ala Ala Val Glu Thr Val Val Leu Lys Val Ala Met Ser Cys Glu
1 5 10 15
Gly Cys Ala Gly Ala Val Arg Arg Val Leu Ser Lys Met Glu Gly Val
20 25 30
Glu Thr Phe Asp Ile Asp Leu Lys Glu Gln Lys Val Thr Val Lys Gly
35 40 45
Asn Val Lys Pro Glu Asp Val Phe Gln Thr Val Ser Lys Ser Gly Lys
50 55 60
Arg Thr Ser Tyr Trp Glu Gly Glu Ala Thr Ala Pro Asp Ala Ala Ala
65 70 75 80
Ala Pro Glu Ala Glu Ala Ala Pro Ser Thr Ala Ala Glu Ala Pro Pro
85 90 95
Ala Ala Ala Pro Ala Ala Pro Glu Ile Thr Pro Ala Lys Xaa Thr Pro
100 105 110
Asp Arg His Ala Ile Ile His Ser His Val Met Leu Arg Leu Arg Leu
115 120 125
Leu Asn Leu Lys Ser Arg Asn Ser Trp Gly Leu Ser Leu His Cys Ile
130 135 140
Val Phe Leu Pro Val
145

(2) INFORMATION FOR SEQ ID NO:3113:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 137 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..137

(D) OTHER INFORMATION: / Ceres Seq. ID 1575591

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3113:

Met Ser Cys Glu Gly Cys Ala Gly Ala Val Arg Arg Val Leu Ser Lys
1 5 10 15
Met Glu Gly Val Glu Thr Phe Asp Ile Asp Leu Lys Glu Gln Lys Val

Thr	Val	Lys	Gly	Asn	Val	Lys	Pro	Glu	Asp	Val	Phe	Gln	Thr	Val	Ser
		35					40					45			
Lys	Ser	Gly	Lys	Arg	Thr	Ser	Tyr	Trp	Glu	Gly	Glu	Ala	Thr	Ala	Pro
		50				55					60				
Asp	Ala	Ala	Ala	Ala	Pro	Glu	Ala	Glu	Ala	Ala	Pro	Ser	Thr	Ala	Ala
		65			70					75				80	
Glu	Ala	Pro	Pro	Ala	Ala	Ala	Pro	Ala	Ala	Pro	Glu	Ile	Thr	Pro	Ala
			85					90					95		
Lys	Xaa	Thr	Pro	Asp	Arg	His	Ala	Ile	Ile	His	Ser	His	Val	Met	Leu
			100					105					110		
Arg	Leu	Arg	Leu	Leu	Asn	Leu	Lys	Ser	Arg	Asn	Ser	Trp	Gly	Leu	Ser
		115				120						125			
Leu	His	Cys	Ile	Val	Phe	Leu	Pro	Val							
		130				135									

(2) INFORMATION FOR SEQ ID NO:3114:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 698 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -

- (B) LOCATION: 1..698

- (D) OTHER INFORMATION: / Ceres Seq. ID 1575592

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3114:

acacatatc	cctacgcctc	gctatcgctc	tccgcgaact	gaggactccc	gagaggccga	60
gaccaccccg	atgtccgcga	tggagaccga	catcaacgcg	ccgccgccg	ccccagccgg	120
cgagggatcc	tcgtcggtc	cgtctcctc	atctcccg	aagcccaaca	agcgcttoga	180
gatcaagaag	tggaaacgcg	tcgcgtctg	ggcatgggat	atcgtcgtcg	acaactgcgc	240
catctgccgc	aaccacatca	tggatctatg	catcgagtgc	caggcggaacc	aaGctagcgc	300
gaccagcgag	gagtgactg	tcgcttgggg	tgtctgtaat	catgcttttc	acttccactg	360
catcagcagg	tggcttaaga	ctcgccaaat	gtgccatta	gataacagtg	agtgaggagt	420
ccagaaatat	ggccactagt	tctctggcac	cgtcatgtga	tgttggggct	tgtctggcac	480
tcaagtgttt	tgtcttgcca	aacagctcca	tctcttactg	ctttcgatgc	tgcacatcat	540
caccgcgtcaa	ttataactag	ctagcagtag	gtacacctgg	gactgtattt	ggacgatcca	600
ttgagaggat	agtagggcca	ttttatcaat	ggtagtgga	tcttcataag	tgagcttgta	660
ttgtgctgtg	gtaccatttt	ctgaagtcac	gttttttt			

(2) INFORMATION FOR SEQ ID NO:3115:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 145 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide

- (B) LOCATION: 1..145

- (D) OTHER INFORMATION: / Ceres Seq. ID 1575593

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3115:

His	Ile	Phe	Pro	Thr	Pro	Arg	Tyr	Arg	Leu	Pro	Arg	Thr	Glu	Asp	Ser
			5					10					15		
Arg	Glu	Ala	Glu	Thr	Thr	Pro	Met	Ser	Ala	Met	Glu	Thr	Asp	Ile	Asn
			20					25					30		
Ala	Pro	Pro	Pro	Ala	Pro	Ala	Gly	Glu	Gly	Ser	Ser	Val	Gly	Pro	Ser
		35					40					45			
Ser	Ser	Ser	Ser	Arg	Lys	Pro	Asn	Lys	Arg	Phe	Glu	Ile	Lys	Lys	Trp
		50				55					60				
Asn	Ala	Val	Ala	Leu	Trp	Ala	Trp	Asp	Ile	Val	Val	Asp	Asn	Cys	Ala
		65			70			75						80	

Ile Cys Arg Asn His Ile Met Asp Leu Cys Ile Glu Cys Gln Ala Asn
85 90 95
Gln Ala Ser Ala Thr Ser Glu Glu Cys Thr Val Ala Trp Gly Val Cys
100 105 110
Asn His Ala Phe His Phe His Cys Ile Ser Arg Trp Leu Lys Thr Arg
115 120 125
Gln Val Cys Pro Leu Asp Asn Ser Glu Trp Glu Phe Gln Lys Tyr Gly
130 135 140
His
145

(2) INFORMATION FOR SEQ ID NO:3116:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 132 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..132

(D) OTHER INFORMATION: / Ceres Seq. ID 1575594

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3116:

Thr Tyr Ser Leu Arg Leu Ala Ile Ala Phe Arg Glu Leu Arg Thr Pro
1 5 10 15
Glu Arg Pro Arg Pro Pro Arg Cys Pro Pro Trp Arg Pro Thr Ser Thr
20 25 30
Arg Arg Arg Pro Pro Gln Pro Ala Arg Asp Pro Pro Ser Val Arg Pro
35 40 45
Pro His Pro Pro Ala Ser Pro Thr Ser Ala Ser Arg Ser Arg Ser Gly
50 55 60
Thr Pro Ser Arg Ser Gly His Gly Ile Ser Ser Ser Thr Thr Ala Pro
65 70 75 80
Ser Ala Ala Thr Thr Ser Trp Ile Tyr Ala Ser Ser Ala Arg Arg Thr
85 90 95
Lys Leu Ala Arg Pro Ala Arg Ser Ala Leu Ser Leu Gly Val Ser Val
100 105 110
Ile Met Leu Phe Thr Ser Thr Ala Ser Ala Gly Gly Leu Arg Leu Ala
115 120 125
Lys Cys Ala His
130

(2) INFORMATION FOR SEQ ID NO:3117:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 122 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..122

(D) OTHER INFORMATION: / Ceres Seq. ID 1575595

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3117:

Met Ser Ala Met Glu Thr Asp Ile Asn Ala Pro Pro Pro Ala Pro Ala
1 5 10 15
Gly Glu Gly Ser Ser Val Gly Pro Ser Ser Ser Ser Arg Lys Pro
20 25 30
Asn Lys Arg Phe Glu Ile Lys Lys Trp Asn Ala Val Ala Leu Trp Ala
35 40 45
Trp Asp Ile Val Val Asp Asn Cys Ala Ile Cys Arg Asn His Ile Met
50 55 60
Asp Leu Cys Ile Glu Cys Gln Ala Asn Gln Ala Ser Ala Thr Ser Glu

65	70	75	80
Glu Cys Thr Val Ala Trp Gly Val Cys Asn His Ala Phe His Phe His			
85	90	95	
Cys Ile Ser Arg Trp Leu Lys Thr Arg Gln Val Cys Pro Leu Asp Asn			
100	105	110	
Ser Glu Trp Glu Phe Gln Lys Tyr Gly His			
115	120		

(2) INFORMATION FOR SEQ ID NO:3118:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 708 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..708
- (D) OTHER INFORMATION: / Ceres Seq. ID 1575596

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3118:

ahtcga	aaaa	agacat	caga	aacca	agta	cagc	accact	gacc	acca	aa	ccacca	atca	60
tgccgc	ccac	tttgcat	ctc	cac	ctcct	cg	tgacc	ctt	ct	ttctg	tcgc	actc	120
tgccct	ctgt	tgccgac	gac	tcgc	ccgc	cg	cacc	caacc	acc	ggc	accg	ccgc	180
ccgcgt	acca	gatcgt	ggag	cggt	aca	caat	tcac	gcag	gg	cat	ctt	gcg	240
cggggt	acgt	ctca	Na	cg	cg	gct	ctc	gag	gt	ac	ctc	ccgc	300
ttccgc	gcgc	gcag	cat	gcg	ggt	cc	agta	c	agc	ag	ccgc	g	360
ctgtcc	atca	cat	ctc	tg	ga	gg	ag	tg	ga	gt	gc	g	420
aagc	agtg	acc	gc	ga	gc	gc	gc	ctc	cg	gt	tt	ctc	480
ttcccc	atgc	acac	att	gc	caac	ag	cccc	caat	gc	ag	ct	gc	540
gga	aaaa	gc	gt	ta	gt	tt	tt	ct	tg	tt	gt	aa	600
caag	ga	tg	ga	tg	ta	ca	ag	ag	at	cc	ag	gc	660
tc	ta	ct	gt	gc	tt	gc	tt	gc	tt	gc	tt	gc	

(2) INFORMATION FOR SEQ ID NO:3119:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 195 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..195
- (D) OTHER INFORMATION: / Ceres Seq. ID 1575597

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3119:

Ser	Lys	Lys	Asp	Ile	Arg	Asn	Gln	Val	Pro	Ala	Pro	Leu	Thr	Lys
1			5					10					15	
Pro	Pro	Ile	Met	Ala	Ala	Thr	Leu	His	Leu	His	Leu	Leu	Val	Thr
			20					25						
Leu	Phe	Val	Ala	Thr	Leu	Thr	Val	Ala	Ser	Val	Ala	Asp	Asp	Ser
			35					40				45		
Pro	Ala	Pro	Thr	Pro	Pro	Ala	Pro	Pro	Gln	Pro	Thr	Ala	Tyr	Gln
			50			55					60			
Leu	Glu	Arg	Tyr	Asn	Phe	Thr	Gln	Gly	Ile	Leu	Pro	Gln	Gly	Val
			65			70			75					80
Gly	Tyr	Val	Leu	Xaa	Arg	Arg	Arg	Leu	Leu	Arg	Gly	Val	Pro	Pro
			85					90					95	
Gly	Leu	Gln	Leu	Pro	Arg	Arg	Gln	His	Ala	Gly	Pro	Val	Gln	Gln
			100				105						110	
Arg	Arg	Arg	Pro	His	Ser	Ala	Ala	Val	His	His	Ile	Pro	Gly	Gly
			115				120						125	
Glu	Gly	Glu	Gly	Ala	Val	Leu	Val	Gly	Arg	Arg	Gln	Ala	Gly	Arg
			130				135						140	

Arg Arg Arg Pro Ala Pro Phe Leu Arg Arg Pro Tyr Val Glu Ile Val
145 150 155 160
Pro His Arg His Ile Cys Gln Gln Pro Pro Met Gln Leu Arg Pro Phe
165 170 175
Gly Arg Leu Arg Lys Lys Ser Leu Leu Val Ser Phe Phe Leu Cys Xaa
180 185 190
Phe Ser Leu
195

(2) INFORMATION FOR SEQ ID NO:3120:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 176 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..176

(D) OTHER INFORMATION: / Ceres Seq. ID 1575598

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3120:

Met Ala Ala Thr Leu His Leu His Leu Val Thr Leu Leu Phe Val
1 5 10 15
Ala Thr Leu Thr Val Ala Ser Val Ala Asp Asp Ser Pro Pro Ala Pro
20 25 30
Thr Pro Pro Ala Pro Pro Gln Pro Thr Ala Tyr Gln Met Leu Glu Arg
35 40 45
Tyr Asn Phe Thr Gln Gly Ile Leu Pro Gln Gly Val Thr Gly Tyr Val
50 55 60
Leu Xaa Arg Arg Arg Leu Leu Arg Gly Val Pro Pro Gly Gly Leu Glu
65 70 75 80
Leu Pro Arg Arg Gln His Ala Gly Pro Val Gln Gln Pro Arg Arg Arg
85 90 95
Pro His Ser Ala Ala Val His His Ile Pro Gly Gly Ser Glu Gly Glu
100 105 110
Gly Ala Val Leu Val Gly Arg Arg Gln Ala Gly Arg Pro Arg Arg Arg
115 120 125
Pro Ala Pro Phe Leu Arg Arg Pro Tyr Val Glu Ile Val Pro His Arg
130 135 140
His Ile Cys Gln Gln Pro Pro Met Gln Leu Arg Pro Phe Gly Arg Leu
145 150 155 160
Arg Lys Lys Ser Leu Leu Val Ser Phe Phe Leu Cys Xaa Phe Ser Leu
165 170 175

(2) INFORMATION FOR SEQ ID NO:3121:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 132 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..132

(D) OTHER INFORMATION: / Ceres Seq. ID 1575599

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3121:

Met Leu Glu Arg Tyr Asn Phe Thr Gln Gly Ile Leu Pro Gln Gly Val
1 5 10 15
Thr Gly Tyr Val Leu Xaa Arg Arg Arg Leu Leu Arg Gly Val Pro Pro
20 25 30
Gly Gly Leu Gln Leu Pro Arg Arg Gln His Ala Gly Pro Val Gln Gln

35	40	45
Pro Arg Arg Arg	Pro His Ser Ala Ala Val His	His Ile Pro Gly Gly
50	55	60
Ser Glu Gly Glu Gly	Ala Val Leu Val Gly Arg	Arg Gln Ala Gly Arg
65	70	75
Pro Arg Arg Arg	Pro Ala Pro Phe Leu Arg Arg	Pro Tyr Val Glu Ile
85	90	95
Val Pro His Arg	His Ile Cys Gln Gln Pro	Pro Met Gln Leu Arg Pro
100	105	110
Phe Gly Arg Leu Arg	Lys Lys Ser Leu Leu Val Ser	Phe Phe Leu Cys
115	120	125
Xaa Phe Ser Leu		
130		

(2) INFORMATION FOR SEQ ID NO:3122:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 588 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..588
- (D) OTHER INFORMATION: / Ceres Seq. ID 1575606

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3122:

gtccgcgcgc	tcogtgttca	ttgccccact	ccctcacgcc	tctcgcgcgc	gccgctccac	60
cacccccac	caogctcagg	gaaagggggt	ctgggttgca	tacaggcgaa	aggcacgcgc	120
cgccgcctgc	gcgcgagcct	ctccgtcccc	atcgccgcgc	agatggatcc	gtcgtcgag	180
ccccgtgaac	cgacaggtcg	gcccgtacac	tccgggttcc	tcaaggtctc	cgatgtccac	240
accatctact	acgagcagtc	cggaaccgcg	caggscatg	cgccggtgtt	tctccacgcg	300
ggtcocggag	ccggcacgct	gcccggcaac	aggaggtttc	ttgacccgca	gttctacagg	360
atcgttctgt	ttgaccagag	gggtgcaggc	agaagcactc	cccatgcttg	tttagagcag	420
aacactactt	gggacttggt	agctgacatt	gagaagctca	gggagcatct	tggcatccct	480
gaatggcagg	tgtttggtgg	ttcatgggga	agcaccttgg	cacttgccata	cagccaggag	540
caccctgata	aggtcactgg	cttgtgtctg	agagggaattt	tcttgctt		

(2) INFORMATION FOR SEQ ID NO:3123:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 196 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..196
- (D) OTHER INFORMATION: / Ceres Seq. ID 1575607

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3123:

Val Arg Pro Leu Arg Val His Cys Pro Thr Pro Ser Arg Leu Ser Arg	
1	5
Pro Pro Leu His His Pro His Pro Arg Ser Gly Lys Gly Gly Leu Gly	10
20	25
Cys Ile Gln Ala Lys Gly Thr Arg Arg Cys Arg Ala Ser Leu Ser	30
35	40
Val Pro Ile Ala Ala Gln Met Asp Pro Ser Ser Glu Pro Leu Tyr Ala	45
50	55
Gln Val Glu Pro Tyr Asp Ser Gly Phe Leu Lys Val Ser Asp Val His	60
65	70
Thr Ile Tyr Tyr Glu Gln Ser Gly Asn Pro Gln Xaa His Ala Val	75
85	90
Phe Leu His Gly Gly Pro Gly Ala Gly Thr Ser Pro Gly Asn Arg	95
100	105
	110

Phe Phe Asp Pro Gln Phe Tyr Arg Ile Val Leu Phe Asp Gln Arg Gly
115 120 125
Ala Gly Arg Ser Thr Pro His Ala Cys Leu Glu Gln Asn Thr Thr Trp
130 135 140
Asp Leu Val Ala Asp Ile Glu Lys Leu Arg Glu His Leu Gly Ile Pro
145 150 155 160
Glu Trp Gln Val Phe Gly Gly Ser Trp Gly Ser Thr Leu Ala Leu Ala
165 170 175
Tyr Ser Gln Glu His Pro Asp Lys Val Thr Gly Leu Val Leu Arg Gly
180 185 190
Ile Phe Leu Leu
195

(2) INFORMATION FOR SEQ ID NO:3124:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 137 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..137

(D) OTHER INFORMATION: / Ceres Seq. ID 1575608

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3124:

Ser Ala Arg Ser Val Phe Ile Ala Pro Leu Pro His Ala Ser Arg Ala
1 5 10 15
Arg Arg Ser Thr Thr Pro Ile His Ala Gln Gly Lys Gly Val Trp Val
20 25 30
Ala Tyr Arg Arg Lys Ala Arg Ala Ala Ala Ala Arg Ala Ser Pro
35 40 45
Ser Pro Ser Pro Arg Arg Trp Ile Arg Arg Arg Ser Pro Cys Thr Arg
50 55 60
Arg Ser Ser Arg Thr Thr Pro Gly Ser Ser Arg Ser Pro Met Ser Thr
65 70 75 80
Pro Ser Thr Thr Ser Ser Pro Gly Thr Arg Arg Xaa Met Arg Arg Cys
85 90 95
Phe Ser Thr Ala Val Pro Glu Pro Ala Arg Arg Pro Ala Thr Gly Gly
100 105 110
Ser Leu Thr Arg Ser Ser Thr Gly Ser Phe Cys Leu Thr Arg Gly Val
115 120 125
Gln Ala Glu Ala Leu Pro Met Leu Val
130 135

(2) INFORMATION FOR SEQ ID NO:3125:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 142 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..142

(D) OTHER INFORMATION: / Ceres Seq. ID 1575609

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3125:

Met Asp Pro Ser Ser Glu Pro Leu Tyr Ala Gln Val Glu Pro Tyr Asp
1 5 10 15
Ser Gly Phe Leu Lys Val Ser Asp Val His Thr Ile Tyr Trp Glu Gln
20 25 30
Ser Gly Asn Pro Gln Xaa His Ala Ala Val Phe Leu His Gly Gly Pro
35 40 45
Gly Ala Gly Thr Ser Pro Gly Asn Arg Arg Phe Phe Asp Pro Gln Phe

50	55	60
Tyr Arg Ile Val Leu Phe Asp Gln Arg Gly Ala Gly Arg Ser Thr Pro		
65	70	75
His Ala Cys Leu Glu Gln Asn Thr Thr Trp Asp Leu Val Ala Asp Ile		
	85	90
Glu Lys Leu Arg Glu His Leu Gly Ile Pro Glu Trp Gln Val Phe Gly		
	100	105
Gly Ser Trp Gly Ser Thr Leu Ala Leu Ala Tyr Ser Gln Glu His Pro		
	115	120
Asp Lys Val Thr Gly Leu Val Leu Arg Gly Ile Phe Leu Leu		
	130	135
		140

(2) INFORMATION FOR SEQ ID NO:3126:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 406 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..406
- (D) OTHER INFORMATION: / Ceres Seq. ID 1575635

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3126:

gacacacctc ccaaacccta cactcccgcc gccggcgccg gccggcgagC agcgccagca	60
gcataccgaag atggtggaagt tcttcaagcc cgrcaaggcc gttatctctcc tccaggcgccg	120
Cttcgccggc aggaaggcag ttatctctgag cgtgttcgag gagggcacc ccgaccgccc	180
ctatggccac tcgctctgctc caggccctgc caagtaccca aagaagtgta tccgcaagga	240
ctctctttac ctgtaaatag ataataggt cttggccaga ttttctgtgt tttgcagctg	300
caggatttgt cctaagacga gtcatgagt taatgtgaag caacttctcc agggatagat	360
ctcaaccaag ttgtgtgsc atacgaatGtt attgaactga atttag	

(2) INFORMATION FOR SEQ ID NO:3127:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 87 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..87
- (D) OTHER INFORMATION: / Ceres Seq. ID 1575636

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3127:

Asp Thr Pro Pro Lys Pro Tyr Thr Pro Gly Gly Gly Gly Ala	
1	5
	10
Ala Ala Ala Ala Ala Ser Glu Asp Gly Glu Val Pro Gln Ala Xaa Gln	
	20
	25
Gly Arg Tyr Pro Pro Pro Gly Pro Leu Arg Arg Gln Glu Gly Ser Tyr	
	35
	40
Pro Ala Arg Val Arg Gly Gly His Pro Arg Pro Pro Leu Trp Pro Leu	
	50
	55
Pro Arg Arg Arg Pro Arg Gln Val Pro Lys Glu Gly Asp Pro Gln Gly	
65	70
	75
Leu Leu Leu Pro Val Asn Arg	
	85

(2) INFORMATION FOR SEQ ID NO:3128:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 84 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..84
(D) OTHER INFORMATION: / Ceres Seq. ID 1575637

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3128:

Thr His Leu Pro Asn Pro Thr Leu Pro Ala Ala Ala Ala Gln
1 5 10 15
Gln Arg Gln Gln His Pro Lys Met Val Lys Phe Leu Lys Pro Xaa Lys
20 25 30
Ala Val Ile Leu Leu Gln Gly Arg Phe Ala Gly Arg Lys Ala Val Ile
35 40 45
Leu Arg Val Phe Glu Glu Gly Thr Arg Asp Arg Pro Tyr Gly His Cys
50 55 60
Leu Val Ala Gly Leu Ala Lys Tyr Pro Lys Lys Val Ile Arg Lys Asp
65 70 75 80
Ser Ser Tyr Leu

(2) INFORMATION FOR SEQ ID NO:3129:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 61 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..61
(D) OTHER INFORMATION: / Ceres Seq. ID 1575638

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3129:

Met Val Lys Phe Leu Lys Pro Xaa Lys Ala Val Ile Leu Leu Gln Gly
1 5 10 15
Arg Phe Ala Gly Arg Lys Ala Val Ile Leu Arg Val Phe Glu Glu Gly
20 25 30
Thr Arg Asp Arg Pro Tyr Gly His Cys Leu Val Ala Gly Leu Ala Lys
35 40 45
Tyr Pro Lys Lys Val Ile Arg Lys Asp Ser Ser Tyr Leu
50 55 60

(2) INFORMATION FOR SEQ ID NO:3130:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 880 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..880
(D) OTHER INFORMATION: / Ceres Seq. ID 1575645

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3130:

caatgtaagt	tcgaacaaca	agaagggggt	gtacagcttg	atcggtgggt	caaatgcgga	60
cgtaaatgtt	tcctacggcc	atacatggtt	caattcgggt	ttgactctgg	gaaaagctct	120
cctctacaa	gagcaatcag	cctctccatc	taacgggaagt	ctagatggtt	ttgaccgcga	180
tccactcga	aagggttgta	ccggggattc	tgtttctcct	gccagccaaa	gcgcccgat	240
agacggtccg	gacgatttat	ttgaagggtt	atctttgctc	catctagcat	gccgcgtcgc	300
gacctggcca	tggttgagct	gctcttcgag	tacggcgcca	atgtaaaccc	cacagattca	360
agagggcgga	cgccgcttca	tcacagcatc	atgaaggggc	gacatgtgta	cgccaagcta	420
ctgctttcca	ggggcgctga	ttctcaagcc	gcggatagag	atggtagaac	agcgttacag	480
tatgcaatcg	acagcggaac	catagaggac	gaagagatcc	ttgttttgc	agagagccca	540
agtagataaa	tcacgtaGgt	gtagtagtcc	aagtctcgag	ttctcggtg	gtgcattgtg	600
gctgcctttt	gcagtcacct	ggcacacaca	ggggccgagg	atgccttgct	agtattcagt	660
ctctgccttt	gtggcaagag	gaagttatag	ttttctag	ctctctcgcg	gttttggtcg	720

(2) INFORMATION FOR SEQ ID NO:3131:

(A) LENGTH: 114 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ix) FEATURE:

(B) LOCATION: 1..114

SEQUENCE DESCRIPTION: SEQ ID NO:3131:

[illegible]

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 86 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ix) FEATURE:

(B) LOCATION: 1..86

SEQUENCE DESCRIPTION: SEQ ID NO:3132:

[illegible]

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 79 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..79
 (D) OTHER INFORMATION: / Ceres Seq. ID 1575648

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3133:

Met	Val	Glu	Leu	Leu	Gln	Tyr	Gly	Ala	Asn	Val	Asn	Pro	Thr	Asp
1			5				10					15		
Ser	Arg	Gly	Arg	Thr	Pro	Leu	His	His	Ser	Ile	Met	Lys	Gly	Arg
			20				25					30		
Val	Tyr	Ala	Lys	Leu	Leu	Leu	Ser	Arg	Gly	Ala	Asp	Ser	Gln	Ala
			35				40					45		
Asp	Arg	Asp	Gly	Arg	Thr	Ala	Leu	Gln	Tyr	Ala	Ile	Asp	Ser	Gly
			50				55					60		
Ile	Glu	Asp	Glu	Glu	Ile	Leu	Val	Leu	Leu	Glu	Asp	Pro	Ser	Arg
			70									75		

(2) INFORMATION FOR SEQ ID NO:3134:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 762 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (ix) FEATURE:
 (A) NAME/KEY: -
 (B) LOCATION: 1..762
 (D) OTHER INFORMATION: / Ceres Seq. ID 1575682

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3134:

accgtgccc	cgccggcctc	tccaccgttc	attctccat	ggcatctact	cacgcaagca	60
gtcctattcc	tgattccttg	ctcggcttgc	gtggcccatg	gattcgatgt	catatcatgt	120
gtgtgtttgt	caaccgcctg	gtcgcagttc	gtgtcggatg	gcgtgttctt	cgcggaatga	180
atgagatgct	cgccgaggac	ggctactccg	gcgtcgaggt	ccgcgtcacc	cccatgtgca	240
tcgagatcat	catccgtgcc	accgcgcgcc	agaacatact	cgcgagaagg	gcccggaggat	300
cagagagctg	gcttctgtga	ttcagaagcg	ctttaactta	tcagaggggtg	gcgttgagct	360
ctacgcagag	aagctgaaca	accgcgggct	ctgcgcacatt	gcccaggccg	agwgcTcccg	420
ctacaagctt	ctcggtgaa	tcgcgcgtgag	aaGggggcatg	ttatgggtgt	ctcttatttg	480
tcacgcagag	tggactaa	ggctgcgaga	tcagtttcaa	tcggaacatg	ccaagctgaa	540
gcgatactca	ctctgcaagga	gcgtcttctc	tgtgtactgc	gtcgaagctt	tacottttta	600
tgtaaattac	gctgtaaatg	tacagtctct	ctggacactg	aatttctaag	ggcttttttt	660
atctttctga	cgcaccattc	actgatagct	ttatcgttgc	atagattttt	cttgaaatta	720
tatgccattc	taacgaacaa	taatatgtga	gtatcattct	tt		

(2) INFORMATION FOR SEQ ID NO:3135:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 105 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

- (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..105
 (D) OTHER INFORMATION: / Ceres Seq. ID 1575683

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3135:

Arg	Ala	Ala	Gly	Leu	Ser	Thr	Val	His	Ser	Pro	Met	Ala	Ser	Thr
1			5				10					15		
His	Ala	Ser	Ser	Pro	Ile	Pro	Asp	Ser	Leu	Leu	Gly	Leu	Arg	Gly
			20				25					30		
Trp	Ile	Arg	Cys	His	Ile	Met	Cys	Cys	Leu	Leu	Thr	Arg	Leu	Val
			35				40					45		
Val	Arg	Val	Gly	Trp	Arg	Val	Leu	Arg	Gly	Xaa	Asn	Glu	Met	Leu
			50				55					60		

Glu Asp Gly Tyr Ser Gly Val Glu Val Arg Val Thr Pro Met Cys Ile
65 70 75 80
Glu Ile Ile Ile Arg Ala Thr Arg Ala Gln Asn Ile Leu Ala Arg Arg
85 90 95

Ala Gly Gly Ser Glu Ser Trp Leu Leu
100 105

(2) INFORMATION FOR SEQ ID NO:3136:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 93 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..93

(D) OTHER INFORMATION: / Ceres Seq. ID 1575684

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3136:

Met Ala Ser Thr His Ala Ser Ser Pro Ile Pro Asp Ser Leu Leu Gly
1 5 10 15
Leu Arg Gly Trp Ile Arg Cys His Ile Met Cys Cys Leu Thr
20 25 30
Arg Leu Val Ala Val Arg Val Gly Trp Arg Val Leu Arg Gly Xaa Asn
35 40 45
Glu Met Leu Ala Glu Asp Gly Tyr Ser Gly Val Glu Val Arg Val Thr
50 55 60
Pro Met Cys Ile Glu Ile Ile Arg Ala Thr Arg Ala Gln Asn Ile
65 70 75 80
Leu Ala Arg Arg Ala Gly Gly Ser Glu Ser Trp Leu Leu
85 90

(2) INFORMATION FOR SEQ ID NO:3137:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 100 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..100

(D) OTHER INFORMATION: / Ceres Seq. ID 1575685

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3137:

Met Val Phe Ser Tyr Leu Ser Ser Arg Val Val Leu Arg Ala Ala Arg
1 5 10 15
Ser Val Ser Ile Gly Thr Cys Gln Ala Glu Ala Ile Leu Thr Cys Lys
20 25 30
Glu Arg Leu Leu Cys Val Leu Arg Arg Ser Phe Thr Phe Leu Cys Lys
35 40 45
Leu Arg Cys Lys Cys Thr Val Pro Leu Asp Thr Glu Phe Leu Arg Ala
50 55 60
Phe Phe Ile Phe Leu Thr His His Ser Leu Ile Ala Leu Ser Leu His
65 70 75 80
Ser Ile Phe Leu Lys Leu Tyr Ala Ile Leu Thr Asn Asn Asn Ile Val
85 90 95

Val Ser Phe Phe
100

(2) INFORMATION FOR SEQ ID NO:3138:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 689 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
 (A) NAME/KEY: -
 (B) LOCATION: 1..689
(D) OTHER INFORMATION: / Ceres Seq. ID 1575704
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3138:
tattgaagtc cattctgtttg gcatcgtccc atctcccttg aaccctttcg cccacaccac 60
agcacccgtg ccgaagtggg aaagaaggcg gcggcgaggg caccggcacc ggcaccgcct 120
aggaaaggaa accgaggaaa ctacagccat ggtggtaagg atccgtctgg cgcggttcgg 180
gtgcgggaat cgccctctct accgggtgat ggcgcgcgat agccgctccc ctccgagacgg 240
caagcacctc gaggctcctg gctactataa cccgctccca gggaaggatg gaggcaagag 300
gatgggctcg aaattcgacc gggtaagta ttggctgtca gttGGGgggg acagccatca 360
gatccgtgac agagtattct ctctcgtgcc ggactctgc caccacctcc attgctagct 420
atggcacgga aggggtgggccc acgtgatagg cgccccattc atccaatgac tggggcgccct 480
ctggatctcg aggggtgtcgc aattattgat aattccaatg ctccgtgaag cgatactgaa 540
gtgcctacag atgaggtggc tcaataagcc ttttgtatta gcatagcata tgtagcggtg 600
ctgcaaaaaga aaactgtttt gatgtgcttg tggcaagact ttgggtactc gtacaaatgtg 660
gcaaaccttt aaacaggtaa ctttcatcc
(2) INFORMATION FOR SEQ ID NO:3139:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 138 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..138
(D) OTHER INFORMATION: / Ceres Seq. ID 1575705
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3139:
Ile Glu Val His Ser Val Gly Ile Val Pro Ser Pro Leu Asn Pro Phe
1 5 10 15
Ala His Thr Thr Ala Pro Leu Pro Lys Trp Glu Arg Arg Arg Arg Arg
20 25 30
Arg His Arg His Arg His Arg Leu Gly Lys Glu Thr Glu Glu Thr Thr
35 40 45
Ala Met Val Val Arg Ile Arg Leu Ala Arg Phe Gly Cys Arg Asn Arg
50 55 60
Pro Phe Tyr Arg Val Met Ala Ala Asp Ser Arg Ser Pro Arg Asp Gly
65 70 75 80
Lys His Leu Glu Val Leu Gly Tyr Tyr Asn Pro Leu Pro Gly Lys Asp
85 90 95
Gly Gly Lys Arg Met Gly Leu Lys Phe Asp Arg Val Lys Tyr Trp Leu
100 105 110
Ser Val Gly Gly His Ser His Gln Ile Leu Cys Arg Val Phe Ser Phe
115 120 125
Val Pro Asp Phe Cys His His Leu His Cys
130 135
(2) INFORMATION FOR SEQ ID NO:3140:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 89 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..89
(D) OTHER INFORMATION: / Ceres Seq. ID 1575706
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3140:

Met Val Val Arg Ile Arg Leu Ala Arg Phe Gly Cys Arg Asn Arg Pro
1 5 10 15
Phe Tyr Arg Val Met Ala Ala Asp Ser Arg Ser Pro Arg Asp Gly Lys
20 25 30
His Leu Glu Val Leu Gly Tyr Tyr Asn Pro Leu Pro Gly Lys Asp Gly
35 40 45
Gly Lys Arg Met Gly Leu Lys Phe Asp Arg Val Lys Tyr Trp Leu Ser
50 55 60
Val Gly Gly His Ser His Gln Ile Leu Cys Arg Val Phe Ser Phe Val
65 70 75 80
Pro Asp Phe Cys His His Leu His Cys
85

(2) INFORMATION FOR SEQ ID NO:3141:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..69
- (D) OTHER INFORMATION: / Ceres Seq. ID 1575707

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3141:

Met Ala Ala Asp Ser Arg Ser Pro Arg Asp Gly Lys His Leu Glu Val
1 5 10 15
Leu Gly Tyr Tyr Asn Pro Leu Pro Gly Lys Asp Gly Lys Lys Arg Met
20 25 30
Gly Leu Lys Phe Asp Arg Val Lys Tyr Trp Leu Ser Val Gly Gly His
35 40 45
Ser His Gln Ile Leu Cys Arg Val Phe Ser Phe Val Pro Asp Phe Cys
50 55 60
His His Leu His Cys
65

(2) INFORMATION FOR SEQ ID NO:3142:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 767 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..767
- (D) OTHER INFORMATION: / Ceres Seq. ID 1575720

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3142:

gtggtgctag aagcaactga aaacagccga gcgatctct ctcctctctc ctctccgatac 60
cattctccag cgcasanang taaacatgtc tgaccgggca aagatgtcgt ggcaggcgta 120
cgtggacgag cacctgatgt gcgagatcga rggccaccac ctccggcgcg cgcccatcgt 180
cggccacgas gntgcgcctt gggcgcaagag caccggcgctt ccagagtcca agaccaggga 240
catggccaac atcatgaagg acttcgacga gccaggggcac ctccgcgccga caggCctggt 300
cctcggacat accaagtaca tggctcatcca aggcgagcct ggtgcctcca tccgtggcaa 360
gaagggatca ggaggcatca cctgaagaa gacaggggcag gcaactcgtcgt ttggcatcta 420
cgacgagcgt atgacgcctg gccagtgcac catggtggtg gaaaggcgtg gcgactacct 480
gcttgaaacg ggcagtgaac tactacgtac cagctggaat gcatgtcgac gacgatgggt 540
tcgagtcttcg acttccaata atagtaacaa caaagcaaa gccctctctc cgccgtattt 600
gctttgtctc ttctctctca cgcataaaga tatctagcaa ttggtgactc gctttaaata 660
gttcgctttg cttttgaggt tgactcgacc attttgctgt agcgtgaatt gcatgcgatg 720
acatgcaacg ctccaatgkc ytttgmmtg tggaattttt ttttttc

(2) INFORMATION FOR SEQ ID NO:3143:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 137 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..137
(D) OTHER INFORMATION: / Ceres Seq. ID 1575721
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3143:

Met Ser Asp Arg Ala Lys Met Ser Trp Gln Ala Tyr Val Asp Glu His
1 5 10 15
Leu Met Cys Glu Ile Xaa Gly His His Leu Ala Ala Ala Ile Val
20 25 30
Gly His Xaa Xaa Ala Ala Trp Ala Gln Ser Thr Ala Phe Pro Glu Phe
35 40 45
Lys Thr Glu Asp Met Ala Asn Ile Met Lys Asp Phe Asp Glu Pro Gly
50 55 60
His Leu Ala Pro Thr Gly Leu Phe Leu Gly Pro Thr Lys Tyr Met Val
65 70 75 80
Ile Gln Gly Glu Pro Gly Ala Val Ile Arg Gly Lys Lys Gly Ser Gly
85 90 95
Gly Ile Thr Val Lys Lys Thr Gly Gln Ala Leu Val Val Gly Ile Tyr
100 105 110
Asp Glu Pro Met Thr Pro Gly Gln Cys Asn Met Val Val Glu Arg Leu
115 120 125
Gly Asp Tyr Leu Leu Glu Gln Gly Met
130 135

(2) INFORMATION FOR SEQ ID NO:3144:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 131 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..131
(D) OTHER INFORMATION: / Ceres Seq. ID 1575722
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3144:

Met Ser Trp Gln Ala Tyr Val Asp Glu His Leu Met Cys Glu Ile Xaa
1 5 10 15
Gly His His Leu Ala Ala Ala Ala Ile Val Gly His Xaa Xaa Ala Ala
20 25 30
Trp Ala Gln Ser Thr Ala Phe Pro Glu Phe Lys Thr Glu Asp Met Ala
35 40 45
Asn Ile Met Lys Asp Phe Asp Glu Pro Gly His Leu Ala Pro Thr Gly
50 55 60
Leu Phe Leu Gly Pro Thr Lys Tyr Met Val Ile Gln Gly Glu Pro Gly
65 70 75 80
Ala Val Ile Arg Gly Lys Lys Gly Ser Gly Gly Ile Thr Val Lys Lys
85 90 95
Thr Gly Gln Ala Leu Val Val Gly Ile Tyr Asp Glu Pro Met Thr Pro
100 105 110
Gly Gln Cys Asn Met Val Val Glu Arg Leu Gly Asp Tyr Leu Leu Glu
115 120 125
Gln Gly Met
130

(2) INFORMATION FOR SEQ ID NO:3145:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 120 amino acids

(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..120
 (D) OTHER INFORMATION: / Ceres Seq. ID 1575723
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3145:
Met Cys Glu Ile Xaa Gly His His Leu Ala Ala Ala Val Gly
1 5 10 15
His Xaa Xaa Ala Ala Trp Ala Gln Ser Thr Ala Phe Pro Glu Phe Lys
 20 25 30
Thr Glu Asp Met Ala Asn Ile Met Lys Asp Phe Asp Glu Pro Gly His
 35 40 45
Leu Ala Pro Thr Gly Leu Phe Leu Gly Pro Thr Lys Tyr Met Val Ile
 50 55 60
Gln Gly Glu Pro Gly Ala Val Ile Arg Gly Lys Lys Gly Ser Gly Gly
65 70 75 80
Ile Thr Val Lys Lys Thr Gly Gln Ala Leu Val Val Gly Ile Tyr Asp
 85 90 95
Glu Pro Met Thr Pro Gly Gln Cys Asn Met Val Val Glu Arg Leu Gly
 100 105 110
Asp Tyr Leu Leu Glu Gln Gly Met
 115 120

(2) INFORMATION FOR SEQ ID NO:3146:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 645 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..645
(D) OTHER INFORMATION: / Ceres Seq. ID 1575729

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3146:

gaggaagaat caggcaggga gctctacccat tcgcatccca ggccaacctc aacccaatc 60
caatcogttg caggtcgca gattgcttcg cgtgagcacc accagcccca ggaggaggag 120
gacacgcgaG cggtcgctcaa gctcatcagc gccgagggct tcgaattcgt cgtcgacaag 180
aaggccgcga tggtctccaa caccctacgc aacatgctca catcgccagg cggcttctcc 240
gagacgcgcc agggcgaggt tcgcttcgcc gagatcccca ccaatatact cgagaagatc 300
tgccagtaet tctattggtc gctccattat tccagctctt gggtcaacac tttggatggc 360
ctgcctattg aagagttatc tgggtccaga ttttgatgtg atggagtctg acaaggccaa 420
taagactgtc acatgtaatg ttatttgatt accaaaacat gaagagcagt caagataggt 480
tgagactgat cgtatatttt gttggttctt aggactcttg gtggaagata tgaggttgct 540
cccaaacatg aatttatgta tggctgaagt aaattcactg ttctgatttt ggtgtccaca 600
ttcttatttg ttccaccatc agcaaaccta agttcagttt gtggt

(2) INFORMATION FOR SEQ ID NO:3147:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 131 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..131
(D) OTHER INFORMATION: / Ceres Seq. ID 1575730

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3147:

Glu Glu Glu Ser Gly Arg Glu Leu Tyr His Ser His Pro Arg Pro Thr

1 5 10 15
Ser Thr Pro Ile Gln Ser Val Ala Gly Arg Arg Met Ala Ser Arg Glu
20 25 30
His His Gln Pro Gln Glu Glu Glu Asp Thr Ala Gly Val Val Lys Leu
35 40 45
Ile Ser Ala Glu Gly Phe Glu Phe Val Val Asp Lys Lys Ala Ala Met
50 55 60
Val Ser Asn Thr Leu Arg Asn Met Leu Thr Ser Pro Gly Gly Phe Ser
65 70 75 80
Glu Thr Arg Gln Gly Glu Val Arg Phe Pro Glu Ile Pro Thr Asn Ile
85 90 95
Leu Glu Lys Ile Cys Gln Tyr Phe Tyr Trp Ser Leu His Tyr Ser Ser
100 105 110
Ser Trp Phe Asn Thr Leu Asp Gly Leu Pro Ile Glu Glu Leu Ser Gly
115 120 125
Pro Glu Phe
130

(2) INFORMATION FOR SEQ ID NO:3148:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 148 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..148

(D) OTHER INFORMATION: / Ceres Seq. ID 1575731

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3148:

Arg Lys Asn Gln Ala Gly Ser Ser Thr Ile Arg Ile Pro Gly Gln Pro
1 5 10 15
Gln Pro Gln Ser Asn Pro Leu Gln Val Ala Gly Trp Leu Arg Val Ser
20 25 30
Thr Thr Ser Pro Arg Arg Arg Thr Pro Gln Ala Ser Ser Ser Ser
35 40 45
Ser Ala Pro Arg Ala Ser Asn Ser Ser Ser Thr Arg Arg Pro Pro Trp
50 55 60
Ser Pro Thr Pro Tyr Ala Thr Cys Ser His Arg Gln Ala Ala Ser Pro
65 70 75 80
Arg Arg Ala Arg Ala Arg Phe Ala Ser Arg Arg Ser Pro Pro Ile Ser
85 90 95
Ser Arg Arg Ser Ala Ser Thr Ser Ile Gly Arg Ser Ile Ile Pro Ala
100 105 110
Leu Gly Ser Thr Leu Trp Met Ala Cys Leu Leu Lys Ser Tyr Leu Val
115 120 125
Gln Asn Phe Asp Val Met Glu Ser Asp Lys Ala Asn Lys Thr Val Thr
130 135 140
Cys Asn Val Ile
145

(2) INFORMATION FOR SEQ ID NO:3149:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 104 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..104

(D) OTHER INFORMATION: / Ceres Seq. ID 1575732

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3149:

Met Ala Ser Arg Glu His His Gln Pro Gln Glu Glu Glu Asp Thr Ala
1 5 10 15
Gly Val Val Lys Leu Ile Ser Ala Glu Gly Phe Glu Phe Val Val Asp
20 25 30
Lys Lys Ala Ala Met Val Ser Asn Thr Leu Arg Asn Met Leu Thr Ser
35 40 45
Pro Gly Gly Phe Ser Glu Thr Arg Gln Gly Glu Val Arg Phe Pro Glu
50 55 60
Ile Pro Thr Asn Ile Leu Glu Lys Ile Cys Gln Tyr Phe Tyr Trp Ser
65 70 75 80
Leu His Tyr Ser Ser Ser Trp Phe Asn Thr Leu Asp Gly Leu Pro Ile
85 90 95
Glu Glu Leu Ser Gly Pro Glu Phe
100

(2) INFORMATION FOR SEQ ID NO:3150:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 330 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..330
- (D) OTHER INFORMATION: / Ceres Seq. ID 1575740

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3150:

atatccgcat ccgctgcctc cgcctctcga gtctcgccca ccgctgctcc tcttagctcc	60
tctactcgcc agtcgccatg ggcaagatta agatcggaat caacggcttc ggaaggatcg	120
gcaggctcgt agaggagctg gtgtctgagg aggacgacga ggaccacgac gattctccgc	180
caaggaaacga gccggctgtt tcgcatcgta gaaaggctgt cgtgtttgat gacagcgacg	240
aggactaaaaa ttgttaaaac cgtatgacga cctgacatgC tacgcttgct ttttctcccc	300
attgttttaa gagaatgatt agttattttt	

(2) INFORMATION FOR SEQ ID NO:3151:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..43
- (D) OTHER INFORMATION: / Ceres Seq. ID 1575741

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3151:

Ile Ser Ala Ser Ala Ala Ser Ala Ser Arg Val Ser Ser Thr Arg Arg
1 5 10 15
Pro Pro Ser Ser Ser Thr Arg Gln Ser Pro Trp Ala Arg Leu Arg Ser
20 25 30
Glu Ser Thr Ala Ser Glu Gly Ser Ala Gly Ser
35 40

(2) INFORMATION FOR SEQ ID NO:3152:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..56
- (D) OTHER INFORMATION: / Ceres Seq. ID 1575742

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3152:

Met Gly Lys Ile Lys Ile Gly Ile Asn Gly Phe Gly Arg Ile Gly Arg
1 5 10 15
Leu Val Glu Glu Leu Val Ser Glu Glu Asp Asp Glu Asp His Asp Asp
20 25 30
Ser Pro Pro Arg Lys Gln Pro Ala Val Ser His Arg Arg Lys Ala Val
35 40 45
Val Phe Asp Asp Ser Asp Glu Asp
50 55

(2) INFORMATION FOR SEQ ID NO:3153:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 710 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..710
- (D) OTHER INFORMATION: / Ceres Seq. ID 1575750

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3153:

atccacaatat taaactcacg cacacacaca attaggtcac atacacacct cccggctgcc 60
tccttagtta gcagcttcta caatggaggc atccaacaag ctgcagctct tgctcctgtg 120
gctgtgctatg gcagctgccca ctgcogtgca cccttctac tctgagaatt cgcctcaaga 180
ctacctcaact ccccaaaaaca gcgcocgtgc gcgcogtggg gttggcccg gtagctggag 240
cacgaagctg cagcagttcg cacagaagta gcgcgcacag agggccggcg actgcctgt 300
ccagcactcg ggcgggccct acggggagaa catcttctgg ggtccgcgg gcttcgattg 360
gaaggcgttg gcgcagctgc gatcgtgggt agacagagaaa cagtgtgtaca actacgccac 420
caacagctgc gcgcgcggca aggtgtgtgg cactacacgc agtgtgtgtg gcgcgccact 480
acaagctatg gCtgcgcggcg cgtcgtgtgc cgcgacaacc gtggcgttct tatcatctgc 540
aactacgagc cccgcggcga cattgccggg atgaagccct actgatatat tgtgcotgag 600
aacgatggca actgatatta tatctagaca cgggcttgtt gcacgcgatg actttccacg 660
tgtatatga ataattttt ataataaat caaagaggtt tgttatttc

(2) INFORMATION FOR SEQ ID NO:3154:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 163 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..163
- (D) OTHER INFORMATION: / Ceres Seq. ID 1575751

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3154:

Met Glu Ala Ser Asn Lys Leu Ala Val Leu Leu Trp Leu Val Met
1 5 10 15
Ala Ala Ala Thr Ala Val His Pro Ser Tyr Ser Glu Asn Ser Pro Gln
20 25 30
Asp Tyr Leu Thr Pro Gln Asn Ser Ala Arg Ala Ala Val Gly Val Gly
35 40 45
Pro Val Thr Trp Ser Thr Lys Leu Gln Gln Phe Ala Glu Lys Tyr Ala
50 55 60
Ala Gln Arg Ala Gly Asp Cys Arg Leu Gln His Ser Gly Gly Pro Tyr
65 70 75 80
Gly Glu Asn Ile Phe Trp Gly Ser Ala Gly Phe Asp Trp Lys Ala Val
85 90 95
Asp Ala Val Arg Ser Trp Val Asp Glu Lys Gln Trp Tyr Asn Tyr Ala
100 105 110
Thr Asn Ser Cys Ala Ala Gly Lys Val Cys Gly Thr Thr Arg Trp
115 120 125

Cys Gly Ala Pro Leu Gln Ala Ser Ala Ala Arg Ala Ser Cys Ala Ala
130 135 140
Thr Thr Val Ala Ser Leu Ser Ser Ala Thr Thr Ser Pro Ala Ala Thr
145 150 155 160
Leu Pro Gly

(2) INFORMATION FOR SEQ ID NO:3155:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 148 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..148

(D) OTHER INFORMATION: / Ceres Seq. ID 1575752

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3155:

Met Ala Ala Ala Thr Ala Val His Pro Ser Tyr Ser Glu Asn Ser Pro
1 5 10 15
Gln Asp Tyr Leu Thr Pro Gln Asn Ser Ala Arg Ala Ala Val Gly Val
20 25 30
Gly Pro Val Thr Trp Ser Thr Lys Leu Gln Gln Phe Ala Glu Lys Tyr
35 40 45
Ala Ala Gln Arg Ala Gly Asp Cys Arg Leu Gln His Ser Gly Gly Pro
50 55 60
Tyr Gly Glu Asn Ile Phe Trp Gly Ser Ala Gly Phe Asp Trp Lys Ala
65 70 75 80
Val Asp Ala Val Arg Ser Trp Val Asp Glu Lys Gln Trp Tyr Asn Tyr
85 90 95
Ala Thr Asn Ser Cys Ala Ala Gly Lys Val Cys Gly Thr Thr Arg Arg
100 105 110
Trp Cys Gly Ala Pro Leu Gln Ala Ser Ala Ala Arg Ala Ser Cys Ala
115 120 125
Ala Thr Thr Val Ala Ser Leu Ser Ser Ala Thr Thr Ser Pro Ala Ala
130 135 140
Thr Leu Pro Gly
145

(2) INFORMATION FOR SEQ ID NO:3156:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 699 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..699

(D) OTHER INFORMATION: / Ceres Seq. ID 1575794

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3156:

actttttctct cctcgtttccc aatttcaagg ctgcaccaacc ctgtgcgcgg taggtggtgg 60
cggtgaggat agagggttac ctgaggaggc agtgaatggcg gccacgattc agtacaaccg 120
gagcaaccgc gcggtgaagc ggatcctgca ggaggtcaag gagatgcagt ccaaccacctc 180
accgacttc atgtccctcc cctcgagga ggacatcttc gagtggcaat ttgctatcct 240
tggtccgaga gacagcgagt ttgagggtgg aatttatcat gccaggatcc agctaCcttc 300
ggattatcca ttcaagccac cgtccttcat gctacttacg ccaagtggac gctttgagat 360
tcagaagaag atttgcttga gcatatccaa ttaccaccct gagcactggc agccttcatg 420
gagtgctcgc acagcttttg tagccttgat tgccttcatg ccgacgaacc caRggtgggg 480
cattgggctc actggattac aaaccagaag acagacgagc acttgctata aaatcacgtg 540
aggtgccscg gaaatttggc tcccacaaac gtcagaaact aattgatgag atccatgagc 600
aaatgctcgt ccggtgtgtag tgttcgtct tctgatccat tgtcgtgct ctgtactcta 660

gtgatcagcg tcaaaataaa gaaatgcctg yccttggtt

(2) INFORMATION FOR SEQ ID NO:3157:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 179 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..179

(D) OTHER INFORMATION: / Ceres Seq. ID 1575795

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3157:

Leu	Phe	Ser	Pro	Arg	Ser	Gln	Phe	Gln	Gly	Cys	Pro	Thr	Leu	Ala	Pro	
1			5						10				15			
Val	Gly	Gly	Gly	Glu	Asp	Arg	Gly	Leu	Pro	Glu	Glu	Ala	Val	Met		
			20				25					30				
Ala	Ala	Thr	Ile	Gln	Tyr	Asn	Arg	Ser	Asn	Pro	Ala	Val	Lys	Arg	Ile	
			35				40				45					
Leu	Gln	Glu	Val	Lys	Glu	Met	Gln	Ser	Asn	Pro	Ser	Pro	Asp	Phe	Met	
			50			55					60					
Ser	Leu	Pro	Leu	Glu	Asp	Ile	Phe	Glu	Trp	Gln	Phe	Ala	Ile	Leu		
65				70					75				80			
Gly	Pro	Arg	Asp	Ser	Glu	Phe	Glu	Gly	Gly	Ile	Tyr	His	Gly	Arg	Ile	
				85					90				95			
Gln	Leu	Pro	Ser	Asp	Tyr	Pro	Phe	Lys	Pro	Pro	Ser	Phe	Met	Leu	Leu	
			100				105						110			
Thr	Pro	Ser	Gly	Arg	Phe	Glu	Ile	Gln	Lys	Lys	Ile	Cys	Leu	Ser	Ile	
			115				120					125				
Ser	Asn	Tyr	His	Pro	Glu	His	Trp	Gln	Pro	Ser	Trp	Ser	Val	Arg	Thr	
			130			135					140					
Ala	Leu	Val	Ala	Leu	Ile	Ala	Phe	Met	Pro	Thr	Asn	Pro	Xaa	Trp	Gly	
				150						155				160		
Ile	Gly	Leu	Thr	Gly	Leu	Gln	Thr	Arg	Arg	Gln	Thr	Ser	Thr	Cys	Tyr	
			165					170						175		
Lys	Ile	Thr														

(2) INFORMATION FOR SEQ ID NO:3158:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 148 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..148

(D) OTHER INFORMATION: / Ceres Seq. ID 1575796

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3158:

Met	Ala	Ala	Thr	Ile	Gln	Tyr	Asn	Arg	Ser	Asn	Pro	Ala	Val	Lys	Arg	
1				5						10			15			
Ile	Leu	Gln	Glu	Val	Lys	Glu	Met	Gln	Ser	Asn	Pro	Ser	Pro	Asp	Phe	
			20				25					30				
Met	Ser	Leu	Pro	Leu	Glu	Glu	Asp	Ile	Phe	Glu	Trp	Gln	Phe	Ala	Ile	
			35				40					45				
Leu	Gly	Pro	Arg	Asp	Ser	Glu	Phe	Glu	Gly	Gly	Ile	Tyr	His	Gly	Arg	
			50			55				60						
Ile	Gln	Leu	Pro	Ser	Asp	Tyr	Pro	Phe	Lys	Pro	Pro	Ser	Phe	Met	Leu	
65				70					75					80		
Leu	Thr	Pro	Ser	Gly	Arg	Phe	Glu	Ile	Gln	Lys	Lys	Ile	Cys	Leu	Ser	
			85					90						95		

Ile Ser Asn Tyr His Pro Glu His Trp Gln Pro Ser Trp Ser Val Arg
100 105 110
Thr Ala Leu Val Ala Leu Ile Ala Phe Met Pro Thr Asn Pro Xaa Trp
115 120 125
Gly Ile Gly Leu Thr Gly Leu Gln Thr Arg Arg Gln Thr Ser Thr Cys
130 135 140
Tyr Lys Ile Thr
145

(2) INFORMATION FOR SEQ ID NO:3159:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 125 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide

- (ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..125
- (D) OTHER INFORMATION: / Ceres Seq. ID 1575797

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3159:

Met Gln Ser Asn Pro Ser Pro Asp Phe Met Ser Leu Pro Leu Glu Glu
1 5 10 15
Asp Ile Phe Glu Trp Gln Phe Ala Ile Leu Gly Pro Arg Asp Ser Glu
20 25 30
Phe Glu Gly Gly Ile Tyr His Gly Arg Ile Gln Leu Pro Ser Asp Tyr
35 40 45
Pro Phe Lys Pro Pro Ser Phe Met Leu Leu Thr Pro Ser Gly Arg Phe
50 55 60
Glu Ile Gln Lys Lys Ile Cys Leu Ser Ile Ser Asn Tyr His Pro Glu
65 70 75 80
His Trp Gln Pro Ser Trp Ser Val Arg Thr Ala Leu Val Ala Leu Ile
85 90 95
Ala Phe Met Pro Thr Asn Pro Xaa Trp Gly Ile Gly Leu Thr Gly Leu
100 105 110
Gln Thr Arg Arg Gln Thr Ser Thr Cys Tyr Lys Ile Thr
115 120 125

(2) INFORMATION FOR SEQ ID NO:3160:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 707 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)

- (ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..707
- (D) OTHER INFORMATION: / Ceres Seq. ID 1575798

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3160:

aaaagaatac ggtttaacaa acaccctacc caaaggggcg gaacccaagc cgccgtgacc 60
gccagaccga agccaacaag caagagcatt actactttct ctccgaccgc aaacottttc 120
tggaacgcga gaagaatccc aaccgccgacc gacctaccct aatcgcgcat ggcgacgggtg 180
gcgatggaca tctcgaagcc cactccagtg gcgtccggcg acgaggcgcg ccgcggccaa 240
ggggaggagc ggcggaggcg gcgaggggct gcggcagtag tacctgcagc acatccacga 300
cctgcagctc cagatccggc agaagaccga caacctcaac cgtctcgagg ccagcgcaa 360
tgacctcaac tcccagtgta gaatgctcag ggaagagttg cagttgcttc aagagcctgg 420
ctcatatgtt ggtgaggttg tgaaggtcat ggggaaatca aaggttctgg tgaaggtaca 480
ccccgaagcc aaatatgttg ttgatataga taagagcatt gatatacaca agatcacacc 540
ttcaacaaga gtgcctcttc gtaatgacag ctatatgctc catctgaccc taccagaaca 600
agttgatcca ttggtcaatc tcatgaaagt tgagaaggtt cctgatttcta catatgatat 660
gattggagcg ctgaccage aaattaaaga gatcaaaagc gtcattg

(2) INFORMATION FOR SEQ ID NO:3161:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 64 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..64
(D) OTHER INFORMATION: / Ceres Seq. ID 1575799

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3161:

Met Ala Thr Val Ala Met Asp Ile Ser Lys Pro Thr Pro Val Ala Ser
1 5 10 15
Gly Asp Glu Ala Ala Gly Gly Gln Gly Glu Glu Arg Arg Arg Gly Arg
20 25 30
Gly Ala Ala Ala Val Leu Pro Ala Ala His Pro Arg Pro Ala Ala Pro
35 40 45
Asp Pro Ala Glu Asp Pro Gln Pro Gln Pro Ser Arg Gly Pro Ala Gln
50 55 60

(2) INFORMATION FOR SEQ ID NO:3162:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 108 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..108
(D) OTHER INFORMATION: / Ceres Seq. ID 1575800

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3162:

Met Leu Arg Glu Glu Leu Gln Leu Leu Gln Glu Pro Gly Ser Tyr Val
1 5 10 15
Gly Glu Val Val Lys Val Met Gly Lys Ser Lys Val Leu Val Lys Val
20 25 30
His Pro Glu Gly Lys Tyr Val Val Asp Ile Asp Lys Ser Ile Asp Ile
35 40 45
Thr Lys Ile Thr Pro Ser Thr Arg Val Ala Leu Arg Asn Asp Ser Tyr
50 55 60
Met Leu His Leu Ile Leu Pro Ser Lys Val Asp Pro Leu Val Asn Leu
65 70 75 80
Met Lys Val Glu Lys Val Pro Asp Ser Thr Tyr Asp Met Ile Gly Gly
85 90 95
Leu Asp Gln Gln Ile Lys Glu Ile Lys Glu Val Ile
100 105

(2) INFORMATION FOR SEQ ID NO:3163:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 86 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..86
(D) OTHER INFORMATION: / Ceres Seq. ID 1575801

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3163:

Met Gly Lys Ser Lys Val Leu Val Lys Val His Pro Glu Gly Lys Tyr
1 5 10 15

Val	Val	Asp	Ile	Asp	Lys	Ser	Ile	Asp	Ile	Thr	Lys	Ile	Thr	Pro	Ser				
		20						25					30						
Thr	Arg	Val	Ala	Leu	Arg	Asn	Asp	Ser	Tyr	Met	Leu	His	Leu	Ile	Leu				
		35				40					45								
Pro	Ser	Lys	Val	Asp	Pro	Leu	Val	Asn	Leu	Met	Lys	Val	Glu	Lys	Val				
		50				55					60								
Pro	Asp	Ser	Thr	Tyr	Asp	Met	Ile	Gly	Gly	Leu	Asp	Gln	Gln	Ile	Lys				
		65				70				75					80				
Glu	Ile	Lys	Glu	Val	Ile														

(2) INFORMATION FOR SEQ ID NO:3164:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 737 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..737

(D) OTHER INFORMATION: / Ceres Seq. ID 1575815

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3164:

atctctctctc	tgttcatagc	ctcccaagaa	acaagagcca	accagcgctt	gcgaactcaa	60
gcgcgcgacg	aatgtctctg	gcccgttcca	tccttccat	caagggtgaag	gtgggggccc	120
tctcggtgcg	tcttccacac	cgtgcatgcc	ggctcttgcg	ggatgatcagg	agctccaagg	180
cagaggggccc	catccggaga	cCtgcggcgc	ctccgCgtgc	gccaccgcca	ccgatgccac	240
ccaagacgccc	ggctctgtcc	actctctcca	cctctgtcca	gctctcgacg	cccgtaagcg	300
ccgctgtctcc	accacagtcg	tgcgagccga	tgccaccttc	tctgagcccg	aagccagttg	360
acgccacacg	ccagatcgcg	aagccggtgg	ctggggccat	gacgctggag	taccagagga	420
aggtggccaa	ggacctcgag	gagtacttca	agaagaagaa	gctggaggag	gccgaccagg	480
gtccgttctt	cgggttcttg	cccaagaatg	agatttccaa	cggaaagttg	gccatttttg	540
ggtttgcagt	agggatgcta	acagagtatg	caacaggctc	ggattttggt	cagcaaatga	600
agatctctct	ctccaatttt	ggaattgtgg	acttggtatta	atggtggact	tttggtgttt	660
tcgttatgta	caagtctttt	aaatgtaatg	tacttacttg	atatggtata	tagaaaaattt	720
catattgcac	gtttgttc					

(2) INFORMATION FOR SEQ ID NO:3165:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 212 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..212

(D) OTHER INFORMATION: / Ceres Seq. ID 1575816

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3165:

Leu	Leu	Ser	Val	His	Ser	Leu	Pro	Arg	Asn	Lys	Ser	Gln	Pro	Ala	Leu				
		5						10				15							
Ala	Asn	Ser	Ser	Ala	Ala	Ala	Met	Ser	Leu	Ala	Pro	Ser	Ile	Pro	Ser				
		20					25				30								
Ile	Lys	Val	Lys	Val	Gly	Ala	Val	Ser	Val	Ala	Pro	Pro	His	Arg	Ala				
		35				40					45								
Cys	Arg	Ser	Phe	Ala	Val	Ile	Arg	Ser	Ser	Lys	Ala	Glu	Gly	Pro	Ile				
		50				55				60									
Arg	Arg	Pro	Ala	Ala	Pro	Pro	Leu	Ser	Pro	Pro	Pro	Pro	Met	Pro	Pro				
		65				70				75				80					
Lys	Thr	Pro	Ala	Leu	Ser	Thr	Pro	Pro	Thr	Leu	Ser	Gln	Pro	Pro	Thr				
		85				90							95						
Pro	Val	Lys	Pro	Ala	Ala	Pro	Pro	Thr	Ser	Ser	Gln	Pro	Met	Pro	Pro				
		100				105						110							

Ser Pro Glu Pro Lys Pro Val Asp Ala Thr Ala Gln Met Arg Lys Pro
115 120 125
Val Ala Gly Ala Met Thr Leu Glu Tyr Gln Arg Lys Val Ala Lys Asp
130 135 140
Leu Gln Glu Tyr Phe Lys Lys Lys Lys Leu Glu Ala Asp Gln Gly
145 150 155 160
Pro Phe Phe Gly Phe Leu Pro Lys Asn Glu Ile Ser Asn Gly Arg Trp
165 170 175
Ala Met Phe Gly Phe Ala Val Gly Met Leu Thr Glu Tyr Ala Thr Gly
180 185 190
Ser Asp Phe Val Gln Gln Met Lys Ile Leu Leu Ser Asn Phe Gly Ile
195 200 205
Val Asp Leu Asp
210

(2) INFORMATION FOR SEQ ID NO:3166:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 189 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..189
- (D) OTHER INFORMATION: / Ceres Seq. ID 1575817

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3166:

Met Ser Leu Ala Pro Ser Ile Pro Ser Ile Lys Val Lys Val Gly Ala
1 5 10 15
Val Ser Val Ala Pro Pro His Arg Ala Cys Arg Ser Phe Ala Val Ile
20 25 30
Arg Ser Ser Lys Ala Glu Gly Pro Ile Arg Arg Pro Ala Ala Pro Pro
35 40 45
Leu Ser Pro Pro Pro Pro Met Pro Pro Lys Thr Pro Ala Leu Ser Thr
50 55 60
Pro Pro Thr Leu Ser Gln Pro Pro Thr Pro Val Lys Pro Ala Ala Pro
65 70 75 80
Pro Thr Ser Ser Gln Pro Met Pro Pro Ser Pro Glu Pro Lys Pro Val
85 90 95
Asp Ala Thr Ala Gln Met Arg Lys Pro Val Ala Gly Ala Met Thr Leu
100 105 110
Glu Tyr Gln Arg Lys Val Ala Lys Asp Leu Gln Glu Tyr Phe Lys Lys
115 120 125
Lys Lys Leu Glu Glu Ala Asp Gln Gly Pro Phe Phe Gly Phe Leu Pro
130 135 140
Lys Asn Glu Ile Ser Asn Gly Arg Trp Ala Met Phe Gly Phe Ala Val
145 150 155 160
Gly Met Leu Thr Glu Tyr Ala Thr Gly Ser Asp Phe Val Gln Gln Met
165 170 175
Lys Ile Leu Leu Ser Asn Phe Gly Ile Val Asp Leu Asp
180 185

(2) INFORMATION FOR SEQ ID NO:3167:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 135 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..135
- (D) OTHER INFORMATION: / Ceres Seq. ID 1575818

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3167:

Met Pro Pro Lys Thr Pro Ala Leu Ser Thr Pro Pro Thr Leu Ser Gln
1 5 10 15
Pro Pro Thr Pro Val Lys Pro Ala Ala Pro Pro Thr Ser Ser Gln Pro
20 25 30
Met Pro Pro Ser Pro Glu Pro Lys Pro Val Asp Ala Thr Ala Gln Met
35 40 45
Arg Lys Pro Val Ala Gly Ala Met Thr Leu Glu Tyr Gln Arg Lys Val
50 55 60
Ala Lys Asp Leu Gln Glu Tyr Phe Lys Lys Lys Leu Glu Glu Ala
65 70 75 80
Asp Gln Gly Pro Phe Phe Gly Phe Leu Pro Lys Asn Glu Ile Ser Asn
85 90 95
Gly Arg Trp Ala Met Phe Gly Phe Ala Val Gly Met Leu Thr Glu Tyr
100 105 110
Ala Thr Gly Ser Asp Phe Val Gln Gln Met Lys Ile Leu Leu Ser Asn
115 120 125
Phe Gly Ile Val Asp Leu Asp
130 135

(2) INFORMATION FOR SEQ ID NO:3168:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 745 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..745
- (D) OTHER INFORMATION: / Ceres Seq. ID 1575822

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3168:

atcaaaatag	agttcacacg	cacaaccgcg	cgcgcacgc	cgggatctcg	atagactctg	60
gctgcgcg	aaagcggaaa	gaaggcagg	atcgtggcca	agatgcagat	cttcgtgaag	120
acgctgtcgt	cgacaaggac	gatcacgctg	gaggttgagc	cttcggacac	ggtggcggac	180
gtgaaggcca	aggtgtacga	gtcggaggcg	gtcccgccgg	ccgagcagcg	cctcatcttc	240
gcggggaagc	agCtgcgcga	cggctgcacg	ctggctgact	acaacatccc	caaggagacg	300
atgctgtcct	tgtgtgcgCg	cctcctcgga	ggcgGcccca	agaagcgcaa	taggaagacg	360
ttcaccactc	ctaagaagg	cacgcacgag	cacaagaacc	ccgggctcga	cgccgtgtct	420
ggcggtgaca	ggatcgatga	ggccacgggg	aaggtggaga	ggCtgcgcgt	gcagtgccct	480
aaaccggagt	gcggcccaRg	gcgtgtctcat	ggcgccgcac	gccgaccgcg	acgtctgcgg	540
cagctgcgcg	ctcaccttcg	tcattccagaa	ctagagcgcg	gcagatagct	aggtcgcttc	600
gtactccccc	catttgaat	gacaaagcgt	ttttaccttt	ctagatatgc	acttatgtct	660
agatacatag	attatcttat	acttttttgc	ttctttttta	tttatcgtgt	tttagttaaa	720
aataaataa	ttgagtgaat	atggt				

(2) INFORMATION FOR SEQ ID NO:3169:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 161 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..161
- (D) OTHER INFORMATION: / Ceres Seq. ID 1575823

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3169:

Met Gln Ile Phe Val Lys Thr Leu Ser Ser Thr Arg Thr Ile Thr Leu
1 5 10 15
Glu Val Glu Pro Ser Asp Thr Val Ala Asp Val Lys Ala Lys Val Tyr
20 25 30
Glu Ser Glu Gly Val Pro Pro Ala Glu Gln Arg Leu Ile Phe Ala Gly

35	40	45	
Lys Gln Leu Arg Asp Gly Cys Thr Leu Ala Asp Tyr Asn Ile Pro Lys			
50	55	60	
Glu Thr Met Leu Ser Leu Cys Cys Arg Leu Leu Gly Gly Pro Lys			
65	70	75	80
Lys Arg Asn Arg Lys Thr Phe Thr Thr Pro Lys Lys Gly Thr His Glu			
	85	90	95
His Lys Asn Pro Gly Leu Asp Ala Val Leu Gly Arg Tyr Arg Ile Asp			
	100	105	110
Glu Ala Thr Gly Lys Val Glu Arg Leu Arg Met Gln Cys Pro Asn Pro			
	115	120	125
Glu Cys Gly Pro Xaa Arg Ala His Gly Gly Ala Arg Pro Ala Arg			
	130	135	140
Leu Arg Gln Leu Arg Pro His Leu Arg His Pro Glu Leu Glu Arg Gly			
	145	150	155
Arg			160

(2) INFORMATION FOR SEQ ID NO:3170:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 95 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..95

(D) OTHER INFORMATION: / Ceres Seq. ID 1575824

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3170:

Met Leu Ser Leu Cys Cys Arg Leu Leu Gly Gly Pro Lys Lys Arg	
1	5
Asn Arg Lys Thr Phe Thr Thr Pro Lys Lys Gly Thr His Glu His Lys	
	20
Asn Pro Gly Leu Asp Ala Val Leu Gly Arg Tyr Arg Ile Asp Glu Ala	
	35
Thr Gly Lys Val Glu Arg Leu Arg Met Gln Cys Pro Asn Pro Glu Cys	
	50
Gly Pro Xaa Arg Ala His Gly Gly Ala Arg Pro Ala Arg Leu Arg	
	65
Gln Leu Arg Pro His Leu Arg His Pro Glu Leu Glu Arg Gly Arg	
	80
	85
	90
	95

(2) INFORMATION FOR SEQ ID NO:3171:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 724 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..724

(D) OTHER INFORMATION: / Ceres Seq. ID 1575825

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3171:

gttttgaaaa aggaacggcc catgttcagg gagaaggctc cgaactgggctc agggaggcgt	60
aggctatcgc cgccggccgcc gttctctcac ctgctgcate gctgcttcgc cctccgcctc	120
acaagGctac accagatgcc cagattttcg tccggttctt Tctccggcaa cgagcagcca	180
ccaggtgtct tggattttgc aaacagtgac aaaaggttct gCttcgctgt agagtcattg	240
ctgcaaaagt accgctagtg atgaagtctt ttatgagcca aagcaaccag gtctcagggc	300
ttatgccatt cacaaaagag attggactac ctgaatcacg agccctgtac accgtgttgc	360
ggtcacctca tatcgataag aagtccaggg aacaattctc gatgcattgc aagaacacgt	420
ttgtggaaca gacagccaaa ccacacgaac ttcacaggaa gttcttctgc ttaaaacgcc	480

tgcggatacc tggggctcag tatgaaatcc aaatttcttt caAgacacgt ctccgatatgg 540
cgagcctaag gtcccaagct ccttgctgac tctcagatct tcttaccgt cctgaatggt 600
tgaagtgact tgtatccatc gacatttcat atgttatgaa gacatgctta ttttgatggc 660
ttttgaaaaa aaatgtacct gctaagtctt cattacccttg acagatcact agtcaagaaa 720
atgc

(2) INFORMATION FOR SEQ ID NO:3172:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 110 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..110

(D) OTHER INFORMATION: / Ceres Seq. ID 1575826

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3172:

Met	Ser	Ala	Lys	Ile	Arg	Val	Val	Met	Lys	Ser	Phe	Met	Ser	Gln	Ser
1			5						10					15	
Asn	Gln	Val	Ser	Gly	Leu	Met	Pro	Phe	Thr	Lys	Lys	Ile	Gly	Leu	Pro
			20						25				30		
Glu	Ser	Arg	Ala	Leu	Tyr	Thr	Val	Leu	Arg	Ser	Pro	His	Ile	Asp	Lys
			35				40					45			
Lys	Ser	Arg	Glu	Gln	Phe	Ser	Met	His	Val	Lys	Lys	Gln	Phe	Val	Glu
			50				55				60				
Gln	Thr	Ala	Lys	Pro	His	Glu	Leu	His	Arg	Lys	Phe	Phe	Trp	Leu	Lys
			65				70				75			80	
Arg	Leu	Arg	Ile	Pro	Gly	Ala	Gln	Tyr	Glu	Ile	Gln	Ile	Ser	Phe	Lys
			85						90				95		
Thr	Arg	Leu	Asp	Met	Ala	Ser	Leu	Arg	Ser	Gln	Ala	Pro	Cys		
			100						105				110		

(2) INFORMATION FOR SEQ ID NO:3173:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 102 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..102

(D) OTHER INFORMATION: / Ceres Seq. ID 1575827

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3173:

Met	Lys	Ser	Phe	Met	Ser	Gln	Ser	Asn	Gln	Val	Ser	Gly	Leu	Met	Pro
1			5						10					15	
Phe	Thr	Lys	Lys	Ile	Gly	Leu	Pro	Glu	Ser	Arg	Ala	Leu	Tyr	Thr	Val
			20						25				30		
Leu	Arg	Ser	Pro	His	Ile	Asp	Lys	Lys	Ser	Arg	Glu	Gln	Phe	Ser	Met
			35				40					45			
His	Val	Lys	Lys	Gln	Phe	Val	Glu	Gln	Thr	Ala	Lys	Pro	His	Glu	Leu
			50				55				60				
His	Arg	Lys	Phe	Phe	Trp	Leu	Lys	Arg	Leu	Arg	Ile	Pro	Gly	Ala	Gln
			65				70				75			80	
Thr	Glu	Ile	Gln	Ile	Ser	Phe	Lys	Thr	Arg	Leu	Asp	Met	Ala	Ser	Leu
			85						90				95		
Arg	Ser	Gln	Ala	Pro	Cys										
			100												

(2) INFORMATION FOR SEQ ID NO:3174:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 96 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..98

(D) OTHER INFORMATION: / Ceres Seq. ID 1575828

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3174:

Met Ser Gln Ser Asn Gln Val Ser Gly Leu Met Pro Phe Thr Lys Lys
1 5 10 15
Ile Gly Leu Pro Glu Ser Arg Ala Leu Tyr Thr Val Leu Arg Ser Pro
20 25 30
His Ile Asp Lys Lys Ser Arg Glu Gln Phe Ser Met His Val Lys Lys
35 40 45
Gln Phe Val Glu Gln Thr Ala Lys Pro His Glu Leu His Arg Lys Phe
50 55 60
Phe Trp Leu Lys Arg Leu Arg Ile Pro Gly Ala Gln Tyr Glu Ile Gln
65 70 75 80
Ile Ser Phe Lys Thr Arg Leu Asp Met Ala Ser Leu Arg Ser Gln Ala
85 90 95
Pro Cys

(2) INFORMATION FOR SEQ ID NO:3175:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 815 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..815

(D) OTHER INFORMATION: / Ceres Seq. ID 1575844

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3175:

catagaactg atggtggggc cagaacatgg gataacacta cacctgtaaa caatgtggat 60
ctctgccaatg ttgtctctgca ggggtggtgaa gctccccgca cagctgcaaa tactactagt 120
gagGatTgca tccaaAcagG tacaccaAag tccaggtagt cctcaggtTg ttTggcaaga 180
caacatTgac cctgacaata tgacatatga ggaactcttg gatttgggtg aggcagttgg 240
aaccacagac cgtgtgtctct cccaagaatg catttctgtg ctctcccatca ctaagtataa 300
gtgtggattc ttttcaagga agaaacacgc ccgtgaaagg tgtgtgattt gccaaatgga 360
gtacaggaga ggaaatttgc agattacgct tccatgcaag catgtatacc atgccagctg 420
cgtgacaaga tggcttagca taaacaaggt atgccctgtt tgctttgctg aagtctctg 480
cgaggattct cagaggcaat gattcatcag ttgtgatgcc actatgaagt tgctgtctgt 540
ggtactgcgc ccccaatgga cgcgatgatt ctttgaagcg agcttgttgt cccacttta 600
gaattgtgta tttagcgcat attaccaaat aggtatttac ttatcagatg tatttagtta 660
gtgtttgtgt tcggaatatg gttagatgga gtcactttgc tctaattta ttgtgtttg 720
aattgtttt atgtaggaca tagtaactct aaaattggaa aaactatgct taaatactga 780
atcatctgac tcccacaaat cttttggacg gagac

(2) INFORMATION FOR SEQ ID NO:3176:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 149 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..149

(D) OTHER INFORMATION: / Ceres Seq. ID 1575845

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3176:

Met Trp Ile Leu Pro Met Leu Ser Cys Arg Val Val Lys Leu Pro Ala

1		5		10		15
Gln	Leu	Gln	Ile	Leu	Val	Arg
		20				25
Ser	Pro	Gly	Ser	Pro	Gln	Val
		35				40
Asn	Met	Thr	Tyr	Glu	Glu	Leu
		50				55
Gln	Ser	Arg	Gly	Leu	Ser	Gln
		65				70
Lys	Tyr	Lys	Cys	Gly	Phe	Phe
			85			
Cys	Val	Ile	Cys	Gln	Met	Glu
			100			105
Leu	Pro	Cys	Lys	His	Val	Tyr
			115			120
Ser	Ile	Asn	Lys	Val	Cys	Pro
			130			135

Asp Ser Gln Arg Gln

145

(2) INFORMATION FOR SEQ ID NO:3177:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 144 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..144
- (D) OTHER INFORMATION: / Ceres Seq. ID 1575846

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3177:

Met	Leu	Ser	Cys	Arg	Val	Val	Lys	Leu	Pro	Ala	Gln	Leu	Gln	Ile	Leu
1			5					10						15	
Leu	Val	Arg	Ile	Ala	Ser	Lys	Gln	Val	His	Gln	Ser	Pro	Gly	Ser	Pro
			20					25						30	
Gln	Val	Val	Trp	Gln	Asp	Asn	Ile	Asp	Pro	Asp	Asn	Met	Thr	Tyr	Glu
			35					40						45	
Glu	Leu	Leu	Asp	Leu	Gly	Glu	Ala	Val	Gly	Thr	Gln	Ser	Arg	Gly	Leu
			50					55						60	
Ser	Gln	Glu	Cys	Ile	Ser	Leu	Leu	Pro	Ile	Thr	Lys	Tyr	Lys	Cys	Gly
			65					70						75	
Phe	Phe	Ser	Arg	Lys	Lys	Thr	Arg	Arg	Glu	Arg	Cys	Val	Ile	Cys	Gln
				85					90					95	
Met	Glu	Tyr	Arg	Arg	Gly	Asn	Leu	Gln	Ile	Thr	Leu	Pro	Cys	Lys	His
				100				105						110	
Val	Tyr	His	Ala	Ser	Cys	Val	Thr	Arg	Trp	Leu	Ser	Ile	Asn	Lys	Val
				115				120						125	
Cys	Pro	Val	Cys	Phe	Ala	Glu	Val	Pro	Gly	Glu	Asp	Ser	Gln	Arg	Gln
				130				135						140	

(2) INFORMATION FOR SEQ ID NO:3178:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 100 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..100

(D) OTHER INFORMATION: / Ceres Seq. ID 1575847

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3178:

Met Thr Tyr Glu Glu Leu Leu Asp Leu Gly Glu Ala Val Gly Thr Gln
1 5 10 15
Ser Arg Gly Leu Ser Gln Glu Cys Ile Ser Leu Leu Pro Ile Thr Lys
20 25 30
Tyr Lys Cys Gly Phe Phe Ser Arg Lys Lys Thr Arg Arg Glu Arg Cys
35 40 45
Val Ile Cys Gln Met Glu Tyr Arg Arg Gly Asn Leu Gln Ile Thr Leu
50 55 60
Pro Cys Lys His Val Tyr His Ala Ser Cys Val Thr Arg Trp Leu Ser
65 70 75 80
Ile Asn Lys Val Cys Pro Val Cys Phe Ala Glu Val Pro Gly Glu Asp
85 90 95
Ser Gln Arg Gln
100

(2) INFORMATION FOR SEQ ID NO:3179:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 923 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..923
- (D) OTHER INFORMATION: / Ceres Seq. ID 1575856

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3179:

gtcatcgctct cgttcctctg ctcccttttg caacctccct tcatataggc cactgtgacc 60
tgcttccctt tcgcagttgc tcatctccat agccacctcg gaagctcgag gccgaggatc 120
cacatatata gcatctgtct tttatactaa taggttttag tttttgggag aatctacaca 180
cgcgagaagc taggtagctt tcttcaataa tctgggtcca gtccagcaag ctccaccttg 240
ccctccatcg accgatcgac ctgctgcggg cccagagaca tccatccatc catcttcctc 300
tccctggctgt aagaagagga gatggtctca tggccgtgat ctacatcGc ggagcGCTcg 360
tcgcggccgt gtcctctctg ctctctctcg Gcgcgcgcac cagcatccGc caccgcgacg 420
ttttccctt ctcaggagaa cctggcggag gacaagtgcg ggctgggggtc gacgcgccgcg 480
atctgccgca accgggtcgag cgctcgcaac ccttcgatcg ccgtgcaggt gacgaccgcg 540
cccgccgggg tcggggcgcg gccccgcgtc accgacgcgc acgcccacgc cgacgcgggtg 600
gcggcttct ccgcctactc cgactacaag ccgctggggg ggaaatgcgg ctgcgacggc 660
cgccctgtag acccttagcc gagcgtgcaa cgccagtga ctctgtcccg gtcgcgttagg 720
gtggggagaga ctggaggcca tccaggttct tcgtgtcatc tgttcttggt ttttgccat 780
gggcatggc ggcttgcttg cattgcagct tgtaccgccc gtacccgtag ccattttttt 840
ttgctctctg ctgaacaat tttactctg cgtgtaaaga gtaaccgtga ccgtgagcac 900
taaaaaattgt agtggttacc gcc

(2) INFORMATION FOR SEQ ID NO:3180:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..129
- (D) OTHER INFORMATION: / Ceres Seq. ID 1575857

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3180:

Met Ala Val Ile Ser His Arg Gly Ala Leu Val Ala Ala Val Ser Leu
1 5 10 15
Cys Leu Leu Leu Gly Ala Ala Thr Ser Ile Pro His Arg Asp Val Phe
20 25 30
Pro Phe Ser Gly Glu Pro Gly Gly Gln Val Ala Ala Gly Val Asp

35	40	45
Ala Ala Asp Leu Pro Gln Pro Val Gln Arg Leu Gln Pro Leu His Ala		
50	55	60
Arg Ala Gly Asp Asp Arg Ala Arg Gly Ala Arg Ala Arg Gly Pro Arg		
65	70	75
His Arg Arg Arg Arg Arg Arg Arg Arg Gly Gly Arg Leu Leu Pro Leu		
85	90	95
Leu Arg Leu Gln Ala Ala Gly Val Glu Met Arg Leu Arg Arg Pro Pro		
100	105	110
Val Arg Pro Leu Ala Glu Arg Ala Thr Pro Val His Ser Ala Pro Val		
115	120	125

Arg

(2) INFORMATION FOR SEQ ID NO:3181:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 904 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..904
- (D) OTHER INFORMATION: / Ceres Seq. ID 1575935

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3181:

gaaggagttc aaggtggagg tggaaagcaat cggctcgtgtt cggcacaaaa atctcgtcag	60
gttgctcggc tactgcgtag aggggtgctta caggatgctt gtgtatgagt atgtggacaa	120
tggtaatctt gaccagtggc ttcattggtga tgttggcgaa gtgagccac tgacatggga	180
catcaggatg aacatcatgc ttgcgaccgc taaagggctg gcctacctcc acgaggggct	240
ggaaccgaa ttgntccacc gcgacatcaa gctagcaac atcctctctg accagcagt	300
gaacgcgaaa gtatcggatt tcgggctcgc gaaGctgttg tgctcggaga gaagctacgt	360
tacgaccogt gtcattggaa mcttcggtta cgtggcgctt gagtacgcca gaacgggcat	420
gctgaacgag aggagcgtat tgatatgctt cggcgctcgt ataatggaga tcatcaccg	480
cagatctcct gtggattaca caagggcgcg tggagagtg cactgggtg agtggctcaa	540
gaacatggtg gccgagagga aagcggagga ggtagtggac agtaagatgg ccgagaggcc	600
tcctcccaag acgtggaagc gggcgctcct ggtgngsstc cgctgcgtgg accctgacgc	660
gaacaagcgg cctaagatgg ggcatgtgat ccacatgctc gaaatggacg acctccagtt	720
ccgagatagg tacagtccta agctaggtgg aggaagggag cctcagcaag cgcgagcacc	780
agcgtcggtg cagatgagat gattgtcatt agagagtac gatattaac atgttatttt	840
tttcccgcta gtaaatatcat tcttcccaa ctcgttccat cgattctcaa tggttytcga	900

ttkt

(2) INFORMATION FOR SEQ ID NO:3182:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 266 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..266
- (D) OTHER INFORMATION: / Ceres Seq. ID 1575936

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3182:

Lys Glu Phe Lys Val Glu Val Glu Ala Ile Gly Arg Val Arg His Lys	
1	15
Asn Leu Val Arg Leu Leu Gly Tyr Cys Val Glu Gly Ala Tyr Arg Met	
20	30
Leu Val Tyr Glu Tyr Val Asp Asn Gly Asn Leu Asp Gln Trp Leu His	
35	45
Gly Asp Val Gly Glu Val Ser Pro Leu Thr Trp Asp Ile Arg Met Asn	
50	60


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Ile Met Leu Ala Thr Ala Lys Gly Leu Ala Tyr Leu His Glu Gly Leu
65      70      75      80
Glu Pro Lys Leu Xaa His Arg Asp Ile Lys Ala Ser Asn Ile Leu Leu
      85      90      95
Asp Gln Gln Trp Asn Ala Lys Val Ser Asp Phe Gly Leu Ala Lys Leu
      100      105      110
Leu Cys Ser Glu Arg Ser Tyr Val Thr Thr Arg Val Met Gly Xaa Phe
      115      120      125
Gly Tyr Val Ala Pro Glu Tyr Ala Ser Thr Gly Met Leu Asn Glu Arg
      130      135      140
Ser Asp Val Tyr Ser Phe Gly Val Leu Ile Met Glu Ile Ile Thr Gly
145      150      155      160
Arg Ser Pro Val Asp Tyr Thr Arg Ala Ala Gly Glu Val His Leu Val
      165      170      175
Glu Trp Leu Lys Asn Met Val Ala Glu Arg Lys Ala Glu Glu Val Val
      180      185      190
Asp Ser Lys Met Ala Glu Arg Pro Pro Lys Thr Leu Lys Arg Ala
      195      200      205
Leu Leu Val Xaa Xaa Arg Cys Val Asp Pro Asp Ala Asn Lys Arg Pro
210      215      220
Lys Met Gly His Val Ile His Met Leu Glu Met Asp Asp Leu Gln Phe
225      230      235      240
Arg Asp Arg Tyr Ser Ser Lys Leu Gly Gly Arg Glu Pro Gln Gln
      245      250      255
Ala Arg Ala Pro Ala Ser Val Gln Met Arg
      260      265

```

(2) INFORMATION FOR SEQ ID NO:3183:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 235 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..235

(D) OTHER INFORMATION: / Ceres Seq. ID 1575937

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3183:

```

Met Leu Val Tyr Glu Tyr Val Asp Asn Gly Asn Leu Asp Gln Trp Leu
1      5      10      15
His Gly Asp Val Gly Glu Val Ser Pro Leu Thr Trp Asp Ile Arg Met
      20      25      30
Asn Ile Met Leu Ala Thr Ala Lys Gly Leu Ala Tyr Leu His Glu Gly
      35      40      45
Leu Glu Pro Lys Leu Xaa His Arg Asp Ile Lys Ala Ser Asn Ile Leu
50      55      60
Leu Asp Gln Gln Trp Asn Ala Lys Val Ser Asp Phe Gly Leu Ala Lys
65      70      75      80
Leu Leu Cys Ser Glu Arg Ser Tyr Val Thr Thr Arg Val Met Gly Xaa
      85      90      95
Phe Gly Tyr Val Ala Pro Glu Tyr Ala Ser Thr Gly Met Leu Asn Glu
      100      105      110
Arg Ser Asp Val Tyr Ser Phe Gly Val Leu Ile Met Glu Ile Ile Thr
      115      120      125
Gly Arg Ser Pro Val Asp Tyr Thr Arg Ala Ala Gly Glu Val His Leu
130      135      140
Val Glu Trp Leu Lys Asn Met Val Ala Glu Arg Lys Ala Glu Glu Val
145      150      155      160
Val Asp Ser Lys Met Ala Glu Arg Pro Pro Lys Thr Leu Lys Arg
      165      170      175
Ala Leu Leu Val Xaa Xaa Arg Cys Val Asp Pro Asp Ala Asn Lys Arg

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180	185	190
Pro Lys Met Gly His Val Ile	His Met Leu Glu Met Asp	Asp Leu Gln
195	200	205
Phe Arg Asp Arg Tyr Ser Ser Lys Leu Gly Gly	Gly Arg Glu Pro Gln	
210	215	220
Gln Ala Arg Ala Pro Ala Ser Val Gln Met Arg		
225	230	235

(2) INFORMATION FOR SEQ ID NO:3184:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 204 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..204

(D) OTHER INFORMATION: / Ceres Seq. ID 1575938

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3184:

Met Asn Ile Met Leu Ala Thr Ala Lys Gly Leu Ala Tyr Leu His Glu	
1 5 10 15	
Gly Leu Glu Pro Lys Leu Xaa His Arg Asp Ile Lys Ala Ser Asn Ile	
20 25 30	
Leu Leu Asp Gln Gln Trp Asn Ala Lys Val Ser Asp Phe Gly Leu Ala	
35 40 45	
Lys Leu Leu Cys Ser Glu Arg Ser Tyr Val Thr Thr Arg Val Met Gly	
50 55 60	
Xaa Phe Gly Tyr Val Ala Pro Glu Tyr Ala Ser Thr Gly Met Leu Asn	
65 70 75 80	
Glu Arg Ser Asp Val Tyr Ser Phe Gly Val Leu Ile Met Glu Ile Ile	
85 90 95	
Thr Gly Arg Ser Pro Val Asp Tyr Thr Arg Ala Ala Gly Glu Val His	
100 105 110	
Leu Val Glu Trp Leu Lys Asn Met Val Ala Glu Arg Lys Ala Glu Glu	
115 120 125	
Val Val Asp Ser Lys Met Ala Glu Arg Pro Pro Pro Lys Thr Leu Lys	
130 135 140	
Arg Ala Leu Leu Val Xaa Xaa Arg Cys Val Asp Pro Asp Ala Asn Lys	
145 150 155 160	
Arg Pro Lys Met Gly His Val Ile His Met Leu Glu Met Asp Asp Leu	
165 170 175	
Gln Phe Arg Asp Arg Tyr Ser Ser Lys Leu Gly Gly Gly Arg Glu Pro	
180 185 190	
Gln Gln Ala Arg Ala Pro Ala Ser Val Gln Met Arg	
195 200	

(2) INFORMATION FOR SEQ ID NO:3185:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 841 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..841

(D) OTHER INFORMATION: / Ceres Seq. ID 1575954

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3185:

acaagcaaaag cagcagcaac agccaacacc taaactaaaag aacagtagta gtccctgtgt	60
acgtctagca acgatccgca ccgagctcgc cagttttgct cgttagtttg grgacrgcga	120
tggcgtccgg tcaggaaagc agggaggagc tggcgccgat ggccaggagg gggcagacgc	180
tcgtcccgcg cggcaccggc ggcaagaccg tcgaggcgca ggagcacctc gccgaarggc	240

gcagtcacgg cgggcagacc cggagtgagc agctggggcca tgagggggtac agcgagatgg 300
gcagcaaggg cgggcagacc cgcaagagc agctggggcca cgaagggtac agcgagatgg 360
ggagggaagg cggtctgagc accatgcagg agtccggcgg cgagcgcgcc gCccgggagg 420
gcacgcagat cgacgagtcc aagttcagga ccaagtccta gatctgatgc gtgccccgcg 480
ttagcatgta gtacgtagct gcaggaatgt agtgtcgtcg tagtagtagg gtatgctgtac 540
gacgtgcgcc tcctcgtttg gcacgtgtgc cctgaataat gtatgctgtg cagtgcgtgt 600
cctagcacgc gtgtaggaga ccatacgtgc gcgtatgac atgcgtgttc gcttcagtta 660
ggtttctgat ttggtcgtcg tcacgtgtt tgaagcaggc aggtctcttc aggtttgttc 720
gtcgtacgag cctgtgttct agctctacga ccccatctc atagcgtgtg gtgtggggtc 780
gtgatgcctt aaggtctcgc agtttgtatc cgtgcttgtt tcgttaaggt agtttggttc 840
t

(2) INFORMATION FOR SEQ ID NO:3186:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..113
- (D) OTHER INFORMATION: / Ceres Seq. ID 1575955

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3186:

Met Ala Ser Gly Gln Glu Ser Arg Glu Leu Ala Arg Met Ala Glu
1 5 10 15
Glu Gly Gln Thr Val Val Pro Gly Gly Thr Gly Gly Lys Thr Leu Glu
20 25 30
Ala Gln Glu His Leu Ala Glu Xaa Arg Ser His Gly Gly Gln Thr Arg
35 40 45
Ser Glu Gln Leu Gly His Glu Gly Tyr Ser Glu Met Gly Ser Lys Gly
50 55 60
Gly Gln Thr Arg Lys Glu Gln Leu Gly His Glu Gly Tyr Ser Glu Met
65 70 75 80
Gly Arg Lys Gly Gly Leu Ser Thr Met Gln Glu Ser Gly Gly Glu Arg
85 90 95
Ala Ala Arg Glu Gly Ile Glu Ile Asp Glu Ser Lys Phe Arg Thr Lys
100 105 110
Ser

(2) INFORMATION FOR SEQ ID NO:3187:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 100 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..100
- (D) OTHER INFORMATION: / Ceres Seq. ID 1575956

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3187:

Met Ala Glu Glu Gly Gln Thr Val Val Pro Gly Gly Thr Gly Gly Lys
1 5 10 15
Thr Leu Glu Ala Gln Glu His Leu Ala Glu Xaa Arg Ser His Gly Gly
20 25 30
Gln Thr Arg Ser Glu Gln Leu Gly His Glu Gly Tyr Ser Glu Met Gly
35 40 45
Ser Lys Gly Gly Gln Thr Arg Lys Glu Gln Leu Gly His Glu Gly Tyr
50 55 60
Ser Glu Met Gly Arg Lys Gly Gly Leu Ser Thr Met Gln Glu Ser Gly
65 70 75 80

Gly Glu Arg Ala Ala Arg Glu Gly Ile Glu Ile Asp Glu Ser Lys Phe
85 90 95

Arg Thr Lys Ser
100

(2) INFORMATION FOR SEQ ID NO:3188:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 620 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..620
- (D) OTHER INFORMATION: / Ceres Seq. ID 1575963

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3188:

atattttcgag	atgaacgaac	agtcacagaac	ccactgctcg	aaaccgcagc	cactggccag	60
tcgatgccca	tgactgcrgt	gccacgagacc	ggcccccggtt	gcctgggggtc	gccgcgggct	120
caggctctgt	cgagctcact	agccgggggtt	caaggcgccc	cgaagcgact	ggcgcatcg	180
aagccgtcgt	ggatcggtcg	cactgagtc	aacgtgagga	gggagagagc	aaaacgacct	240
gatccctctt	gcaccatctg	caagggcaca	gggagaatag	actgccgcaa	ctgctttggc	300
cgaggaaaga	caaaccatgc	cgatgtggcc	atgcttcga	acggcgaaatg	gccacaatgg	360
tgtcgaaatt	gtgtgtgtag	tggactggat	tactgcctcc	ggtgccaatg	aactgtgtg	420
tatcgtgaac	ccatgggctt	ccaattcact	gtccaaagaa	aatgagttag	gtgggatggc	480
cttgatgct	acgatgcagc	gcaGcTgvgN	gggacatcgt	agCccactca	gcattgttct	540
ccactgtctc	tcagaactca	gatgatttat	gtctaggsst	aacgctgtaa	taacgttgct	600
tcataaaagg	aaaaaatgtc					

(2) INFORMATION FOR SEQ ID NO:3189:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 154 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..154
- (D) OTHER INFORMATION: / Ceres Seq. ID 1575964

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3189:

Ile	Phe	Arg	Asp	Glu	Arg	Thr	Val	Gln	Asn	Pro	Leu	Leu	Glu	Thr	Ala
1		5						10					15		
Ala	Thr	Gly	Gln	Ser	Met	Pro	Met	Thr	Xaa	Val	Pro	Arg	Thr	Gly	Pro
		20					25					30			
Gly	Cys	Leu	Gly	Ser	Pro	Pro	Ala	Gln	Ala	Leu	Ser	Ser	Ser	Leu	Ala
		35					40				45				
Gly	Val	Gln	Gly	Ala	Pro	Lys	Arg	Leu	Gly	Ala	Ser	Lys	Pro	Ser	Trp
		50				55				60					
Ile	Val	Arg	Thr	Glu	Ser	Asn	Val	Arg	Arg	Glu	Arg	Ala	Lys	Arg	Pro
65						70				75			80		
Asp	Pro	Pro	Cys	Thr	Ile	Cys	Lys	Gly	Thr	Gly	Arg	Ile	Asp	Cys	Arg
			85					90					95		
Asn	Cys	Phe	Gly	Arg	Gly	Arg	Thr	Asn	His	Ala	Asp	Val	Ala	Met	Leu
			100				105					110			
Pro	Asn	Gly	Glu	Trp	Pro	Gln	Trp	Cys	Arg	Ile	Cys	Gly	Gly	Ser	Gly
		115				120					125				
Leu	Asp	Tyr	Cys	Leu	Arg	Cys	His	Gly	Thr	Gly	Glu	Tyr	Arg	Glu	Pro
		130				135					140				
Met	Gly	Phe	His	Phe	Thr	Val	Gln	Arg	Lys						
145						150									

(2) INFORMATION FOR SEQ ID NO:3190:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 133 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..133
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1575965
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3190:

Met Pro Met Thr Xaa Val Pro Arg Thr Gly Pro Gly Cys Leu Gly Ser
1 5 10 15
Pro Pro Ala Gln Ala Leu Ser Ser Ser Leu Ala Gly Val Gln Gly Ala
20 25 30
Pro Lys Arg Leu Gly Ala Ser Lys Pro Ser Trp Ile Val Arg Thr Glu
35 40 45
Ser Asn Val Arg Arg Glu Arg Ala Lys Arg Pro Asp Pro Pro Cys Thr
50 55 60
Ile Cys Lys Gly Thr Gly Arg Ile Asp Cys Arg Asn Cys Phe Gly Arg
65 70 75 80
Gly Arg Thr Asn His Ala Asp Val Ala Met Leu Pro Asn Gly Glu Trp
85 90 95
Pro Gln Trp Cys Arg Ile Cys Gly Gly Ser Gly Leu Asp Tyr Cys Leu
100 105 110
Arg Cys His Gly Thr Gly Glu Tyr Arg Glu Pro Met Gly Phe His Phe
115 120 125
Thr Val Gln Arg Lys
130

(2) INFORMATION FOR SEQ ID NO:3191:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 131 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..131

- (D) OTHER INFORMATION: / Ceres Seq. ID 1575966
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3191:

Met Thr Xaa Val Pro Arg Thr Gly Pro Gly Cys Leu Gly Ser Pro Pro
1 5 10 15
Ala Gln Ala Leu Ser Ser Ser Leu Ala Gly Val Gln Gly Ala Pro Lys
20 25 30
Arg Leu Gly Ala Ser Lys Pro Ser Trp Ile Val Arg Thr Glu Ser Asn
35 40 45
Val Arg Arg Glu Arg Ala Lys Arg Pro Asp Pro Pro Cys Thr Ile Cys
50 55 60
Lys Gly Thr Gly Arg Ile Asp Cys Arg Asn Cys Phe Gly Arg Gly Arg
65 70 75 80
Thr Asn His Ala Asp Val Ala Met Leu Pro Asn Gly Glu Trp Pro Gln
85 90 95
Trp Cys Arg Ile Cys Gly Gly Ser Gly Leu Asp Tyr Cys Leu Arg Cys
100 105 110
His Gly Thr Gly Glu Tyr Arg Glu Pro Met Gly Phe His Phe Thr Val
115 120 125
Gln Arg Lys
130

(2) INFORMATION FOR SEQ ID NO:3192:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 855 base pairs

- (B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:

(A) NAME/KEY: -
(B) LOCATION: 1..855
(D) OTHER INFORMATION: / Ceres Seq. ID 1575992

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3192:

attataaaaaa	aaaggaaaag	ggaggccagc	cggtgggct	gctatcagcg	cttttggccg	60
agctagcccca	cggtctagca	cttcctctatg	gcaccagaaa	gccaagcgta	vnnngtgaca	120
gagaaggag	tagcgaagag	gaggttgct	tccttggcg	cggtcgctga	agccgtttct	180
ttcggcgctc	gcaatcttct	cgccggttct	tgccgcaacct	cttcaaggac	gctcctctaa	240
gtatggagac	aagctccctg	ctaaggatca	ggcacaggac	acagcctatg	agcaattaca	300
atcatacccc	tcataaaagt	ttacaacaac	gactcaagct	cttatggact	aaaaggacat	360
tctatcttta	agtcagtttg	taattccgaa	gcttcatgaa	cggcaccctt	cggtatcacg	420
tacagacagc	ttcagccgaa	gctgtttctt	cttcgaggac	cttcagcgac	gaagcatggt	480
cccaacagt	gttaactcca	ccccaggaga	tacagcagcg	caccagtcct	gatgggaaat	540
ggtgttccgg	cagcagttcg	aggtactgga	caggtctacc	tgaagttaac	ttcaggaaga	600
acgctcgttc	tgaaggacat	actctatgtg	ccatcgatga	gcgggaacct	catattagtg	660
tcgctgctat	gtcgcacagg	tctcaaatga	gtgtttgagt	ctaataaagt	ggtcctgtct	720
aagtttgcta	ctttgttgga	aagtcatatg	agtcaggcgg	ttgttccgt	ctttctgttt	780
tgaataatca	ttcttctac	catgttaagt	tggtctgtaa	taacgattcc	attaataata	840
tatggcattc	cggtt					

(2) INFORMATION FOR SEQ ID NO:3193:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1..50
(D) OTHER INFORMATION: / Ceres Seq. ID 1575993

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3193:

Met	Ala	Pro	Arg	Ser	Gln	Ala	Xaa	Xaa	Xaa	Thr	Glu	Lys	Gly	Val	Ala	
1				5						10				15		
Lys	Arg	Arg	Leu	Pro	Ser	Leu	Ala	Ala	Ala	Leu	Glu	Ala	Gly	Ser	Phe	
			20					25					30			
Gly	Ala	Arg	Asn	Leu	Leu	Ala	Gly	Phe	Cys	Ala	Thr	Ser	Ser	Arg	Thr	
			35				40						45			
Pro	Pro															
	50															

(2) INFORMATION FOR SEQ ID NO:3194:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 100 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1..100
(D) OTHER INFORMATION: / Ceres Seq. ID 1575994

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3194:

Met	Asn	Gly	Thr	Leu	Arg	Tyr	His	Val	Gln	Thr	Ala	Ser	Ala	Glu	Ala	
1				5						10				15		
Val	Ser	Ser	Cys	Arg	Thr	Phe	Ser	Asp	Glu	Ala	Trp	Ser	Gln	Gln	Trp	
			20					25					30			
Leu	Thr	Pro	Pro	Gln	Gly	Ile	Gln	Gln	Arg	Thr	Ser	Leu	Asp	Gly	Lys	

cgcacatctc	ccgcgcgcgc	gacgccttc	ctccctccct	tcctccgtc	catcgctcgc	60
cgtcgacacg	ttctgccgac	ttaacacttc	gatgcgcgc	cgtccgcga	taccgcgcgt	120
ctcgcggggt	gtgcttcccc	aaaccttct	atcccccg	tcgcgcgcgc	cgcaggctgc	180
acgcgtggcc	tcctcatcc	cgcggcttc	ctgttgctg	tcctccctgc	ggatcactca	240
caataatccc	ccgcctgatg	caagtgcga	agctgcgaa	cgcgagcctg	tcactgcttc	300
agatgaatcc	gaagaggagg	tgggcgcagg	gtctctcgt	gtggcgcgag	gggaagaacc	360
gacgcgcgcg	acgaacgcga	agGttaatg	cggcgaaata	atggggatc	tgaataatcc	420
gtctcattga	gaggctcaga	agcgaagac	tgtacccgat	ctbagccctg	gcgataatcc	480
tgagcttagg	atgcacgcgg	ccacaaaaa	gagattgtgc	ctctttaagg	ccataatcat	540
cgcgaagcac	aaagctggtg	ttcacaccac	aatccgtgtc	agaagaaata	ttgctgggtg	600
aggagtgttg	attaccttcc	cagtgctatc	accaggatc	aaggaaatac	cggttatcag	660
gcacaaagaa	gtgaggagag	caaatgtgta	ctacctgaaa	gcagaacttc	ccgctcttcc	720
aaacttcaag	tgaatacaga	tatgtcgaca	gaacgacttc	tttcaccacc	atctcagttt	780
ctcttcaaaa	tttttttttc	accttccctt	cgatatcatt	atatttcaac	gtaatcctgt	840
tgatctcagt	gtgtaatact	tacagcttta	tatcatactt	ggcttagtgc	aatgttttgt	900
tttdttctct	gtacaaaatt	ctactactac	acctttttat	tgaataattg	caaatgacaa	960

gttatgc

(2) INFORMATION FOR SEQ ID NO:3197:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 243 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..243

(D) OTHER INFORMATION: / Ceres Seq. ID 1576003

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3197:

Pro	Ile	Leu	Pro	Pro	Xaa	Arg	Arg	Leu	Pro	Leu	Pro	Pro	Ser	Ser	Val
1			5					10					15		
Pro	Cys	Ser	Ala	Ala	Asp	Thr	Leu	Ala	Arg	Leu	Asn	Leu	Thr	Met	Ala
			20				25					30			
Ala	Ala	Ser	Ala	Ile	Thr	Ala	Val	Ser	Gly	Val	Val	Leu	Pro	Gln	Thr
			35				40					45			
Phe	Leu	Ser	Pro	Arg	Ser	Pro	Pro	Gln	Val	Leu	Ala	Val	Ala	Ser	
			50			55				60					
Ser	Phe	Arg	Arg	Leu	Ser	Leu	Cys	Ala	Ser	Pro	Arg	Arg	Ile	Thr	His
65					70					75				80	
Ile	Ile	Pro	Arg	Ala	Asp	Ala	Ser	Ala	Glu	Ala	Gly	Glu	Pro	Glu	Pro
					85				90					95	
Val	Thr	Ala	Ser	Asp	Glu	Ser	Glu	Glu	Glu	Val	Ala	Glu	Gly	Ser	Val
			100					105					110		
Ala	Val	Ala	Glu	Gly	Glu	Glu	Pro	Thr	Pro	Pro	Ser	Lys	Pro	Lys	Val
			115				120					125			
Lys	Phe	Gly	Glu	Ile	Ile	Gly	Ile	Leu	Asn	Lys	Gln	Phe	Ile	Glu	Glu
			130			135					140				
Ala	Glu	Lys	Val	Lys	Thr	Val	Pro	Asp	Leu	Arg	Pro	Gly	Asp	Ile	Ile
145					150				155					160	
Glu	Leu	Arg	Met	Gln	Arg	Pro	Asn	Lys	Arg	Arg	Leu	Ser	Leu	Phe	Lys
			165					170						175	
Gly	Ile	Ile	Ile	Ala	Lys	His	Lys	Ala	Gly	Val	His	Thr	Thr	Ile	Arg
			180					185						190	
Val	Arg	Arg	Ile	Ile	Ala	Gly	Val	Gly	Val	Glu	Ile	Thr	Phe	Pro	Val
			195				200					205			
Tyr	Ser	Pro	Arg	Ile	Lys	Glu	Ile	Thr	Val	Ile	Arg	His	Lys	Lys	Val
			210			215					220				
Arg	Arg	Ala	Lys	Leu	Tyr	Tyr	Leu	Lys	Asp	Lys	Leu	Pro	Arg	Phe	Ser
225					230					235				240	
Thr	Phe	Lys													

(2) INFORMATION FOR SEQ ID NO:3198:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 213 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..213

(D) OTHER INFORMATION: / Ceres Seq. ID 1576004

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3198:

Met	Ala	Ala	Ala	Ser	Ala	Ile	Thr	Ala	Val	Ser	Gly	Val	Val	Leu	Pro
1				5				10						15	
Gln	Thr	Phe	Leu	Ser	Pro	Arg	Ser	Pro	Pro	Pro	Gln	Val	Leu	Ala	Val
			20				25					30			

Ala Ser Ser Phe Arg Arg Leu Ser Leu Cys Ala Ser Pro Arg Arg Ile
35 40 45
Thr His Ile Ile Pro Arg Ala Asp Ala Ser Ala Glu Ala Gly Glu Pro
50 55 60
Glu Pro Val Thr Ala Ser Asp Glu Ser Glu Glu Val Ala Glu Gly
65 70 75 80
Ser Val Ala Val Ala Glu Gly Glu Glu Pro Thr Pro Pro Ser Lys Pro
85 90 95
Lys Val Lys Phe Gly Glu Ile Ile Gly Ile Leu Asn Lys Gln Phe Ile
100 105 110
Glu Glu Ala Glu Lys Val Lys Thr Val Pro Asp Leu Arg Pro Gly Asp
115 120 125
Ile Ile Glu Leu Arg Met Gln Arg Pro Asn Lys Arg Arg Leu Ser Leu
130 135 140
Phe Lys Gly Ile Ile Ile Ala Lys His Lys Ala Gly Val His Thr Thr
145 150 155 160
Ile Arg Val Arg Arg Ile Ile Ala Gly Val Gly Val Glu Ile Thr Phe
165 170 175
Pro Val Tyr Ser Pro Arg Ile Lys Glu Ile Thr Val Ile Arg His Lys
180 185 190
Lys Val Arg Arg Ala Lys Leu Tyr Tyr Leu Lys Asp Lys Leu Pro Arg
195 200 205
Phe Ser Thr Phe Lys
210

(2) INFORMATION FOR SEQ ID NO:3199:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 967 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..967
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576026

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3199:

cttaaaaaacc	tctgctcggg	cctagggttt	cctcccagtc	gtcatcgctt	ggcgctcgcc	60
ttagccccgcc	gccaggagag	ccggctcggt	cggttcgtcg	aagatcccgg	atctgctctg	120
tcacgaggctc	tctcgccggg	tgttgtctcg	cgaggtgtag	cgagccaagg	tctggtcgcc	180
ttttcaggag	agtttcgaga	agctgaaatg	gtctcctaaag	ctgctcctgc	caagaagggt	240
gatgccaaaga	cccaggcctt	gaagggttgc	aaggctgtga	agtctgggtc	agtaagaaga	300
accaagaaga	tccgcacgtc	cgtagacatt	caccgcccca	agaccctgaa	gaaggctagg	360
gaccccaagt	accacaagaat	cagcactacc	ggaaggaaca	agcttgatca	gtaccaaat	420
ctcaagtatc	ccctcaccac	agaatcggcg	atgaagaaga	ttgaagataa	caacactctt	480
gtcttctattg	tgcacctcaa	ggcagacaag	ragaagatca	Aggctgctgt	caagaagatg	540
tatgacattc	agggccaaga	ggctcaacacc	ctgatcaggc	ctgatggaaa	gaagaaggct	600
tacgtgaagc	ttatgctgta	ctatgatgct	cttgatgtgg	ccaacaaaat	cgggcatcatc	660
taaaagtacc	ggctcaggca	tctgctgtgc	tctatttcca	tgtgaaacca	gagtttttgt	720
agctatggct	cagtggtctc	atgacctatg	cttatgcaca	cttacgaatt	tgatatcatc	780
caagtcacag	gttgctctca	tcaatacttg	gatactatca	cttattcgta	tggggttggt	840
ctttggctct	cacatttctt	tgtattgggt	tgggtgtttg	atctcacctt	tcttcgcatt	900
gggttggtct	ttgggaattg	gaactcggcc	tgatagctgt	tggagtatag	tgtatggatc	960
tgcgttc						

(2) INFORMATION FOR SEQ ID NO:3200:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 220 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1..220
(D) OTHER INFORMATION: / Ceres Seq. ID 1576027

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3200:

Leu Lys Asn Leu Cys Ser Gly Leu Gly Phe Pro Pro Ser Arg His Arg
1 5 10 15
Leu Ala Ser Ala Leu Ala Arg Arg Gln Glu Ser Arg Leu Gly Arg Phe
20 25 30
Val Glu Asp Pro Gly Ser Ala Leu Ser Arg Gly Leu Ser Ala Gly Val
35 40 45
Val Ser Arg Gly Val Ala Ser Gln Gly Leu Val Ala Phe Ser Gly Glu
50 55 60
Phe Arg Glu Ala Glu Met Ala Pro Lys Ala Ala Pro Ala Lys Lys Gly
65 70 75 80
Asp Ala Lys Thr Gln Ala Leu Lys Val Ala Lys Ala Val Lys Ser Gly
85 90 95
Ser Val Lys Lys Thr Lys Lys Ile Arg Thr Ser Val Thr Phe His Arg
100 105 110
Pro Lys Thr Leu Lys Lys Ala Arg Asp Pro Lys Tyr Pro Arg Ile Ser
115 120 125
Thr Thr Gly Arg Asn Lys Leu Asp Gln Tyr Gln Ile Leu Lys Tyr Pro
130 135 140
Leu Thr Thr Glu Ser Ala Met Lys Lys Ile Glu Asp Asn Asn Thr Leu
145 150 155 160
Val Phe Ile Val Asp Leu Lys Ala Asp Lys Xaa Lys Ile Lys Ala Ala
165 170 175
Val Lys Lys Met Tyr Asp Ile Gln Ala Lys Lys Val Asn Thr Leu Ile
180 185 190
Arg Pro Asp Gly Lys Lys Lys Ala Tyr Val Lys Leu Met Pro Asp Tyr
195 200 205 210 215 220

(2) INFORMATION FOR SEQ ID NO:3201:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 151 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide
(ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1..151
(D) OTHER INFORMATION: / Ceres Seq. ID 1576028

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3201:

Met Ala Pro Lys Ala Ala Pro Ala Lys Lys Gly Asp Ala Lys Thr Gln
1 5 10 15
Ala Leu Lys Val Ala Lys Ala Val Lys Ser Gly Ser Val Lys Lys Thr
20 25 30
Lys Lys Ile Arg Thr Ser Val Thr Phe His Arg Pro Lys Thr Leu Lys
35 40 45
Lys Ala Arg Asp Pro Lys Tyr Pro Arg Ile Ser Thr Thr Gly Arg Asn
50 55 60
Lys Leu Asp Gln Tyr Gln Ile Leu Lys Tyr Pro Leu Thr Thr Glu Ser
65 70 75 80
Ala Met Lys Lys Ile Glu Asp Asn Asn Thr Leu Val Phe Ile Val Asp
85 90 95
Leu Lys Ala Asp Lys Xaa Lys Ile Lys Ala Ala Val Lys Lys Met Tyr
100 105 110
Asp Ile Gln Ala Lys Lys Val Asn Thr Leu Ile Arg Pro Asp Gly Lys
115 120 125
Lys Lys Ala Tyr Val Lys Leu Met Pro Asp Tyr Asp Ala Leu Asp Val

130 135
Ala Asn Lys Ile Gly Ile Ile
145 150

140

(2) INFORMATION FOR SEO ID NO:3202:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- ```
(A) NAME/KEY: peptide
(B) LOCATION: 1..115
```

(D) OTHER INFORMATION: / Ceres Seq. ID 1576029

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3202:

[illegible]

(2) INFORMATION FOR SEO ID NO:3203:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1041 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..1041

(D) OTHER INFORMATION: / Ceres Seq. ID 1576041

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3203:

|             |             |             |             |             |             |      |
|-------------|-------------|-------------|-------------|-------------|-------------|------|
| atcaactgac  | tgcgcagaga  | cgcggcgctca | cgtcggcgctc | ataaatgtgt  | tcgtagacta  | 60   |
| tcgacacaca  | gtttgcgaga  | ggggagagag  | tagaggtttc  | gaggtagaga  | gatcanganag | 120  |
| mgacagaagra | gggggaaggcg | goggatccgt  | caactcggtc  | ttctcccgta  | atctggagga  | 180  |
| aggargcgarg | gggagtgtgca | aatcatcaca  | tggccacatc  | aaccacacta  | tcagtcgcga  | 240  |
| tattctcgca  | gaccacacaa  | tatgaagcgt  | gggtgggtg   | gacacagat   | ttggccagcg  | 300  |
| aactcgcagga | dggagagacg  | acgcgtgamt  | ctrtcgcgca  | cacgcagaaa  | gtcgcgcga   | 360  |
| atgtaccctt  | ggagtcacgc  | taccccgctg  | tgtgartcac  | gtctgcacag  | aatgcagact  | 420  |
| aggtgtccaag | ggaagacaaat | gtgGaccacg  | ataaatgtGt  | catatgcGagc | aactacaagc  | 480  |
| atattggggaa | cgagtagaag  | ttcaagtcgct | agggttatct  | gatgagctga  | tattctattt  | 540  |
| ggagccattt  | agggaacaagt | gcacttttct  | ctccaggaaa  | agaagacact  | aggaaattgt  | 600  |
| gtgtctcaag  | acaacatata  | gaagccgcga  | gaatttgata  | agactacctc  | cgagcgaact  | 660  |
| ttatcacgcga | gattgcataa  | ctctgttggt  | taagatcaac  | aaggcatgcc  | cagctgtcaa  | 720  |
| cgaggagagc  | tttggatgaa  | ctcgaaagtt  | ctcggcgat   | gtcgcggtt   | actcgttact  | 780  |
| tcgtctgcgcg | atgcttttga  | gaagacgttt  | gaacgataag  | gtcactgtt   | tgtgatgatg  | 840  |
| tttgtgacct  | agttttgtgc  | cttttgctta  | agagagactg  | ctcgtcccat  | gcagtggctg  | 900  |
| gtctacagct  | gtgctagtta  | ctgcgaacag  | tcgcggtttg  | tgtatgcctg  | atcatctctt  | 960  |
| gttttatcac  | aaattgatag  | atctgttgtg  | tgggtagtgt  | ggttgcggtt  | ttctgaatat  | 1020 |
| aatggaatgt  | gtttttgcc   | c           |             |             |             |      |

(2) INFORMATION FOR SEQ ID NO:3204:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 91 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..91
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576042

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3204:

Met Ala Thr Pro Thr Thr Tyr Ser Val Arg Ile Ser Ser Glu Thr His  
1 5 10 15  
Lys Ile Glu Ala Trp Val Val Ser Asp Glu Ala Leu Ala Arg Gln Leu  
20 25 30  
Gln Xaa Glu Glu Asn Thr Arg Xaa Ala Asp Thr Arg Glu Val  
35 40 45  
Xaa Gly Asn Val Pro Leu Glu Ser Ser Ser Pro Ala Val Xaa Tyr Arg  
50 55 60  
Xaa Ala Gln Asn Ala Ala Gln Val Ala Arg Glu Asp Asn Val Asp Pro  
65 70 75 80  
Asp Asn Met Val Ile Trp Ser Asn Tyr Lys His  
85 90

(2) INFORMATION FOR SEQ ID NO:3205:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..53
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576043

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3205:

Met Tyr Pro Trp Ser His Arg His Arg Leu Leu Xaa Thr Xaa Leu His  
1 5 10 15  
Arg Met Gln Leu Arg Leu Gln Gly Lys Thr Met Trp Thr Gln Ile Ile  
20 25 30  
Trp Ser Tyr Gly Ala Thr Thr Ser Ile Arg Gly Ser Ser Arg Asn Ser  
35 40 45  
Val Gln Arg Val Ile  
50

(2) INFORMATION FOR SEQ ID NO:3206:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 91 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..91
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576044

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3206:

Met Glu Gln Leu Gln Ala Leu Gly Glu Ala Val Gly Ile Gln Ser Arg  
1 5 10 15  
Gly Leu Ser Asp Glu Leu Ile Ser Tyr Leu Glu Pro Phe Arg Asn Lys  
20 25 30  
Cys Thr Phe Phe Ser Arg Lys Lys Asn Ser Glu Glu Cys Val Ile Cys

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |     |
| Lys | Thr | Thr | Tyr | Arg | Ser | Arg | Gln | Lys | Leu | Ile | Arg | Leu | Pro | Cys | Ser |
| 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |
| His | Cys | Tyr | His | Ala | Asp | Cys | Ile | Thr | Arg | Trp | Leu | Lys | Ile | Asn | Lys |
| 65  |     |     |     | 70  |     |     |     |     |     | 75  |     |     |     |     | 80  |
| Ala | Cys | Pro | Val | Cys | Asn | Glu | Glu | Val | Phe | Gly |     |     |     |     |     |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     |     |

(2) INFORMATION FOR SEO ID NO:3207:

## (1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 769 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(1x) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..769  
(D) OTHER INFORMATION: / Ceres Seq. ID 1576045

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3207:

|             |            |            |             |             |            |     |
|-------------|------------|------------|-------------|-------------|------------|-----|
| cccaaaacgc  | ccaacacgcc | gccacttcga | accgcacaac  | agccctcgcg  | accaccaccg | 160 |
| acgtcgacga  | cgtgcagatg | ggaggttcgc | gcgcgctcac  | ctgtcgcgtg  | ctcggcgccg | 170 |
| ggcccgggccc | ccacgctccc | gaccaaaggc | gaagtcgcgc  | gcactcctgag | atccgtcaag | 180 |
| gcgcagggtg  | aggaggacgc | ctctcgacgc | Gtctcgccc   | ctctagaggc  | taaggacatc | 190 |
| gcgcagctga  | tcgcacacgg | cggggagcat | ctcgccctacg | cgccctcagg  | taagcgctgc | 200 |
| gcgcctcgtt  | ccaactctcg | cgctcgcgag | ctcgaggagg  | aggccacaga  | ggaggaagat | 210 |
| gaggacacgc  | ccctctctaa | ctctctcgac | tgatcgtgca  | acctcactag  | ccgtccggga | 220 |
| ccgcggcgcaa | ccaaaggaca | gtgcgcgcga | taaccgcaca  | tgaccacagg  | acacggccaa | 230 |
| gcacacaggc  | ccaagctgcc | ctcgatgatc | tactctctc   | ctgtcgtctt  | gcattgcgat | 240 |
| gtaatctata  | ggctgtgcga | tgcactcata | catgatacat  | gcgcgtgact  | tggatcgccg | 250 |
| gtactcgtat  | gcactctttc | atactagtat | attactacta  | ctactactct  | tcctgtcttc | 260 |
| ctactgtgtg  | cccaaaagtc | agaggggaga | catgcattgc  | gatgacatct  | cgtgttatgt | 270 |
| gcactgcgcg  | ccacttgccc | aggtcataat | tcactctctg  | tgtattatg   |            | 280 |

(2) INFORMATION FOR SEQ ID NO:3208:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 130 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(1x) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..130  
(D) OTHER INFORMATION: / Ceres Seq. ID 1576046

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3208:

[illegible]

130

(2) INFORMATION FOR SEQ ID NO:3209:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 76 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..76
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576047

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3209:

```
Gln Asn Ala His His Ala Ala Thr Arg Asn Arg Thr Pro Ala Leu Ala
1 5 10 15
Thr His His His Val Arg Asp Val Arg Asp Gly Val Pro Arg Arg Val
 20 25 30
Pro Ala Ala Val Pro Gly Arg Arg Pro Gly Pro His Ala Pro Asp Gln
 35 40 45
Gly Arg Arg Ala Ser His Pro Glu Ile Arg Gln Arg Arg Gly Gly Gly
50 55 60
Gly Pro Pro Arg Pro Gly Leu Arg Pro Pro Arg Gly
65 70 75
```

(2) INFORMATION FOR SEQ ID NO:3210:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..104
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576048

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3210:

```
Met Glu Phe Leu Ala Ala Tyr Leu Leu Pro Cys Leu Gly Ala Gly Pro
1 5 10 15
Ala Pro Thr Leu Pro Thr Lys Asp Asp Val Arg Arg Ile Leu Arg Ser
 20 25 30
Val Ser Ala Glu Val Glu Glu Asp Arg Leu Asp Leu Val Phe Ala Leu
 35 40 45
Leu Glu Val Lys Asp Ile Ala Glu Leu Ile Ala Thr Gly Gly Glu His
50 55 60
Leu Ala Tyr Ala Pro Ser Gly Ala Ala Ala Val Val Ala Thr Pro
65 70 75 80
Ala Ala Ala Glu Val Glu Glu Glu Ala Thr Lys Glu Glu Asp Glu Asp
 85 90 95
Ile Ala Leu Phe Asn Leu Phe Asp
100
```

(2) INFORMATION FOR SEQ ID NO:3211:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 999 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..999
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576049

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3211:

|            |            |            |            |            |             |     |
|------------|------------|------------|------------|------------|-------------|-----|
| gagtagcaat | cactgctgcg | cccgataggg | ggcagcgagc | cagcdhmcga | mccgactctg  | 60  |
| ttccaacgag | cctwccccc  | caaacttgca | cgtgcgcgcc | gctctcgcc  | cgcgcgcgcga | 120 |
| tccagatcca | gggtggaata | gggaacggcc | atacaccatg | gggatttct  | ccaaggaatc  | 180 |
| ttgccctctc | gtgaagaaca | ttttacttct | ggattctgaa | ggaaagcgty | ttgctgtaaa  | 240 |
| gtattttcca | gatgattggc | cgactaatgc | atcaaatgta | gcctacgaaa | agctctgttt  | 300 |
| tactaaaact | ctaaaagaca | atgcacggac | agaagctgag | ataacattgt | ttgatgggta  | 360 |
| tattgwcgk  | tacaagtgtt | tactgacct  | tcacttkttt | gtcaccgctg | gagatgatga  | 420 |
| gGaatgagct | catcttagca | agtgtactac | atgggttttc | tgattctggt | ggctctctac  | 480 |
| tcagggggga | tgttggaag  | cggactgcgc | ttgagaactt | ggatttgata | cttctctgca  | 540 |
| tcgatgaat  | tgtagatggg | ggaatcatcc | tgaaaacaga | tgcaaacacc | attgctggta  | 600 |
| aggttgcaac | caatgctgtt | gatggttctg | tgcccttttc | tgagcagacg | atatctcaag  | 660 |
| cactagcaoc | agctagggag | caccttgcaa | gatctctact | gaaatgaaca | accagcaata  | 720 |
| tgtatgacgt | attatatgac | atatatgtgt | gtaggttggg | ctactgaaat | ttgaggggtc  | 780 |
| ttgtagacgt | tattgtcccc | aaagtgcctc | tgtgacagag | cctagttgaa | tatccgaggg  | 840 |
| attggtcaca | tgctcgttaa | attttttttt | tgaaccagtg | agtttgtagc | tgccaatttt  | 900 |
| caggtaaaaa | ataaaataaa | gagttgtaat | gggtgtgta  | ataattttca | ccatacaaaa  | 960 |
| aaaattcat  | ctcaactatc | aaaccatggt | aaaagttc   |            |             |     |

(2) INFORMATION FOR SEQ ID NO:3212:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 117 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..117

(D) OTHER INFORMATION: / Ceres Seq. ID 1576050

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3212:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Val | Ile | Leu | Xaa | Xaa | Thr | Ser | Leu | Tyr | Xaa | Thr | Phe | Thr | Xaa | Leu |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Ser | Pro | Leu | Glu | Met | Met | Arg | Asn | Glu | Leu | Ile | Leu | Ala | Ser | Val | Leu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| His | Gly | Phe | Ser | Asp | Ser | Val | Gly | Leu | Leu | Leu | Arg | Gly | Asp | Val | Xaa |
|     |     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |
| Lys | Arg | Thr | Ala | Leu | Glu | Asn | Leu | Asp | Leu | Ile | Leu | Leu | Cys | Ile | Asp |
|     |     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |
| Glu | Ile | Val | Asp | Gly | Gly | Ile | Ile | Leu | Glu | Thr | Asp | Ala | Asn | Thr | Ile |
|     |     |     | 65  |     |     |     | 70  |     |     |     | 75  |     |     | 80  |     |
| Ala | Gly | Lys | Val | Ala | Thr | Asn | Ala | Val | Asp | Gly | Ser | Val | Pro | Phe | Ser |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Glu | Gln | Thr | Ile | Ser | Gln | Ala | Leu | Ala | Thr | Ala | Arg | Glu | His | Leu | Ala |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Arg | Ser | Leu | Leu | Lys |     |     |     |     |     |     |     |     |     |     |     |
|     |     |     | 115 |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:3213:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 97 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..97

(D) OTHER INFORMATION: / Ceres Seq. ID 1576051

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3213:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Met | Arg | Asn | Glu | Leu | Ile | Leu | Ala | Ser | Val | Leu | His | Gly | Phe | Ser |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Asp | Ser | Val | Gly | Leu | Leu | Leu | Arg | Gly | Asp | Val | Xaa | Lys | Arg | Thr | Ala |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |

Leu Glu Asn Leu Asp Leu Ile Leu Leu Cys Ile Asp Glu Ile Val Asp  
35 40 45  
Gly Gly Ile Ile Leu Glu Thr Asp Ala Asn Thr Ile Ala Gly Lys Val  
50 55 60  
Ala Thr Asn Ala Val Asp Gly Ser Val Pro Phe Ser Glu Gln Thr Ile  
65 70 75 80  
Ser Gln Ala Leu Ala Thr Ala Arg Glu His Leu Ala Arg Ser Leu Leu  
85 90 95  
Lys

(2) INFORMATION FOR SEQ ID NO:3214:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 96 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..96
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576052

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3214:

Met Arg Asn Glu Leu Ile Leu Ala Ser Val Leu His Gly Phe Ser Asp  
1 5 10 15  
Ser Val Gly Leu Leu Arg Gly Asp Val Xaa Lys Arg Thr Ala Leu  
20 25 30  
Glu Asn Leu Asp Leu Ile Leu Leu Cys Ile Asp Glu Ile Val Asp Gly  
35 40 45  
Gly Ile Ile Leu Glu Thr Asp Ala Asn Thr Ile Ala Gly Lys Val Ala  
50 55 60  
Thr Asn Ala Val Asp Gly Ser Val Pro Phe Ser Glu Gln Thr Ile Ser  
65 70 75 80  
Gln Ala Leu Ala Thr Ala Arg Glu His Leu Ala Arg Ser Leu Leu Lys  
85 90 95

(2) INFORMATION FOR SEQ ID NO:3215:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 655 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..655
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576067

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3215:

gcccgctcat tgcctgcctc cagctccagc agaacgcgat ttgttctgtt gttcggtccc 60  
caatcttcgc ctccgctccg cccgcgccga cccagatcag gagctgagag atggacgcga 120  
acagcgccca aggtgggagt cagcagttgc tggctgcgga gCaggaggct cagcaaatgt 180  
tgaatgcggc tagagctgct aagtcagcaa gccttaggca agcgaagag gaggcagaga 240  
gggaaatagc cgaatacgtg gccagatagg aggtgagtt ccagaggaag gtgcgacaga 300  
gcagtggtga ctctggtgcg aacgtcaagc gtctcgagga agagacaacg gcgaaaatcg 360  
aacagctcaa ccagcagcgt gcaagcatct ccccagatgt cattcagatg ctctcgagcg 420  
atgtcaccac cgtgaagaac tgagaagtgc tgctcccaaa ctatggctat cggctctattt 480  
attttttgta gagcaggtga ggaataataa tatggccctt gtaccagtaa ttcttttttt 540  
aactacggaa taagccgcag cagcttttagc ggcaaccgtg actgttacta ccagaacctg 600  
ccattatttg gtataatcgg caaataataa atattgttt tatattggat ttttg

(2) INFORMATION FOR SEQ ID NO:3216:

(i) SEQUENCE CHARACTERISTICS:



- (A) LENGTH: 60 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..60  
(D) OTHER INFORMATION: / Ceres Seq. ID 1576068

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3216:

Ala Arg Ser Leu Leu Ala Ser Ser Leu Gln Arg Thr Arg Phe Val Leu  
1 5 10 15  
Leu Phe Gly Pro Gln Ser Ser Pro Pro Leu Arg Pro Pro Arg Pro Arg  
20 25 30  
Ser Gly Ala Glu Arg Trp Thr Pro Thr Gly Ala Lys Val Gly Phe Ser  
35 40 45  
Ser Cys Trp Leu Arg Ser Arg Arg Leu Ser Lys Leu  
50 55 60

(2) INFORMATION FOR SEQ ID NO:3217:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 63 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..63  
(D) OTHER INFORMATION: / Ceres Seq. ID 1576069

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3217:

Pro Ala His Cys Leu Pro Pro Val Ser Arg Glu Arg Asp Leu Phe Cys  
1 5 10 15  
Cys Ser Val Pro Asn Leu Arg Leu Arg Ser Ala Arg Pro Asp Pro Asp  
20 25 30  
Gln Glu Leu Arg Asp Gly Arg Gln Gln Ala Pro Arg Trp Asp Ser Ala  
35 40 45  
Val Ala Gly Cys Gly Ala Gly Gly Ser Ala Asn Cys Glu Cys Gly  
50 55 60

(2) INFORMATION FOR SEQ ID NO:3218:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 110 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..110  
(D) OTHER INFORMATION: / Ceres Seq. ID 1576070

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3218:

Met Asp Ala Asn Arg Arg Gln Gly Gly Ile Gln Gln Leu Leu Ala Ala  
1 5 10 15  
Glu Gln Glu Ala Gln Gln Ile Val Asn Ala Ala Arg Ala Ala Lys Ser  
20 25 30  
Ala Arg Leu Arg Gln Ala Lys Glu Glu Ala Glu Arg Glu Ile Ala Glu  
35 40 45  
Tyr Arg Ala Gln Met Glu Ala Glu Phe Gln Arg Lys Val Ala Glu Ser  
50 55 60  
Ser Gly Asp Ser Gly Ala Asn Val Lys Arg Leu Glu Glu Glu Thr Thr  
65 70 75 80  
Ala Lys Ile Glu Gln Leu Asn Gln Gln Ala Ala Ser Ile Ser Pro Asp

85 90 95  
Val Ile Gln Met Leu Leu Arg His Val Thr Thr Val Lys Asn  
100 105 110

(2) INFORMATION FOR SEQ ID NO:3219:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 892 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..892
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576075

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3219:

|            |             |            |             |            |            |     |
|------------|-------------|------------|-------------|------------|------------|-----|
| accgcagcca | cacccaaca   | tcaaaacct  | cccatctctt  | cccctccgcc | gccgtctctg | 60  |
| ctctcaagat | cgccatggcg  | tcagaaaaga | agcagtcgaa  | cccgatgcgg | gagatcaagg | 120 |
| tgcagaagct | cgtgctcaat  | atctccgttg | gagagagtgg  | agatcgactc | accgcgcgcc | 180 |
| ccaaggtgtt | ggagcagttg  | agtgggcagt | ctccggtttt  | ctccaaggca | aggfatactg | 240 |
| tgaggtcttt | cggtattctg  | cgtaatgaga | agattgcatg  | ctatttcaat | cgtgctgtat | 300 |
| gcttcttgaa | attgggaaaa  | catgatgaga | ccattaaaAg  | aatgctcaaa | agcacttgag | 360 |
| ctcaatccaa | catacctgaa  | agccctgctt | cggaggggcag | aagcgcgatg | aaagcttgaa | 420 |
| cattatgatg | aagctattgc  | cgatatgaaa | aagggtgttg  | aagtggatcc | ttcaaatcaa | 480 |
| caagccacga | ggtctctttt  | ccgacttgag | cccctggcag  | ctgagaagag | ggaaaagatg | 540 |
| aaggaagaaa | tgattgcaaa  | gctgaaaagt | ctgggggaact | ctgtgctggg | ccgcttcggg | 600 |
| atgagtgttg | acaatttcaa  | agctgtcaaa | gatccaaaca  | ctggctctta | cagcattcaa | 660 |
| ttccaaaagt | aacacgacgt  | gaagaaagac | atggatgaat  | atggctgggg | ggcatatttc | 720 |
| agttgtaatt | gttcaaaggaa | ctgtgctgtc | acatacctgg  | acaatatcca | aacagatatc | 780 |
| tgcaaatcga | tctgaagggt  | ggacatggaa | gaggaattgg  | agtattcggt | cgcggttgca | 840 |
| tttgtcgac  | gttagactgt  | tagagatgct | ttctcgagtg  | cgaacttgca | tg         |     |

(2) INFORMATION FOR SEQ ID NO:3220:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 118 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..118
- (D) OTHER INFORMATION: / Ceres Seq. ID 1576076

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3220:

|                                                                 |  |
|-----------------------------------------------------------------|--|
| Arg Ser His Thr Pro Thr Ser Lys Pro Ser His Leu Phe Pro Ser Ala |  |
| 1 5 10 15                                                       |  |
| Ala Val Ser Ala Leu Lys Ile Ala Met Ala Ser Glu Lys Lys Gln Ser |  |
| 20 25 30                                                        |  |
| Asn Pro Met Arg Glu Ile Lys Val Gln Lys Leu Val Leu Asn Ile Ser |  |
| 35 40 45                                                        |  |
| Val Gly Glu Ser Gly Asp Arg Leu Thr Arg Ala Ala Lys Val Leu Glu |  |
| 50 55 60                                                        |  |
| Gln Leu Ser Gly Gln Ser Pro Val Phe Ser Lys Ala Arg Tyr Thr Val |  |
| 65 70 75 80                                                     |  |
| Arg Ser Phe Gly Ile Arg Arg Asn Glu Lys Ile Ala Cys Tyr Ser Asn |  |
| 85 90 95                                                        |  |
| Arg Ala Val Cys Phe Leu Lys Leu Gly Lys His Asp Glu Thr Ile Lys |  |
| 100 105 110                                                     |  |
| Arg Met Leu Lys Ser Thr                                         |  |
| 115                                                             |  |

(2) INFORMATION FOR SEQ ID NO:3221:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 116 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..116

(D) OTHER INFORMATION: / Ceres Seq. ID 1576077

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3221:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Arg | Pro | Leu | Lys | Glu | Cys | Ser | Lys | Ala | Leu | Glu | Leu | Asn | Pro |
| 1   |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Thr | Tyr | Leu | Lys | Ala | Leu | Leu | Arg | Arg | Ala | Glu | Ala | His | Glu | Lys |
|     |     |     | 20  |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Glu | His | Tyr | Asp | Glu | Ala | Ile | Ala | Asp | Met | Lys | Lys | Val | Val | Glu |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |
| Asp | Pro | Ser | Asn | Gln | Gln | Ala | Thr | Arg | Ser | Leu | Phe | Arg | Leu | Glu |
|     |     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |
| Leu | Ala | Ala | Glu | Lys | Arg | Glu | Lys | Met | Lys | Glu | Glu | Met | Ile | Ala |
|     |     |     | 65  |     |     |     | 70  |     |     |     | 75  |     |     | 80  |
| Leu | Lys | Asp | Leu | Gly | Asn | Ser | Val | Leu | Gly | Arg | Phe | Gly | Met | Ser |
|     |     |     | 85  |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Asp | Asn | Phe | Lys | Ala | Val | Lys | Asp | Pro | Asn | Thr | Gly | Ser | Tyr | Ser |
|     |     |     | 100 |     |     |     | 105 |     |     |     |     |     | 110 |     |
| Gln | Phe | Gln | Lys |     |     |     |     |     |     |     |     |     |     |     |
|     |     |     | 115 |     |     |     |     |     |     |     |     |     |     |     |

- (2) INFORMATION FOR SEQ ID NO:3222:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide

- (ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..115

(D) OTHER INFORMATION: / Ceres Seq. ID 1576078

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3222:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Arg | Pro | Leu | Lys | Glu | Cys | Ser | Lys | Ala | Leu | Glu | Leu | Asn | Pro | Thr |
| 1   |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |     |
| Tyr | Leu | Lys | Ala | Leu | Leu | Arg | Arg | Ala | Glu | Ala | His | Glu | Lys | Leu | Glu |
|     |     |     | 20  |     |     |     | 25  |     |     |     |     | 30  |     |     |     |
| His | Tyr | Asp | Glu | Ala | Ile | Ala | Asp | Met | Lys | Lys | Val | Val | Glu | Val | Asp |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Pro | Ser | Asn | Gln | Gln | Ala | Thr | Arg | Ser | Leu | Phe | Arg | Leu | Glu | Pro | Leu |
|     |     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |
| Ala | Ala | Glu | Lys | Arg | Glu | Lys | Met | Lys | Glu | Glu | Met | Ile | Ala | Lys | Leu |
|     |     |     | 65  |     |     |     | 70  |     |     |     | 75  |     |     | 80  |     |
| Lys | Asp | Leu | Gly | Asn | Ser | Val | Leu | Gly | Arg | Phe | Gly | Met | Ser | Val | Asp |
|     |     |     | 85  |     |     |     | 90  |     |     |     |     | 95  |     |     |     |
| Asn | Phe | Lys | Ala | Val | Lys | Asp | Pro | Asn | Thr | Gly | Ser | Tyr | Ser | Ile | Gln |
|     |     |     | 100 |     |     |     | 105 |     |     |     |     |     | 110 |     |     |
| Phe | Gln | Lys |     |     |     |     |     |     |     |     |     |     |     |     |     |
|     |     |     | 115 |     |     |     |     |     |     |     |     |     |     |     |     |

- (2) INFORMATION FOR SEQ ID NO:3223:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1206 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)

- (ix) FEATURE:

(A) NAME/KEY: -  
(B) LOCATION: 1..1206  
(D) OTHER INFORMATION: / Ceres Seq. ID 1576102

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3223:

|             |             |             |             |             |             |      |
|-------------|-------------|-------------|-------------|-------------|-------------|------|
| aaagrararav | ggggaggtcg  | acgagacaga  | gagagaaggc  | caagaggett  | cctctcccca  | 60   |
| ttctctccctt | ccgtgcacct  | gccgagccag  | ccgcgaggaa  | ggagggcatcc | cgcgctctcg  | 120  |
| ccctggcgccc | gcccgcgcgc  | cgacctctcg  | ccgcgagcttc | caattgtataa | aagatcatag  | 180  |
| atttttgtgc  | aagagcgagt  | ggatatggaa  | ccatccccctc | agcctatggg  | tgctgctgoc  | 240  |
| gggtgggtcac | aagtgtatcc  | tgccctctgcc | tatccgcctg  | cagcaaacagt | agctccctgt  | 300  |
| tctgtgtgat  | ctgctgggtt  | acagtcaggg  | cagccattcc  | cagccaatcc  | tggtcatagt  | 360  |
| agtgctcagc  | accagattgt  | ctaccaacaa  | gctcaacaat  | tccaccaaca  | gctccagcag  | 420  |
| caaccaacaac | agcagcttca  | cgagttctgg  | gttgaacgca  | tgaactgaaat | tgaggcgacg  | 480  |
| actgattttca | agaaccacaa  | cttgcacact  | gcgaggataa  | agaagatcat  | gaagggccgat | 540  |
| gaagatgttc  | gcatgatctc  | agctgaagct  | ctgtagtctt  | ttgcaaaagc  | ttgtgagata  | 600  |
| ttcatactgg  | agctgacact  | taVggtcgtg  | gatgcmcaact | gaggwgwaca  | agcgccgcac  | 660  |
| yttgcwaamg  | aatgacattg  | cagcagcgat  | cactaggact  | gacatttatg  | acttcttggt  | 720  |
| cgacattgtt  | cccaggggwtg | agatgaagga  | ggmcgggaatt | gggcttccca  | gggctggtct  | 780  |
| gccaccctatg | ggagccccag  | ctgatgcata  | tccatactac  | tacatgccac  | agcagcaggt  | 840  |
| gctctggtct  | ggaatgggtt  | atgggtgccc  | gcaagggcac  | ccagtgactt  | attgtggcca  | 900  |
| ggagcctcac  | caacagcagg  | agcaagctcc  | tgaagagcag  | caatctgcac  | gaaagtggtc  | 960  |
| gagaattattg | ctcagaagct  | atcacctgat  | tcagagttct  | catttttaggt | tggtccaaact | 1020 |
| gcaggtttttc | ttagttaatat | cggtgtgtat  | caactgaaa   | caggcgattc  | taagtagggt  | 1080 |
| gtagcatcat  | gttagtttca  | ttctcgtgtg  | tgatgttagt  | tgaagagata  | atgattagt   | 1140 |
| gctagtggtat | taaagttacc  | ataccatttc  | cttctatttc  | gaaagtgdgy  | ttccwtgwgw  | 1200 |

(2) INFORMATION FOR SEQ ID NO:3224:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 150 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..150

(D) OTHER INFORMATION: / Ceres Seq. ID 1576103

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3224:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Arg | Xaa | Xaa | Gly | Arg | Ser | Thr | Arg | Gln | Arg | Glu | Lys | Ala | Lys | Arg | Leu |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Pro | Leu | Pro | Ile | Pro | Pro | Phe | Arg | Ala | Leu | Ala | Glu | Pro | Ala | Ala | Arg |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     | 30  |     |     |     |
| Lys | Glu | Ala | Ser | Arg | Arg | Leu | Ala | Trp | Arg | Pro | Pro | Val | Gly | Arg | Pro |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ser | Ala | Ala | Ala | Ser | Asn | Cys | Lys | Lys | Ile | Ile | Asp | Phe | Cys | Ala | Arg |
|     |     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |
| Ala | Ser | Gly | Tyr | Gly | Thr | Ile | Pro | Ser | Ala | Tyr | Gly | Cys | Arg | Cys | Arg |
|     |     |     | 65  |     |     |     | 70  |     |     |     | 75  |     |     | 80  |     |
| Trp | Val | Thr | Ser | Val | Ser | Cys | Leu | Cys | Leu | Ser | Ala | Cys | Ser | Asn | Ser |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     | 95  |     |     |     |
| Ser | Ser | Cys | Phe | Cys | Cys | Ile | Cys | Trp | Phe | Thr | Val | Arg | Ala | Ala | Ile |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     | 110 |     |     |     |
| Pro | Ser | Gln | Ser | Trp | Ser | Tyr | Glu | Cys | Ser | Ala | Pro | Asp | Cys | Leu | Pro |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Thr | Ser | Ser | Thr | Ile | Pro | Pro | Thr | Ala | Pro | Ala | Ala | Thr | Thr | Thr | Ala |
|     |     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |
| Ala | Ser | Ala | Val | Leu | Gly |     |     |     |     |     |     |     |     |     |     |
|     |     |     | 145 |     |     |     | 150 |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:3225:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 145 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..145

(D) OTHER INFORMATION: / Ceres Seq. ID 1576104

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3225:

```
Met Glu Pro Ser Pro Gln Pro Met Gly Val Ala Ala Gly Gly Ser Gln
1 5 10 15
Val Tyr Pro Ala Ser Ala Tyr Pro Pro Ala Ala Thr Val Ala Pro Ala
 20 25 30
Ser Val Val Ser Ala Gly Leu Gln Ser Gly Gln Pro Phe Pro Ala Asn
 35 40 45
Pro Gly His Met Ser Ala Gln His Gln Ile Val Tyr Gln Gln Ala Gln
 50 55 60
Gln Phe His Gln Gln Leu Gln Gln Gln Gln Gln Gln Leu Gln Gln
 65 70 75 80
Phe Trp Val Glu Arg Met Thr Glu Ile Glu Ala Thr Thr Asp Phe Lys
 85 90 95
Asn His Asn Leu Pro Leu Ala Arg Ile Lys Lys Ile Met Lys Ala Asp
 100 105 110
Glu Asp Val Arg Met Ile Ser Ala Glu Ala Pro Val Val Phe Ala Lys
 115 120 125
Ala Cys Glu Ile Phe Ile Leu Glu Leu Thr Leu Xaa Val Val Asp Xaa
 130 135 140
```

His  
145

(2) INFORMATION FOR SEQ ID NO:3226:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 138 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..138

(D) OTHER INFORMATION: / Ceres Seq. ID 1576105

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3226:

```
Met Gly Val Ala Ala Gly Gly Ser Gln Val Tyr Pro Ala Ser Ala Tyr
1 5 10 15
Pro Pro Ala Ala Thr Val Ala Pro Ala Ser Val Val Ser Ala Gly Leu
 20 25 30
Gln Ser Gly Gln Pro Phe Pro Ala Asn Pro Gly His Met Ser Ala Gln
 35 40 45
His Gln Ile Val Tyr Gln Gln Ala Gln Gln Phe His Gln Gln Leu Gln
 50 55 60
Gln Gln Gln Gln Gln Gln Leu Gln Gln Phe Trp Val Glu Arg Met Thr
 65 70 75 80
Glu Ile Glu Ala Thr Thr Asp Phe Lys Asn His Asn Leu Pro Leu Ala
 85 90 95
Arg Ile Lys Lys Ile Met Lys Ala Asp Glu Asp Val Arg Met Ile Ser
 100 105 110
Ala Glu Ala Pro Val Val Phe Ala Lys Ala Cys Glu Ile Phe Ile Leu
 115 120 125
Glu Leu Thr Leu Xaa Val Val Asp Xaa His
 130 135
```

(2) INFORMATION FOR SEQ ID NO:3227:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 773 base pairs

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:

(A) NAME/KEY: -  
(B) LOCATION: 1..773  
(D) OTHER INFORMATION: / Ceres Seq. ID 1576110

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3227:

|            |            |            |            |             |             |     |
|------------|------------|------------|------------|-------------|-------------|-----|
| arcgctcgtg | gaaaggagac | gtctctgaac | cgaggctgcg | actgcgaggg  | cagcgaggga  | 60  |
| gatcgagcca | cgcttcttgt | cgctgtaatc | ccctcgagag | ccgcccggcg  | ascatggcgc  | 120 |
| ggccccagcg | cgctctctcc | tcctctacac | cggacagcac | gggatccctc  | tcgactcag   | 180 |
| Gctccacctc | ctcggaatc  | gaccgccgcc | gccacagcgc | ggagcggcgg  | cggtccgcgt  | 240 |
| cggacgacga | cagctacagc | acaagctctt | atgacagtga | ccgtgaggtg  | tctggcagat  | 300 |
| ctcgaaaca  | taagaagagc | agcagatcaa | gaaagtctag | ggagagggag  | cggagCaaag  | 360 |
| atagacatca | taaacgagac | aagagtaaac | acaaagagaa | gaaagagagt  | gagcatgtctg | 420 |
| atggccctgt | ccagctttcc | aagtttcttg | gacgggacaa | agaaaaaggaa | gaaggtactc  | 480 |
| aacggagtgc | aatatcttgt | aaaaagataa | tgatgaagct | tgagaagaca  | aaggaagaca  | 540 |
| aggcagcaga | gagcaagcga | aacgaactgt | tgaagtttct | gaatgccagt  | tacgattgat  | 600 |
| gtgttcgaat | yGctgacgcg | gaaagtgcag | watgcccttt | tttatcgctc  | ttgcactcgt  | 660 |
| gcttttgtgt | atacttaagt | tataaacggt | ttgtttcttg | tctataactt  | ggccaccaaa  | 720 |
| gtttttttat | gctcaactag | cgaactgagt | aaggtctaca | tgcaattgat  | ttg         |     |

(2) INFORMATION FOR SEQ ID NO:3228:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 198 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide  
(B) LOCATION: 1..198  
(D) OTHER INFORMATION: / Ceres Seq. ID 1576111

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3228:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Arg | Ser | Trp | Lys | Gly | Asp | Val | Ser | Glu | Pro | Arg | Leu | Arg | Leu | Arg | Gly |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     | 15  |     |     |     |     |
| Gln | Arg | Gly | Arg | Ser | Ser | His | Ala | Ser | Cys | Arg | Val | Asn | Pro | Leu | Glu |
|     |     |     | 20  |     |     |     | 25  |     |     |     | 30  |     |     |     |     |
| Xaa | Arg | Arg | Xaa | Xaa | Met | Ala | Arg | Ser | Pro | Ala | Ala | Ser | Ser | Ser | Ser |
|     |     |     | 35  |     |     | 40  |     |     |     | 45  |     |     |     |     |     |
| Tyr | Thr | Asp | Ser | Thr | Gly | Ser | Ser | Ser | Asp | Ser | Gly | Ser | Thr | Ser | Ser |
|     |     |     | 50  |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Gly | Ile | Asp | Arg | Arg | Arg | His | Glu | Arg | Glu | Arg | Arg | Ser | Ala | Ser |     |
|     |     |     | 65  |     |     | 70  |     |     | 75  |     |     |     | 80  |     |     |
| Asp | Asp | Asp | Ser | Tyr | Ser | Thr | Ser | Ser | Tyr | Asp | Ser | Asp | Arg | Glu | Val |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     | 95  |     |     |
| Ser | Gly | Arg | Ser | Arg | Lys | His | Lys | Lys | Ser | Ser | Arg | Ser | Arg | Lys | Ser |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     | 110 |     |     |     |
| Arg | Glu | Arg | Glu | Arg | Ser | Lys | Asp | Arg | His | His | Lys | Arg | Asp | Lys | Ser |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Lys | His | Lys | Glu | Lys | Lys | Glu | Ser | Glu | His | Ala | Asp | Gly | Pro | Val | Gln |
|     |     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |
| Leu | Ser | Lys | Phe | Leu | Gly | Arg | Asp | Lys | Glu | Lys | Glu | Glu | Gly | Thr | Gln |
|     |     |     | 145 |     |     | 150 |     |     | 155 |     |     |     |     |     | 160 |
| Arg | Ser | Ala | Ile | Ser | Gly | Lys | Lys | Ile | Met | Met | Lys | Leu | Glu | Lys | Thr |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Lys | Glu | Asp | Lys | Ala | Ala | Glu | Ser | Lys | Arg | Asn | Glu | Leu | Leu | Lys | Phe |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Leu | Asn | Ala | Ser | Tyr | Asp |     |     |     |     |     |     |     |     |     |     |
|     |     |     | 195 |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:3229: